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Foreword

Welcome to the 5th Australasian Dairy Science Symposium.

It is my privilege to be chairing the Australasian Dairy Science Symposium 2012. This Symposium is held once every two years, rotating between Australia and New Zealand and is considered the premier gathering for information exchange and professional development of the dairy science communities of these two great dairying countries.

I am proud to be working with an exceptional editorial committee who together share a vision for this event being one that nurtures the careers of young dairy scientists. As a consequence of this strategy we are delighted to see a strong contingent of dairy science students delivering both full papers and posters.

We have spearheaded the program with a mixture of international and ANZAC keynote speakers that will compel attendance and deliver provocative, challenging papers – ensuring that all delegates view this event as a quality contribution to their science.

Through our call for abstracts and the subsequent review process, we encouraged authors to push boundaries and use this event to have their science critiqued by colleagues – while all the time keeping a focus on our responsibility for shaping the future production systems of the Australasian dairy industry.

The resulting peer-reviewed proceedings comprises full papers from invited speakers, and shorter papers from those to whom we offered an oral presentations and those displaying posters. I trust you find this an invaluable reference source.

Meanwhile, we have brought a new dimension to the 2012 event, by introducing a 'speaking workshop' as part of our working program on Tuesday evening. Our coach, Ann Burbrook has worked with science communicators, farmers and members of the agri-sector, journalists, performers and students from primary to tertiary level. She specialises in helping people focus their message as well as ensuring that the delivery is both easy to watch and invigorating to hear.

For experienced professionals and novices alike this workshop will help remind participants of the importance of good communication skills and how they can be used not only to get your message across but also to stimulate your audience to action.

I look forward to welcoming you to Australasian Dairy Science Symposium 2012.

Dr Joe Jacobs
Chair ADSS 2012
Principal Scientist – Dairy
Future Farming Systems Research
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Warrnambool, Victoria
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From the Editors

Editorial processes adopted for Australasian Dairy Science Symposium 2012

The invited reviews published in this volume were commissioned by the organising committee for Australasian Dairy Science Symposium 2012. In selecting author teams for each topic, the organising committee applied criteria related to the scientific achievements of the prospective authors and their standing in the discipline. The organizing committee also sought a balance in the number of invitations issued to New Zealand and Australian scientists and where-ever possible, sought to invite early-career scientists to lead the author team – providing of course the criteria of scientific achievement and standing were met.

Each offered paper published in this volume was selected following review of an abstract submitted for consideration under one of the themes of the symposium. The final selection was made by the organising committee based on the quality of the research presented and its relevance to the Symposium themes and objectives.

The editors also chose to publish papers submitted by authors who were allocated poster space in lieu of an oral presentation. These papers are shorter in length but help contribute towards the production of a significant Symposium volume for 2012.

Papers included in the publication were refereed by at least one anonymous reviewer. Authors were required to amend their papers accordingly and amended papers were re-reviewed by the editors before acceptance for publication.

**Joe Jacobs**

Editor 2012
Program

Day One – November 13

11.00am Registration open
12.00-1.00pm Lunch

Theme 1: Biotechnology in Dairying – Animals

Invited papers

1.00pm Use of molecular technologies for the advancement of animal breeding – Richard Spelman (LIC) with Ben Hayes (DPI Victoria) and Donagh Berry (Teagasc)
1.30pm The symbiotic microbiome and dairy cattle performance – Ben Cocks (DPI Victoria and La Trobe University) and Mark Morrison (CSIRO)

Offered papers and open discussion

2.00pm genomic evaluation of Jersey in Australia – Gert Nieuwhof (ADHIS DPI Victoria)
2.12pm Toward using rumen metagenomic profiles to predict feed conversion efficiency and methane emissions levels – Elizabeth Ross (DPI Victoria and La Trobe University)
2.24pm Combining gene expression data with SNP association studies to identify genes affecting bovine milk production traits - Christy Vander Jagt (DPI Victoria and University of Melbourne)
2.36pm Dietary nucleotides affect the microbial diversity of the pre-rumen of young calves – Cesar Guzman (La Trobe University)
2.48pm Discussion
3.15-3.45pm Break

Theme 1: Biotechnology in Dairying – Plants

Invited papers

3.45pm Use of plant biotechnologies to improve animal production outcomes - German Spangenberg (DPI Victoria)
4.15pm Use of plant biotechnologies to improve efficiency and sustainability of the dairy industry – Zac Hanley (Pastoral Genomics)

Offered Papers and open discussion

4.45pm Cumulative potential net benefits of transgenic white clover for dairy production in Southern Australia and New Zealand – Claire Lewis (DPI Victoria)
4.57pm Systems biology analysis of Gametophytic self-incompatibility in PRG – Hiroshi Shinozuka (DPI Victoria)
5.09pm Phenotypic assessment of yield and nutritive values of Italian ryegrass from a spaced plant Field trail – Junping Wang (DPI Victoria)
5.21pm Computational tools for genomic assisted forage plant breeding – Luke Pembleton (DPI Victoria)
5.33pm Discussion
6.00pm Break
6.30pm Working Dinner: The art of speaking science in the Gen Y era. Professional speaking coach Ann Burbrook demystifies the task of communicating science to a modern audience. “Quite possibly, the most valuable professional development session I’ve ever undertaken” – A delegate participating in the Ann Burbrook workshop, Invigorating Agriculture Conference, Adelaide 2012
## Program (Cont)

### Theme 2: Dairy Production Systems

#### Invited papers

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
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<tr>
<td>8.00am</td>
<td>Dairying in the Antipodes: recent past and near prospects - Dave Clark (DairyNZ), with Bill Malcolm (DPI Victoria) and Joe Jacobs (DPI Victoria)</td>
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<tr>
<td>8.30am</td>
<td>Performance, risk and returns of different dairy systems - Christie Ho (DPI Victoria), with Matthew Newman (DairyNZ), Dawn Dalley (DairyNZ), Steve Little (Dairy Australia) and Bill Wales (DPI Victoria)</td>
</tr>
<tr>
<td>9.00am</td>
<td>Precision Dairying: Adoption, risks and opportunities – Jenny Jago (DairyNZ) with Kendra Davis (University of Sydney), Ian Yule (Massey University) and Callum Eastwood (University of Melbourne)</td>
</tr>
<tr>
<td>9.30am</td>
<td>The Extension challenge with evolving Dairy systems – Chris Murphy (Dairy Australia), with Mark Paine (DairyNZ), Brad Granzin (DPI Victoria) and Ruth Nettle (University of Melbourne)</td>
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<td>10.00am</td>
<td>Break</td>
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### Theme 2: Dairy Production Systems (cont)

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<th>Time</th>
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<tr>
<td>10.30am</td>
<td>Influence on spring post-grazing height on dairy cow production performance and grass production – Emer Kennedy (Teagasc)</td>
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<tr>
<td>10.42am</td>
<td>Modeling the effects of increasing dietary white clover content on milk production, nitrogen excretion and profitability of a Waikato dairy farm – Edith Khaembah (DairyNZ)</td>
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<tr>
<td>10.54am</td>
<td>Economic analysis of options available to irrigated dairy farmers in northern Victoria under increased water availability – Ben Myers (DPI Victoria)</td>
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<td>11.06am</td>
<td>Nutrient losses from intensive dairy grazing systems in SW Australia – Martin Staines (DAFWA)</td>
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<td>11.18am</td>
<td>Evaluation of urinary nitrogen output prediction models from cows with low and high breeding worth – Paul (Long) Cheng (Lincoln University)</td>
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<td>11.30am</td>
<td>Differentiation between organic and conventional milk – Heike Schwendel (Massey University/AgResearch/Fonterra)</td>
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<tr>
<td>11.42am</td>
<td>Impact of pre vs. post-milking supplementation on milking interval of cows milked in a pasture-based automatic milking system – Nicolas Andres Lyons (University of Sydney)</td>
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<tr>
<td>11.54am</td>
<td>Discussion</td>
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<td>12.20pm</td>
<td>Lunch</td>
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### Theme 3: Animals – Animal Health and well being

#### Invited papers

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<th>Time</th>
<th>Session</th>
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<tr>
<td>1.30pm</td>
<td>Behavioural Welfare – R&amp;D outcomes to help the farmer in the face of increasing scrutiny? - Andrew Fisher (University of Melbourne) with Jim Webster (AgResearch)</td>
</tr>
<tr>
<td>2.00pm</td>
<td>Functional Welfare – Using biochemical and molecular technologies to understand an animal’s welfare state better - Juan Loo (University of Illinois) with Giuseppe Bertoni (University of Piacenza), Afshin Hosseini (University of Illinois), John Roche (DairyNZ), and Erminio Trevisi (University of Piacenza)</td>
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#### Offered papers

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<th>Time</th>
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<tr>
<td>2.30pm</td>
<td>The effect of feed trough space and feed barriers on behaviour and welfare of partial mixed ration fed cows on a feed pad – Anoma Hetti Arachchige (University of Melbourne)</td>
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<tr>
<td>2.43pm</td>
<td>Impact of wintering system in the Southern South Island on the lying behaviour of dairy cows – Dawn Dalley (DairyNZ)</td>
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<tr>
<td>2.55 pm</td>
<td>Break</td>
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</table>
Theme 3: Animals – Animal health and well being

Offered papers

3.25pm Comparing the rumen pH of pasture-based dairy cows fed supplement in the dairy ors a PMR on a feedpad, using indwelling rumen pH meters – Joanne Coombe (University of Melbourne)

3.37pm Automated assessment of animal health and welfare using infrared thermography – Mairi Stewart (AgResearch)

3.49pm Discussion

4.30pm Close

6.15pm Symposium Dinner at Aitkin Hill. Buses depart 6.15pm, dinner commencing 7.00pm

Session Day Three – November 15

Theme 4: Animals – Reproduction

Invited papers

8.00am Reproductive technologies for the future – a role for epigenetics – Murray Mitchell (University of Queensland) with Caroline Walker (DairyNZ)

8.30am Heat stress challenges in getting cows pregnant – Frank Dunshea (University of Melbourne), with Michael McGowan (University of Queensland) and Karin Schutz (AgResearch)

Offered papers and open discussion

9.00am Supplementation of hand-reared calves from birth to 3 weeks of age with nucleotides and effects on health and immunity – Claire Kentler (La Trobe University)

9.12am Treatment of subclinical endometritis in dairy cows with a non-steroidal anti-inflammatory drug – Nicola Priest (DairyNZ)

9.24am Innate immune proteins as biomarkers for mastitis and endometritis – Tom Wheeler (AgResearch)

9.36am Advantages of using lactation length, mating and pregnancy data to improve genetic evaluation for fertility based on calving interval – Mekonnen Haile-Mariam (DPI Victoria)

9.44am Reproductive performance of dairy cows in a pasture based, automatic milking system research farm: a five year retrospective analysis – Saranika Talukder (University of Sydney)

9.56am Discussion

10:30am Break

Theme 4: Feedbase and Nutrition

Invited papers

11.00am Complimentary forage systems – integration at a farm level – Richard Rawnsley (TIA), with Dave Chapman (DairyNZ), Joe Jacobs (DPI Victoria), Yani Garcia (University of Sydney), Mark Callow (Agri-Science QLD, DAFF), Grant Edwards (Lincoln University) and Keith Pemberton (TIA)

Offered papers and open discussion

11.30am Increasing the starch availability of sorghum grain for ruminants through dry heat popping – Amy Anstis (Agri-Science Queensland, DAFF)

11.42am New Developments in our knowledge of 25, oH Vitamin D requirements for dairy and beef cattle – Joseph McGrath (University of New England)

11.54 am Feed type affects liveweight gain in non-lactating pregnant dairy cows – Kristina Mandok (DairyNZ)

12.06pm Commercial reality of integrating for forage crops on pasture-based dairies – Michael Campbell (University of Sydney)

12.18pm Discussion

12.45pm Lunch
Program (Cont)

<table>
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<tr>
<th>Session</th>
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<tr>
<td></td>
<td><strong>Theme 4: Feedbase and Nutrition</strong></td>
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<tr>
<td>Invited papers</td>
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<tr>
<td>1.45pm</td>
<td>Using changes in dairy cow behaviour to predict health challenges in the transition dairy cow - Pilar Sepulveda-Varas with Juliana Huzzey, Daniel Weary and Marina von Keyserlingk (University of British Columbia)</td>
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<tr>
<td>2.15pm</td>
<td>Transition Feeding – John Roche (DairyNZ) with Alan Bell (CSIRO), Tom Overton (Cornell) and Juan Loor (University of Illinois)</td>
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<td>Offered papers and open discussion</td>
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<tr>
<td>2.45pm</td>
<td>Chicory and plantain defoliation management to increase herbage yield, quality and plant survival – Julia Lee (Dairy NZ)</td>
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<tr>
<td>2.57pm</td>
<td>Impact of lax and intense grazing on chicory utilisation and survival – Katherine Tozer (AgResearch)</td>
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<tr>
<td>3.09pm</td>
<td>Irrigated mixed sward of annual ryegrass (Lolium multiflorum) and kikuyu (Pennisetum clandestinum) exceeds 20 t DM/ha/yr utilisation for dairy production - Mark Callow (Agri-Science Queensland, DAFF)</td>
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<tr>
<td>3.21pm</td>
<td>Discussion</td>
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<tr>
<td>3.45 pm</td>
<td>Symposium close</td>
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</table>
BIOTECHNOLOGY IN DAIRYING - ANIMALS
Use of molecular technologies for the advancement of animal breeding: Genomic selection in dairy cattle populations in Australia, Ireland and New Zealand

R. SPELMAN¹, B. HAYES², D. BERRY³

¹Livestock Improvement Corporation, Private Bag 3016, Hamilton, New Zealand.
²Department of Primary Industries, Victoria, Australia
³Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland.

ABSTRACT

The New Zealand, Irish and Australian dairy industries have used genomic information to enhance their genetic evaluations over the last 2-4 years. The improvement in the accuracy obtained by including genomic information on thousands of animals in the national evaluation system has revolutionised the dairy breeding programmes in the three countries. The genomically-enhanced breeding (GEBVs) of young bulls are more reliable than BVs based on parent average, thus allowing them to be reliably selected and used in the national herd. Traditionally, use of young bulls was limited and bulls were not used extensively until they were five years old when the more reliable progeny test results became available. Using young sires, as opposed to progeny-tested sires in the breeding programme dramatically reduces the generation interval, thereby increasing the theoretical rate of genetic gain by 40%-50%. Young sires have been marketed on their GEBVs in the three countries over the last 2-4 years. Initial results have shown that the genomic estimates were over-estimated in both New Zealand and Ireland. Adjustments have since been introduced into their national evaluations to reduce the bias. Sequencing of the dairy cattle population has just commenced in an effort to further improve the genomic predictions and also to detect causative mutations that underlie traits of economic performance.

INTRODUCTION

Genomic selection is a new technology that allows the breeding value of young bulls and heifers to be predicted reliably from a DNA sample. While some traits such as complex vertebral malformation (CVM; Thomsen et al. 2006), bovine leukocyte adhesion deficiency (BLAD; Shuster et al. 1992) and deficiency of uridine monophosphate synthase (DUMPS; Robinson et al. 1984) are each controlled by a single gene, most traits of importance for profitability of dairy cattle (such as milk production, fertility, longevity, mastitis resistance and others) are affected by many genes of small effect (Cole et al. 2010, Hayes et al. 2010). Genomic selection can capture the effect of these genes, by using thousands of genome wide DNA markers associated with the genes affecting the trait. Implementing genomic selection is a two step process. First the effect of the genome wide DNA markers on the trait of interest must be estimated in a reference population. Because the effect of each DNA marker will be small, reference populations must be very large to estimate these effects accurately. Secondly, GEBVs are calculated for young bulls or heifers, by summing across all the DNA markers times their effect.

In this review, we compare and contrast how the genomic selection technology has been applied in Australia, Ireland, and New Zealand, both at the bull breeding company level and at the farm level. Results for the performance of young bulls, which were evaluated for their GEBV, and then subsequently had milking daughters, are presented. Finally, likely future improvements in genomic selection are outlined.

DEVELOPMENT OF GENOMIC SELECTION IN AUSTRALIA, IRELAND, AND NEW ZEALAND

Derivation of genomic predictions, irrespective of the population or species, requires a large reference population (also referred to as training population) of animals with both DNA marker information and phenotypic records for the traits for which GEBV are required. In cattle, commercial genotyping technology allows an animal to be genotyped reasonably cheaply for 54,000 DNA markers. The DNA markers here are single nucleotide polymorphism (SNPs) - a tiny piece of DNA (i.e., one base) where variation exists among animals.

The reference or training population of most dairy cattle populations used to estimate the effect of the different genetic markers (i.e., SNPs) consist of AI sires. In New Zealand genomic predictions use only AI sires with daughters producing in the country itself (Harris and Johnson, 2010). Other countries like Ireland, exploit both domestic and daughter records from other countries, for the bulls in the reference population (Berry et al. 2009). Ireland also includes information from natural mating bulls with progeny in their genomic predictions (Kearney et al. 2010).
Although male animals can obviously not express female traits (e.g., milk production) their daughter’s performance contribute to the traditional estimated breeding value of the sire thereby providing a more accurate estimate of the true genetic merit of the individual; this is especially true for low heritability traits such as fertility and health. Therefore, for the same number of animals genotyped (i.e., the same cost) genomic predictions will be more accurate when bulls with progeny are included in the training population compared to when cows are included in the training population; the difference is greatest for low heritability traits like fertility and health. Moreover, including bulls with many progeny (ideally from a structured progeny test) in the training population will minimise the effect of preferential treatment that can bias the genomic predictions. If the progeny test program is well structured, using progeny test bulls could also minimise the impact of genotype-by-environment interactions.

The disadvantage, however, of using just AI sires in the training population are: 1) the number of new proven AI sires available annually is limited thereby limiting the ability to increase the size of the training population, and 2) estimated breeding values on AI sires are generally limited to traits routinely recorded nationally or as part of a structured breeding program. It is for this reason that some genomic predictions (e.g., USA, Australia, Livestock Improvement (LIC)) now include cows in their training population, as well as AI sires (Wiggans et al. 2011, Pryce et al. 2012). However, when including cows in the training population care must be taken to avoid the inclusion of preferential treatment of particular cows in the genomic predictions via their performance records. In many instances it is the elite cows that are genotyped, and these cows may be subjected to preferential treatment.

The benefit of including females in the training population will be a function of the heritability of the trait. In Holsteins born in Australia, the reliability of genomic predictions increased by 4% to 8% (varied by trait) when 10,000 cows were added to the Australian reference population of 3,100 bulls (Pryce et al. 2012). The cows were selected from the commercial population (i.e., unlikely to be preferentially treated), and the bias due to adding the cows was minimal. For Jersey cattle, gains in reliability were even larger (up to 10%) when 4200 Jersey cows were added to the reference population.

**IMPLEMENTATION OF GENOMIC SELECTION PROGRAMS IN INTERNATIONAL DAIRY CATTLE POPULATIONS**

Genomic selection has been the official national genetic evaluation of dairy cattle in some countries since 2009. It has, however, been used by breeding companies as a bull pre-selection tool for many years.

Integration into national genetic evaluations

Genomic predictions are either undertaken by commercial companies (e.g., LIC) or by national genetic evaluation bodies (Berry et al. 2009). In all dairy cattle populations a “two-step” approach is undertaken although research on a single-step approach for genomic predictions is in an advanced stage of research in New Zealand (Harris et al. 2012). The theoretical studies have examined the genetic gain from 25% to over 100% (Pryce et al. 2012). However, when including cows in the training population care must be taken to avoid the inclusion of preferential treatment of particular cows in the genomic predictions via their performance records. In many instances it is the elite cows that are genotyped, and these cows may be subjected to preferential treatment.

Breeding Scheme Designs

Prior to the implementation of genomic selection, dairy cattle breeding schemes were heavily reliant on progeny testing to identify the superior sires for use in commercial herds. Progeny testing is time consuming and the sires are 5 to 6 years of age before their daughters have completed a lactation and thus provide data for the genetic evaluation. The large costs associated with progeny testing include incentivising farmers to record data and the feed and capital costs associated with retaining the bull for several years until proven. With the ability to evaluate an animal from its DNA profile the structure of breeding schemes has changed markedly. Theoretical estimates, based on simulations representative of population parameters, indicate a rate of increase in genetic gain from 25% to over 100% (Pryce et al. 2010, Winkelman and Spelman 2010, McHugh et al. 2011). The theoretical studies have examined the technology being applied to two of the four selection paths; i) selection of elite dams to generate sons and ii) selection within the group of young bulls.
The primary exploitation of genomic technology within the LIC breeding scheme in New Zealand, has been for the pre-selection of young sires. Prior to the introduction of the genomic selection technology in 2008, LIC progeny tested approximately 300 bulls annually. In 2008, the number of bulls progeny tested was reduced to approximately 160 and has remained at this size since then. The 160 bulls that enter progeny testing are selected from a group of 2000 to 3000 candidate bulls born from elite sires and dams that have been genotyped. The young bulls have been genotyped on different genotyping panels: a custom-made 384 SNP panel in the first year (2008) and a 50K panel for the next three years. A low-density (LD, approximately 12K SNPs) panel will likely be used in 2012.

Genotyping of elite bull dams was undertaken in the first two years of the application of genomic selection in the LIC breeding scheme with the genotyping focusing on yearlings. Since yearling heifers had yet to lactate, the genomic information would have the greatest impact in increasing reliability of breeding value estimation. Given a fixed budget it was decided that pre-screening more young bulls was a better investment than elite dam genotyping. This will be reviewed in the near future with the availability of the low-density marker panel that allows affordable genotyping in the elite cow population.

Genotyping of embryos (Humblot et al. 2010, Fisher et al. 2012) has the potential to further increase the rate of genetic gain and also increase the economic benefits of genomic technology. The efficiencies from this technology come from only implanting embryos of sufficient genetic merit and thus removing the cost and time of bearing and rearing animals that are not of sufficient genetic merit. Gender of the embryo can also be determined through the same genomic approach. A further step would be the extraction and screening of foetal blood cells for cows that are pregnant to artificial insemination rather than embryo transfer. Foetal blood screening is becoming possible in humans (Hayden 2011) although there are a number of biological hurdles to overcome for it to be successful in bovine.

Sires used by commercial farmers are either one or two-year old genomically evaluated bulls or progeny tested bulls. In New Zealand over 40% of the inseminations are from genomically selected bulls. This proportion is consistent with the rate of use of genomic bulls in a number of other countries, including Australia (though slightly less) and Ireland (Pryce et al. 2010, Cromie et al. 2010). A structured progeny test continues in New Zealand to service the proportion of the market that prefers that product. In France, a formal progeny test is no longer undertaken. It is expected that, through time, other dairy breeding schemes will move to this scenario once a greater degree of confidence is reached with genomic technology.

Breeding companies are continually faced with an interesting investment decision about progeny testing. It costs approximately $NZ30-40,000 to progeny test a bull and the return on the investment is not realised until 5 years later. Predicting the number of genomically selected and progeny tested bulls that will be demanded by farmers 5 years from now is difficult and thus investing approximately $NZ5-6 million dollars today may be for a market that has moved totally to genomic bulls.

**INBREEDING**

Dairy cattle breeding must achieve a balance between increasing genetic gain for traits affecting profitability, and increasing inbreeding, as inbreeding reduces future genetic gains. Genomic selection has the potential to actually decrease the rate of inbreeding. Consider the following scenario. An AI company is purchasing bull calves for future progeny testing, and two full brothers are available. Without genomic information, their breeding values will be based on sire and dam breeding values only, and so would be exactly the same. So both brothers would end up on the progeny test team. With genomic information, they will have inherited different chromosomes from their sire and dam, so their genomic breeding values will be different, and only one brother would end up on the progeny test team. So it is now very unlikely that both brothers will become AI sires of the future. However while genomic selection will decrease the rate of inbreeding per generation, the generations are now turned over more quickly. (De Roos et al. 2011) concluded that the net effect of genomic selection would be a slight increase in the rate of inbreeding per year.

Furthermore the genomic information can be used to control the rate of inbreeding with a high degree of precision. (Pryce et al. 2012) described genomic mate allocation schemes; that is sires and dams were chosen for mating to each other on the basis of their relationship at the genome level. (Pryce et al. 2012) demonstrated these strategies could considerably reduce the rate of inbreeding in progeny (1-2% per year), with only a slight penalty in performance.

**On-Farm exploitation**

Above we have described the application of genomic selection for AI sires. As the price of genotyping falls, it will become increasingly
attractive for farmers to genotype their heifers to select those to retain in the herd. Other advantages of genotyping heifers include accurate parentage assignment, avoiding genetic defects (e.g., BLAD, CVM and many others), and genomic mate allocation as described above. The cost of genomic selection with the Illumina Bovine50 Beadchip (50K) genotyping platform is currently prohibitively expensive for routine use in females for on-farm decisions. Decreasing the number of genetic markers genotyped in conjunction with a strategy called imputation, however, has dramatically reduced the cost of genomic selection. By exploiting simple inheritance theory we know that half the DNA of the sire and half the DNA of the dam is transmitted to the offspring. By being able to “tag”, with a lower genotype density, which DNA segments of the offspring originated from which parent, the higher density DNA complement of the offspring can be imputed. This is achieved by exploiting knowledge on the entire DNA complement of both parents. The accuracy of imputing the Illumina Bovine50 54,001 SNPs from 6,909 SNPs is 97-99% in US, Australian and Irish dairy cows (Boichard et al. 2012, Berry and Kearney, 2011); the lower number of SNPs means a lower cost thereby making it more amenable to on-farm use.

The effect of imputed genotypes on the resultant estimated genomic breeding values was tested using 50K SNP chip data for 2000 bulls and their dams that were pre-screened in 2011 for the LIC breeding scheme. Only using the low-density markers that are on 50K panel (i.e. discarding the other 40K SNPs), the animals were imputed to back to 50K SNP data and then evaluated using the imputed data. The correlation between genomic breeding worth (GBW) was approximately 99% when calculated from the two different marker panels (Table 1). The rank correlation for the animals is also very high between the two marker sources (Table 1). Similar accuracy of genomic predictions from imputed genotypes was documented also for Irish cattle (Berry and Kearney, 2011).

The threshold price a farmer can pay for genomic selection is dependent on the accuracy of the genomic predictions as well as what proportion of the females the farmer selects as replacements. As well as increasing genetic gain, genomic selection on-farm can aid in mating programs as well as potentially demanding a greater price for their sold replacement females.

Ireland embarked on an initiative in 2012 incentivising farmers, through a slightly reduced cost, to genotype maiden heifers with the view of including them in the training population from 2013 on. To-date almost 5,000 heifers have been genotyped by farmers. Maiden heifers were targeted to avoid any possible selection bias since only high producing, fertile cows remain to later lactations. To avail of the incentive the whole herd of maiden heifers had to be genotyped.

**Retrospective analysis of performance of GEBV**

Prior to implementing genomic evaluations, the accuracy in estimating genetic merit achievable through exploiting genomic information is ascertained. This research is generally achieved by attempting to predict the breeding values of recently daughter-proven sires using only the genomic information of their back-ancestry. This approach mimics reality for genomic selection breeding programs in that genomic information is available to predict the genetic merit of candidate young bulls. Because the “candidate” bulls in the testing phase are already daughter proven, the accuracy of the genomic predictions can be accurately quantified.

However, many countries now have several years experience with genomic selection and many of the AI bulls proven in the recent 1 to 2 years were genomically selected many years previous. Although this analysis is not completely valid since it generally does not include candidate young bulls which, based on their genomic proofs, did not enter the progeny test, it can provide an good indication of the success of genomic selection.

<table>
<thead>
<tr>
<th>Table 1: Relationship between true 50k and imputed-to-50k GBWs and imputation accuracies for 2011-born bulls</th>
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<tr>
<td><strong>Correlation of GBWs</strong></td>
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<tr>
<td>Across all 2011-born bulls</td>
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<td>Top 100 bulls for 50k GBW</td>
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<td>Bottom 100 bulls for 50k GBW</td>
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GBW= genomic breeding worth, where breeding worth is the economic index in NZ.
Ireland released official genomic proofs for dairy cattle in Spring 2009. Bulls that were in layoff awaiting their first-crop daughter proofs in summer 2009 and 2010 were genomically tested and re-released for widespread use; they were already proven for calving difficulty and congenital defects since their progeny had been born 2 years previous. In 2012, there will be progeny entering their second, third and fourth lactation for bulls tested in 2007, 2008, and 2009, respectively. Because the genetic evaluation model for fertility traits changed dramatically in 2011 it was only possible to compare the genomic proofs for the milk production traits attributed to these bulls in 2009, 2010 and 2011 relative to their (reliable) daughter proofs today.

The mean performance of 136 Irish Holstein-Friesian bulls with first crop daughters in 2009 to 2011 in Ireland are detailed in Table 2 and are compared to their predictions based on genomics or on traditional parental average at the time of sale. On average, both the parental average and genomic selection overestimated the mean performance of the candidate bulls. However the correlation with daughter-based estimated breeding values was greater when the genomic information was utilised implying more accurate predictions. In 2009, only 985 bulls were included in the genomic selection training population for Ireland and this increased to over 4,500 in 2011. Clear improvements in the accuracy of genomic predictions (as measured by the correlation between the genomic proofs and the daughter-based proofs) exists across time reflecting the increase in training population, or in other words, more accurate prediction of genetic marker effects. In 2011, to counteract the over-prediction of genetic merit, an adjustment was made to the genomic proofs.

New Zealand Animal Evaluation Limited (NZAE), which oversees the national dairy genetic evaluation, first included genomic information in the national evaluation in 2009. The method used, is described by Harris and Johnson (2010). Subsequent analysis by NZAE in 2010 identified that the genomic estimates were biased upwards. At that time, NZAE advised removing the bias by subtracting 15-30 BW units from the GEBVs. In 2011, the genomic bias adjustment factor was further refined so that it accounted for the breed, ancestry and genetic merit of the animal. The majority of the adjustment factors now range from 20 to 40 BW units. Also in 2011, NZAE decided to remove genomics from the main index (Breeding Worth) but continue to publish a secondary index that includes genomic information.

The first two crops of DNA-proven sires, used in 2008 and 2009, have now received their progeny test proofs. The initial GEBVs of these sires were found to be over-estimated and thus the use of genomically-proven sires did not result in the expected genetic advantage. Therefore, as a gesture of appreciation to the early adopters of genomic evaluation, LIC credited the $5 premium that the farmers paid. Since 2009 the genomic adjustments have been in place and thus the level of over-estimation observed in the 2008 and 2009 teams should not occur in the coming years.

### On-farm uptake of genomic selection

Genomic selection for Holstein-Friesian dairy cattle was officially launched in Ireland in Spring 2009 immediately prior to the breeding season. Table 3 summarises the uptake of genomic selection by Irish dairy farmers since its release in 2009. In 2009, 34% of the semen sold was genomically selected and this has increased consistently to 47% in 2011; usage

### Table 2: Mean performance of 136 Irish Holstein-Friesian bulls with first crop daughters in 2009 to 2011 for milk yield, fat yield and protein yield based on daughter information compared to mean predicted performance prior to progeny test based on parental average and genomics. Also included is the correlation with the daughter-based estimated breeding value for parental average and genomic predictions.

<table>
<thead>
<tr>
<th></th>
<th>Milk yield Mean</th>
<th>Correlation</th>
<th>Fat yield Mean</th>
<th>Correlation</th>
<th>Protein yield Mean</th>
<th>Correlation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Daughter proof</td>
<td>108</td>
<td>0.73</td>
<td>10.37</td>
<td></td>
<td>7.30</td>
<td></td>
</tr>
<tr>
<td>Parental Average</td>
<td>176</td>
<td>0.73</td>
<td>12.32</td>
<td>0.52</td>
<td>9.71</td>
<td>0.60</td>
</tr>
<tr>
<td>Genomic</td>
<td>163</td>
<td>0.78</td>
<td>12.43</td>
<td>0.63</td>
<td>9.50</td>
<td>0.72</td>
</tr>
</tbody>
</table>
in 2012 is expected to be considerably greater due to a disease outbreak at one of the major breeding companies resulting in the destruction of all bulls. On average farmers used 4 to 5 genomic bulls per year to minimise the risk associated with the lower reliability of these genomic bulls relative to their proven counterparts. The EBI (economic breeding index for Ireland) of the genomically selected bulls, which is the total merit index in Ireland, has been consistently one genetic standard deviation greater than the EBI of the proven bulls. The semen price was the same for both genomically selected bulls and proven bulls. This is the main reason for the high update of genomic selection in Ireland.

Table 3: Usage of different categories of bulls (Use), the number of bulls used per farm (Bulls) and the mean EBI and associated reliability in parenthesis of these different bulls in Ireland

<table>
<thead>
<tr>
<th>Proof(^1)</th>
<th>2009 Use (%)</th>
<th>Bulls</th>
<th>EBI (Rel)</th>
<th>2010 Use (%)</th>
<th>Bulls</th>
<th>EBI (Rel)</th>
<th>2011 Use (%)</th>
<th>Bulls</th>
<th>EBI (Rel)</th>
</tr>
</thead>
<tbody>
<tr>
<td>DP-IRL</td>
<td>37</td>
<td>3</td>
<td>120(86)</td>
<td>25</td>
<td>3</td>
<td>146(76)</td>
<td>29</td>
<td>3</td>
<td>143(75)</td>
</tr>
<tr>
<td>DP-INT</td>
<td>29</td>
<td>3</td>
<td>133(56)</td>
<td>34</td>
<td>3</td>
<td>155(47)</td>
<td>24</td>
<td>3</td>
<td>155(47)</td>
</tr>
<tr>
<td>GS</td>
<td>34</td>
<td>4</td>
<td>179(55)</td>
<td>40</td>
<td>4</td>
<td>218(56)</td>
<td>47</td>
<td>5</td>
<td>218(57)</td>
</tr>
</tbody>
</table>

\(^1\) DP-IRL: bulls with daughter producing in Ireland; DP-INT: bulls with daughters producing in some foreign country but not Ireland; GS: genomically tested bulls.

As previously mentioned the uptake for young genomic sires in New Zealand is approximately 40% and in Australia thirty-five percent.

**GENOMIC SELECTION VERSION II**

Research underpinning traditional BLUP evaluations has been underway for many decades. Research on genomic selection therefore is expected to continue for some time.

**Genomic selection for difficult to measure traits**

GEBV in Australia, Ireland, and New Zealand are currently calculated for all routinely recorded traits, using data from herd recording and linear type evaluations. For traits that are not routinely recorded but either do or will contribute to profit, large reference populations of individuals measured for these traits must be assembled. Such traits include feed conversion efficiency, methane emissions, and some health traits. For feed conversion efficiency, New Zealand (LIC, Dairy NZ) and Australia have collaborated on a large-scale project to assemble a reference population. Two thousand growing dairy heifers (1000 in each country) were measured for feed efficiency, and GEBV with an accuracy of 0.42 can be produced for this trait (Pryce et al. 2012). Recently, the growing heifer trait has been demonstrated to predict cow feed efficiency (Pryce et al. 2012 this proceedings). While selection on GEBV for feed efficiency with this accuracy has considerable economic benefit (Hayes et al. 2010), the benefits would increase if accuracy could be improved. A major international consortium has now been established to pool records for dry matter intake, and feed efficiency in the near future, from Ireland, Australia, the US, the Netherlands, the UK and Germany (Veerkamp et al. 2012). (De Haas et al. 2012) recently demonstrated this strategy will improve the accuracy of GEBV for dry matter intake within each country.

**FUTURE IMPROVEMENTS IN GENOMIC SELECTION**

The value of genomic selection to dairy farmers depends on the reliability of the GEBV for young bulls and heifers (the correlation with true breeding value squared). As discussed above, the reliabilities of GEBV can be improved by increasing the size of the reference populations – this was the motivation for the 10,000 Holstein cow and 4,200 Jersey cow projects in Australia. Further improvement in reliability will be achieved by improving the information generated by the DNA markers. The ultimate DNA information is the full genome sequence, all 3 billion bases for an individual cow or bull!

Using full genome sequence data in genomic prediction could be advantageous in at least three situations. If associations between SNP on standard arrays and causative mutations affecting the quantitative trait are not 100%, accuracy of GEBV could be improved by including the causative mutations in the data set. Secondly, if genomic predictions are made across breeds, using full sequence data is likely to be particularly advantageous, as there is no longer the need to rely on marker- associations that may not persist across
breeds. Thirdly, persistence of accuracy of genomic predictions across generations should be improved with full sequence data. Unfortunately the cost of sequencing is such that it is unlikely that the entire reference population will be sequenced. An alternative strategy is to sequence key ancestors of the population, then impute the genotypes for the sequence variants into much larger reference sets with phenotypes and SNP panel genotypes. The 1000 Bull Genomes Project aims to build this database of sequenced key ancestor bulls for the bovine research community. A similar project is underway in New Zealand. Thus far the data set consists of 250 full genome sequences of Holstein, Jersey, Fleckvieh, Angus bulls, sequenced at an average of 11.3 fold coverage. There were approximately 25 million sequence variants detected in the sequences; a small proportion of which will be the causative mutations actually affecting dairy traits. The next challenge will be to use this vast amount of information in genomic evaluations.

CONCLUSIONS

Genomic selection exploiting information on the DNA of an animal is now the official method of genetic evaluations in many dairy cattle populations. Retrospective analysis of data shows that the accuracy of identifying genetically elite animals can be increased by utilising DNA information. Furthermore, the accuracy of prediction is expected to increase further with future developments in genomic technologies and mathematical algorithms.

REFERENCES


The symbiotic microbiome and dairy cattle performance

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INTRODUCTION

The dairy cow, like all ruminants, relies on the microbes within the rumen to enzymatically deconstruct and ferment the plant material it ingests, to ultimately provide energy- and protein-yielding nutrients that support animal maintenance, growth and lactation. The rumen microbiota has evolved over millions of years, and is comprised of bacteria, archaea, protozoa, fungi and viruses. The symbiotic relationships between host and microbes, and between the microbes themselves, offer many opportunities to productively affect the performance of the host; and warrant greater examination using the latest advances in life sciences research.

During the last 5-10 years, the importance of gut microbes in affecting host phenotype has been highlighted by studies of the human gut microbiota, including US NIH’s Human Microbiome Project and the EU-Framework project MetaHIT. The human microbiome has ten times the number of cells as does the human body. Many of those microbes are found in the gut, and are thought to play a role

SUMMARY

The rumen of the dairy cow retains a rich and diverse collection of microbes that, during feed digestion, produce significant quantities of methane gas as well as ammonia, both of which ultimately contribute to the greenhouse gas emissions arising from these production systems. As such, strategies that help to redirect rumen carbon and nitrogen metabolism away from these products provide opportunities for significant productivity improvements in dairy systems not only by improved nutrient retention, but also by reducing greenhouse gas emissions.

To address the regulation of methane emissions in dairy cattle the Department of Primary Industries Victoria (DPI Vic) has used a combination of approaches including massively parallel DNA sequencing, microarrays, and gene specific quantitative polymerase chain reaction (PCR) to identify microbes involved in metabolism underpinning methane production. Similar work has been performed by scientists in Queensland and New South Wales with beef cattle, as part of the most recent Beef Cooperative Research Centre (CRC) program. The conclusion from both studies was that the abundance of methane producing microbes (methanogens) in animals producing “high” and “low” levels of methane does not correlate particularly well with methane emission levels. These results suggest that many microbes other than the methanogens affect the amounts of methane formed by individual animals, presumably by affecting the quantities of substrate pools (e.g. CO2 and H2) needed for methane production.

With respect to rumen nitrogen metabolism, whole genome sequencing and metabolic characterisation of some of the key microbes involved with nitrogen transactions have improved our understanding of the processes controlling the fate of dietary proteins, ammonia production, and intraruminal nitrogen recycling. Recent findings suggest that some of the alterations in the rumen microbiota that favour relatively less amounts of methane formed tend to favour groups of bacteria that are known to be important to the process of rumen protein digestion. Further studies are needed to quantify the implications of these microbiota changes with respect to nitrogen metabolism and retention in livestock.

Advances in genomics technologies have provided new opportunities for large scale, in depth analysis of entire microbial communities, including the large percentage of microbes that are not readily cultured and studied in the laboratory. These recent “metagenomics” studies with both human and rodent models implicate the gut microbiota as an important influence on host phenotype; e.g. obesity and other metabolic diseases in humans. There is also emerging evidence from these studies that host genotype may also play a critical role in the configuration of the gut microbiota. In that context, the integration of animal and microbial genetics and genomics as a new opportunity for the selection of superior animals is an attractive hypothesis. Efforts are now underway in Australia and abroad to examine the rumen microbiota of dairy cattle and other ruminants, with a view to better understand and possibly select animals with superior traits leading to improvements in feed efficiency, methane emissions, and nitrogen retention.
in obesity and malnutrition; diabetes; multiple sclerosis; asthma and eczema; numerous diseases of the intestines, including colon cancer; and autism (Louis 2012, Lozupone et al. 2012 and references within, Maynard et al. 2012). We can extrapolate from this with the assumption that the microbiome, or the “second” genome of the ruminant, which is estimated to outnumber the host cells by 100 times (Attwood et al. 2008) is just as integral to its health and performance. Indeed, much has been learned since the mid 1950’s about the degradative and metabolic properties of rumen microbes, including the establishment of core principles of anaerobic metabolism, such as interspecies hydrogen transfer and the role of methane formation in gut ecosystems (reviewed in Hobson and Stewart, 1997).

It has been estimated by (Gill et al. 2010) that only between 6-26% of dietary energy was recovered in ruminant food products, indicating the digestion process of ruminants has room for gains in efficiency. Methane emissions have also been calculated to be a loss of significant energy to the system (2 to 12% of gross energy intake; Johnson and Johnson, 1995), and therefore potentially targeted as a way to boost production. Recent studies suggest there are differences in the rumen microbiota of cows determined to possess “high” or “low” feed conversion efficiencies (Guan et al. 2008, Zhou et al. 2009). Therefore, looking for differences in microbial populations, which may be linked to changes in the cows feed conversion efficiency (FCF) or their methane emissions, gives us the opportunity to find rumen phenotypes that identify more efficient and productive animals.

Similarly, changes in ruminal nitrogen metabolism could result in productive alterations in nitrogen utilization efficiencies. Unless feed proteins are naturally resistant or pretreated to “escape” rumen digestion, the kinetics of protein degradation occur very rapidly in the rumen; more rapidly than its recapture in microbial protein (Wallace et al. 1997). If these processes could be slowed down, there is the potential to reduce nitrogen losses from the animal. The intensification of food production systems in developed countries has resulted in the practice of feeding protein-rich forages to ruminant animals. The bacteria convert the protein to ammonia, but when ammonia exceeds that which can be used by the rumen microbes, the excess is excreted as significant amounts into the environment, and lost from the animal (Madeira et al. 1997), and references within.

Given that dairy cattle provide sustenance for millions of people worldwide, and consumption is increasing along with populations, that economically in 2010/2011 the Australian dairy industry was worth 3.9 billion at the farm-gate, and was the third largest rural industry in this country (Dairy Australia, 2012), and that greenhouse gas emissions from livestock are an environmental problem worldwide - increasing the performance of the dairy cow remains a priority. Therefore, in order to identify methods by which the rumen microbes might be manipulated, with the aim of increasing production, reducing greenhouse emissions, and increasing nitrogen retention in livestock, all of which have significant economical impacts, we need to continue to study the rumen microbes, and how they interact with each other, but also with the host animal. Microbial ecology enabled by metagenomics approaches will play a large part in this.

**TECHNOLOGY IMPROVEMENTS AND APPLICATION**

Much of our knowledge of the rumen microbes has in the past come from culturing the microorganisms in the laboratory. Unfortunately the bacteria that have been able to be cultured only make up around 10% of the bacterial species found in the rumen (Edwards et al. 2004, Whitford et al. 1998), and don’t represent the dominant or functionally significant populations present. It has been through the evolution of non-culturing molecular techniques, such as small subunit rRNA (ssrRNA) PCR surveys, that we have been able to get a better idea of the true diversity of species present in the rumen.

Other techniques, such as restriction fragment length polymorphism (RFLP) analysis and denaturing gradient gel electrophoresis (DGGE) have also been used to profile the complex communities of the rumen reviewed in (Morrison et al. 2005 and McSweeney et al. 2007). They are useful for identifying the dominant members of a population and for discovering new microbial taxa, but in large part inadequate for detection and quantification of rare species.

In order to quantify the different populations of the rumen several techniques have been used. Fluorescent in-situ hybridization (FISH) involved using fluorescently labelled oligonucleotide probes that would hybridize to the targeted 16S rRNA gene, allowing the targeted organism to be visualized and quantified. Then from 16S rRNA studies, PCR progressed to both competitive PCR, and the more popular quantitative real time polymerase chain reaction (qPCR). Quantitative PCR is a powerful technique that has become the gold standard to accurately quantify nucleic acids and the abundance of microorganisms in a given sample. It has been applied to rumen studies over quite a numbers of years now, usually to monitor the shifts in bacterial

At DPI (Vic) qPCR has been used to identify potential biomarkers that could be indicators of FCE or methane emissions in dairy cattle. Initial qPCR data from FCE assessed dairy cattle (albeit a small number, n=32) has shown in multiple regression analysis that 33% of the variation in RFI data is associated with numbers of species related to Selenomonas ruminantium, Fibrobacter succinogenes, and Prevotella species. The overall bacterial numbers (16S rDNA) present in the rumen and the S. ruminantium abundance appear to be a reasonable indicator, although further studies are required to confirm this relationship (unpublished data).

One hypothesis would be that there is a direct correlation between the number of methanogens and the amount of methane emissions, though various researchers have been unable to find a clear relationship. (Williams et al. 2009) found that methanogen numbers, measured by qPCR of the 16S rDNA, failed to show any correlation with methane production, while (Zhou et al. 2009), by using 16SrRNA gene clone libraries and qPCR, found that methanogen numbers did not significantly change between efficient and inefficient cattle. In our work too, we have not yet seen a correlation. At this stage it seems more likely that other microbes may play a key role by regulating the metabolism determining methane levels. Our early data suggests some of the fibrolytic bacteria may correlate reasonably well (unpublished data), whereas others have found that protozoan numbers correlate with emissions (Morgavi et al. 2010).

Although qPCR is generally used to quantify select microbes at a species or genus level, microarray techniques afford the opportunity to screen and monitor literally thousands of targets from any one sample. The use of phylogenetic and functional microarrays for analysis of rumen samples has been relatively limited to date e.g. (Krause et al. 2004). Rather than be limited to species that have been cultured, or sequenced in some way, DPI Victoria has been able to use microarrays representing hundreds of contigs obtained from metagenomic sequencing. This profiling technique was used on rumen samples of dairy cows on a monensin feeding trial. Despite monensin not inducing significant changes in rumen parameters such as the volatile fatty acids (VFA) (Grainger et al. 2010), microarray profiling was clearly able to distinguish global differences in microbial composition induced by monensin (Cocks et al. 2010). This indicates that the rumen microarray provides a sensitive diagnostic tool.

With the advances in next generation sequencing, 16S rRNA gene surveys have been taken to another level, not to mention the ease at which a single genome can now be fully sequenced. The technology development has enhanced metagenomics approaches and this has the potential to help unravel many microbiome environments, such as the rumen. Others have used the technology to analysed the fibre-degrading enzymes of the bacteria (Brulc et al. 2009, Hess et al. 2011) or to compare the gut microbes of other animals to the rumen (Pope et al. 2010, Pope et al. 2011). (Ross et al. 2012) have compiled a database of rumen microbiome sequence in excess of 100Gbp, which serves as a reference for reliably profiling individual animal’s rumen sequence in order to predict both FCE and methane emission levels. Whole metagenome sequencing provides a profiling method useful in measuring rumen microbial diversity and genetic potential. Analogous to the many genes of small effect identified for complex traits by genome-wide association studies, the rumen metagenomic approach can measure the many microbes of small effect for regulating methane emission. This may assist in improved selection of dairy animals and development of productive rumen interventions (Ross et al. 2012).

The latest research efforts that have focused on either inhibiting the growth/activity of rumen methane producing microbes, or selecting animals with a “low methane” phenotype have revealed that Prevotella spp. are often the predominant group of ruminal bacteria that increase in response to these interventions. In addition to their fermentation schemes favouring a redirection of hydrogen towards products other than methane (i.e. succinate and propionate) it is well recognised that ruminal Prevotella spp. are a principal source of enzymes controlling the rate and extent of rumen proteolysis, peptide formation, and subsequent ammonia production. Previous studies by (e.g. Yang and Russell 1993) have demonstrated that the rapid rates of rumen proteolysis to peptides and then ammonia, and the role of Prevotella spp. in these processes, results in as much as 20% of feed protein being “wasted” via rumen ammonia production and its metabolism and excretion in urea. Subsequently, Morrison and colleagues at CSIRO has previously shown that a specific class of enzymes, called diaminopropetyl peptidases (hereafter referred to as DAPs), are produced by Prevotella spp., and DAP activity accelerates amino acid fermentation and ammonia production by rumen bacteria (Madeira et

al. 1997). For these reasons, we contend that strategies that seek to reduce ruminal proteolysis, by reducing DAP activity, might improve nitrogen utilization efficiency in animals consuming protein rich diets. Furthermore, one of the “unintended consequences” of livestock methane mitigation strategies, which elevate the abundance of Prevotella spp. might be an increased rate of ruminal proteolysis via DAPs and changes in nitrogen utilization efficiency, including urea excretion and consequently nitrous oxide emissions. Whole genome sequencing of Prevotella spp. e.g. (Purushe et al. 2010) integrated with metabolic characterisation and mutagenesis methods will improve our understanding of the key individual microbes that regulate rumen protein digestion as well as how best to antagonize this process, with a view to improve rumen nitrogen transactions and nitrogen utilization efficiency. It will be through the information obtained from metagenomics, allowing us to determine a more complete phenotype of the rumen microbes, how they are regulated and how they function, that will lead us to better understand the rumen ecosystem, and therefore how it can best be measured, managed and manipulated to provide a more productive animal.

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Validation of genomic evaluations in Australian Jersey cattle using a reference set that includes cows

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ABSTRACT

Genomic breeding values (ABVg) can be used to select young dairy bulls and heifers for breeding, provided they are sufficiently reliable. The aim of the “Jer-nomics” project was to assemble a large reference population of cows and progeny-tested bulls, to enable the calculation of ABVg for Australian Jersey cattle. A reference set consisting of 4,200 cows and 1,000 bulls was created. To demonstrate the value of ABVg calculated from this reference set, ABVg were calculated for a validation set of Jersey bulls (where the records of these bulls were omitted when DNA marker effects were calculated), either using a reference set of bulls only or bulls and cows. For young validation bulls, inclusion of cows in the reference set generally led to higher correlations of ABVg with actual daughter performance compared with conventional breeding values based on parent average for yield, workability traits and SCC, with results being similar for ABVg based on a bulls only reference set, except for fertility. There was a tendency for ABVg based on bulls+cows to reduce the overestimation of daughter performance compared with Parent Average (PA) for most traits considered, but this was not the case for fertility and overall type. Reliabilities of ABVg for young bulls were approximately double the PA, and will be a useful tool to increase the rate of gain for traits affecting profit in the Jersey breed.

Keywords: Genomics; Jersey; cows; reference set.

INTRODUCTION

Genomic evaluations have the potential to increase the reliability of breeding values (BV), especially for young animals without records and offspring. This effect may lead to large increases in the rate of genetic gain, as the bulls can be used at a much younger age than following progeny testing. The increase in reliability that can be achieved depends largely on the size of the reference set (animals with both genotypes and phenotypes) used to estimate the effect of DNA markers.

Following the successful introduction of genomic breeding values (ABVg) for Holstein cattle, the “Jer-nomics” project was undertaken to enable the reliable estimation of ABVg for this breed by increasing the reference set for Jersey cattle. The aim of this study was to determine the increase in BV reliability for young Jersey bulls and to investigate whether there was any bias from genomic evaluations based on a reference set that included cows.

MATERIALS AND METHODS

By April 2012, the ADHIS database held 1,017 genotyped Jersey bulls and 4,237 genotyped Jersey cows. The majority of genotyped cows (4,202) was from the Dairy Futures CRC Jer-nomics project, consisting of cows with extensive records for a variety of traits; the remainder were cows genotyped by breeding companies and farmers. The majority (n=4110) of cows were genotyped with the 50K Illumina SNP chip, but in some cases the 7K chip (n = 92) was used.

The methodology used for predicting ABVg in Holstein cattle was used. Briefly, genotypes were received on the 50K or 7K Illumina chip and after quality checks (minimum values for call rate of a sample, genetrain score for each marker in a batch and heterozygotes) were imputed to 50K if any markers were missing. Marker effects were estimated using the RR-BlUp program described by (Moser et al. 2009), with phenotypes based on the daughter yield deviation concept (e.g. Szyda et al. 2008, phenotypes corrected for fixed effects and parent BV) and called Daughter Trait Deviations (DTDs) for bulls and Trait Deviations (TDs) for cows. In the marker effect estimation, DTDs and TDs were weighted according to the amount of information they were based on (i.e. number of daughters, number of lactations); this was adapted from the method described by (Garrick et al. 2009). For example, for milk yield, a bull DTD based on 6 daughters has the same weight as a cow TD based on 1 lactation.

Direct Genomic Values (DGV) were a simple sum of marker effects across all markers for an animal. Direct Genomic Values and conventional BV were combined in a blending step based on Harris and Johnson (2010), but adjusted to account for the fact that markers do not account for the full genetic variance (Haile-Mariam et al. 2012).

In the Jersey breed, it was noted that for yield traits, the parent average (PA) – which is the conventional BV for bulls without daughters – tended
to overestimate the BV calculated from daughter information. The conventional BV for bulls with less than 10 daughters was, therefore, multiplied by the regression coefficient of DTD on PA prior to blending.

In order to investigate the value of ABVg for Jerseys (in terms of reliability and bias), an Interbull style test was performed. For this test, ABVg were calculated for a group of 125 validation bulls that had no daughters in 2007 and at least 20 daughters in April 2012. The Interbull test consisted of calculating ABVg for these bulls, using SNP effects and their conventional ABV (in this case parent average) from 2007, and comparing these to their DTD based on daughter information in 2012, in terms of correlations and regression coefficients. The regression coefficients of DTD on PA or ABVg are a measure of bias, with values less than 1 indicating that the PA or ABVg overestimates the BV. The reference set consisted of 673 bulls and 1,460 cows that had BV as well as DTD or TDs in August 2007. Only about a third of the cows could be used, as the majority did not get records until after 2007. When ABVg are predicted in routine analyses, all the genotyped bulls with DTD and cows with TD are used in the reference set.

RESULTS

Correlations between DTD and ABVg were very similar for ABVg based on bulls only or bulls+cows for all traits except fertility (Table 1). The ABVg based on bulls+cows had a higher correlation with DTD than the PA for yield traits, workability traits (temperament and likability) and SCC. This increase ranged from 0.05 to 0.11 and was not statistically significant (the s.e. of the correlation based on a sample of 125 bulls is 0.089). For Overall Type, survival and fertility, PA and ABVg based on cows+bulls had similar correlations with DTD, suggesting that the PA is as effective as an ABVg in predicting the DTD.

Regression coefficients for DTD on ABVg based on bulls+cows were higher than for DTD on PA and DTD on ABVg (bulls only) for the yield traits and survival, although not significantly. The highest regression coefficient for SCC was with the ABVg based on bulls only, while for Overall Type and fertility the highest regression coefficient was for PA on DTD. For likability and temperament all regression coefficients were very close to or over 1.

DISCUSSION AND CONCLUSION

The addition of genomic information to the BV of young bulls resulted in BV that were more highly correlated with performance of daughters than the parent average for yield and workability traits and SCC. Although this effect was not significant, it is in line with results in Holstein and in other countries.

Except for fertility, there was little difference in the use of a bulls only or a bulls+cows reference set in correlations with daughter performance. The main advantage of the bulls+cows reference set was in an improvement in regression coefficients for many traits, compared with both the PA and the ABVg based on bulls only. While it was expected that bias might increase with the inclusion of cows in the reference set, this only happened for SCC, suggesting that the process of including cows with good quality records in the reference set resulted in cows being selected for better SCC performance. The very low regression coefficient of DTD on ABVg based on bulls only for fertility would suggest a selection of bulls for better fertility, but it is unclear how this would have happened in practice. For fertility and Overall Type it is possible that a cows only reference set would outperform the PA.

The main aim of the introduction of genomics was to increase the reliability of BV for young bulls with no daughters. Based on the above analysis, marker effects were re-estimated using all bulls and cows in the reference set to produce ABVg for April 2012. Table 2 gives an overview based on 105 young bulls. Without genomics, the average reliability for PA for these bulls varied from 20 to 28%. With genomic information added, this increased to 35 to 60%. The highest genomic APR for a young bull was 299, which was similar to the highest Publishable bull with genomics (308), indicating that young bulls with genomics can compete with proven bulls in terms of genetic merit and reliability.

Genomic evaluations for Jersey cattle were recently included in ADHIS’ August 2012 release of BV and the Good Bulls Guide. These ABVg will be a valuable tool for increasing the rate of genetic gain for traits affecting profit in Australian Jersey cattle.

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**Table 1**: Comparison of Daughter Trait Deviation (DTD) in 2012 with Parent Average (PA) and genomic breeding value (ABVg) estimated from 2007 data using either a bulls only or bulls+cows reference set

<table>
<thead>
<tr>
<th>Trait*</th>
<th>OT</th>
<th>Fert</th>
<th>SCC</th>
<th>Surv</th>
<th>Like</th>
<th>Temp</th>
<th>Fat</th>
<th>Milk</th>
<th>Prot</th>
</tr>
</thead>
<tbody>
<tr>
<td>DTD v PA</td>
<td></td>
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</tr>
<tr>
<td>Correlation DTD, PA</td>
<td>0.33</td>
<td>0.19</td>
<td>0.59</td>
<td>0.14</td>
<td>0.35</td>
<td>0.35</td>
<td>0.62</td>
<td>0.52</td>
<td>0.53</td>
</tr>
<tr>
<td>Regression coeff. DTD on PA</td>
<td>0.88</td>
<td>1.14</td>
<td>0.79</td>
<td>0.65</td>
<td>0.97</td>
<td>1.27</td>
<td>0.82</td>
<td>0.66</td>
<td>0.71</td>
</tr>
<tr>
<td>DTD v ABVg bulls only</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Correlation DTD, ABVg</td>
<td>0.28</td>
<td>0.03</td>
<td>0.66</td>
<td>0.14</td>
<td>0.45</td>
<td>0.41</td>
<td>0.67</td>
<td>0.61</td>
<td>0.64</td>
</tr>
<tr>
<td>Regression coeff. DTD on ABVg</td>
<td>0.71</td>
<td>0.19</td>
<td>0.90</td>
<td>0.64</td>
<td>1.09</td>
<td>1.29</td>
<td>0.71</td>
<td>0.62</td>
<td>0.69</td>
</tr>
<tr>
<td>DTD v ABVg bulls + cows</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Correlation DTD, ABVg</td>
<td>0.30</td>
<td>0.19</td>
<td>0.66</td>
<td>0.15</td>
<td>0.44</td>
<td>0.42</td>
<td>0.68</td>
<td>0.61</td>
<td>0.65</td>
</tr>
<tr>
<td>Regression coeff. DTD on ABVg</td>
<td>0.69</td>
<td>0.66</td>
<td>0.76</td>
<td>0.76</td>
<td>1.13</td>
<td>1.20</td>
<td>0.85</td>
<td>0.76</td>
<td>0.89</td>
</tr>
<tr>
<td>Increase in correlation</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bulls only vs PA</td>
<td>-0.05</td>
<td>-0.16</td>
<td>0.07</td>
<td>0</td>
<td>0.10</td>
<td>0.06</td>
<td>0.05</td>
<td>0.09</td>
<td>0.11</td>
</tr>
<tr>
<td>Bulls + cows vs PA</td>
<td>-0.02</td>
<td>0</td>
<td>0.07</td>
<td>0.01</td>
<td>0.09</td>
<td>0.07</td>
<td>0.06</td>
<td>0.09</td>
<td>0.12</td>
</tr>
</tbody>
</table>

*OT=overall type; Fert=fertility; SCC=Somatic Cell Count; Surv=survival; Like=likability; Temp=temperament; Fat=lactation fat yield (kg); Milk=lactation milk yield (l), Prot=lactation protein yield (kg)

**Table 2**: Reliability (%) of Breeding Values for young bulls based on Parent Average or genomic Breeding Value (ABVg) based on bulls and cows in the reference set

<table>
<thead>
<tr>
<th>Trait*</th>
<th>OT</th>
<th>Fert</th>
<th>SCC</th>
<th>Surv</th>
<th>Work</th>
<th>Yield</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parent Average</td>
<td>21</td>
<td>20</td>
<td>28</td>
<td>22</td>
<td>24</td>
<td>28</td>
</tr>
<tr>
<td>ABVg</td>
<td>47</td>
<td>35</td>
<td>49</td>
<td>40</td>
<td>47</td>
<td>60</td>
</tr>
<tr>
<td>difference reliability ABVg-Parent Average</td>
<td>26</td>
<td>15</td>
<td>21</td>
<td>18</td>
<td>23</td>
<td>32</td>
</tr>
</tbody>
</table>

*OT=overall type; Fert=fertility; SCC=Somatic Cell Count; Surv=survival; Work=workability traits (likability, temperament, milking speed); Yield=yield traits (milk yield, protein yield, fat yield)
Toward using rumen metagenomic profiles to predict methane emissions from dairy cows

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ABSTRACT

The immense microbial population in the dairy cow rumen has long been thought to affect the phenotype of the host animal, particularly for traits which are primarily rumen derived, such as feed conversion efficiency and methane production. Here a method is proposed that uses rumen metagenome profiles, which have been obtained by using massively parallel sequencing technology to quantify the abundance of thousands of DNA markers (each of which represents a microbial species), to predict quantitative traits. In a similar way to which genomic predictions have used the cow’s DNA profile to predict traits, the method proposed here uses these metagenome profiles to predict methane production. The workflow for these predictions is presented. Two proof of principle experiments were performed to test this method. Both experiments showed a positive relationship between the predicted and measured trait ($r^2=0.478$ and 0.959). By developing alternative methods to predict methane production it may be possible to greatly increase the number of animals which can be individually phenotyped for greenhouse gas emissions.

Keywords: methane production; rumen metagenome; microbial profiling.

INTRODUCTION

Ruminants such as dairy cattle are herbivores which ferment vegetation in the reticulo-rumen, a section of the stomach. The rumen of cattle contains between $10^{10}$ to $10^{11}$ micro-organisms per millilitre including bacteria, archaea, fungi and protozoa (Dehority 2003), which break down the consumed vegetation to provide nutrients such as volatile fatty acids (VFA) and bacterial protein for the host animal. The rumen micro-organism community allows ruminants to access nutrients from sources which would otherwise be unavailable (e.g. cellulose), as well as being the source of 87% of methane produced by the animal (Murray et al. 1976). Therefore investigating the diversity, ecology and abundance profile of these rumen micro-organisms should be considered an important part of dairy research.

DNA based methods mostly utilising polymerase chain reaction (PCR), form the majority of recent investigations into rumen microbial communities. These studies have attempted to find associations between microbial species or groups, with varying levels of success (Hegarty 1999; Hart et al. 2009, Zhou et al. 2009, Zhou et al. 2011). A limitation of this technology is that it may overlook population wide community patterns.

With recent advances in massively parallel sequencing it is now possible to obtain millions of sequences from the DNA of thousands of different rumen microbiota (Brulc et al. 2009, Hess et al. 2011, Ross et al. 2012). Associating this data with traits such as methane (a greenhouse gas over 20 times stronger than CO₂) is as yet an unachieved challenge.

This study will report the proposed workflow for using metagenomic profiles for predicting traits such as methane production and will use the method on two proof of principle examples. Firstly predicting the type of sample (rumen fluid or faeces) and secondly predicting host disease state.

MATERIALS AND METHODS

A graphical outline of the proposed method is outlined in Figure 1. As a proof of principle experiment for this method, data from an earlier study (Ross et al. 2012) was used. The samples were taken from eight lactating Holstein dairy cattle located at the Department of Primary Industries’ Ellinbank centre (Victoria, Australia). A second proof of principle experiment was also performed on human faecal data from (Qin et al. 2010). The data consisted of 38 samples, including some from patients in clinical remission from inflammatory bowel disease (IBD).

Firstly, samples and phenotypes (traits) must be obtained from a reference population of animals. Metagenomic DNA was extracted from the samples and sequenced on a massively parallel sequencer. This DNA sequence was used to produce a metagenomic profile of the sample (Ross et al. 2012), which resulted in an $n \times m$ matrix $X$ with elements $x_{ij}$, the log transformed and standardised count for sample $i$ for contig $j$, with $n$ samples and $m$ contigs. These profiles were then compared to make a rumen microbiome
relationship matrix (calculated as $G = XX'/m$). Best linear unbiased prediction (Henderson 1984) was then used to predict phenotypes for validation samples. A mixed model was fitted to the data: $y = 1_n \mu + Zg + e$; where $y$ is the a vector of phenotypes, with one record per sample, $1_n$ is a vector of ones, $\mu$ is the overall mean, $Z$ is a design matrix allocating records to samples, and $g$ is a random effect estimate $\sim N(0, G \sigma^2_g)$. Using ASReml (Gilmour et al. 2006), phenotype of the samples $(\hat{g})$ were predicted as:

$$
\begin{bmatrix}
\hat{\mu} \\
\hat{g}
\end{bmatrix} = \left(\begin{bmatrix} 1_n & 1_n \\
Z'1_n & Z'Z + G^{-1} \sigma^2_g \
\end{bmatrix}\right)^{-1} \begin{bmatrix} 1_n'y \\
Z'y
\end{bmatrix}
$$

Figure 1: Methodology for using metagenome profiles to predict phenotypes (traits) such as methane production.

As the phenotypes used in this study are qualitative, they are assigned a value of 1 (rumen fluid) or 0 (faeces) for the sample type comparison. Samples with a value of $< 0.5$ are assigned to faeces; samples with a value of $> 0.5$ are assigned to rumen. Leave out two cross validation was used to obtain predictions for each animal. Samples were assigned a phenotype value of 1 (normal) or 0 (affected) of the IBD study. Low assignment values are assigned to having IBD; high values are assigned to no IBD. A small subset of phenotypes was predicted using a model built on all other samples.

**RESULTS**

Using the methodology outlined above, all 7 rumen fluid and 8 faeces samples were successfully allocated to the correct metagenome type ($r=0.959$; Figure 2A). Predicted disease state of IBD patients was also positively correlated with actual disease state ($r=0.478$; Figure 2B). Therefore the method was successful in predicting phenotypes in both experiments.

![Figure 2](image)

**DISCUSSION AND CONCLUSION**

This study has illustrated how microbial metagenomic profiles can be used to correctly identify the phenotype of samples. This experiment was chosen as a proof of principle due to the large differences observed between faecal and ruminal metagenome profiles (Ross et al. 2012). Due to these large differences, it is not surprising that all samples were able to be correctly allocated to their sample type. This method was then applied to a more subtle trait, disease phenotype of IBD patients in clinical remission. The success of the disease state predictions suggests that this method is a promising candidate for modelling other subtle traits that are closely linked to the gut microbiome, such as methane production or feed conversion efficiency. This method will be expanded to include the ability to predict quantitative traits that are of high importance to the dairy industry including methane production from lactating dairy cattle.

The trait prediction methodology presented in this study mirrors genomic predictions, however it uses metagenome DNA markers, in the form of
counts mapping to each contig, in place of the host animal’s genotype. By integrating metagenomic predictions with genomic predictions it may be possible to surpass current accuracy of predictions for rumen-centric traits, such a methane prediction and feed conversion efficiency.

ACKNOWLEDGEMENTS

The authors are very grateful to the Dairy Futures Co-operative Research Centre and the Gardiner Foundation for supporting this work and to their colleagues for support and encouragement.

REFERENCES


Identifying candidate genes affecting milk production traits by combining gene expression studies and genome wide association studies

Combining microarrays and GWAS

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ABSTRACT

Although complex traits, such as milk production, are thought to be controlled by many genes there has been little success in identifying them. Two different types of experiments that may help identify these genes are microarray experiments and genome-wide association studies (GWAS). Few systematic studies have been performed to determine if these two approaches identify the same genes. In this study, we compared genes that are differentially expressed in mammary cells in response to treatments affecting milk synthesis, to genes containing single nucleotide polymorphisms (SNPs) significantly associated with milk production traits. We found that genes differentially expressed in multiple microarray experiments contain significantly more SNPs associated with milk production traits than expected by chance. It is probable that these genes containing significant SNP have a functional role in milk synthesis. This approach can identify new candidate genes that are important in the functioning of the mammary gland and this may improve selection of dairy cattle for milk production.

Keywords: Microarray; genome-wide association study; GWAS; single nucleotide polymorphism; SNP; association; milk production trait; lactation.

INTRODUCTION

While the physiology of milk production and secretion in the dairy cow is well established, regulation at the gene level has yet to be clearly defined. Milk production is a complex trait, controlled by many genes and the relationship between the genetic variation and phenotypic variation seen in dairy cows is non-linear (environmental variation affects phenotype). Identifying the genes and genetic polymorphisms involved in regulating these milk production traits would provide valuable information for dairy cattle breeding programs.

Two methodologies that could help identify genes involved in regulating milk production in the dairy cow are DNA microarray experiments and genome-wide association studies (GWAS). DNA microarrays measure changes in transcript expression levels between two conditions. There have been many studies utilising microarrays to examine bovine milk production traits (Singh et al. 2008, Swanson et al. 2009, McCord et al. 2010). GWAS are a more recent technology and have become a popular methodology to identify genomic regions containing variants affecting complex traits. GWAS have also been used to study milk production in the dairy cow and have successfully identified genomic regions effecting bovine milk protein production (Cole et al. 2010, Cole et al. 2011) and milk fat (Cole et al. 2011, Wang et al. 2012). Recently, a study integrating both GWAS and microarray data identified several putative candidate pathways and genes involved in inflammatory responses to mastitis across ruminant host species (including dairy cattle), pathogens and cell systems (Lewandowska-Sabat et al. 2012). Findings from this study supported previous results (Genini et al. 2011) and suggest that this integrative approach is effective for identifying novel candidate genes for further functional studies.

There have been few systematic studies comparing results between microarray experiments and GWAS studies. In this study, we compare genes that are differentially expressed in multiple bovine lactation microarray experiments to genes that contain SNPs significantly associated with milk production traits (using the results of a series of GWAS). Results may reveal putative gene candidates involved in the regulation of milk production traits in the cow, potentially leading to improved selection of dairy cattle.

MATERIALS AND METHODS:

Microarray experiments

A series of cDNA microarray experiments were conducted as part of a collaboration between the Department of Primary Industries (DPI) Victoria
and AgResearch (New Zealand), examining gene expression changes in the bovine mammary gland during lactation under different conditions. For this analysis, eight experiments were examined, very briefly outlined below:

1) *In vivo* bromocriptine-mediated prolactin loss experiment
2) *In vitro* bovine mammary epithelial cells in response to prolactin and extracellular matrix.
3) Extended lactation program in cows examining the difference between:
   a. Early and late lactation
   b. Persistent and non-persistent dairy cows
   c. Cows in extended lactation with low, medium or high nutritional status
4) Genetic merit experiment: comparing cows of high and low genetic merit under normal conditions, when fasted for 36 hours and when on 50% rations for 7 days.
5) Time course involution experiment involving the induction of involution by termination of milking and transcript profiling at 6, 12, 18, 24 and 36 hours post-milking. Full methods for this experiment are described in (Singh *et al.* 2008).
6) Streptococcus uberis-induced mastitis experiment. Full methods for this experiment are described in (Swanson *et al.* 2009).
7) Once a day milking versus twice daily milking experiment.
8) Growth hormone treatment experiment. Animals and treatment described in detail in (Hayashi *et al.* 2009).

Independent experimental validation of the microarray expression results was performed by Northern analysis and quantitative real-time PCR for a subset of significantly differentially regulated expressed sequence tags (ESTs) and for ESTs representing housekeeping genes. Genes corresponding to ESTs with a minimum fold change value of 1.5 and $P<0.1$ in two or more of these microarray experiments were identified and added to a gene list (referred to as the “common-set” in this article).

**Genome-wide association studies (GWAS)**

Using the Illumina BovineHD BeadChip, 12,685 Holstein and 5,240 Jersey bulls and cows were genotyped for each SNP. An association analysis was used to determine the relationship between polymorphisms and the milk production traits: protein yield, fat yield and milk volume. Statistical analyses were performed using ASReml (Gilmour *et al.* 2002).

All SNP falling either in our common-set genes or within 50 kb either side of these genes (accounting for regulatory regions) were identified (using a cut-off $p$-value of $1 \times 10^{-5}$). This was repeated for all 24,616 genes in the bovine genome (UMD 3.1).

The observed proportion of significant SNP in the common-set for each milk production trait was compared to the proportion of significant ($p < 1 \times 10^{-5}$) SNP for the same trait in all genes in the bovine genome using a Chi-square test (degrees of freedom = 1). The false discovery rate (FDR) was calculated using the formula: $m(p/s)$, where $m$ is the total number of SNPs, $p$ is the probability of the F-test and $s$ is the proportion of significant SNP at $p < 1 \times 10^{-5}$.

**RESULTS**

We found 1,683 ESTs were significantly differentially regulated in at least two different microarray experiments. These ESTs corresponded to 797 annotated bovine genes (termed the “common-set”). The number of SNP falling in ($\pm$ 50 kb) the common-set genes totalled 23,818. Using the proportion of significant SNP in all bovine-genes (24,616), the number of expected significant SNP in the common-set was calculated (see Table 1). Applying a Chi-square test (degrees of freedom = 1), we compared the actual number of significant SNP in the common-set to the expected proportion of significant SNP and found that for every milk production trait tested, the number of significant SNP in genes ($\pm$ 50 kb) from the common-set outweighed the number of significant SNP we would expect to see by chance alone ($P<1x10^{-5}$) (Table 1). Genes from the common-set containing significant SNP for protein yield, fat yield and milk volume (the numbers of which are outlined in Table 1) were added to a candidate gene list.

**DISCUSSION**

In this study we combined the results of a series of microarray experiments with a series of GWAS and identify candidate genes hypothesised to be involved in the production of milk in the dairy cow. Individually, microarray experiments and GWAS both allow unbiased identification of candidate genes involved in milk production, however, each of these methodologies have their associated advantages and disadvantages. When microarray experiments are of a sufficient size or when multiple experiments are pooled in a meta-analysis, they can have the statistical power to detect minute expression changes. However, because genes are often involved in more than one pathway, differential expression of an individual gene may induce a ‘ripple effect’ on multiple downstream targets, complicating the identification of causal genes. In general, this is not an issue with GWAS.
However, GWAS do not perform well when there are many genes with a small effect and they inadequately identify relationships between genes.

Candidate genes identified by this study include the suppressor of cytokine signalling 2 (SOCS2) and E74-like factor 5 (ELF5) genes. Both SOCS2 and ELF5 were significantly differentially regulated in three of the eight microarray experiments (experiments 1, 2 and 5 outlined in the methods section). The SOCS2 gene contained three significant SNP for milk volume, whereas ELF5 contained two SNP for fat yield. SOCS2 and ELF5 are important mediators of prolactin action in the mammary gland and may regulate the expression of milk protein genes (Harris et al. 2006, Anderson et al. 2007).

Our results indicated that there is a significant overlap between genes identified as differentially regulated during lactation from microarray experiments and those identified by the GWAS as containing SNPs significantly associated with milk production traits. Results of our analyses also suggests that combining both microarray expression and genotype (GWAS) data may provide a more effective approach of establishing biological context than when using one technology alone. This multifaceted approach enables the generation of more-informed hypotheses and can refine the identification and prioritise candidate genes.

**Table 1: SNPs significantly associated with the milk production traits: protein yield, fat yield and milk volume in genes (± 50 kb) in the common-set and all genes in the bovine genome (UMD 3.1)**

<table>
<thead>
<tr>
<th>Gene set</th>
<th>Total number of SNP</th>
<th>Protein yield</th>
<th>Fat yield</th>
<th>Milk volume</th>
</tr>
</thead>
<tbody>
<tr>
<td>All bovine genes (24,616 genes)</td>
<td>377,656</td>
<td>377,656</td>
<td>377,656</td>
<td></td>
</tr>
<tr>
<td>Number of significant SNP</td>
<td>9,693</td>
<td>5,863</td>
<td>9,296</td>
<td></td>
</tr>
<tr>
<td>Percent of SNP significant</td>
<td>2.57%</td>
<td>1.55%</td>
<td>2.46%</td>
<td></td>
</tr>
<tr>
<td>False discovery rate</td>
<td>3.90E-04</td>
<td>6.44E-04</td>
<td>4.06E-04</td>
<td></td>
</tr>
</tbody>
</table>

| Common-set (797 genes)               | 23,818             | 23,818        | 23,818    |
| Total number of SNP                  | 612                | 369           | 586       |
| Number of expected significant SNP   | 927                | 551           | 1,053     |
| Number of actual significant SNP     | 3.89%              | 2.31%         | 4.42%     |
| Percent of actual SNP significant    | 146                | 186           |
| Number of genes with significant SNP | 178.57             | 96.58         | 406.56    |
| False discovery rate                 | 2.57E-04           | 4.32E-04      | 2.26E-04  |

The number of SNPs significantly associated with milk production traits in genes (± 50 kb) in the common-set and all genes in the bovine genome (UMD 3.1) were counted. A SNP was considered significant if its f-statistic corresponded to a p-value of less than 1 \times 10^{-5}. A Chi-squared test (degrees of freedom = 1) was used to test significance of the common-set results against results from all bovine genes. Results indicated for all milk production traits investigated, the common-set contained more significant SNP than expected by chance (p < 1 \times 10^{-5}). The false discovery rate was also calculated.

**ACKNOWLEDGEMENTS**

We would like to thank the Dairy Futures CRC for their continued support for this project.

**REFERENCES**


Dietary nucleotides affect the microbial diversity of the developing rumen in young calves

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ABSTRACT

Methane mitigation is possible by examining the interaction between developing rumen microorganisms and their reduction of methanogenic archaea, and subsequently by manipulating the developing microbial ecosystem in the developing rumen of calves to alter the microbiota of the cow rumen. The aim of this study was to determine the effects of a nucleotide feed additive (Ascogen®) and restricted feed intake on the microbial population in the developing rumen of calves. Ten calves were assigned to each of four treatments: Control unrestricted diet (CU), control restricted diet (CR), nucleotides and unrestricted diet (NU) and nucleotides and restricted diet (NR). Samples from the developing rumen were taken at 7, 14, and 20 days of age with a stomach tube 3 hours after feeding.

Quantitative polymerase chain reaction (PCR) was used to quantify the genes encoding 16S and 18S ribosomal DNA of the rumen cellulolytic (Fibrobacter succinogenes and Ruminococcus flavefaciens), non-Fibrolytic (Selenomonas ruminantium), proteolytic bacteria (Prevotella ruminicola), methanogenic (Methanobrevibacter spp and Methanobacterium spp) and protozoic (Entodinium spp) organisms. Cloning was used to confirm the specificities of the primer pairs. Our studies showed that Ascogen® significantly increased the concentration of nucleic acids from P. ruminicola and decreased the concentration of nucleic acids from Methanobrevibacter spp and Methanobacterium spp. This interaction between microorganisms suggests that increases in P. ruminicola is associated with the reduction of methanogenic microorganisms and thus may be a mechanism to reduce methane production in ruminants.

Keywords: nucleotides; microorganisms; calf; developing rumen; methane; Prevotella; methanogenic archaea;

INTRODUCTION

During the past twenty years, additives have been extensively used in the developing rumen of calves to improve health (Chaucheyras-Durand and Durand 2010; Fooks and Gibson 2002), to decrease intestinal disorders (Casas and Dobrogosz 2000), to enhance body condition (Oyetayo and Oyetayo 2005), and to reduce feed costs (Chaucheyras-Durand and Fonty 2002). Some research has found that nucleotides affect microorganisms in the small intestine (Carver et al. 1998, Kulkarni et al. 1986) However; very few studies have examined the effect of feed additives on microorganisms in the developing rumen. The rumen is a remarkable environment that houses thousands of species of bacteria, methanogenic archaea, protozoa, fungi and viruses (Stewart et al. 1988). This complex community of organisms interact to play an important role in the digestion of feed and the supply of energy and protein to the host in the form of volatile fatty acids (VFA) and microbial protein (Martinez et al. 1997). Until now there is no known work that involves young calves and that determines the presence of microorganisms in the developing rumen with molecular techniques, or examines the effect on the microbiota incurred by a nucleotide feed additive in the diet. Thus, the aim for this study was to determine the effects of a nucleotide feed additive (Ascogen®) and a restricted diet on the presence and relative concentration of nucleic acids from fibrolytic, non-fibrolytic, methanogenic archaea and protozoa in the developing rumen of young calves.

MATERIALS AND METHODS

Rumen samples and treatments

The animal experiment involved 40 friesian bull calves and was conducted according to a protocol approved by the Animal Care and Use Committee, Research Animal Resource Centre, La Trobe University, Australia. From 3 days of age the calves were fed twice daily according to the manufacturer’s instruction at 8.00 am and 4.00 pm with one commercial calf-milk replacement (CMR) product, Veanavite® full cream (Rivalea). All calves had ad libitum access to water and oaten hay. The factorial experiment consisted of four treatments given to calves from 5 to 20 days of age: ‘control unrestricted’ (CU), ‘control restricted’ (CR), ‘nucleotides unrestricted’ (NU) and ‘nucleotides restricted’ (NR). Calves given nucleotide treatments were given Ascogen® (1 g per feed, 2g/day), whereas calves receiving the control treatments were not. Ascogen® (Chemoforma, Switzerland) is a product containing a minimum of 15% RNA/Nucleotides. Calves given restricted treatments were allowed access to calf
meal (Southern Livestock Nutrition, Murgheboluc, Victoria, Australia) daily at 60% of the unrestricted ration (0.2 kg per day). Ruminal samples were taken at 7, 14, and 20 days of age.

**DNA preparation and extraction**

The fluid was filtered through two layers of cheesecloth, collected in 15 ml sterile plastic tubes, immediately stored on ice and then kept at -80 °C until DNA extraction. DNA was extracted from 1.5 ml of frozen ruminal fluid using the method of (Skillman et al. 2004) and Stevenson and Weimer (2007). The DNA was extracted from the rumen samples with a ZR Fungal/Bacterial DNA Kit (Zymo Research, Australia) and stored at -20 °C. The concentration and purity of the extracted DNA were assessed spectrophotometrically by calculating $A_{260}/A_{280}$.

**Real-time PCR condition.**

Primers used were based on those employed to identify presence of *Methanobacterium* spp. and *Methanobrevibacter* spp in lambs (Skillman et al. 2004); *Prevotella ruminicola*, *Ruminococcus flavefaciens* and *Selenomonas ruminantium* in lactating dairy cows (Khafipour et al. 2009); *Fibrobacter Succinogenes* in lactating cows (Stevenson and Weimer 2007); and Protozoa *Entodinium* spp. (Skillman et al. 2006). The primers were made by Geneworks Pty Ltd Australia. Real time polymerase chain reaction (qPCR) was performed in a Cycler in a Stratagene Mx 3000P qPCR (Agilent Technologies, Australia) and analysis was carried out using Brilliant II SYBR Green QPCR Master Mix (Stratagene, Integrated Sciences).

**Statistical analysis**

The data were analysed using the generalized linear model (GLM). Treatment means were compared using one-way ANOVA post hoc multiple comparisons with the Tukey’s HSD test. All statistical analyses was conducted using version 8.0 SPSS (IBM). Results were considered significant at the $P < 0.05$ level.

**RESULTS**

**Developing rumen parameters and qPCR analysis by the threshold cycle (Ct) method.**

For the protozoa, *Entodinium* spp, the concentration of nucleic acids was lower than it was for the bacteria and archaea. At day 7, the concentration of nucleic acids in *Methanobrevibacter* and *Methanobacterium* were significantly increased on the NU and NR treatments ($P < 0.05$), and at day 14 and 20, *Methanobrevibacter* spp and *Methanobacterium* spp were significantly decreased and *Prevotella ruminicola* was significantly increased on the NU and NR treatments ($P < 0.05$; Table 1). The bacteria, *F. succinogenes*, *R. flavefaciens*, *S. ruminantium*, and Protozoa, *Entodinium* spp, were not significantly different between the treatments ($P>0.05$).

**DISCUSSION AND CONCLUSION**

This study aimed to determine the effects of Ascogen® and a restricted diet on the microbial population in the developing rumen of calves. The results show that at 7 days of age, after two days of treatment the nucleotide feed additive (Ascogen®)

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**Table 1:** Threshold cycle (Ct) values (Mean ± SD, N= 10) of three developing rumen microorganisms in rumen fluid in showing significant treatment effects 7, 14 and 20 day old calves fed four different diets.

<table>
<thead>
<tr>
<th>Treatments</th>
<th>7</th>
<th>14</th>
<th>20</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>CU</td>
<td>CR</td>
<td>NU</td>
</tr>
<tr>
<td><strong>Microorganisms</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Methanobrevisbacter</em> spp</td>
<td>28.72±2.32</td>
<td>27.86±2.53</td>
<td>25.51±2.09</td>
</tr>
<tr>
<td><em>Methanobacterium</em> spp</td>
<td>31.67±1.70</td>
<td>31.04±2.45</td>
<td>26.29±1.52</td>
</tr>
<tr>
<td><em>Prevotella ruminicola</em></td>
<td>17.77±1.30</td>
<td>17.56±1.34</td>
<td>16.50±1.39</td>
</tr>
</tbody>
</table>

1Treatments: Control unrestricted (CU), Control restricted (CR), Nucleotide unrestricted (NU), Nucleotide restricted (NR). 4Means within a row are different (7, 14 and 20 days) at the level of significant $P < 0.05$. 

---
increased the concentrations of nucleic acids in the methanogenic archaea (\textit{Methanobrevibacter spp} and \textit{Methanobacterium spp}), but this is unlikely to be directly in response to the nucleotides because methanogenic archaea do not use protein as a nutrient source, instead they use hydrogen (Hobson 1988, Janssen and Kirs 2008, Morvan et al. 1996). The nucleotide feed additive had no effect on \textit{P. ruminicola} at day 7, even though \textit{P. ruminicola} can use nucleotides as a protein nutrient source. It is possible that at day 7 there was no increase in the \textit{P. ruminicola} because the nucleotide and milk passed through the oesophageal groove into the abomasum and thus by-passed the developing rumen (Abe et al. 1979). At day 14 and 20, \textit{Methanobrevibacter spp} and \textit{Methanobacterium spp} were significantly decreased and \textit{P. ruminicola} significantly increased, which suggests that \textit{P. ruminicola} has a positive interaction and that decreased the methanogenic archaea. These results could be supported by other studies that show that \textit{P. ruminicola} concentration was significantly increased when the levels of dietary crude protein were increased and subsequently reduced methane production (Chanthakhoun et al. 2012, Firkins et al. 2007). When the unrestricted and restricted diets were compared, they showed no significant difference in the concentration of nucleic acids from any of the measured microorganisms. These results indicate that the nucleotide feed additive and not the restriction of calf meal is responsible for the change in the proportions of microorganisms within the developing rumen. In addition in this study, it was shown that the nucleotides did not affect the concentrations of nucleotide acids of the bacteria \textit{F. succinogenes}, \textit{R. flavefaciens}, \textit{S. ruminantium}, and Protozoa, \textit{Entodinium} spp. In support of this finding, Chanthakhoun (2012) reported that various levels of crude protein did not change the populations of \textit{R. flavefaciens}, \textit{S. ruminantium}, and Protozoa, However, in contrast the population of \textit{F. succinogenes} was significantly increased. These comparisons are between mature ruminal animals (buffalo) and developing ruminants (calves) which are not necessarily valid, and illustrate the importance of further research in developing ruminants.

The results of this study show that nucleotide feed additives could have an effect on the interaction between microorganisms in the developing rumen of calves. Nucleotides in the diet increased the concentration of nucleic acids of \textit{P. ruminicola} and decreased those of \textit{Methanobrevibacter spp} and \textit{Methanobacterium spp}. Further research is required to understand the interaction between microorganisms within the pre-rumen of the young ruminant.

ACKNOWLEDGEMENTS

This study was financially support by the La Trobe University Department of Agricultural Science Victoria.

REFERENCES


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Calves selected for divergence in feed conversion efficiency for growth also exhibit divergence in feed conversion efficiency in lactation

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ABSTRACT

Research indicates that feed conversion efficiency (measured by residual feed intake; RFI), is heritable in growing heifer calves. In this experiment, 108 heifers that were divergent for RFI were tested to determine if the difference was maintained during their first lactation. The experiment was conducted with two animal cohorts over two years. The combined cohort dataset indicated a difference in RFI between the RFI groups \((P<0.05)\), although this difference was not evident in cohort 1. Using a small dataset, RFI in calves was demonstrated to be a predictor of RFI in lactating cows. However, more data are required to understand the genetic consequences of selecting on growing heifer RFI. This important result indicates that DNA markers for RFI derived from growing heifers can be used to predict genetic merit for RFI during lactation.

Keywords: Feed conversion efficiency; residual feed intake; dairy.

INTRODUCTION

Feed makes up a large proportion of the variable costs in dairying. For this reason, selection for traits associated with feed conversion efficiency (FCE) could be economically useful. Residual feed intake (RFI) is the difference between actual and predicted dry matter intake (DMI) and is used to select for improved FCE. However, measuring DMI on a large scale is prohibitively expensive. A panel of DNA markers explaining genetic variation in RFI would enable cost-effective genomic selection for this trait.

The hypothesis tested was that lactating primiparous cows previously identified as being divergent in RFI as growing calves (Williams et al. 2011) would still differ in RFI during lactation. If confirmed, the genomic prediction of RFI in growing heifers (Pryce et al. 2012) could be used to select breeding animals with higher genetic merit for RFI as lactating cows.

MATERIALS AND METHODS

The lactating experiment consisted of two cohorts calving in the Spring of two consecutive years. Cohort 1 consisted of 28 lactating primiparous cows identified as high RFI for growth (i.e. inefficient) at 6-9 months and 26 identified as low RFI (i.e. efficient). Cohort 2 consisted of 24 efficient and 30 inefficient animals. The experiment commenced at, on average, 197 and 90 days in milk in cohort 1 and 2, respectively. Diets fed to both the growing heifers and lactating cows were based on lucerne cubes (85% DM, 28 mm). For lactating cows, the diet was formulated to provide sufficient metabolisable energy and protein to support 20 litres of milk per cow/day.

Milk yield was recorded twice daily for 31 and 32 days for cohort 1 and 2, respectively. Milk was sampled 4 times weekly (2x AM and 2x PM samples) and analysed for fat, protein, lactose and somatic cell count. Average milk yields were 16.3 and 19.7 litres for cohort 1 and 2, respectively. Cows were weighed daily to determine live weight (LWT). Change in LWT \((\text{LWT}_\text{g})\) over the experimental period was calculated as the linear regression of LWT on days in milk.

Individual RFI was calculated within each cohort as the residual term from a linear model fitted to measured DMI and predicted DMI from requirements for daily milk, fat, lactose and protein yields, LWT and \(\text{LWT}_\text{g}\).

\[
\text{DMI} = \text{milk} + \text{fat} + \text{protein} + \text{lactose} + \text{LWT} + \text{LWT}_\text{g} + \text{RFI}
\]

A t-test was used to evaluate whether heifers that were extreme for RFI as calves were also divergent as lactating cows; the model also included days in milk nested within cohort. Within group phenotypic correlations between calf RFI and lactating cow RFI were performed after correcting the phenotypes for days in milk and cohort. The reason why the correlations were estimated within group is because there were two discrete groups, so it is statistically not valid to estimate the correlation across groups.

RESULTS

The combined cohort dataset indicated a difference in RFI between the RFI groups \((P<0.05)\), although this difference was not evident in cohort 1 (Figure 1).
The correlations between calf and lactating cow RFI were $r=0.34$ (efficient group; $n=47$; $P<0.01$) and $r=0.17$ (inefficient group; $n=57$; $P=0.10$).

**DISCUSSION AND CONCLUSION**

This analysis indicates that selection for RFI derived from measurements made in young growing heifers will, on average, lead to improvements in RFI in primiparous cows. However, the experiment was based on relatively small numbers of cows. More data are required to understand the genetic relationship between growing heifer and lactating cow RFI and, consequently, enable calculations of the response to selection expected in lactating cow RFI from selecting on growing heifer RFI. Before it is possible to implement this trait as a selection objective, genetic correlations with other traits of economic importance are required, most notably fertility, which may be unfavourable if the calculation of RFI does not sufficiently capture variation in body tissue mobilisation.

**Figure 1:** A box-plot of residual feed intake (RFI) in lactating primiparous cows grouped by their RFI as growing heifers across both cohorts.

**ACKNOWLEDGEMENTS**

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**REFERENCES**


Calibration of somatic-cell counting machines is vital for the Australian dairy industry

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ABSTRACT

High somatic-cell count (SCC) can result in farmers receiving a lower price for their milk, reduced cheese yield, and reduced heat stability and organoleptic properties of milk powders. The SCC of raw milk collected in Australia is generally measured by automatic counting machines. These machines need to be calibrated against standards to ensure accuracy and consistency of results over time and between laboratories. Cell-Cal, a product of the Department of Primary Industries, Ellinbank, Victoria, Australia (DPI Ellinbank) has provided this standard since 1990. Variation between cell-counting machines has declined from 15% at the introduction of the Cell-Cal standard to about 5% today. Maintaining this level of accuracy requires ongoing vigilance and is dependant on the existence of accurate somatic-cell standards.

Keywords: somatic-cells; ring test; dairy.

INTRODUCTION

Cows with a mammary infection secrete white blood cells (a type of somatic cell) from their blood into their milk. High SCC in milk can result in farmers receiving a lower price for their milk, reduced cheese yield, and reduced heat stability and organoleptic properties of milk powders (Auldist and Hubble, 1998). Farmers can identify which cows in their herd are shedding large numbers of somatic cells by sending milk samples from individual cows to a laboratory for SCC analysis. Cows identified with a high SCC can be treated or culled from the herd. Thus for economic, production and herd health reasons, the SCC of milk needs to be determined accurately, and most importantly the counting needs to be consistent over time and between laboratories.

In Australia, both bulk and individual-cow samples of raw milk are generally measured for SCC by automatic counting machines which need to be calibrated against standards to ensure accuracy and consistency of results. Cell-Cal, a product of the Department of Primary Industries - Victoria (Ellinbank, Australia) has provided this standard since 1990. The Cell-Cal service consists of physical standards of low, medium and high cell-count milks that are sent to all subscribing laboratories (currently 12 laboratories). Laboratories count the somatic cells in these samples, and the averages of the cell counts for each of the low, medium and high standards are the consensus counts for the cell-count standards. In addition, the DPI Ellinbank laboratory performs direct microscopic cell counts for each of the standards.

The objective of this study was to investigate the accuracy and consistency between cell-counting laboratories.

MATERIALS AND METHODS

The coefficient of variation between cell-counting machines was calculated from test results reported to and collated by Cell-Cal. Quarterly data for untreated milk samples were retrieved for 52 machines in 24 Australian laboratories from June 1993 to May 2012. Data could not be recovered for the period June 2001 to May 2004. Summary statistics for 1990 and 1991 were taken from a Cell-Cal report (T. Clark, Department of Primary Industries – Victoria, unpublished).

RESULTS

Before Cell-Cal began, in extreme cases the error in counting somatic cells by cell-counting machines in some laboratories was up to 50% (T. Clark, Department of Primary Industries – Victoria, unpublished). Within the first year of Cell-Cal operating (1990) the average coefficient of variation of cell-count for all machines in Australia was 0.15. This declined to 0.10 by 1991 and has ranged from 0.04 to 0.11 over the last year (Figure 1).

Figure 1: Coefficient of variation in cell-count results for up to 52 counting machines in 24 Australian laboratories from 1993 to May 2012.
DISCUSSION AND CONCLUSION

Variation in cell-count results between counting machines has been consistently low since the introduction of Cell-Cal. Two factors have likely contributed to this low variation. One is the increased awareness of laboratory staff regarding factors that affect accuracy of somatic-cell counting. The other is the existence of the Cell-Cal standard which provides an inter-laboratory reference, enabling laboratories to identify and correct malfunctioning machines.

Coefficient of variation in cell-count between Australian laboratories is averaged 0.07 over the last year. This means farmers can be confident that their cell count results accurately reflect their milk quality, and is not biased by differences between cell-counting machines. In contrast to the high accuracy of Australian cell-counting laboratories, a bulletin of the International Dairy Federation (IDF, 2008) reported that European laboratories performing direct microscopic cell-counts had a coefficient of variation of about 15%.

The mean SCC for the Australian dairy herd was estimated at 300,000 cells/ml in 1990 and has declined to 220,000 cells/ml in 2010 (ADHIS, 2011). While much of this decline can be attributed to the launch in 1998 of Countdown Downunder (www.countdown.org.au/), an Australia wide mastitis control program, it is highly likely that this reduction could not have been achieved if cell-counts were not being accurately measured. It is interesting to note that in Germany, where the accuracy in measurement of SCC is lower than in Australia, the average SCC of selected dairy herds for 2001 was reported as 366,000 cells/ml (Köster et al. 2006) while the Australian SCC for the same period was 213,000 cells/ml (ADHIS, 2002).

In conclusion, whilst there have been many campaigns and activities targeting the reduction of SCC within the Australian dairy industry the existence of an accurate and consistent somatic-cell standard have contributed to these improvements.

ACKNOWLEDGEMENTS

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REFERENCES


BIOTECHNOLOGY IN DAIRYING - PLANTS
Cumulative potential net benefits of transgenic white clover for dairy production in southern Australia and New Zealand

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ABSTRACT

Transgenic white clovers (Trifolium repens L.) with alfalfa mosaic virus resistance (‘AMV Res.’) and delayed leaf senescence (‘DLS’) have been developed and are undergoing field evaluation with the aim of improving white clover DM production and persistence. As these novel white clovers are yet to be tested under commercial farming conditions, we developed an economic model to estimate the potential net benefit from including transgenic white clovers in a mixed pasture sward used for dairy production under both southern Australian and New Zealand conditions. The replacement cost technique was applied to indirectly value any DM production benefits of the transgenic white clovers. Partial budget analysis was used to estimate the annual extra potential benefits minus the annual extra potential costs from growing novel white clovers compared to an existing white clover cultivar over time. Real net present value was estimated at a discount rate of 10 per cent. Probability distributions were developed and stochastic simulation was used for analysis of uncertain variables. Under Australian conditions the traits showed the greatest median potential net benefit, and the greatest variability of potential net benefit, when deployed in combination compared to single traits. Incorporating decline in white clover content in mixed swards over time reduced the potential net benefit from the ‘AMV Res.’ trait for the New Zealand scenario, however the potential benefit remained positive. The use of economic models accompanying molecular breeding programs can inform the prioritisation of traits deployed and also assist in determining required trait efficiencies.

Keywords: replacement cost technique, economic modelling, stochastic analysis, pasture

INTRODUCTION

Transgenic white clover with alfalfa mosaic virus resistance (‘AMV Res.’) and delayed leaf senescence (‘DLS’) have been developed and are undergoing field evaluation with the aim of improving white clover production and persistence (Forster et al. 2012). The traits can be deployed in white clover individually or together as a trait stack.

There is no direct method for estimating the economic value of changes in DM yield in a mixed pasture sward as a result of the improved white clover, as the affects on animal production and hence milk income cannot be estimated without conducting complex whole farm analysis. An approach was developed based on the replacement cost technique, as described by Sinden and Thampapillai (1995), to indirectly value any DM production benefits through valuing the major production components of estimated metabolisable energy (ME)(MJ/kg DM) and crude protein (CP) (% DM). This technique estimates the minimum value of a benefit. There are a number of different ways to utilise additional ME and CP produced by the improved white clover within a farm system. For this analysis it was assumed that it acts as a direct substitute for ME and CP that would have otherwise been brought into the system as supplementary feed.

Using this approach two mixed pasture swards used for dairy production were modelled and analysed: 1) a dryland sward located in the high rainfall zone of Australia with an average annual rainfall of approximately 1000 mm, and 2) an irrigated sward located in the Canterbury plans region of the south island of New Zealand. Perennial ryegrass (Lolium perenne L.) was used as the companion species for white clover in both scenarios. Pasture swards from these two locations were selected as they represented significant yet differing dairy production regions and systems.

For both these regions it is expected that by including the AMV resistance trait, susceptibility of white clover to virus will be eliminated, and individual clover plants will show increased vigour and improved DM production. The AMV virus can cause reductions in white clover DM yield of approximately 30-50 per cent (Gibson 1981, Johnstone and Chu 1993, Kalla et al. 2000). Incidence levels of 30-100 per cent across pure white clover trial swards and mixed pastures have been
reported in Australia (Garrett 1991, McKirdy and Jones 1997, Panter et al. 2011, Smith et al. 2007). In the South Island of New Zealand, incidence of AMV in white clover pastures ranges from 0-82 per cent with the virus estimated to be 16 times more likely to occur in irrigated pastures (Denny and Guy 2009). The increased summer survival characteristic of the DLS trait was expected to translate into increased clover plant survival between years, with the ‘Improved’ white clover showing reduced plant death by approximately 50 per cent compared to the control, and a stolen death percentage of 5 per cent compared to 25 per cent, under induced drought stress in glasshouse trials (Forster et al. 2012).

The benefits of the ‘AMV Res.’ and ‘DLS’ traits are likely to improve the survival and persistence of white clover when compared to a current common cultivar, and result in a cumulative increase in white clover contribution to the sward over time as a greater proportion of white clover plants are anticipated to survive from one year to the next.

For the purpose of this analysis white clover with the transgenic trait improvements is referred to as ‘Improved’ white clover. The objective of this work was to apply the replacement cost technique to estimate the potential net benefit of ‘Improved’ white clover for dairy production.

**MATERIALS AND METHODS**

It was assumed that any extra ME and CP produced by the ‘Improved’ white clover is substituted for purchased supplementary feed ME and CP, and valued at market price accordingly. This assumption is valid whether the extra ME and CP are achieved through DM yield improvements (i.e. increased total white clover DM production in the mixed pasture sward), or through nutritive value improvements (i.e. increased concentrations of ME and/or CP per kg/DM).

It was assumed that any additional white clover DM produced had an ME value of 11 MJ/kg DM and a CP percentage of 25 per cent. The supplementary feed substitutes used for each system are described in Table 1.

**Table 1: Summary of supplementary feed ME and CP replacement cost substitutes for each system**

<table>
<thead>
<tr>
<th>Component</th>
<th>Australian dairy system</th>
<th>New Zealand dairy system</th>
</tr>
</thead>
<tbody>
<tr>
<td>ME</td>
<td>Feed barley</td>
<td>Palm kernel expeller (PKE)</td>
</tr>
<tr>
<td>CP</td>
<td>Canola meal</td>
<td>Good pasture silage</td>
</tr>
</tbody>
</table>

To estimate the potential value of the ‘Improved’ white clover it was compared to a current common mixed pasture sward in each location termed the ‘Base Case’.

Partial budget analysis was used to estimate the potential net present value (NPV) of the ‘Improved’ white clover compared to a current common practice ‘Base Case’. Real NPV was calculated after tax with a discount rate of 10 per cent. The NPV at a particular discount rate is the value of all future net benefits from an investment. This represents the potential addition to wealth above what could be earned from an investment that earned a return equivalent to the discount rate (Malcolm et al. 2005). In this analysis, the NPV at 10 per cent discount rate from growing a hectare of the ‘Improved’ white clover in a mixed pasture sward was compared to the NPV at 10 per cent discount rate from growing a hectare of the ‘Base Case’ mixed pasture sward over the same time period. NPV results were converted to annuity figures to reflect the potential net benefit on a per annum basis (Malcolm et al. 2005).

Stochastic simulation was carried out using @Risk, an add-in package to Microsoft Excel, which allows uncertain variables to be described by probability distributions (Palisade Corporation 2012). Monte Carlo simulation randomly selects sets of input parameters, based on their specified probability distributions, and a potential value is estimated based on the partial budget analysis. Each outcome from a random set of inputs is termed an ‘iteration’. The results reported in this analysis for white clover are based on 10,000 iterations, or 10,000 runs of 10 years.

A 10 year time period was selected to capture the variation in white clover DM yield as part of a mixed pasture sward over time for the temperate high rainfall zone of Australia ‘Base Case’. In the model, white clover content could either increase or decrease from year to year, and it was assumed that it would ultimately decline to contribute less than five percent of total sward DM by year 10 (Lewis et al. 2012). In DM terms this equated to a decline from 3.7 t DM/ha in Year 1 to a median DM yield of 0.6 t DM/ha in Year 10. A summary of the production and price probability distributions used for the Australian ‘Base Case’ analysis can be found in Table 2.
For the irrigated New Zealand ‘Base Case’ it was assumed that white clover yield periodically oscillated in accordance with the findings of Schwinning and Parsons (1996), with a high white clover DM yield year followed two years later by a low white clover DM yield year. A 12 year time period was selected to capture four cycles of periodic oscillation in white clover DM yield as part of a mixed pasture sward over time (Schwinning and Parsons 1996).

Whilst Schwinning and Parsons (1996) found no ultimate decline in white clover content over time, N fertiliser was not applied to the trial data set analysed. Modern management practices, including those resulting from the use of N fertiliser, have been shown to have detrimental impacts on white clover performance over time (Ball et al. 1978, Eckard and Franks 1998, Frame 1994, Ledgard et al. 1995, Mundy 1997). The irrigated New Zealand ‘Base Case’ was analysed both with and without white clover decline over time. A summary of the production and price probability distributions used for the New Zealand ‘Base Case’ analysis can be found in Table 3.

For the Australian temperate high rainfall scenario, potential net benefit of the ‘AMV Res.’ and ‘DLS’ traits were analysed as individual trait improvements and combined together as a trait stack. When the two traits were stacked together in white clover for the Australian scenario, a multiplication factor was included. This factor was used to reflect the phenomenon that potentially the total impact of the traits together will differ from the sum of the traits as individual improvements i.e. the impact may be smaller or greater.

The potential net benefit of the ‘AMV Res.’ trait was investigated for the New Zealand irrigation scenario. As irrigation was available for the New Zealand ‘Base Case’, and the risk of high temperature limiting white clover performance is low for the South Island, it was assumed for this analysis that the ‘DLS’ trait would only provide a potential benefit for the Australian high rainfall analysis.

Further description of the assumptions used for each trait in each analysis are shown in Table 4 and Table 5. These assumptions were based on available literature, experimental results, and expert opinion.

### Table 2: Summary of the probability distributions used for the Australian temperate high rainfall ‘Base Case’. The 2nd percentile (P2), the median (P50) and the 98th percentile (P98) for each distribution are described. The ‘Distribution type’ refers to the shape of each distribution.

<table>
<thead>
<tr>
<th>Distribution</th>
<th>Distribution type</th>
<th>P2</th>
<th>P50</th>
<th>P98</th>
</tr>
</thead>
<tbody>
<tr>
<td>Production</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Percentage of white clover content (DM yield) transferred from one year to the next</td>
<td>Weibull</td>
<td>15%</td>
<td>-25%</td>
<td>-65%</td>
</tr>
<tr>
<td>Price</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Feed grain ($AU/t)</td>
<td>Gamma</td>
<td>$165</td>
<td>$290</td>
<td>$480</td>
</tr>
<tr>
<td>Canola meal ($AU/t)</td>
<td>Gamma</td>
<td>$265</td>
<td>$398</td>
<td>$580</td>
</tr>
</tbody>
</table>

### Table 3: Summary of the probability distributions used for the New Zealand irrigated ‘Base Case’. The 2nd percentile (P2), the median (P50) and the 98th percentile (P98) for each distribution are described. The ‘Distribution type’ refers to the shape of each distribution.

<table>
<thead>
<tr>
<th>Distribution</th>
<th>Distribution type</th>
<th>P2</th>
<th>P50</th>
<th>P98</th>
</tr>
</thead>
<tbody>
<tr>
<td>Production</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>No Decline in white clover over time (percentage of annual total DM yield)</td>
<td>Normal</td>
<td>20%</td>
<td>30%</td>
<td>40%</td>
</tr>
<tr>
<td>‘High’ white clover (yrs 1&amp;2, 5&amp;6, 9&amp;10)</td>
<td>Normal</td>
<td>20%</td>
<td>30%</td>
<td>40%</td>
</tr>
<tr>
<td>‘Low’ white clover (yrs 3&amp;4, 7&amp;8, 11&amp;12)</td>
<td>Normal</td>
<td>10%</td>
<td>15%</td>
<td>20%</td>
</tr>
<tr>
<td>Decline in white clover over time (percentage of annual total DM yield)</td>
<td>Normal</td>
<td>20%</td>
<td>30%</td>
<td>40%</td>
</tr>
<tr>
<td>Yrs 1&amp;2: ‘High’ white clover</td>
<td>Normal</td>
<td>20%</td>
<td>30%</td>
<td>40%</td>
</tr>
<tr>
<td>Yrs 4&amp;6: ‘Low’ white clover</td>
<td>Normal</td>
<td>10%</td>
<td>15%</td>
<td>20%</td>
</tr>
<tr>
<td>Yrs 5&amp;8: ‘High’ white clover</td>
<td>Normal</td>
<td>15%</td>
<td>25%</td>
<td>35%</td>
</tr>
<tr>
<td>Yrs 7&amp;9: ‘Low’ white clover</td>
<td>Normal</td>
<td>5%</td>
<td>10%</td>
<td>15%</td>
</tr>
<tr>
<td>Yrs 9&amp;10: ‘High’ white clover</td>
<td>Normal</td>
<td>10%</td>
<td>20%</td>
<td>30%</td>
</tr>
<tr>
<td>Yrs 11&amp;12: ‘Low’ white clover</td>
<td>Normal</td>
<td>2%</td>
<td>5%</td>
<td>10%</td>
</tr>
<tr>
<td>Price</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Good pasture silage ($NZ/bale)</td>
<td>LogLogistic</td>
<td>$50</td>
<td>$90</td>
<td>$200</td>
</tr>
<tr>
<td>PKE ($NZ/t)</td>
<td>ExtValue</td>
<td>$101</td>
<td>$245</td>
<td>$541</td>
</tr>
</tbody>
</table>
For both analyses, it was assumed that the first full year of grazing occurred in Year 1 with pasture establishment completed prior to the start of the analysis period. Additional establishment costs (e.g. seed costs) that may be required for sowing the ‘Improved’ white clover compared to a current common cultivar were ignored.

**Table 4:** Potential percentage increase in white clover content carried from one year to the next in the Australian scenario due to ‘AMV Res.’ and ‘DlS’, and the multiplication factor for the two traits stacked together. Uniform distribution asserts equal probability of occurrence to all values on the distribution.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Min</th>
<th>Max</th>
<th>Distribution</th>
</tr>
</thead>
<tbody>
<tr>
<td>‘AMV Res’</td>
<td>10%</td>
<td>40%</td>
<td>Uniform</td>
</tr>
<tr>
<td>‘DlS’</td>
<td>10%</td>
<td>60%</td>
<td>Uniform</td>
</tr>
<tr>
<td>Trait stack multiplication factor</td>
<td>0.8</td>
<td>1.2</td>
<td>Uniform</td>
</tr>
</tbody>
</table>

**Table 5:** Potential increase in annual white clover DM yield in the irrigated New Zealand scenario due to ‘AMV Res’. Uniform distribution asserts equal probability of occurrence to all values on the distribution.

<table>
<thead>
<tr>
<th>Age of sward</th>
<th>Min</th>
<th>Max</th>
<th>Distribution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Year 1 - 4</td>
<td>0%</td>
<td>5%</td>
<td>Uniform</td>
</tr>
<tr>
<td>Year 5 - 8</td>
<td>5%</td>
<td>15%</td>
<td>Uniform</td>
</tr>
<tr>
<td>Year 9 - 12</td>
<td>15%</td>
<td>30%</td>
<td>Uniform</td>
</tr>
</tbody>
</table>

**RESULTS**

Based on the ‘what if’ assumptions used in this analysis the traits showed the greatest median potential net benefit, and greatest variability of potential net benefit, when stacked compared to single traits for the Australian temperate high rainfall scenario (Figure 1). The level of variability of potential net benefit increased when the two traits were stacked together.

**Figure 1:** Potential value of ‘Improved’ white clover per year for 10 years (annuity of NPV @ 10 per cent for one hectare of mixed pasture) for the Australian temperate high rainfall scenario.

Median white clover contribution to total DM after 10 years was two percent for the ‘Base Case’, five and six per cent for ‘AMV Res.’ and ‘DlS’ as individual traits respectively, and 12 per cent when the two traits were combined as a trait stack.

For the New Zealand irrigated scenario, the ‘AMV Res.’ trait showed the greatest median potential benefit when no decline in white clover content over time was assumed (Figure 2). When decline in white clover DM yield was included the potential NPV at a discount rate of 10 per cent remained positive, and the variability of potential value over time was reduced.

**Figure 2:** Potential value of ‘Improved’ white clover per year for 12 years (annuity of NPV @ 10 per cent for 1 ha of mixed pasture) for the irrigated New Zealand scenario.

**DISCUSSION AND CONCLUSION**

The net benefit of ‘Improved’ white clover was estimated using the replacement value technique to provide an initial indication of the
potential net benefit of trait improvements, with all scenarios investigated returning positive NPV. For the Australian scenario, the trait stack option resulted in a greater median potential net benefit of approximately $460 per hectare per year for the 10 year period, compared to approximately the $150 to $230 per hectare median for traits individually based on the assumptions used in this analysis. The potential net benefits estimated for the ‘AMV Res.’ trait in the New Zealand scenario ranged from a median of approximately $220 to $340 per hectare per year over the 12 year period, depending on the assumption made regarding white clover decline over time. The higher the estimated median potential net benefit, the greater the variability of potential net benefit for all scenarios investigated. This increase in variability is consistent with economic theory regarding concomitant increasing risk and return. The replacement cost technique provided an adequate framework to explore the potential net benefits from deploying the trait improvements in white clover, including the sensitivity testing of parameters.

It must be noted that all potential net benefit results in this analysis are a direct product of the ‘what if’ assumptions used, and therefore any potential value figures reported are purely indicative. Stronger conclusions cannot be drawn regarding the value of the ‘Improved’ legume forage options for dairy producers until these assumptions have been refined through further scientific research, and then rigorously analysed as part of a whole farm system.

Whole farm economic modelling will be performed in the next stage of analysis to capture additional considerations from including the ‘Improved’ white clover in the farm system. At the sward level these considerations include, but are not limited to, the impact of additional white clover on the ryegrass proportion of the sward (Chapman et al. 1996) and the implications for biological N fixation (Care 1996, Denny and Guy 2009, Ledgard et al. 2001, Panter et al. 2011). Trait specific considerations include the nature of the spread and decay caused by the AMV over time (Denny and Guy 2009; McKirdy and Jones 1995; McKirdy and Jones 1997; Panter et al. 2011), and the impact of delayed leaf senescence on the seasonal nutritive value of white clover. Other dairy farm system impacts that may result from introducing the ‘Improved’ white clover include changes in grazing rotation to optimise ‘Improved’ white clover production, DM intake, milk production and composition and supplementary feed rations as a result of increased white clover content in the diet. Fertiliser regimes due to potentially increased N fixation in the system may also be influenced. The whole farm approach is the most appropriate framework to capture and analyse the impact of introducing ‘Improved’ white clover on these elements of the farm system (Malcolm et al. 2005).

The use of economic models accompanying molecular breeding programs can inform the prioritisation of traits deployed and also assist in determining required trait efficiencies.

ACKNOWLEDGEMENTS

The authors would like to gratefully acknowledge the input from Professor G. Spangenburg and the Dairy Futures CRC to this work.

REFERENCES


Perennial ryegrass, which is an important pasture grass crop in temperate climates, possesses a gametophytic self-incompatibility (SI) system controlled by two loci (S and Z). Although the SI system is believed to contribute to the maintenance of genetic diversity in populations, it provides major obstacles to targeted molecular breeding. A comprehensive approach using a systems biology paradigm has been initiated to enable the identification of both the S and Z genes. For the purpose of genetic mapping in perennial ryegrass, 17 (S) and 10 (Z) SI-linked DNA-based markers were developed using comparative genetic means. A large-scale mapping population composed of 567 individuals was established. The perennial ryegrass SI loci were fine-structure mapped by genotyping and phenotyping of this population. The S and Z loci were mapped on linkage groups (LGs) 1 and 2, respectively. A comparative approach with the SI-linked markers revealed gene-based microsyntenic relationships for both loci between perennial ryegrass and model grass plant species, such as Brachypodium distachyon and rice. This microsyntenic information supported the fine-scale genetic and physical mapping processes. Additional DNA-based markers were developed based on microsyntenic information to dissect the probable intervals containing the two loci. For physical mapping, BAC clones representing the target regions were isolated from a perennial ryegrass genomic library and sequenced with a high-throughput second-generation sequencing system. BAC-derived sequences were aligned based on microsyntenic information, and gene-like sequences were identified. In addition, high-throughput deep transcript sequencing of target reproductive tissues has been performed to assist identification and ranking of candidate genes for further investigation. The generation of transgenic perennial ryegrass plants for targeted modification of the expression of candidate genes for S and Z has also been progressed for highly qualified candidate sequences.

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Phenotypic Assessment of Yield and Nutritive Values of Italian ryegrass \((Lolium multiflorum)\) from a Spaced-Plant Field Trial

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Italian ryegrass \((Lolium multiflorum)\) is an agronomically important pasture grass. Molecular breeding of Italian ryegrass for yield and quality through marker-assisted selection (MAS) has progressed little beyond the stage of QTL identification by trait-dissection. In order to effectively implement MAS for complex outcrossing species like Italian ryegrass, genomic selection strategies may be required. Genomic selection uses information on sequence variation across the whole genome to provide prediction equations for phenotypic performance for complex quantitative traits such as yield. The objective of this study was to provide data for genome-wide association analysis and to identify superior genotypes for selection in breeding. A total of 960 Italian ryegrass genotypes were assessed for herbage yield and nutritive values in a field-based nursery experiment located at Hamilton in south-western Victoria, Australia, in 2010-2011. The experimental design was a randomised complete block with four replicates resulting in total 3840 plants in the trial. Herbage yields were recorded from 5 cuttings over the year. Nutritive values including crude protein, water-soluble carbohydrate, acid and neutral detergent fibre, and digestibility were assessed using near infra-red reflectance spectroscopy on vegetative samples harvested in May 2011. A broad range of phenotypic variation was observed. There were significant genotypic variance components for yield and nutritive values. Moderate heritability estimates were obtained for nutritive values, as compared to low to high heritability estimates for yields from different cuttings. Target plants were also genotyped using single nucleotide polymorphism (SNP) markers. While preserving all SNP allele variants, genotypes with high yield were selected for pair-crossing and evaluation of the derived families is being progressed. Phenotypic measurements from this study are amenable to genome-wide association studies, given provision of sufficient marker coverage over the genome, and investigation of the feasibility of genomic selection in Italian ryegrass breeding.

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Computational Tools for Genomics-Assisted Forage Plant Breeding

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With the advent of next-generation genotyping platforms, the ability to rapidly and cost-effectively genotype plants in commercial breeding nurseries has become realistic and practical. This capacity not only paves the way for future integrated genomics-assisted breeding programs for forages, but already has direct application in current breeding programs. Maintenance of genetic diversity in breeding nurseries is fundamental for achievement of continual genetic gain in breeding lines. Loss of rare beneficial alleles can be common when intense phenotypic selection for several key traits is applied, which can present significant issues in future breeding cycles. In addition, the ability to perform population identification and seed purity analysis from genotype data for a quality-assured seed supply chain also provides benefits to breeders. However, rates of development in genotyping technology have not been matched by corresponding advances in computational tools to assist and enable their application. Selection while Conserving Diversity (SeConD), is a software package that assists breeders to select a sub-set of phenotypically elite individuals from a breeding nursery, whilst ensuring that all molecular marker alleles identified within the nursery are present in the selection. Statistical Analysis of Mixed Ploidy Populations (StAMPP) allows users to calculate Nei’s genetic distance and pairwise Fst values with confidence intervals and p-values from single nucleotide polymorphism genotypic datasets derived from samples of mixed ploidy levels. Previously unavailable to mixed ploidy genotype analysis, StAMPP allows breeders to develop cultivar catalogues, explore breeding history, examine population structure and perform population differentiation, to protect the genetics of proprietary cultivars and to provide confidence on seed purity to farmers. These two packages provide an effective link between genotype data and its application in commercial plant breeding.

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Analysis of Compatibility and Stability in Designer Endophyte-Grass Associations between Tall Fescue and *Neotyphodium coenophialum*

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*Neotyphodium* fungal species form endophytic symbioses with agronomically important pasture grasses. Tall fescue (*Lolium arundinaceum* [Schreb.] Darbysh syn. *Festuca arundinacea* Schreb.) is generally reported to associate with the endophyte *Neotyphodium coenophialum*. Both beneficial and detrimental agronomic properties result from the association, including improved tolerance to water and nutrient stress and resistance to invertebrate pests. Invertebrate resistance is provided by specific metabolites produced by the endophyte, in particular loline alkaloids and peramine. Other metabolites produced by the endophyte, such as ergot alkaloids, are toxic to grazing animals and reduce herbivore feeding. Genetically novel endophyte strains with favourable alkaloid profiles have been identified in a study of global genetic diversity using expressed sequence tags (EST)-derived simple sequence repeats (SSR) markers combined with metabolic profiling. Novel endophytes have been isolated for inoculation into an isogenic host plant genotype panel selected from elite tall fescue germplasm to assess endophyte compatibility, and vegetative stability, with the host plant genotype. Nine out of 10 novel endophytes strains were successfully inoculated into four host genotypes representing a broad range of tall fescue cultivars. Following inoculation, in-depth characterisation of the designer symbiota (i.e. endophyte-host associations) can be performed independent of effects due to host genotype variation.

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Analysis of Compatibility and Stability in Designer Endophyte-Grass Associations between Perennial Ryegrass and Neotyphodium Species

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Fungal species of the genus Neotyphodium form endophytic symbioses with agronomically important pasture grass species such as perennial ryegrass (Lolium perenne L.) and tall fescue (Festuca arundinacea Schreb.). The fungal mycelium proliferates within the vascular tissue of aerial tissues, especially the leaf base and leaf sheath, and is asexually propagated through colonisation of seeds. Fungal grass endophytes produce both beneficial (tolerance to abiotic stresses such as drought, deterrence of invertebrate herbivores) and deleterious effects (toxicity to mammalian herbivores) for pasture grass production. Herbivore toxicity effects are associated with production of alkaloids such as lolitrem B and ergovaline (producing mammalian toxicity syndromes such as ryegrass staggers and fescue toxicosis) and peramine (deterrence of feeding by insect pests such as the Argentine stem weevil). A genetic diversity study based on gene-associated simple sequence repeat (SSR) markers has identified the range of limited but significant global variation within N. lolii. This variation can be correlated with both geographical origin in Eurasia and major toxin profiles. Using genotypic data as a predictor of likely toxin profile, a germplasm collection resource established on the basis of geographical targeting and genotypic analysis identified a discrete number of previously unidentified endophyte strains, some of which also have favourable toxin profiles. These novel endophytes have been deployed into a novel method for inoculation of multiple strains into common genetic backgrounds of host grass, providing a panel of symbiota suitable for isogenic comparisons based on identity of either the grass or endophyte genotype. Members of the isogenic inoculation panel have been used to assess compatibility and intergenerational stability of the symbiota dissecting endophyte and host plant genotype effects.

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Metabolic Profiling of Novel Neotyphodium Endophytes in Tall Fescue (Lolium arundinaceum Schreb.)

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Tall Fescue (Lolium arundinaceum [Schreb.] Darbysh syn. Festuca arundinacea Schreb.), which is one of the most economically important forage grasses in temperate regions of the world, is known to form associations with Neotyphodium species endophytes, of which Neotyphodium coenophialum is the most highly characterised taxon. In addition, endophytes belong to other groupings such as FaTG-2, FaTG-3 (Festuca arundinacea Taxonomic Group) and other uncharacterised taxa have also been identified to reside within tall fescue. Endophyte symbiosis confers protection from mammalian and insect herbivory through the production of a range of secondary metabolites in planta. Among them, peramine, ergot alkaloids, lolines and lolitrems provide protection to the host plant from insects while lolitrems and ergot alkaloids are also toxic to grazing animals. Knowledge of the alkaloid composition of the symbiotum metabolome is consequently an essential component for selection of agronomically favourable endophytes which do not produce mammalian toxins, but still synthesise beneficial alkaloids for resistance to invertebrate herbivory as well as ecological fitness. Twenty novel tall fescue endophyte strains from five taxa were characterised for in planta production of the above four alkaloids using liquid chromatography-mass spectrometry (LC-MS). The results revealed diverse alkaloid profiles between strains and endophyte taxa. Six endophyte strains were identified as lacking production of both ergovaline and lolitrem B. Endophytes belonging to the presently unclassified ‘non-EPichloë outgroup’ failed to produce any of the known alkaloids. Novel endophytes with favourable alkaloid profiles have been isolated and inoculated into an isogenic host plant genotype panel in order to perform detailed characterisation of the metabolic profiles of novel endophytes independent of effects due to host genotype variation.

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Systems biology of alkaloid biosynthesis in fungal endophytes of tall fescue

(Lolium arundinaceum Schreb.)

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Symbiotic associations between tall fescue grasses and endophytic fungi of Neotyphodium species manifest enhanced resistance to several biotic stress factors, including protection from mammalian and insect herbivory and resistance to both nematode pests and some fungal pathogens. The ability of endophytes to synthesise a range of secondary metabolites in planta plays a major role in obtaining protection from mammalian and insect herbivores. Grasses infected with endophytes predominantly produce four varieties of alkaloids: pyrrolopyrazine alkaloids (e.g. peramine); ergot alkaloids (e.g. ergovaline); pyrrolizidine (e.g. lolines); and indole diterpenes (lolitrems). However, different endophyte strains have diverse alkaloid production capabilities. In this systems biology (genome-metabolome) study, whole genome sequencing of several novel tall fescue endophyte strains that exhibit phenotypic differences, including diverse alkaloid production profiles, was performed using the HiSeq2000 (Illumina) DNA sequencing platform, to identify sequence polymorphisms. For instance, the content of genes that involved in alkaloid biosynthesis was compared between novel endophyte strains, including the taxa N. coenophialum, FaTG-2, FaTG-3 (Festuca arundinacea Taxonomic Group) and a currently uncharacterised ‘non-Epichloë out-group’. Deletions were observed in regions harbouring genes associated with alkaloid production that correlated with variation for known alkaloid profiles. Further analysis is ongoing to relate other phenotypic differences observed among these endophyte strains and their sequence variation.

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Pan-Genome Analysis of Perennial Ryegrass Endophytes

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Neotyphodium species are fungal endophytes that form symbioses with agronomically important pasture grasses. N. lolii is the predominant endophyte of perennial ryegrass (Lolium perenne L.), but other non-N. lolii taxa, such as LpTG-2, are also detected. Within- and between-taxon diversity provides a source of variation for production of secondary metabolites (in particular lolitrem B, ergot alkaloids and peramine) which are either toxic to grazing animals or reduce feeding by invertebrate herbivores. A selection of 23 perennial ryegrass endophytes was assembled in order to sample diversity across the range of variation for the various taxa, and high-throughput DNA sequencing technology has been performed on each strain. Furthermore, the genome of the commonly identified ‘Standard Toxic’ (ST) N. lolii endophyte has been assembled into a reference genome, in order to facilitate this cross-taxon pan-genome analysis. Results from the analysis include: an enhanced understanding of the genomic variation amongst various perennial ryegrass endophytes; improved insights into mitochondrial and nuclear genomic changes that have occurred during the endophyte evolution; and an increased ability to associate genetic variation with phenotypic differences, such as presence and absence of key genes in alkaloid biosynthesis.

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A High-resolution Method for the Localization of Proanthocyanidins in Plant Tissues

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Histochemical staining of plant tissues with 4-dimethylaminocinnamaldehyde (DMACA) or vanillin-HCl is widely used to characterize spatial patterns of proanthocyanidin accumulation in plant tissues. These methods are limited in their ability to allow high-resolution imaging of proanthocyanidin deposits. Tissue embedding techniques were used in combination with DMACA staining to analyze the accumulation of proanthocyanidins in *Lotus corniculatus* and *Trifolium repens* tissues. Embedding of plant tissues in LR White or paraffin matrices, with or without DMACA staining, preserved the physical integrity of the plant tissues, allowing high-resolution imaging that facilitated cell-specific localization of proanthocyanidins. A brown coloration was seen in proanthocyanidin-producing cells when plant tissues were embedded without DMACA staining and this was likely to have been due to non-enzymatic oxidation of proanthocyanidins and the formation of coloured semiquinones and quinones. This report presents a simple, high-resolution method for analysis of proanthocyanidin accumulation in organs, tissues and cells of two plant species with different patterns of proanthocyanidin accumulation, namely *Lotus corniculatus* (birdsfoot trefoil) and *Trifolium repens* (white clover). This technique was used to characterize cell type-specific patterns of proanthocyanidin accumulation in white clover flowers at different stages of development.

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Targeted Expression of Malate Dehydrogenase in Transgenic White Clover (Trifolium repens) Enhances Tolerance to Aluminium

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Aluminium (Al) toxicity is a major environmental limitation of plant production in acid soils which represent more than one third of the world’s agricultural land. Most agricultural soils are deficient in phosphorus (P), and most soluble P, incorporated by addition of non-renewable P-fertilisers, is rapidly fixed into unavailable forms. Al-induced secretion of organic acids (OA) by roots, such as malate and citrate, has the capacity to chelate the toxic Al cation, excluding it from the root, which is also associated with enhanced P-use efficiency. An endogenous white clover (Trifolium repens) OA biosynthetic gene, the nodule enhanced malate dehydrogenase (TrneMDH), was identified, isolated and genetically characterized. In order to increase OA production and secretion, thus enhance Al resistance, the TrneMDH gene was over-expressed in white clover plants under the control of a root-prevalent white clover phosphate transporter gene promoter (TrPT1), using transgenic modification. The sequence corresponding to the TrPT promoter was isolated following screening of a clover BAC library, and its spatial expression pattern confirmed molecularly and physiologically. Molecular analysis of independent transgenic white clover plants confirmed the stable integration and expression of the chimeric TrPT::TrneMDH transgene. Selected transgenic white clover was subjected to growth performance analysis in the presence and absence of Al, to assess the extent of Al tolerance. This research provided evidence that modification of OA metabolism in white clover can lead to enhanced Al-tolerance by a mechanism that excludes Al from root tips.

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Molecular Breeding of Transgenic White Clover (*Trifolium repens* L.) with Field Resistance to Alfalfa Mosaic Virus through the Expression of its Coat Protein Gene

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Viral diseases, such as alfalfa mosaic virus (AMV), cause significant reductions in the productivity and vegetative persistence of white clover plants in the field. Transgenic white clover plants ectopically expressing the viral coat protein gene encoded by the sub-genomic RNA4 of AMV were generated. Lines carrying a single copy of the transgene were analysed at the molecular, biochemical and phenotypic levels under glasshouse and field conditions. Field resistance to AMV infection, as well as mitotic and meiotic stability of the transgene, were confirmed by phenotypic evaluation of the transgenic plants at two field sites in Australia. The T₀ and T₁ generations of transgenic plants showed immunity to infection by AMV under glasshouse and field conditions, while the T₄ generation in elite genetic background, showed a very high level of resistance to AMV in the field. An extensive biochemical study of T₄ plants, aiming to evaluate the level and composition of natural toxicants and key nutritional parameters, showed that the composition of the transgenic plants was within the range of variation seen in non-transgenic populations.

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Gene Discovery and Molecular Marker Development Based on High-Throughput Transcriptome Sequencing in *Brachiaria brizantha* Hochst ex A. Rich.

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*Brachiaria* is an economically-important forage grass genus in Central and South America. Productivity per hectare and weight gain per head are both significantly higher in cattle grazed on *Brachiaria* pastures compared with those grazing native savana. *B. brizantha* Hochst ex A. Rich is an apomictic tetraploid species, which does also have a diploid sexual form that is not currently used in agricultural systems. The *B. brizantha* cv. ‘Marandu’ has been widely adopted due to its resistance to spittlebug as well as displaying good persistence under grazing and resistance to water deficit. However, *B. brizantha* still has opportunities for improvement in digestibility and nutritive value. The species would benefit significantly from an enabling molecular breeding program for varietal development. To generate initial resources a pooled cDNA library was prepared from RNA samples from different tissues and subsequently sequenced using GS FLX Titanium technology. A total of 445,357 sequence reads were obtained, corresponding to c. 130 Mbp, which were assembled using Newbler software v 2.3, generating 12,005 contigs of a combined length of 6,373,398 nucleotides. The transcript sequence contigs generated were also analysed for the presence of simple sequence repeats (SSRs). A total of 1,699 SSR motifs were identified and primer pairs were designed for SSR amplification for 1,446 contigs using the batch Primer3 software. This molecular marker resource will enable molecular breeding efforts in *Brachiaria* species.

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Characterisation of a Phosphate Transporter Gene from White Clover (*Trifolium repens* L.)

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Acid soils, pH 5.5 or lower, are one of the most significant limitations to agricultural production worldwide, affecting approximately 30% of the total land area. The primary site of root growth inhibition by Aluminium (Al) toxicity is focussed at the root apex, which is also the region most actively involved in Al tolerance responses mediated by organic acid secretion. Root secretion of organic compounds represents a net loss of carbon to the organism, making an inducible, localised mechanism of Al tolerance mediated by root tip secretion the most effective means to confer Al tolerance. Transgenic modification offers the potential to enable targeted gene expression in desired tissue types under specific conditions for maximal effect with minimal fitness penalty. Plant gene promoters are the key to enable such a precision strategy. A phosphate transporter gene (*Tr*PT1) from white clover has been identified and fully sequenced along with its 5’ regulatory sequences to putatively direct root-specific gene expression inducible under low inorganic phosphate conditions, found under acidic Al-rich soils. An in depth *in silico* analysis of the *Tr*PT1 promoter has been performed revealing a high level of conservation of the transcription factor binding sites indentified in *Arabidopsis thaliana* and *Medicago truncatula* PT1 and PT2 promoter sequences. From a collection of characterised transcription factor binding site motifs the PIBS element, which regulates response to P deprivation, was identified in all of the PT promoter regions along with other sites associated with root and nodule expression and auxin induction. The detailed characterisation of the DNA sequence of the *Tr*PT1 promoter demonstrates its suitability and specificity as an inducible and root tip cell-specific promoter for deployment in transgenic approaches for engineering Al tolerance in forage legumes such as white clover and alfalfa.

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Characterisation of a Nodule Enhanced Malate Dehydrogenase Gene from White Clover
(Trifolium repens L.)

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Aluminium (Al) toxicity is a major environmental limitation for plant production in acid soils which represent more than one third of the world’s agricultural land. Most agricultural soils are deficient in phosphorus (P), and most soluble P, incorporated by addition of non-renewable P-fertilisers, is rapidly fixed into unavailable forms. Al-induced secretion of organic acids (OA) by roots, such as malate and citrate, has the capacity to chelate the toxic Al cation, excluding it from the root, which appears also associated with enhanced P-use efficiency. A white clover EST was identified as the putative orthologue of a Medicago sativa nodule enhanced malate dehydrogenase gene (MsneMDH). The EST sequence of the putative TrnemDH was then used to identify a white clover bacterial artificial chromosome (BAC) clone that would contain the complete gene. The identified BAC clone was subjected to sequencing using the GS FLX Titanium platform and assembled using Newbler v 1.0.52 software. A contig of c. 36 kbp was identified that contained the complete TrnemMDH gene sequence as well as adjacent genes in both 5’ and 3’ directions. Extensive micro-synteny was identified and characterised between the white clover BAC sequence and the reference genome sequences of Glycine max, Lotus japonicus and to lesser extent Arabidopsis thaliana. The TrnemMDH gene sequence was also subjected to in vitro SNP discovery and genetic mapping in an F1 population, enabling its mapping to linkage group 8.

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Structure-Function Analysis of Caffeic Acid O-Methyltransferase from Perennial Ryegrass
(Lolium perenne L.)

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Lignin forms from the polymerization of phenylpropanoid-derived building-blocks (the monolignols); the modification through hydroxylation and O-methylation of the monolignols modulates the chemical and physical properties of the lignin polymer. The enzyme caffeic acid O-methyltransferase (COMT) is central to lignin biosynthesis, and is often targeted transgenically to alter plant lignin composition. Despite intensive investigation, the structural determinants of the regiospecificity and substrate selectivity of COMT remain poorly defined. Reported here are X-ray crystallographic structures of perennial ryegrass (Lolium perenne L.) COMT (LpOMT1), in open conformational-state, apo- and holo-enzyme forms; and most significantly, in a closed conformational-state complexed with the products S-adenosyl-L-homocysteine and sinapaldehyde. The product-bound complex reveals for the first time the post-methyl-transfer organization of COMT’s catalytic groups with reactant molecules, and the fully formed phenolic-ligand binding site. The core scaffold of the phenolic ligand forges a hydrogen-bonding network involving the 4-hydroxy group that anchors the aromatic ring and thereby permits only meta hydroxyl-groups to be positioned for transmethylation. While distal from the site of transmethylation, the propanoid-tail substituent governs the kinetic preference of ryegrass COMT for aldehydes over alcohols and acids due to a single hydrogen-bond donor for the C9 oxygenated moiety dictating the preference for an aldehyde.

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Lignin Biosynthesis in Paspalum dilatatum: Isolation and Characterisation of Cinnamoyl CoA Reductase

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Dallisgrass (Paspalum dilatatum Poir) is a highly productive C4 grass native to South America and naturalized in Australia with special relevance for dairy and animal production. However, digestibility of warm-season grasses is poor compared with most temperate grasses. The main factor limiting digestibility is lignin deposition in plant cell walls which causes resistance to digestion by ruminant microbes. During the transition of the vegetative to the reproductive stage of development, lignin composition in monocots changes with an increase in syringyl (S) lignin and decrease in guaiacyl (G) lignin that negatively correlates with digestibility. The aim of this work is the identification of genes associated with lignin biosynthesis and the isolation and characterisation of cinnamoyl CoA reductase (CCR) gene in P. dilatatum. Lignification-related candidate genes were identified by transcriptome sequencing using the Roche GS FLX sequencing platform. A novel PdCCR with a coding sequence of 1,293 bp from P. dilatatum was isolated. Phylogenetic analysis shows that PdCCR is closely related to other monocotyledonous CCRs revealing with high homology to SbCCR. Deduced aminoacid sequence sequence analysis showed that the catalytic site for CCR enzymatic activity and the conserved NAD/ NADP(H)-dependent dehydrogenase and reductase binding fold domains were present in PdCCR. The genomic analysis revealed that CCR belong to a multicopy gene family in P. dilatatum. The spatio-temporal profile of lignin deposition shows an increase in S lignin and G lignin deposition in cell walls and the accumulation of cells enriched in S lignin during plant maturity. The expression profile of PdCCR correlates with plant maturation and lignin deposition. This work describes the characterisation of a CCR gene in P. dilatatum for the first time contributing to the knowledge base of the functional characterisation of lignin related genes in warm-season grasses.

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Gene Discovery and Molecular Marker Development Based on High-Throughput Transcriptome Sequencing in *Paspalum dilatatum* Poir

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Dallisgrass (*Paspalum dilatatum* Poir.) is a highly productive C4 grass with a wide distribution within temperate-warm regions and has a growing season from late spring to late summer. It is a native grass species of South America, with special relevance for dairy and red meat production. The forage quality of *Paspalum* is higher than other C4 forage species and the species exhibits other desirable traits such as frost tolerance and tolerance of water stresses. However, there are still significant opportunities for molecular breeding to improve the productivity of this species. With the ongoing reductions in cost and resources required to deliver genomic tools to underpin molecular breeding strategies, opportunities now arise for many species to rapidly benefit from these developments. A cDNA library was prepared from pooled RNA of different tissues (stems, roots, leaves and inflorescences) from the final reproductive stage of *P. dilatatum* ‘Primo’ and subsequently sequenced using GS FLX Titanium technology. A total of 324,695 sequence reads were obtained, corresponding to c. 102 Mbp, which were assembled using Newbler software, generating 20,169 contigs of a combined length of 9,336,138 nucleotides. The generated contigs were subjected to BLAST sequence analysis against the full genome sequences of *Oryza sativa* subsp. *japonica*, *Sorghum bicolor* and *Brachypodium distachyon* as well as against the UniRef 90 protein database. The transcript sequence contigs generated were also analysed for the presence of simple sequence repeats (SSRs). A total of 2,339 SSR motifs were identified and primer pairs were designed for SSR amplification for 1,989 contigs using the batch Primer3 software. Empirical validation of a cohort of 96 SSRs has been performed, with acceptable performance confirmed for 64% of the markers tested. This molecular marker resource will enable molecular breeding efforts in *Paspalum* species.

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Biosynthesis of Proanthocyanidins in White Clover Flowers: Cross Talk within the Flavonoid Pathway

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Proanthocyanidins and anthocyanins are produced by closely related branches of the flavonoid pathway and utilize the same metabolic intermediates. Previous studies have shown a flexible mechanism of flux diversion at the branch-point between the anthocyanin and proanthocyanidin pathways, but the molecular basis for this mechanism is poorly understood. Floral tissues in white clover (Trifolium repens) plants produce both proanthocyanidins and anthocyanins. This makes white clover amenable to studies of proanthocyanidin and anthocyanin biosynthesis and possible interactions within the flavonoid pathway. Results of this study show that the anthocyanin and proanthocyanidin pathways are spatially co-localized within epidermal cells of petals and temporally overlap in partially open flowers. A correlation between spatio-temporal patterns of anthocyanin and proanthocyanidin biosynthesis with expression profiles of putative flavonoid-related genes indicates that these pathways may recruit different isoforms of flavonoid biosynthetic enzymes. Furthermore, in transgenic white clover plants with down-regulated expression of the anthocyanidin reductase gene, levels of flavan 3-ols, anthocyanins, and flavonol glycosides and the expression levels of a range of genes encoding putative flavonoid biosynthetic enzymes and transcription factors were altered. This is consistent with the hypothesis that flux through the flavonoid pathway may be at least partially regulated by the availability of intermediates.

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Assessment of Gene Flow in White Clover (Trifolium repens L.) under Field Conditions in Australia Using Phenotypic and Genetic Markers

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White clover is one of the most important pasture legumes in global temperate regions. It is an outcrossing, insect-pollinated species with gene flow occurring naturally between plants. A 2-year study was conducted to assess the relationship between gene flow and physical distance in white clover under field conditions in southern Australia. White clover plants exhibiting a red leaf mark phenotypic trait acted as pollen donors to recipient plants lacking leaf markings at distances up to 200 m distant from the donor plants. Progeny were scored for the dominant red-leafed phenotype and gene flow was modelled. Paternity was confirmed using simple sequence repeat markers. A leptokurtic pattern of gene flow was observed under conditions designed to measure maximised gene flow with the majority of pollination occurring in the first 50m from the donor pollen source.

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Antifungal Activities of Ryegrass and Fescue Endophytes


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Fungi of the genus *Neotyphodium* form endophytic symbioses with agronomically important pasture grass species such as perennial ryegrass (*Lolium perenne* L.) and tall fescue (*Lolium arundinaceum* [Schreb.] Darbysh syn. *Festuca arundinacea* Schreb.). *Neotyphodium* endophytes produce both beneficial (tolerance to abiotic stresses such as drought, deterrence of invertebrate herbivores) and deleterious effects (toxicity to mammalian herbivores) for pasture grass production. However, fungal endophytes in general have been unexplored in terms of their production of novel antimicrobial agents. Although some *Épichloë*/*Neotyphodium* endophytes have been shown to inhibit *in vitro* the growth of plant pathogenic fungi, the inhibitory substances produced have not been identified. Endophytes with anti-fungal properties may benefit host plants by preventing pathogenic organisms from colonisation and disease development. To determine whether *Neotyphodium* endophytes produce anti-fungal compounds *in vitro* and *in planta*, strains of *N. lolii*, *Lp*TG-2, *N. coenophialum*, *Fa*TG-2, *Fa*TG-3, *N. uncinatum* and two novel endophytes were tested for anti-fungal activity against eight phytopathogenic fungi. Tall fescue endophytes exhibited high anti-fungal activity against *Colletotrichum graminicola*, *Drechslera brizae* and *Rhizoctonia cerealis*. Bioassay results showed that endophytes exhibit variation for *in vitro* anti-fungal activity that does not correlate with known toxin production (specifically, lolitrem B, ergovaline and peramine). Variation was also observed between genetically distinct strains within *N. lolii*. Inhibition of fungal growth by endophyte was also demonstrated *in planta* using plant extracts from endophyte-inoculated host plants. Mass spectrometry (LCMS) was used to determine a relationship between anti-fungal activity and expression of metabolites to identify potential compounds that are active against plant pathogenic fungi.

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Development of a Transcriptome Atlas for Perennial Ryegrass (Lolium perenne L.)

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The current generation of DNA sequencing platforms permits significant resources and data to be generated rapidly at relatively low cost. A single genotype of perennial ryegrass has been subjected to transcriptome analysis through deep sequencing of cDNA samples derived from multiple distinct tissue types. A total of 0.6 billion sequencing reads from the Illumina HiSeq2000 platform have been generated from 11 different vegetative samples, including leaf, pseudostem and root samples for both terrestrial and subterranean aspects of gene expression. DNA sequence assembly has been performed on the resulting data from each individual tissue sample, as well as an overall assembly using the SOAP de novo package version 1.05. The assembly generated between c. 23,000 and 29,000 scaffolds from each tissue type, and the combined assembly obtained 57,480 scaffolds, summing to in excess of 47 Mb, with an average length of 820 bp. The resulting contigs have been compared, using a BLAST analysis pipeline, to the gene complement from the related model grass species Brachypodium distachyon L. In excess of 85% of all predicted genes and splice variants of the fully sequenced model grass species have been identified in the assembled ryegrass data set. In addition, analysis of the data has enabled tissue specific patterns of expression to be identified, with over 23,000 genes attributed to a broad expression profile, along with smaller cohorts that display tissue-specific expression. The identification of specific transcription regulation patterns will be valuable for candidate gene identification for agronomically relevant traits.

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Whole Genome Sequencing of Perennial Ryegrass (*Lolium perenne* L.) Supports Exome Assembly for Gene and SNP Catalogue Development

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The current generation of DNA sequencing platforms enables significant resources and data to be generated rapidly at relatively low cost. Although determination of whole genome sequence for a complex plant genome is still a significant undertaking, generation and assembly of the exome (gene-encoding) component is possible with the use of more modest resources. A single plant genotype of perennial ryegrass has been sequenced to approximately 70 X coverage, with c. 2 billion sequencing reads of 100 bp paired-end sequence reads on the Illumina HiSeq2000 platform. The generated sequence data has been assembled using the SOAP \textit{de novo} software package v 1.05. The sequence assembly has been empirically optimised through iterative assessment of performance based on a range of input kmer sizes, in terms of number of bases assembled, and the average length of assembled contigs and scaffolds. An optimal assembly has generated 1.9 million scaffolds covering c. 1.7 Gb, while all contigs and singletons cover c. 3.5 Gb. Comparison of the contigs and scaffolds to the coding sequences from *Brachypodium distachyon* L. has permitted identification of putative perennial ryegrass orthologues to c. 86% of all predicted genes and alternate transcripts from the model grass species. Development of this exome sequence library has enabled assembly and identification of a large collection of genic contigs, along with the corresponding regulatory elements. The collection is accessible to interrogation to characterise and document complete sets of gene families, along with provision of reference assemblies to identify sequence polymorphisms.

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High-throughput Automated Low-Cost Quantification of Individual Water Soluble Carbohydrates and Protein in Grass Herbage

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Quantification of forage quality is essential for the identification of elite genotypes and the continued advancement of pasture grass breeding. A number of methods for quantification of water soluble carbohydrates (WSC) and plant protein are available, such as near-infra red spectroscopy (NIRS) and high performance liquid chromatography (HPLC). However, such methods are labour intensive, low-throughput and cost-prohibitive for commercial breeding programs, which typically need to assess thousands of samples annually. An accurate high-throughput micro-plate-based protocol has been developed and validated, with the ability to simultaneously process and quantify WSC and plant protein with a high level of automation. This protocol represents an important throughput improvement in pasture plant phenotyping, with an increase in sample processing of c. 11-fold compared to commonly-used methods. As WSC and protein are extracted simultaneously and quantified within micro-plates, consumable costs are minimised with optimal reagent use efficiency, resulting in a low cost per sample that is suitable for commercial pasture breeding companies. This represents a first high-throughput, low cost herbage quality phenotyping protocol suitable for broad-scale application which allows breeders to select elite genotypes based not only on visual assessment but also on WSC-to-protein ratios for improved ruminant nutrition.

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Genome-Wide SNP Identification in Multiple Morphotypes of Allohexaploid Tall Fescue

(Festuca arundinacea Schreb.)

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As an outbreeding allohexaploid species, the agronomically important pasture grass tall fescue (Festuca arundinacea Schreb. syn. Lolium arundinaceum (Schreb.) Darbysh.) provides an example of a plant species with a complex genome. Furthermore, three distinct morphotypes of tall fescue have been identified (Continental, Mediterranean and rhizomatous) which differ with respect to geographical origin, growth patterns and morphological features. A bioinformatic pipeline was developed that successfully identified SNPs within genotypes from distinct tall fescue morphotypes, following the sequencing of 414 polymerase chain reaction – generated amplicons using GS FLX Titanium technology. Equivalent amplicon sets were derived from representative genotypes of each morphotype, including six Continental, five Mediterranean and one rhizomatous. A total of 8,584 and 2,292 SNPs were identified with high confidence within the Continental and Mediterranean morphotypes respectively. The success of the bioinformatic approach was demonstrated through validation (at a rate of 70%) of a subset of SNPs using both SNAPSHOT™ and GoldenGate™ assay chemistries. Furthermore, the quantitative genotyping capability of the GoldenGate™ assay revealed that approximately 30% of the putative SNPs were accessible to co-dominant scoring, despite the hexaploid genome structure. The sub-genome-specific origin of each SNP validated from Continental tall fescue was predicted using a phylogenetic approach based on comparison with orthologous sequences from predicted progenitor species. This SNP collection may now be refined and used in applications such as cultivar identification, genetic linkage map construction, genome-wide association studies and genomic selection in tall fescue.

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Comparative Genomic Analysis of Five Diploid Grasses from the Festuca-Lolium Species Complex

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Species belonging to the Festuca-Lolium complex comprise many agriculturally important cool-season forage grasses including perennial ryegrass (L. perenne L.), Italian ryegrass (L. multiflorum Lam.), meadow fescue (F. pratensis Huds. syn. L. pratense Huds. [Darbysh.]) and tall fescue (F. arundinacea Schreb. syn. L. arundinaceum Schreb. [Darbysh.]). A fully sequenced and annotated genome from each species would be ultimately desirable to permit major advances in forage grass genetics and breeding, through the provision of a complete catalogue of gene and regulatory regions of a species, as well as tools for evaluation of genome-wide variation. However, the genomes of important Festuca-Lolium species are both large (haploid genome sizes = 2-4 Gb) and complex (as tall fescue is an allohexaploid) when compared to model grasses such as rice (Oryza sativa L. – 389 Mb) and Brachypodium distachyon L. (270 Mb), for which complete genome sequences are available. Lower coverage survey-sequencing of multiple species offers an alternative method for obtaining gene catalogues and also enables inter-specific genomic comparisons. Low-coverage whole genome sequence was obtained from five diploid species of the Festuca-Lolium complex: L. perenne, L. multiflorum, F. pratensis, F. altissima and F. ovina. Sampling was designed to include agriculturally important forage grasses, along with representatives of each major sub-genus within the species complex. Following de novo assembly, sampling of c. 80% of the gene-space was estimated, based on a comparison with predicted genes from B. distachyon. The complete chloroplast genome was also assembled for each species, enabling phylogenomic analysis of included taxa. This work has generated sequences for many functionally significant protein-coding genes and will enable an insight into the pan-genome of the Festuca-Lolium species complex. The generated sequence will also provide a framework for assembly of the hexaploid tall fescue genome in the future.

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Accelerated Genomics in Allotetraploid White Clover (*Trifolium repens* L.) Based on High-Throughput Sequencing

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White clover is an important forage legume in temperate grassland agriculture, which would benefit from a broader uptake of molecular breeding technologies to deliver the next generation of elite cultivars. However, as a complex outbreeding allotetraploid (2n = 4x = 32) species, white clover presents significant challenges with respect to development of genomic resources. Significant efforts have led to the characterisation of the sequence diversity within and between the two constituent sub-genomes of this species. In addition, extensive comparative genomics with the model legume species *Medicago truncatula* and *Lotus japonicas* has delivered a rationalised linkage group nomenclature system, as well as translational genomics data for the prediction of gene order and content. Proof-of-concept work has been performed in SNP discovery, with amplicons from selected genes undergoing cloning, sequencing and validation to differentiate genuine allelic (homologous) variation from homoeologous and paralogous sequence variation. In order to validate a reduction-to-practice for a high-throughput SNP discovery pipeline, large-scale resequencing of genic amplicons has been performed. A total of 195 gene amplicons were selected based on two rounds of primer design, initially from genes of potential agronomic significance, and subsequently on the basis of predicted genetic map location based on comparative genomics. The parental plants from two biparental mapping populations were used as the template DNA source, and amplified products were pooled and sequenced using GS FLX Titanium technology. The sequence data was reference assembled using Mosaik software, and a collection of 9,610 putative SNP loci were identified. These SNP loci represent an important resource for the development of a highly-multiplexed SNP assay system to correlate genotypic diversity with phenotypic variation.

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Molecular Characterisation and Analysis of Genetic Diversity within a Globally Distributed Collection of Tall Fescue (*Festuca arundinacea* Schreb.)

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Tall fescue (*Festuca arundinacea* Schreb. syn. *Lolium arundinaceum* (Schreb.) Darbysh.), is an outbreeding allohexaploid (2n = 6x = 42) cultivated for pasture worldwide. The majority of tall fescue cultivars are classified as Continental types, and have arisen from northern European ecotypes that display maximum growth over summer periods. All additional cultivars can generally be categorized as either Mediterranean or rhizomatous, which differ from Continental cultivars with respect to geographical origin, growth patterns and morphological features. Previous sequencing of a chloroplast genome-derived gene and the internal transcribed spacer region of ribosomal DNA from each of the three tall fescue morphotypes and related tall fescue cytotypes, has identified diagnostic nucleotides capable of characterising tall fescue germplasm. This approach has been used to screen a large collection of tall fescue and meadow fescue accessions held and maintained by the United States Department of Agriculture through the Germplasm Resource Information Network. Results have identified the presence of each three tall fescue morphotypes as well tall fescue sub-species of varying ploidy levels in both collections. Characterisation of these accessions has enabled biogeographical analysis of each tall fescue morphotype and sub-species and as expected, has revealed a North African distribution of Mediterranean tall fescue and a wider European distribution of Continental tall fescue from Spain through to western China. Genetic structure within Continental, Mediterranean and rhizomatous tall fescue was investigated further through the amplification of 34 SSR markers. This analysis supports the divergence between Continental and Mediterranean tall fescue and also identifies subpopulations within the Continental germplasm that reflect morphological differences and geographical distribution. This work has provided an insight into the phylo-geographical history of tall fescue whilst comprehensively characterising and dissecting a complex germplasm resource for the benefit of plant breeding.

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Differentiation of Perennial and Italian Ryegrasses at Both Species- and Variety-Specific Levels Using Multiplexed SNP Markers

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The Lolium species L. perenne (perennial ryegrass) and L. multiflorum (Italian ryegrass) are widely cultivated as forage grasses and they are closely related, such that natural and artificial hybridisation produces fully fertile F1 progeny. Cultivars from both species and interspecies hybrid (L. x. boucheanum) are represented in the current pasture seed market. Differentiation at both the species- and varietal levels are not readily undertaken by morphological comparison and enzyme electrophoresis. The objective of this study was to differentiate L. perenne and L. multiflorum at both species and cultivar levels by discovery and implementation of multiplexed single nucleotide polymorphisms (SNP) marker genotyping assays. Genomic amplicon sequencing from L. perenne permitted SNP prediction and validation to allow assembly of a 384-plex Illumina GoldenGate™ assay panel. The panel was used to genotype plants from cultivars of each non-hybrid and hybrid taxon. High transferability of SNP marker performance was observed between L. perenne and L. multiflorum. Neighbor-joining (NJ) tree analysis based on pair-wise genetic distances between cultivars revealed that clustering of perennial and Italian ryegrass varieties into two distinct groups, with intermediate positioning of the hybrid variety. At the varietal level within species, the NJ tree generally reflected breeding history and pedigree. Tetraploid varieties could also be distinguished from diploid types based on SNP data, which exhibited 5 and 3 distinct genotypic classes, respectively. These results demonstrated that multiplexed SNP markers could differentiate L. perenne and L. multiflorum at both the species and variety-specific levels. The primary catalogue of current varieties from both species will provide valuable information for cultivar choice on farm and direction for future varietal development in breeding.

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Genetic Diversity and Host Specificity of Fungal Endophyte Taxa in Fescue Pasture Grasses

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A number of pasture and turf grass species form mutually beneficial symbiotic associations with endophytic fungal species. Within the fescue grasses, diploid meadow fescue interacts with Neotyphodium uncinatum, while allohexaploid tall fescue has been reported to associate with N. coenophialum and two other morphologically distinct taxa (FaTG-2 and FaTG-3). The evolutionary history of hexaploid tall fescue is complex, as it is part of a species group with varying ploidy levels, and exhibits distinct ecogeographical morphotypes. In order to evaluate both naturally occurring variation and host grass taxon specificity, diversity was determined in collections representing multiple meadow fescue and tall fescue accessions. Initial screening with a minimal set of endophyte-specific SSR genetic markers detected endophyte incidence in 33% of 701 tested accessions. Subsequent analysis identified N. coenophialum genotypes within Continental and rhizomatous hexaploid and octoploid tall fescue accessions. FaTG-2 and FaTG-3 endophytes appeared to be restricted to Mediterranean hexaploid and decaploid tall fescue hosts. Endophytes of meadow fescue were confirmed as belonging to N. uncinatum. This study has elucidated host specificity of fescue endophyte taxa and supported models for host-symbiont co-evolution.

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Biosynthesis of Proanthocyanidins in White Clover: Single Cell Omics for Designing Pathway Re-programming

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Proanthocyanidins and anthocyanins are produced by closely related branches of the flavonoid pathway and utilize the same metabolic intermediates. Previous studies have shown a flexible mechanism of flux diversion at the branch-point between the anthocyanin and proanthocyanidin pathways, but the molecular basis for this mechanism is poorly understood. Floral tissues in white clover (Trifolium repens) plants produce both proanthocyanidins and anthocyanins. Foliar tissues do not appear to produce condensed tannins with the exception of trichomes. This makes white clover amenable to studies of proanthocyanidin and anthocyanin biosynthesis and possible interactions within the flavonoid pathway. The aim of this study is to better understand the pathway intermediates present in different white clover tissues and thus indicate how genetic manipulation of the pathway might be achieved. Two different white clover cultivars (‘Mink’ and ‘NZRLM’) are under study which includes the generation of transgenic plants with tissues-specific expression of fluorescent markers. We are applying LCMS analysis to whole tissues, specifically enriched tissues (trichomes, epidermis and mesophyll) and single cells isolated using different techniques including FACS.

Approaches for single cell ‘omics (transcriptome and metabolome analyses) in white clover leaves for re-programming flavonoid biosynthesis have been initiated as part of PhD student project (Samira Rahimi-Ashtiani). Metabolomics data based on analysis of whole leaf samples from 2 different cultivars of white clover (‘Mink’ and ‘NZRLM’) has been generated as a reference study. Methods for enrichment and purification of specific leaf tissue types have been developed including FACS capability. Tissue-specific promoters for generation of reporter gene cassettes have been isolated for evaluation in white clover cvs. ‘Mink’ and ‘NZRLM’. Constructs derived from these cassettes will now be used to generate transgenic plants for attempts at purification of epidermal tissue-derived protoplasts using FACS.

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Metabolome Analysis of Symbiota Established with Novel Neotyphodium Endophytes in a Diverse Panel of Isogenic Perennial Ryegrass Host Genotypes

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Perennial ryegrass (Lolium perenne L.), the most important temperate forage grass on a global basis, can form a mutualistic association with the endophytic fungus Neotyphodium lolii. The presence of this fungus can protect the host plant from a variety of environmental stresses. Both beneficial and detrimental agronomic properties result from the association. Invertebrate resistance is provided by specific metabolites produced by the endophyte, in particular peramine. Other metabolites produced by the endophyte, such as lolitrems and ergot alkaloids, are toxic to grazing animals and reduce herbivore feeding. Novel endophyte strains that lack either or both of the toxins detrimental to animal welfare have been identified. The stability of toxin levels is very important for future deployment of these novel endophytes. In this study, the products of a novel method for inoculation of multiple endophyte strains into common host grass genotypic backgrounds have been subjected to detailed metabolome characterisation. The metabolome of these novel host grass-endophyte symbiota was analysed using liquid chromatography-mass spectrometry (LC-MS) to gain a comprehensive understanding of lolitrems, ergovaline, peramine and janthitrem production including intermediates in their biosynthesis for host-endophyte combinations grown under controlled conditions, and hence to unambiguously assess the genotypic contributions of each partner in the symbiosis.

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Pan-genome Analysis of *Brachiaria* Endophytes

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*Brachiaria* is a pan-tropical grass genus comprising c. 100 species, of which several are economically important forage pasture crops. Seed-transmitted endophytic *Acremonium* fungi have been reported to form mutually beneficial associations with *Brachiaria brizantha*, but limited genomic resources are currently available to investigate these symbiotic relationships. A total of 29 *Acremonium* endophytes were isolated from 12 different *Brachiaria/Urochloa* accessions representing four species, *B. brizantha*, *B. decumbens*, *B. humidicola* and *B. stolonifera*. Ribosomal DNA (rDNA) sequence analysis of the internal transcribed spacer (ITS) and 18S regions from all 29 *Acremonium* isolates identified 4 distinct clusters. Interestingly, in two separate accessions, multiple endophytes isolated from a single plant belonged to three different rDNA clusters, suggesting co-existence of 3 different species. To elucidate the genuine level of diversity within and between each cluster, genome survey sequencing of seven isolates from each group was conducted. Genome sequence assembly statistics were similar for isolates within a given cluster, but substantially different between clusters. Sequence analysis of the GAPDH gene also revealed sequence conservation among isolates within the same ITS-based grouping, but significant variation among isolates from different clusters. Phylogenetic analysis of GAPDH protein structure confirmed that isolates from different ITS clusters belonged to Clavicipitaceae different species. Furthermore, none of the *Acremonium* isolates showed identity to the GAPDH protein from other Ascomycetes, suggesting evolutionary divergence. Sequence analysis of the *Epichloë festucae* peramine biosynthetic gene (*perA*) homologue, however, identified variation among *Acremonium* isolates within the same group, suggesting higher levels of within-cluster variation than previously described. Phylogenetic analysis of the perA protein provided further evidence distinct specific status. Whole genome sequence comparisons within and between *Acremonium* isolates will expand these inferences and enable discovery of single nucleotide polymorphisms (SNPs) and simple sequence repeats (SSRs) to develop molecular markers specific for *Brachiaria* endophytes.

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Novel Endophyte Discovery and Characterisation in Brachiaria Species

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The Brachiaria-Urochloa species complex is a component of the grass family Poaceae, with representatives distributed throughout the tropics, particularly in Africa. Brachiaria brizantha is an economically significant C4 tropical forage grass. It forms associations with seed-transmitted endophytic fungi of the genus Acremonium. Although widely used for pasture-based agriculture in tropical regions of South America, Asia and Australia, Brachiaria exhibits a number of shortcomings that constrain both its use and genetic improvement. Improvement of this species is limited due to its apomictic (clonal) nature. Endophytes provide an excellent mechanism for novel trait delivery in Brachiaria improvement. Global diversity in Acremonium endophytes from multiple Brachiaria/Urochloa accessions was sampled for novel endophyte discovery and characterisation to identify candidate endophytes for their delivery into the Brachiaria improvement process. Fifteen accessions representing four different species (B. brizantha, B. decumbens, B. humidola and U. mosambicensis) were subjected to genetic and metabolite-content analysis. Genetic diversity analysis using simple sequence repeat markers (SSRs) revealed no variation within accessions of the same species, as expected due to apomictic reproduction, although two sub-populations were detected within several accessions of B. humidicola. Metabolite profiling of mature plants similarly discriminated all four species, and identified two sub-populations of B. humidicola. No lolitrem, loline, ergovaline or janthitrem metabolites were detected. However, a peramine-like compound was identified in the U. mosambicensis accessions. A total of 31 endophytes were successfully isolated from 12 Brachiaria/Urochloa accessions, of which 29 were Acremonium morphotypes. Ribosomal DNA sequence analysis identified four distinct clades, with members matching a variety of Ascomycete species. Antifungal activity was assessed for all isolates, very high, broad-spectrum activity being detected for one isolate. Methods for inoculation of Acremonium endophytes into B. brizantha are being optimised.

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De Novo Generation of Genetic Diversity in Neotyphodium Grass Fungal Endophytes Based on X-Ray Mutagenesis

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The fungal endophyte Neotyphodium lolii is a common symbiont of perennial ryegrass (Lolium perenne L.). In this study, a method for generating novel endophyte genetic diversity using ionising radiation is described. Liquid cultures of N. lolii were exposed to a single or double dose of ionising radiation (from the radioisotope Cesium-137) ranging from 10–30 Gray (Gy). After a period of recovery, protoplasts were prepared from irradiated mycelia and then used to regenerate single fungal colonies. More than 5,000 irradiation-mutagenised (IRM) colonies were regenerated from protoplasts. Nine IRM colonies, which were subjected to different doses of radiation, were selected for further analysis. All 9 IRM colonies exhibited reduced in vitro growth compared to the non-irradiated standard toxic (ST) endophyte. However, in a dual-culture in vitro assay, these IRM colonies showed similar activity against several fungal pathogens as the ST endophyte. The genomes of the 9 IRM colonies were sequenced using the HiSeq 2000 Sequencing System. Sequence analysis revealed that three IRM strains contained large (>250 bp) deletions, including those within genes encoding proteins of predicted function. Three other IRM strains contained partial duplications of chromosomal regions. Compared to the ST endophyte reference genome, all IRM strains contained approximately 3-5 single nucleotide polymorphisms (SNPs) and ≥ 100 small insertions/deletions (INDELs) per Mb across genic regions. The effect of radiation dose on the mutagenesis index was also compared among the IRM strains. A repeated dose of 10 Gy on endophyte mycelia created the highest number of SNPs and INDELs per Mb across genic regions. Use of ionising radiation consequently has the potential for de novo generation of genetic variation in Neotyphodium endophytes.

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De Novo Generation of Genetic Diversity in Neotyphodium Grass Fungal Endophytes Based on Colchicine Treatment

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Colchicine inhibits chromosome segregation during mitosis and has been widely used for induction of chromosome doubling in plants, but limited to very few fungal species. This study has developed a method for putative induced polyploidisation in endophytic symbiotic fungi of perennial ryegrass (Lolium perenne L.). The Neotyphodium endophyte strain PT (non-N. lolii taxonomic group) was grown in potato dextrose broth in the presence of 0.1-0.2% (w/v) colchicine. Protoplasts were prepared from colchicine-treated (CT) mycelia and then used to regenerate single fungal colonies. Over one hundred CT colonies were regenerated from protoplasts, of which 20 were randomly selected for further analysis. SYBR Green staining of nuclei and flow cytometric analyses indicated that the majority (80%) of CT strains contained similar DNA content to the PT (parental) endophyte. Four CT strains exhibited an increase in nuclear DNA content, although whole genome duplication was not observed. In vitro growth assays showed that, when compared to PT endophyte, one strain exhibited enhanced growth, while two CT colonies showed reduced growth. Four of the 20 CT colonies showed increased antifungal activity against several plant fungal pathogens. The genomes of 10 CT strains were sequenced using the HiSeq 2000 Sequencing System. No large partial duplications events were detected in any of the strains. However, genome assembly produced contigs that were greater in abundance but smaller in size compared to the assembled PT genome. It is speculated that the increased abundance of smaller contigs in CT strains may be caused by increased transposon prevalence. Differences in genome assembly statistics indicate that genomic changes caused by colchicine treatment have occurred in CT strains. The use of colchicine may hence be applicable to the de novo generation of genetic diversity in Neotyphodium endophytes including the production of artificial polyploid endophytes exhibiting novel traits such as enhanced growth and host colonization and increased antifungal activity.

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A systems approach to a promising species: Biserrula pelecinus L

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*Biserrula pelecinus* L. is a Mediterranean annual pasture legume which performs best on well-drained sandy loams and medium loams with a pH 4.5 – 7. Diversity analysis of a germplasm collection containing 279 accessions using 18 agro-morphological traits, 22 eco-geographical datasets from the collection sites, and amplified fragment length polymorphism (AFLP) markers was conducted to develop a core collection constituting c. 10% of the original collection. This core collection adequately represented the diversity of the whole collection. A previous comparison, chiefly between pasture legume species, revealed significant variation for in vitro methane production, *Biserrula pelecinus* showed particularly low methanogenic potential. It has been proposed that the core collection of *B. pelecinus* may exhibit variation for fermentability traits. The Biserrula core, comprising 30 accessions from seven different countries, in addition to subterranean clover and bladder clover control samples, was examined for variability of *in vitro* rumen fermentation, including methane production by rumen microbes, and possible association of these traits to variation for plant morphological characters. Significant variability in fermentability profiles was revealed between accessions. The methanogenic potential of the accessions showed a 90% broad-sense heritability value. Although all of the tested accessions showed low gas pressure and methanogenic potential, they also sustained volatile fatty acid (VFA), which indicates low digestibility and high nutritive value. Metabolomic profiles of five high and five low methanogenesis accessions were developed, and correlations between metabolites and methanogenic potential were investigated. These correlations may be used for selection of an environmentally friendly cultivar of *B. pelecinus* in the near future.
DAIRY PRODUCTION SYSTEMS
Dairying in the Antipodes: Recent Past, Near Prospects

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\textbf{ABSTRACT}

The majority of dairy farmers and processors in Australia and New Zealand are considered world class because they produce and sell dairy product on export markets without subsidy assistance from taxpayers or consumers. International and domestic forces beyond the farm will influence the international competitiveness of Antipodean dairy systems, as much or more than, the within-farm characteristics of the systems. Critical external forces include: world population growth, protein demand from increasingly wealthy developing countries, dairy supply from domestic and international producers, international dairy prices and exchange rate volatility. Within farm, the keys to persistent profitability and business survival and growth will continue to be management ability and labour skill as well as the relationship between milk solids (MS; milk fat + milk protein) produced per system and the cost of production including capital and the efficient use of feed. Domestic forces will be competition for resources such as land and water, quality labour, capital and public expectations that farms will meet the costs of public environmental and welfare objectives. Public and industry investment in research, development and extension (R, D & E) in innovations that increase productivity is essential if dairying is to remain competitive. The operation of the principle of comparative advantage determines which industries thrive, or decline, in an economy. New Zealand dairying has a strong comparative advantage over other alternative pastoral industries which will continue. In Australia, the comparative advantage of dairy farming over alternative activities is less clear-cut. History shows that the best farmers and processors handle risks such as market and climate volatility and other challenges better than others, and their prospects are positive. However, these world class performers will certainly not be all, or even the majority, of the current population of dairy farmers.

\textbf{Keywords:} comparative advantage; farm business performance; feed base; land price

\textbf{INTRODUCTION}

The world economy has been wracked by the Global Financial Crisis (GFC) of 2007-08 and its continuing after-shocks, evidenced in the financial calamities besieging European economies. Meanwhile industrialisation in China, India and Brazil, and continuing but slow economic reforms in some countries, has led to high rates of economic growth in the ‘emerging economies’. The late 2000s saw agricultural prices reach very high levels as world demand outstripped supply due in part to droughts, grain demand for biofuel, and capital flight from equities. Grain and milk prices rapidly returned to trend as consumers looked for alternative protein sources and better seasonal conditions encouraged more supply world-wide. Agricultural land values declined but generally held up well compared with other property sectors through the GFC, supported by investment from international capital funds and local investors.

While improvements within the farm systems will be critical to ensure sustained profitability, a theme in this paper is that for dairying in the Antipodes it will be forces external to individual dairy systems that will influence the competitiveness and structure of those systems, as much or more than, their technical and economic factors within the farm. In the external environment a number of expectations are identifiable:

- World population will grow to 9 billion by 2050
- Income of a large proportion of this population will grow from very low and low to middle income levels, especially in China, India, SE Asia, Indonesia, South America and Russia
- Demand for protein, including dairy protein, will grow with rising incomes
- In the long term, the climate is likely to become generally warmer and drier, although more variable, especially with regard to high intensity rainfall events and heatwaves
- Exchange rates will remain volatile
- International dairy prices, input costs and technical advances will change the structure of the Australian and New Zealand dairy industries

In summary, these expectations point to a potential slow increase in aggregate international demand for dairy products. Although some of the extra milk will be produced within countries it is
highly likely that there will be an increase in the volume of international dairy commodity trade. The average annual growth rate for 2011-2020 is projected to be 1.9% (an increase in world milk production of 153 Mt, with 73% coming from developing countries) (OECD – FAO 2011).

**DAIRYING IN NEW ZEALAND AND AUSTRALIA: RECENT PAST**

**Comparative advantage**

The current shape of dairying in New Zealand and Australia is a result of both within-farm and external factors. Type of farm activity is determined not only by technical factors such as climate, topography, soils, scientific knowledge, but also by economic factors such as costs, returns and risks of the activity and the alternative activities that compete for the land, labour, capital and management. What is done, and how it is undertaken, depends on the goals, skills, preferences and attitudes to risk of the respective farmers. Collectively, these factors, including risk attitudes and risk bearing capacity, form the resource endowments of a country.

Comparative advantage determines the ability of businesses to be competitive and profitable, and to endure. Comparative advantage for a dairy farm business anywhere in the world, is that dairying is better than the next best use (opportunity cost) of the same resources (e.g. intensive lamb grazing or cropping), by a greater margin than is the case faced by competing farmers elsewhere. Comparative advantage has determined the shape and persistence of Australian and New Zealand dairy industries, and will determine the extent to which future their dairy farmers will be producing more, the same or less, dairy product than they do currently. Historically, comparative advantage and the resources of Australia and New Zealand have meant that farmers in both countries have shaped dairy industries that are large in terms of total agricultural production with farm gate values of AUD$3.9 and NZ$11.6 billion for Australia (Dairy Australia 2011) and New Zealand (DairyNZ 2011) respectively.

On a world scale, dairying is often categorised as low, medium and high cost in different countries with both Australia and New Zealand considered as low-medium cost. An alternative categorisation is ‘world class’ and ‘not world class’, with the test for ‘world class’ being ‘the ability to sell dairy product on export markets without domestic assistance’. Most dairy farmers in both countries are then, by definition, world class.

Dairy industry commentators often focus mistakenly on absolute advantage as a guide to future prospects. Absolute advantage compares the business costs (not opportunity costs) and profit of dairying in one region with business costs and profits of dairying in another region, and draws conclusions about the relative absolute business costs of production. This approach is incorrect when considering why and how businesses survive and prosper under competition over time: it is businesses with a large advantage in their activity over their next best alternative, with the lowest opportunity costs compared with their competing suppliers, that has comparative advantage and determines that they will prevail and endure as costs rise and real prices decline.

Thus, to contemplate the future shape of dairy systems in Australia and New Zealand, the theoretically valid ‘framework of thinking’ is the advantage of the activity over other uses relative to the situation of (i) competing dairy farmers in other countries (ii) competing dairy farmers in other parts of their own country, (iii) competitors for the same resources for different types of activities in their own country.

(i) Competing dairy farmers in other countries – European Union milk producers will be unable to meet the expired (2015) quota level even by 2020 because of increased costs. United States milk production is expected to grow 1.4% p.a. as yield gains more than offset a small decline in cow numbers. Argentinian milk production is expected to grow at 3% p.a. over the next decade as capital investment and management efficiency increase, with higher land prices and competition from soybeans being the main constraint. Brazil milk production is projected to grow at 1.7% p.a as a consequence of increased domestic demand, reduced feed costs and productivity gains. Chinese and Indian milk production growth is projected to slow to 3-3.3% p.a.; for the former, an increased emphasis on milk quality has constrained growth (OECD – FAO Agricultural Outlook 2011).

(ii) Competing dairy farmers in other parts of their own country – In New Zealand, farmers on east coast regions of both islands may benefit from a Government intention to support new irrigation schemes. However, in other districts (e.g. Upper Waikato catchment and Southland), dairy expansion may be restricted by regional council requirements for catchments to meet water quality targets.

In Australia, changes in the total permanent water allocation available for irrigation in northern Victoria and the Riverina region, and reliability of supply are leading to significant shifts in feedbases and risk profiles within dairy systems in these areas. Conversely, massive
public investment in infrastructure for irrigation dairying in Northern Victoria means that the capital spent on water delivery and on-farm irrigation systems that, whilst never earning a return on that capital, will provide water delivery services for the next 30-40 years. Meanwhile, growth in dairying regions with higher and more predictable rainfall patterns (South west Victoria and Tasmania) continues. Dairy farm numbers and production in Western Australia, Queensland and northern NSW continue to decline due to the relatively high cost of year round production systems to meet domestic supply, lower premiums for domestic milk and increasing transport costs of fresh milk.

(iii) Competitors for the same resources for different types of activities in their own country – In New Zealand, irrigation water could be used by horticultural enterprises, but the recent \textit{Pseudomonas syringae} pv. actinidiae (PsA) damage to the kiwifruit industry has meant that substantial capital will be needed by existing kiwifruit farmers to rebuild their enterprises. Conversion of \textit{Pinus radiata} forests to dairying ceased around 2008 due to uncertainties over liabilities related to any future Emissions Trading Scheme (ETS). Until some certainty is achieved it is unlikely that existing forests will be converted to dairy, or pasture land converted to forest.

In Australia, while horticultural industries in N Victoria remain a major competitor for irrigated water, continuing water use reforms will divert water from agriculture to the environment. Urban encroachment remains a reality for dairying close to major population centres. Sheep and cropping systems may compete with dairying in south west Victoria if lamb and grain prices increase.

**Situation updates (2007-2012) New Zealand and Australia**

**New Zealand**

In 2002, sheep-beef, forestry and dairy occupied 69%, 14% and 12% of New Zealand’s land used for primary production, by 2009 this had changed to 66%, 12% and 15% respectively. These values underestimate dairy farming’s recent expansion because 1 million dairy cattle are now grazed for at least part of the year on farms classified as sheep-beef (Statistics New Zealand 2012). Figure 1 summarises the changes in pasture use, livestock numbers and production for beef, sheep and dairy from 2002 to 2009 (MPI 2012). These changes illustrate the consequences of the comparative advantage that milk production has had over sheep meat or beef production in parts of New Zealand over the past decade.

![Figure 1](image1.png)

**Figure 1:** Changes (%) in pasture use, livestock numbers and production for beef, sheep and dairy from 2002 to 2009 (MPI 2012).

Dairy expansion has been accompanied by increased intensification of land use (Figure 2). Milksolids, number of dairy cows and debt per ha have increased by 9, 5 and 139% respectively from 2002-2009. Labour, potassium and phosphorus inputs per hectare have decreased by 25%, 38%, 27% respectively over the same period, while nitrogen input per hectare has increased slightly by 1.2% (MPI 2012).

![Figure 2](image2.png)

**Figure 2:** Changes (%) in outputs and inputs per ha on New Zealand dairy land from 2002-2009 (MPI 2012).

In New Zealand the labour required to produce one kg of MS has decreased markedly, by 18%, since 2002. The MPI (2012) report suggests that this may be because of the greater use of automation on dairy farms. It is more likely that it is a result of farm amalgamation and large scale conversions using rotary rather than herringbone dairies. Rotary dairies have more automatic technology installed than herringbones (Figure 3; from Cuthbert 2008); though for both dairy types there is low (0-20%) uptake of: EID tags, automatic drafting, weighing or heat detection, in line milk meters or mastitis detectors.
In both New Zealand and Australia, dairy systems are classified according to technical criteria about the feeding system, for the purposes of answering questions about the feed base\(^1\). In New Zealand there is less difference in supplements fed, between system 1 and system 4/5 farms, than is commonly assumed (Table 1). As expected, given the direct relationship between feed input and MS output, the systems with high feed purchases such as System 4/5 farms achieve higher operating profit when payout is $7.36/kg MS. There is greater variation in operating profit within each system than between them, because profit is the result of the combination of all the system components, including owner goals and management capacity. Providing sufficient milk is produced to keep overhead costs per unit low, many different types of systems can earn competitive returns on capital if managed well.

In 2010/11 New Zealand farmers spent 30% of their operating expenditure on feed, and all systems are prepared to use off farm supplements. From 2007-2011 use of Palm Kernel Expeller (PKE) by New Zealand dairy farmers increased from 0.4 m to 1.4 million t (Statistics NZ 2012). It appears the impetus for this was a severe drought in all major North Island dairy regions in 2008, but imports are predicted to be 1.6 million t for 2011/12. The level of use by many farmers and the past volatility of price from NZ$150-370/t suggest increasing exposure to this feed source will also increase exposure to price risk.

**Table 1:** Production and financial characteristics of New Zealand System 1-5 farms in 2010/11 (Dairy NZ Economic Survey 2010-11)

<table>
<thead>
<tr>
<th>Farm System</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4 &amp; 5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Description</td>
<td>Low input grass based</td>
<td>4-14% feed imported for dry cows</td>
<td>10-20% feed imported for dry cows and to extend lactation</td>
<td>&gt;20% feed imported</td>
</tr>
<tr>
<td>Herds per category (% of total)</td>
<td>13</td>
<td>30</td>
<td>35</td>
<td>22</td>
</tr>
<tr>
<td>Stocking rate (cows/ha)</td>
<td>2.6</td>
<td>2.6</td>
<td>2.8</td>
<td>3.0</td>
</tr>
<tr>
<td>Milksolids (fat + protein) (kg/ha)</td>
<td>845</td>
<td>835</td>
<td>1007</td>
<td>1190</td>
</tr>
<tr>
<td>Milksolids (fat + protein) (kg/cow)</td>
<td>329</td>
<td>318</td>
<td>353</td>
<td>397</td>
</tr>
<tr>
<td>Supplementary feed (t DM/ha)(^1) (% of total DM in brackets)</td>
<td>1.5 (12%)</td>
<td>1.9 (16%)</td>
<td>3.0 (21%)</td>
<td>3.9 (23%)</td>
</tr>
<tr>
<td>Gross farm revenue ($/ha)</td>
<td>6523</td>
<td>6520</td>
<td>7983</td>
<td>9406</td>
</tr>
<tr>
<td>Operating expenses ($/ha)</td>
<td>3970</td>
<td>4072</td>
<td>5009</td>
<td>5954</td>
</tr>
<tr>
<td>Operating profit ($/ha)</td>
<td>2553</td>
<td>2448</td>
<td>2974</td>
<td>3452</td>
</tr>
</tbody>
</table>

\(^1\) Calculated from assumed constant cost of supplementary feed across systems of NZ$0.3/kg DM, survey data on cost of supplement per kg MS and DairyNZ feed tables.
Focussing on sources of feed as a criterion to classify dairy systems, Australian dairy systems are classified into five broad categories namely:

System 1 – Pasture + other forages + up to 1 t grain or concentrates/cow fed in the dairy

System 2 - Pasture + other forages + more than 1 t grain or concentrates/cow fed in the dairy

System 3 – Pasture + partial mixed ration (PMR) (grain+ forages) on a feed pad ± grain/concentrate in the dairy

System 4 – Hybrid (pasture grazed < 9 months/hr + PMR on a feed pad ± grain/concentrate in the dairy, with TMR or supplements at other times

System 5 – Total mixed ration (zero grazing)

Note: these categorisations are somewhat arbitrary; there is a continuum of feed combinations in practice.

Over the past decade feeding systems in mainland Australia have become more sophisticated and complex; a feature accelerated by recent severe droughts which forced many farmers to purchase non-traditional feeds and higher volumes of traditional feeds. It is estimated that on a national basis in 2010 (Dairy Australia 2010) the proportions of farms in systems 1-5 were 30%, 50%, 11%, 5%, and 3% respectively (a small proportion classed as ‘other’). Of these, the northern irrigation region of Victoria and Riverina of NSW which had been affected by severe droughts and very low water allocations, had 33% of farm systems using some form of mixed ration (Systems 3-5). In contrast, farming systems in Tasmania remain predominantly based on pasture (66% of farms classed as system 1) with relatively low grain inputs (Table 2).

Mainland dairy systems while in general still based mostly on perennial ryegrass have experienced reduced persistence of pasture and stability of production, hence further options are being sought (e.g. Chapman et al. 2006). Across Australia, purchased feed is considered the largest single cost for dairy farmers, representing 25% of farm cash costs in 2011/12 (Dairy Australia 2012), down from 37% in 2007/08 at the height of the drought. The annual average use of grain supplement has increased from 0.5 t/cow in 1990 to 1.5 t/cow in 2011. The primary supplements remain high energy cereal grains, although by-products are accessed where transport costs are low and protein supplements used to balance rations.

Table 2: Contribution of grain, grain mixes and concentrates to dairy diets in Australia – percentage of producers (2010-11) (Dharma 2012)

<table>
<thead>
<tr>
<th></th>
<th>&lt; 0.5 t/cow</th>
<th>0.5-1.0 t/cow</th>
<th>1.0-2.0 t/cow</th>
<th>&gt;2.0 t/cow</th>
<th>Ave. (t/cow)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Australia</td>
<td>10</td>
<td>16</td>
<td>52</td>
<td>12</td>
<td>1.47</td>
</tr>
<tr>
<td>N NSW and Queensland</td>
<td>0</td>
<td>3</td>
<td>48</td>
<td>31</td>
<td>2.52</td>
</tr>
<tr>
<td>N Victoria and Riverina</td>
<td>20</td>
<td>0</td>
<td>57</td>
<td>7</td>
<td>1.32</td>
</tr>
<tr>
<td>Tasmania</td>
<td>23</td>
<td>29</td>
<td>38</td>
<td>6</td>
<td>1.00</td>
</tr>
<tr>
<td>W Australia</td>
<td>0</td>
<td>18</td>
<td>66</td>
<td>8</td>
<td>1.57</td>
</tr>
<tr>
<td>S Australia</td>
<td>0</td>
<td>2</td>
<td>44</td>
<td>38</td>
<td>2.01</td>
</tr>
<tr>
<td>Gippsland</td>
<td>0</td>
<td>46</td>
<td>43</td>
<td>10</td>
<td>1.27</td>
</tr>
<tr>
<td>W Victoria</td>
<td>18</td>
<td>14</td>
<td>59</td>
<td>3</td>
<td>1.19</td>
</tr>
<tr>
<td>S and Central NSW</td>
<td>0</td>
<td>0</td>
<td>60</td>
<td>31</td>
<td>1.85</td>
</tr>
</tbody>
</table>
Farm business performance in Australia and New Zealand

The similarity in nominal price received by dairy farmers for Australian and New Zealand milk and the volatility in annual price is demonstrated in Figure 4. Prices for 2008-12 have been higher than in the early 2000s in both nominal and real terms.

![Figure 4: Nominal milksolids price (A$/kg) for Australia and New Zealand (2002-2012) (Dairy Australia 2012).](image)

The financial performance of Australian and New Zealand dairy farms for 2009/10 and 2010/11 is shown in Table 3. The high operating profit in 2010/11 for farms in both countries reflects the exceptional milk price received. The high interest payments for New Zealand farms, demonstrates the increased debt that many farms have associated with recent land purchase and conversion, plus extra capital required through intensification e.g. larger dairy sheds, stand-off pads and housing. The importance to growth of wealth of farming efficiently and real increases in land values, particularly on New Zealand farms, is also demonstrated.

Industry mean measures of performance are not always instructive, rather it is the distributions of performance by individual businesses that give a more accurate description. Industry structure, the distribution of performance and the potential of firms in an industry are important in determining future performance of an industry. For example, New Zealand dairy farms have farm operating expenses from $3.00-7.80/kg MS; operating profit from zero to $6200/ha and return on dairy assets of <0 -> 14%. Over thirty per cent of Australian farms returned an operating loss of > A$50 000 in 2010/11, while 18% returned a profit of > A$50 000 (Figure 5). For New Zealand farms, 25% had operating profit of < NZ$1500 per ha while 25% returned > NZ$4500 per ha (Figure 6). Despite the higher milk prices there is a significant proportion of farms that in recent years have generated poor cash flows, operating profit and returns to capital compared to other dairy farmers. However, the opposite also exists, allowing some farmers to repay some term debt.

Empirical evidence of dairy businesses earning rates of return to capital of 7% - > 10%, from the farming operation, can be found in almost every year, in such sources as the Dairy Industry Farm Monitor (2011), DairyNZ Economic Farm Survey (2011) and the Dairy Business of the Year (2012) competition. Farm businesses in these recording schemes year in and year out find their performance comes into and drops out of the top proportion, for reasons to do with the random luck of the external environment. This highlights the point that farmers make their best-bet input use decisions based on their expected milk price, which itself derives from expected international prices, and then output and overall firm performance is determined subsequently, influenced by the coincidence of timing of rainfall and other weather events. The combination of farmer input decisions and external circumstances in some years suit particular systems and result in good outcomes; in other years the combinations suit less well.
The fascinating history of unprecedented rises in real prices of dairy land in New Zealand, and subsequent realignment to the long-term trend is documented by Eves and Painter (2008). Recent changes in dairy farm land prices in both countries are shown in Figure 7. The major increase in land price from 2002-2008 was driven by low real interest rates, ready availability of credit and strong demand for dairy land by local and overseas interests, together with positive medium term forecasts for dairy product prices. By 2012, the average New Zealand dairy farm business had 60% equity, but 20% of businesses had <30% equity.

The prices dairy businesses pay for land expresses buyer expectation about future business prospects. Land prices are determined by the interaction of many agricultural and non-agricultural factors. The value of dairy assets is confounded by proximity to major centres of population and urban real estate values. In Australian irrigation areas, land values are confounded by the separation of water right and land. Selling permanent water right for other uses became an option through the 2000s, and the high value of environmental water made it an option for dairy farmers to adjust their risk profiles and balance sheets.

**Table 3:** Average financial performance from Australia and New Zealand dairy farms for 2009/10 and 2010/11

<table>
<thead>
<tr>
<th></th>
<th>Australia</th>
<th>New Zealand</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total Return on Capital (%)</td>
<td>1.8</td>
<td>4.6</td>
</tr>
<tr>
<td>Return to Capital from owning farmland (%)</td>
<td>0.2</td>
<td>0.1</td>
</tr>
<tr>
<td>Return on Capital from farming (%)</td>
<td>1.6</td>
<td>4.5</td>
</tr>
<tr>
<td>Return on Equity (%)</td>
<td>0.12</td>
<td>1.90</td>
</tr>
<tr>
<td>Operating Profit ($/farm)</td>
<td>55880</td>
<td>262972</td>
</tr>
<tr>
<td>Interest ($/farm)</td>
<td>59540</td>
<td>214357</td>
</tr>
<tr>
<td>Growth in wealth from farming (pre-tax) ($/farm)</td>
<td>-3660</td>
<td>48615</td>
</tr>
<tr>
<td>Growth in wealth from owning farmland ($/farm)</td>
<td>7230</td>
<td>5789</td>
</tr>
<tr>
<td>Total Growth in wealth (pre-tax) ($/farm)</td>
<td>3570</td>
<td>54405</td>
</tr>
<tr>
<td>Net Cash Flow (NCF) after interest (before family labour and management) ($/farm)</td>
<td>75110</td>
<td>168637</td>
</tr>
<tr>
<td>Interest % of NCF before interest</td>
<td>0.44</td>
<td>0.56</td>
</tr>
</tbody>
</table>

**Figure 5:** Distribution of annual operating profit per farm for Australian dairy farms in 2010/11 (ABARE 2011).

**Figure 6:** Distribution of annual operating profit per farm for New Zealand dairy farms (2010/11) (DairyNZ Economic Survey 2010/11).
Dairy systems in Australia and New Zealand

**DAIRYING IN NEW ZEALAND AND AUSTRALIA: NEAR FUTURE**

**General**

A critical factor determining the shape of the dairy industry and dairy systems in both countries will be the performance of their economies, which will be influenced by the economic performance of trading partners and the world economy. Exchange rates critically affect export returns and imported input costs. The way the exchange rate, inflation, interest rate nexus is managed is critically important.

Policy matters. Dairy farmers in both countries are unique in that they operate in deregulated environments with virtually zero producer subsidies. Ironically, the absence of subsidy and the necessity to sell at world prices has created economically efficient dairying. The US could contribute to the projected world increase in milk demand but will be hindered by slow policy changes and demand for corn for biofuel. Similarly, W Europe and India are constrained by protectionist policies. There remains a substantial time lag between the recognition by investors of the genuine potential for major expansions of dairy production in Eastern Europe and South America and the establishment of the economic, political and scientific settings that are required to nurture the growth of the dairying industry and for this potential to be fulfilled. In the meantime, the pre-existing competitive advantages of dairying in New Zealand and Australia can, with continued sound investment in R, D & E, be maintained and improved.

World demand factors will assist dairy farmers everywhere, encouraging the growth of dairying in developing countries, as well as providing incentives for the major exporting nations. The increased supply could moderate the increase in milk prices. If oil prices rise in real terms and pressure grain prices upwards, grain-based suppliers of dairy product such as the US will be more adversely affected than grass-based suppliers.

Some observers consider that the scope for Australian and New Zealand dairy farmers to make significant further contributions to world supply is constrained by the limits of pasture based systems. The argument goes that extra production will incur higher marginal cost, and reduce comparative advantage. In Australia, water supply for irrigation is constrained by competing demands, and in New Zealand the best conversion opportunities have been taken.

Certainly, beyond gains from intensification of systems, further expansion needs to come from extensification by dairy competing resources away from non-dairy farming activities. One of the most significant constraints to growth of the dairy industry from both intensification and extensification is management capacity, allied to the operation of the principle of increasing financial risk dictating management and risk related constraints to financiers financing expansion.

The rising profile in public awareness of the state of the natural environment and the welfare of farm animals is here to stay. Dairy farmers will adapt to these external demands, reaping some productivity gains from more efficient use of inputs (e.g. nitrogen and energy). To these ends though, serious and prolonged commitment to agricultural R, D & E is required.

A price on carbon will cause costs of reducing carbon emissions to be incurred in supply chains, in the short term costs will fall more on producers, but longer term, consumers will pay a greater share. Farmers will need to be adroit, but putting added costs of carbon emissions in the perspective of annual productivity gains shows that an extremely small annual average increase in farm productivity compounding over a planning horizon of 20-30 years easily offsets any extra annual cost burden from carbon emission pricing. A price on carbon emissions...
should be no cause for alarm, provided sound and significant investment in producing the R,D & E knowledge to help lift productivity is continued.

**Australia**

**Water**

Current water reform policies relating to the Murray Darling Basin will result in less water being available for irrigated agriculture as more volume is assigned to the environment. This is likely to increase competition for available water and will lead to some adjustment within the dairy industry. Some farms may exit the industry and others alter their feed base from irrigated pastures to annual pastures grown from winter rainfall, combined with conserved forages, to high supplement use with possibly a changed calving pattern. Progressively more farm systems will shift from feeding systems 1 to those using more forms of supplementary feeding.

A notable development in irrigated dairy systems management has been the realignment of the sources of water and exposure to the risk of fluctuating water supply by irrigation businesses. Dairy farmers have (i) sold permanent water right and shored up balance sheets, moving to greater reliance on temporary water or alternatives to irrigated feed sources; (ii) increased holdings of permanent water to reduce exposure to the volatility of supply and prices of temporary water and non-irrigated feed sources; (iii) done elements of both (i) and (ii), along with carrying unused water over from one season to the next.

**Climate**

Future climatic projections for the south eastern dairy regions of Australia indicate that the region will become warmer with either a decrease or no change in annual rainfall (CSIRO 2007), with the likelihood of droughts, heatwaves and high intensity rainfall events increasing. Australia was influenced by a prolonged El Niño until 2010, and since then as a result of La Niña has received almost record rainfall in most regions. While such variability is likely to challenge dairy systems it may also provide opportunity, especially if predictive models provide adequate prior warning to inform sound decisions about feed supply.

**Feed**

Feed is one of the major inputs to dairying, and requirements for feed input per unit of MS do not decrease much once medium scale is reached. From a technical perspective, there are limits to production of milk per cow and per hectare from grown and grazed pasture. Further product per farm system then comes from feed brought into the system and from expansion of the size of the key components of the system, cows and land. Expression of improved genetic potential in expanded systems is constrained by limits set by the production environment: both natural, human and risk elements. In Australia, since 2000, the rate of increase in MS production per system from improved pasture growth and consumption and from increased use of supplement has slowed. Research evidence suggests that some further gains in MS per system are possible in the characteristics of the supplementary feeds supplied.

There are concerns about the constraints that Australian dairy farmers face in terms of land and water to grow dairy pastures and the limitations of the traditional perennial ryegrass based pastures. However, the notion that some limit to growth has been reached neglects the whole farm view in which there are substitutes for inputs that become expensive. It also overlooks the extent to which the potential pasture production and consumption is actually being achieved in many dairy systems, and overlooks the role of well-balanced supplementary feed in dairy systems. With current knowledge there is still scope to lift the standard of grass-fed dairy management of many businesses to the level of the best, as evidenced by the performance of the ryegrass only farmlet system reported by (Cullen et al. 2012). Many combinations of sources and types of inputs to dairy systems can be combined to earn returns on capital that are competitive with those earned in the rest of the economy. The climatic variability of the past decade has highlighted the challenges associated with managing dairy systems based predominantly on perennial ryegrass and a move to greater reliance on both alternate forages and supplement use is highly likely. The key challenge is to successfully integrate these options into more flexible farming systems.

Dairying in southern Australia will continue to rely on perennial ryegrass for 60-70% of the lactating cow’s diet. (Chapman et al. 2008) looked at summer and winter crops and alternative grasses such as tall fescue to overcome some of the problems of ryegrass persistence and drought tolerance in non-irrigated regions. They identified some potential gains from cropping but emphasised the challenges of designing new systems to accommodate alternative feeds. In all regions, challenges exist in how best to integrate a large array of supplements with a changing pasture base to maintain and increase profitability. In the medium to long term, it is likely that the DM production potential of perennial ryegrass will be reduced due to the shortening of the growing season and as such other perennial and annual forages will become more common place.
Debt

Seventy five per cent of dairy farm businesses have more than 70% equity. In 2009-10, 14% of farms were at risk of insolvency, having less than 70% equity and negative cash flow after debt servicing. This figure was 7% in 2010-2011. Movement in farm debt and land values are shown in Figure 7. Debt for Australian farms, on average, is much less than on New Zealand farms, but there is a group of farms where high debt is an important component of high total risk.

Structural adjustment

The Australian dairy industry is characterised by a bi-modal distribution of contribution to total output, and by returns to total capital. Thirty per cent of dairy farms account for over 50% of total milk supply, while the smallest 28% of producers supply 8% of total milk (Dairy Australia 2011). Only a small proportion of businesses earn competitive returns to total capital from farming and from owning farmland. Therefore, for the majority of owners the comparative advantage over alternative resource use is not high. This suggests that small, relatively unprofitable businesses will be subsumed by larger, more profitable dairy operations or by alternative enterprises, as happened to Australian dairying in the 1960s.

Economic growth will continue to see labour competed away from farming, with rising real costs to retain labour. These costs, and declining real costs of capital substitutes for labour, mean that labour saving technology will become more feasible; although the industry is likely to remain a slow adopter.

Overseas and internal competition

The major exporters of dairy products are New Zealand and the EU with 27% each of total exports, and Australia and the US contribute 12 and 9% of traded milk products respectively. However, while New Zealand and Australia impose no restrictions on trade, the EU and the US impose high tariffs on dairy imports, and can opportunistically reinstate subsidies to dairy exporters when threatened by more efficient producers. Less than 10% of the total trade in dairy products is free of barriers. The net effect of dairy farmer protection around the world is to adversely affect both the prices received, and the volumes exported, by Australia and New Zealand. Any progress in trade liberalisation has potentially large benefits for efficient dairy producers and processors in both countries. Domestically, the biggest threat to dairy farmers is their fellow dairy farmers who can do it better, in the long term this gives them an advantage in competing for scarce resources such as capital, land and labour. This applies within every region, and is subject to the protection provided by freight costs of liquid milk, between regions.

Dairy Research, Development and Extension

The key to having a positive view of future dairy farming is a belief that sound and substantial investment in agricultural R, D & E will continue, in Australia and New Zealand, and world-wide, as many innovations are imported. Will the strong performance of such investment over the past 50 years be a good guide to the future 50 years? The high returns to investment in agricultural R, D & E of the past will still apply in the future but continued investment must be made. Investment in agricultural R, D & E remains one of the best-returning investments in the economy. It is an investment in which the market failure case for it remains very strong. Looming threats to continued and successful investment in agricultural R, D & E are competing demands on public finances and a serious and growing shortage of young scientists.

How are the benefits of R, D & E investment shared amongst farmers, processors and consumers? Analysis of the distribution of benefits of research through the Australian dairy industry by (Liu et al. 2012) calculated that a 1% reduction in farm costs of supply across the whole industry, once the effects had worked through the economy, would generate total annual benefits of over AUD$40 m (Figure 8). Of this, $7.5 m went to the dairy farmers, $1 m to processors, $31 m to domestic consumers and $0.5 m to overseas consumers. The estimate of $40 m benefits p.a. generated from a 1% reduction in farm costs does not take account of the costs of achieving the cost savings nor the cost of the research. Domestic consumers and farmers received 80% and 20% of the total benefits of the R, D & E respectively. A 1% gain in processing efficiency provided total benefits of $30 m, with $3 m going to farmers and $25 m to domestic consumers. In the Australian situation, the return to farmers from their contribution to total investment in R, D & E is effectively doubled as the public matches their contributions. From the dairy farmers’ viewpoint, if 10% of farmers achieved a 10% reduction in their costs this too would generate benefits of $40 m. Ten per cent of farmers (700 farmers) would be sharing $7 m benefits p.a., or $10,000 per farmer p.a.
New Zealand

Water

Future increases in milk production from grazed pasture will rely substantially on investment in new irrigation schemes on the east coasts of both islands but particularly the South Island. Water resources are available but limiting factors are likely to be capital for infrastructure and dairy conversions, and public resistance to the environmental and social implications of large scale irrigation schemes. Water allocation for dairy expansion interacts with the impact of current and new dairy farms on water quality. In some catchments it is likely that dairy production will be constrained at current levels, in others there will be significant extra costs to converting sheep, beef or forest land to dairy because of the need to implement management and mitigation procedures to reduce N, P and sediment losses.

The keys to further expansion of the New Zealand dairy industry are water allocation for irrigation and other farm uses and the control of water degradation in catchments associated with dairy activity. Less than 5% of New Zealand’s renewable freshwater resource is currently allocated for use, which is low by international standards (MFE 2009). The current National government has recently issued a National Policy Statement on freshwater management to set a consistent, nationwide regulatory framework for setting water quantity and quality limits to govern allocation and use of freshwater. It has set up an Irrigation Acceleration Fund of NZ$35 m over 5 years and a proposal for up to NZ$400 m of Crown equity investment in water infrastructure schemes. In the current absence of economically viable options for mitigating nitrogen losses from intensive dairying, it is difficult to see how new large scale irrigation schemes can avoid contributing increased N to groundwater, river and lake ecosystems. Based on the river water quality data for 2003-2007, over 50% of sites in Auckland, Waikato, Canterbury and Southland regions had median total N levels that exceeded the New Zealand guideline value and over 50% of sites in Northland, Auckland, Waikato and Southland had median total P levels that exceeded the guideline value (MFE 2009).

A recent report (NZIER 2010) on the economic benefits of 14 irrigation projects throughout New Zealand calculated $2.7 billion off-farm and $8.7 billion on-farm costs to 2026. An additional 347 000 ha of irrigated land (52% in dairying) could, by 2035, produce agricultural exports of $4 billion in real 2010 prices. The majority of this land would be in Canterbury, and would mean that by 2020-2025 South Island milk production would exceed that from the North Island. The increased area in dairy support, arable and horticulture would also provide an additional feed base for Canterbury dairying.

Land

Large areas of unirrigable land suitable for dairy conversion exist throughout New Zealand. Much of this challenges preconceived notions about milking frequency, a fixed farm dairy, cow breed and mixed farm enterprises. Many such areas are currently used as dairy support land but some could easily be converted, especially if technology such as once daily milking, mobile dairies and mixtures of sheep and lactating cows were considered.
Environment Southland now has new dairy conversion rules making dairying a discretionary activity which requires consent, and in June 2012 a Southland farm received consent to convert. This required a farm management plan which includes a soil assessment, a nutrient management plan and a winter grazing plan. This decision indicates firstly, that consent requests that meet specifications will be granted, but secondly, the cost of future conversions will be increased as a consequence of the extra planning required. In this case the applicant obviously calculated that the extra cost for dairy conversion was still a better option than carrying on with the previous beef grazing enterprise.

Recent modelling exercises have shown the potential for improving the technical efficiency of dairy farming to achieve both profit and environmental goals (Beukes et al. 2011). Such changes involve an integrated redesign of dairy systems to use higher genetic merit cows at lower stocking rates, and limited grain feeding, with reduced N fertiliser, standing off to collect and spread urine more evenly, and nitrification inhibitors. The success of these systems will depend on managers with the skills to manage pastures and nutrition at a standard above current industry norms.

Climate
Dairy extension in New Zealand has developed a range of management recommendations to manage the inevitable droughts, excessive rainfall and temperature variation associated with the El Niño/Southern Oscillation cycle. From October 2007 - April 2008 rainfall was 10-50% lower than average in all major dairy regions. There was a 1 in 100 year drought in Waikato; but despite very difficult farming conditions everywhere, national MS per ha production decreased by only 5.1%. Climatic challenges will test dairy systems but are unlikely to have serious long term consequences for production or profitability.

Emissions Trading Scheme
Under current ETS settings, agriculture sector participants must report their emissions and face full surrender obligations from 2015 although the Government wishes to extend this to 2018. An independent review will report back in 2014 on technologies and international action to reduce greenhouse emissions. The Government supports the entry of agricultural emissions into the scheme under two conditions –that there are practical technologies to reduce emissions and our international competitors take sufficient action to reduce their total emissions. The New Zealand Government is currently funding $20 m per year for research to reduce New Zealand’s agricultural greenhouse gas emissions. Current research by the New Zealand Agricultural Greenhouse Gas Research Centre and the Pastoral Greenhouse Gas Research Consortium is aimed at reducing methane and nitrous oxide emissions, increasing soil carbon accumulation and designing practical and profitable farm systems that reduce greenhouse gas emissions.

It is unlikely that dairy expansion in the next decade will be constrained by either current or future ETS settings. The uncertainty around forest harvesting will mean that this route to dairy conversion is likely to remain closed, but this would likely be the case in the complete absence of an ETS because of more stringent regional council consent processes in those areas with major forests. Longer term, there will be direct and indirect tax on carbon emissions which will impact on dairy profitability but these will also affect other primary industries so that little shift in comparative advantage will occur, with the possible exception of forestry.

Feed
Although sound data are difficult to find it is likely that at least 80 - 85% of New Zealand milk comes from pasture or conserved pasture diets. The industry has long realised that perennial ryegrass and white clover pastures have been unable to deliver the feed quantity and nutritive value demanded by modern dairy farmers. Poor pasture persistence associated with drought, insect pests, treading damage, weed competition and suboptimal nutrition are well documented (e.g. Clark, 2011). There is now a substantial joint programme between the pasture seed and dairy industries to understand the mechanisms responsible for poor pasture persistence and to provide a Forage Value Index (FVI) that will allow farmers to select ryegrass cultivars suitable for the environment and management system (Chapman et al. 2011). Although protection of DM yield from the ryegrass- white clover feed base is critical, it is even more important to increase the intake potential of pastures because without this advance the industry will become increasingly reliant on imported low-medium quality supplements. These supplements, e.g. PKE, may become less available through either policy or price changes. Farmers find it difficult to revert to lower input systems because of non-recoverable costs in building, equipment, staff and livestock and consequently incur increased financial risks. The challenge is to find home-grown or imported substitutes for PKE that are relatively low cost.

Debt
Access to capital for further dairy development is likely to be a challenge for those 20% of farmers with
<30% equity. There are however, 32% of farmers with >70% equity and many of these will be able to access capital for further expansion. A recent Agri Insight (2012) survey of 750 farmers found 24% had plans to acquire more dairy land. Banks are likely to be more cautious in lending for farm purchase than in the past decade, but in the absence of alternative investment options, proposals for dairy expansion by proven dairy businesses will find support.

Overseas competition
The Agri Insight (2012) survey found 44% of farmers were concerned about the effect of exchange rate movement on their business and 43% about the effect of milk commodity price movements. The latter reflects concerns about competition from other countries in supplying milk, these issues are dealt with in the Australian section, but the past decade has shown that New Zealand can be exposed to a ±25% variation about mean milk price without serious effects on long term growth. The growth of New Zealand exports to China and recent agreement on free trade arrangements with China represent significant developments, as too does the parallel growth of milk output in China.

Processing
For perishable dairy products, the capacity of the processing sector to achieve economies of size is a key component of a nation’s comparative advantage in dairy farming. For dairy processing co-operatives the perennial challenge is capitalisation for the growth that is necessary to remain competitive. The June 2009 vote by Fonterra suppliers in support of the Trading amongst Farmers (TAF) proposal has introduced a new era for New Zealand’s largest dairy company. The proposal will reduce the risk the company faces of having to redeem farmer shares. However, a more important outcome is the slow acceptance that the company will need to access outside capital if it is to fulfil ambitions to become a truly global dairy company. New Zealand farmers have invested in farms in Australia, USA, China, Russia, Chile and Brazil over the past decade and Fonterra has established joint ventures with farming, processing or marketing companies in these and other countries. It will be fascinating to see where the balance of New Zealand dairy farmers invests capital over the next decade.

CONCLUDING COMMENT
When it is recognised what the best dairy farmers and their processors in both countries are capable of doing in their businesses under volatile and changing circumstances, there is ample reason to be positive about the prospects of these businesses in their respective industries. The industry challenge is maintaining and enhancing comparative advantage and competitiveness. World-wide growth in demand for dairy products will create the need for an overall increase in world supply. This will create opportunity for the best dairy farmers in Australia and New Zealand. As ever, high prices will encourage increased supply that will put downward pressure on price and volatility in price will remain. This creates challenges for all and opportunities for the best farmers.

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Performance, return and risk of different dairy systems in Australia and New Zealand

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ABSTRACT

Changes in the farm operating and policy environments, and a need to remain profitable under a cost-price squeeze have contributed to dairy systems in Australia and New Zealand becoming more intensive and complex over the last two to three decades. Farm systems in both countries are now very diverse, varying from pasture-based with little use of purchased supplements, to a high dependence on feed supplements and even zero grazing. The performance (defined in this paper as production or technical performance), return (return on assets or profit) and risk (variation in economic performance over time) as dairy systems increase in intensity, were examined using farm survey data, case studies and existing published studies. Technical performance measures, such as milk production, feed conversion efficiency and pasture consumption were individually poor indicators of farm return on assets or operating profit. In addition, when survey data was grouped by return on assets, few farms were in the top 25% in successive years. The farms that were able to perform consistently were characterised by good, but not extreme, technical performance in a range of areas, which translated to favourable business return (return on asset and profit). Farm manager knowledge and skills are critical, and mean that many different systems can operate successfully. Risk and system intensity was explored, and alternative future options that resulted in larger and more intensive systems generally resulted in higher net wealth for the farm owner, but almost always at increased risk. The best system for a farmer to operate is one which best meets their preferences, goals and aspirations, regardless of system type.

Key words: Economic performance, profit, system intensity

INTRODUCTION

Dairy farmers operate in a complex and changing environment from both economic and physical production perspectives. Deregulation, decline in terms of trade, variability in seasonal conditions and extreme events have contributed to significant changes in the dairy industry and dairy production systems in Australia and New Zealand compared with 20 or 30 years ago. In both countries, farm numbers have declined while milk production has increased. Cow numbers have decreased slightly in Australia since the early 1980s, and doubled in New Zealand, but in both countries average milk production per cow has increased markedly (Table 1). The diversity of feeding systems on dairy farms has also increased. For example, prior to the 1980s, milk production systems in Victoria were predominantly pasture based with concentrate feeding at less than 0.2 t/cow per year (Doyle et al. 2000). By 2011/12, average grain usage in Victoria had increased to 1.5 t/cow, and in a national survey of dairy farmers in Australia, average grain and concentrates usage was 1.7 t/cow (Dairy Australia 2012a). Feed consumption of a milking herd in Australia now varies between 100% grazed pasture or home grown feed and no purchased feed to little or no grazed pasture and high dependence on purchased feed (Armstrong et al. 2000, Doyle et al. 2000, Dairy Australia 2009). While New Zealand dairy farmers use less purchased feed and concentrates, than their Australian counterparts, dairy systems in New Zealand have also become more intensive in the use of feed inputs over the last decade, with increased use of nitrogen fertiliser, maize silage and palm kernel expeller (MacLeod and Moller 2006; Booker 2009; Cameron and Bell 2012). This is evident in increased stocking rates from 2.6 to 2.8 over the last decade.
Table 1: Australian and New Zealand dairy industry statistics for 1979/80 and 2010/11 (Dairy Australia 2011a; DairynZ 2011)

<table>
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<th>Australia 2010/11</th>
<th>New Zealand 1979/80</th>
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<td>No. of herds (New Zealand)</td>
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<td>16,500</td>
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<td>Cow numbers (million head)</td>
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<td>Total milk production (million L)</td>
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<td>9.1</td>
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<td>5,700 L</td>
<td>260 kg protein + fat</td>
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</table>

The feeding and production systems on dairy farms in Australia and New Zealand have been categorised, somewhat arbitrarily, into five types according to characteristics of key feed inputs used. In practice, if an industry comprises 7,500 dairy businesses, there are 7,500 individual dairy systems, once all inputs, including regional specific features, management, operator stage of career and family situation, and timing and quality of operations are taken into consideration, i.e. no two systems are the same. The five feeding systems defined in Australia cover a broad spectrum with regard to proportions of grazing and supplementary feed use, ranging from largely grazing and little use of supplementary feed to zero grazing and predominantly reliant on purchased feeds. The five Australian systems are (Dairy Australia 2012b):

Aust. System 1: Low bail system – Grazed pasture + other forages + up to 1.0 t/cow of grain and/or concentrates fed in the dairy shed during milking;

Aust. System 2: Moderate-high bail system – Grazed pasture + other forages + more than 1 t/cow grain and/or concentrates fed in the dairy shed during milking;

Aust. System 3: Partial mixed ration system – Pasture grazed for most or all of the year + partial mixed ration on feed pad ± grain and/or concentrates fed in the dairy shed;

Aust. System 4: Hybrid system – Pasture grazed for less than nine months per year + partial mixed ration on feed pad ± grain and/or concentrates fed in the dairy shed;

Aust. System 5: Total mixed ration system – Zero grazing. Cows housed and fed a total mixed ration.

The New Zealand five production systems are similarly arbitrary, defined by the amount, timing, and intended use (milking or dry cows) of purchased or imported feed. The five New Zealand systems are (DairynZ 2012):

NZ System 1: All grass, self contained. No supplement fed to the milking herd except supplement harvested off the milking area and no cows grazing off the milking area;

NZ System 2: Dry cow feed purchased. Approximately 4-14% of total feed imported and fed to dry cows including dry cows grazing off the milking area;

NZ System 3: Feed purchased for dry cows and to extend lactation. Approximately 10-20% of total feed is imported to the milking area to extend lactation (usually autumn feed) and for dry cows;

NZ System 4: Feed purchased for dry cows and to extend both ends of lactation. Approximately 20-30% of total feed purchased at both ends of lactation and for dry cows;

NZ System 5: Feed purchased for year round feeding. At least 30% of total feed imported including for dry cows.

The range in feeding systems in New Zealand is narrower than for Australia with the system that is classified as the most intensive potentially still being largely pasture based. Around 5 to 10% of farms included in the DairynZ Economic Survey in 2010/11 comprised the most intensive type of system (DairynZ 2012). Placed side by side, the New Zealand production systems would overlap most with Systems 1 and 2 for Australia. While the Australian and New Zealand systems are classified largely by feed base and amount of purchased feed, there are also other differences in dairy systems, including once a day milking, organic farming and different wintering systems. Few farms are likely to fit neatly into a particular feeding system, however the two arrangements described above provide a broad indicator of proportions of dairy farms with common feeding system characteristics. These categories of farms by feeding system have been used in this paper to investigate how performance, return and risk change across the range of farm system intensity in Australia and New Zealand.
**PERFORMANCE, RETURN AND RISK – SOME DEFINITIONS**

Performance, return and risk with respect to farm businesses can be interpreted in many ways. In the following discussion, the terms have been taken to refer to the following:

**Performance**

Production or technical performance of the farm business and the factors that contribute to it, such as pasture consumption per hectare, labour efficiency, water use efficiency, feed conversion efficiency, amount of purchased feed per cow, milk production per cow.

Production economic theory states that any of a wide range of partial average technical efficiency ratios can be consistent with high or low whole farm economic efficiency. Farm performance in a production system context is essentially about the differences in milk production and the inputs and costs incurred to produce extra milk i.e. the contribution of marginal additional inputs to marginal output, marginal costs and marginal returns; assessed and understood in the context of risk. Partial average efficiency ratios, whether technical or economic, are used widely and can represent shorthand proxies for what is happening at the farm level when the user has a thorough and sound knowledge of the whole system. The technical efficiency of a component of a business, measured by the ratio of physical output to a physical input, is a determinant of economic efficiency (income/costs), but is not, as at times implied, a proxy for economic efficiency. Information about a partial technical efficiency ratio, such as average output per unit of input, can be useful when comparing the technical aspects of a change to a system within a farm, such as alternative new technologies that are designed to perform the same task in a system.

**Return**

Return on assets and operating profit. Return relates to economic performance over a defined period, normally a year.

Return on assets is calculated by dividing operating profit by the value of total assets managed, and is the return from operating the dairy portion of the business, excluding income and costs from other enterprises and capital gains from land or asset appreciation. While returns on capital from owning dairy assets that may experience capital gain, such as land and water, is valuable and important, the focus is the farming operation. Return on assets indicates how efficiently resources are being used and managed. Operating profit, also known as earnings before interest and tax (EBIT), is calculated as gross income minus variable costs and overhead costs. Gross income is quantity of output multiplied by output price, plus gains (or minus losses) from stock and feed inventories, and other sources of income related directly to the farm business, such as dividends on milk company shares. Variable costs are those that contribute directly to output, and change in proportion to the amount of output produced. These costs include feed, shed, herd, permanent labour and management, and repairs and maintenance costs. Overhead costs are costs that do not vary as the level of production changes, for example depreciation and administration costs. A critical element in calculating operating profit is costs associated with imputed labour and management, which are allocated at the market rate based on opportunity cost. Operating profit measures the annual return to, and efficiency of, all capital managed in the business for a year, but excludes interest paid.

**Risk**

Fluctuations in economic performance over a period of time as a result of business risk and financial risk and how these risks are managed. Business risk arises from:

- Production risk: due to climate variability, pests, genetic variation, and diseases – factors beyond the farmer’s control.
- Personal risk: illness or death of the owner or injury to a farm worker which may affect production or costs, and risk associated with labour availability and quality.
- Price risk: fluctuations in milk price, supplementary feed price and other inputs and outputs.
- Institutional risk: changes in legislation that affect farm production, including environmental regulation.

Business risk is independent of how a business is financed, and therefore refers to effects present regardless of equity level. Financial risk refers to the variability of returns to the owner’s equity resulting from meeting interest charges, financial obligations or debt servicing. Financial risk results from the gearing of the farm, with the higher the proportion of debt to total input, the higher the financial risk (Boehlje and Eidman 1988, Makeham and Malcolm 1993, Hardaker et al. 2004).
INFLUENCES ON SYSTEM PERFORMANCE

Some of the key technical and institutional influences and shaping factors for the five Australian feeding systems have been explored by Little and Murphy (2009), and encompass climate, irrigation, stocking rate, preferred focus on forage production or milk production, cow type, milk production, milk company supplied and pricing system. From a farm technical performance and economic return perspective, the importance and implications of these factors vary depending on feeding system, as well as other factors, such as availability and skill level of employed labour, animal health and welfare, economies of size, and farm owner/manager skill, knowledge, ability and attitude to risk. Both intensive and less intensive systems require good management and ability to bear and manage the risk involved, for successful farm performance. Newman and Smeaton (2011) note that ‘farm profitability is directly related to how well your business handles risk’. Predominantly pasture-based systems require many skills to run the business; knowledge is needed about a range of disciplines, such as animal production, soil science, fertiliser management, agronomy, irrigation, human resources and business management. As systems become larger and more intensive, employed labour is generally needed and specialisation of tasks and activities is often possible, however good labour management skills become increasingly important in larger teams. Knowledge and management of cow nutrition also becomes more important in highly intensive systems.

FARM INTENSITY, PERFORMANCE AND RETURN

In Australia and New Zealand farm level survey data for the dairy industry is collected through projects such as the Victorian Dairy Industry Farm Monitor project, the Tasmanian Institute of Agriculture benchmarking service, TasMilk60, RedSky, the Dairy Business of the Year award, the Queensland Dairy Accounting Scheme, DairyBase and the Dairy NZ Economic Survey. While these surveys are not necessarily representative of the whole dairy populations in Australia and New Zealand, they provide useful data sets to examine if technical and economic performances change as dairy systems move towards greater intensification and complexity. In a recently published study, Shadbolt (2012) used the physical and financial data of dairy businesses in DairyBase for the three years between 2006/07 and 2008/09 to compare the financial performance across the five New Zealand production systems.

Some typical technical and partial efficiency measures used to assess the technical performance of farms are milk production (per cow or per hectare), pasture consumption or utilisation per hectare, stocking rate, feed conversion efficiency and operating profit per cow or per hectare. Even though correlation is not causation, strong correlations are often demonstrated by plotting feed eaten per cow versus milk production per cow, pasture consumed per hectare versus stocking rate, feed conversion efficiency versus feed intake, or cost of production versus pasture consumed. In addition, correlations for individual farms between partial technical measures for levels of single inputs (e.g. nitrogen per hectare) and system output or economic measures (e.g. milk per hectare or operating profit per hectare), are often mistakenly thought to suggest that better performance in these single input measures on other farms should lead to higher return on assets or operating profit.

Using data from the Victorian Dairy Industry Farm Monitor project between 2006/07 and 2010/11, the TasMilk60 project (2006/07 to 2008/09), the Queensland Dairy Accounting Scheme (2008/09 to 2010/11), and DairyBase (2010/11), the relationships between some of these partial measures and profit were analysed. It is important to note that different surveys use different terminology or descriptors unique to that particular survey. For the TasMilk60 data, a partial indicator ‘Dairy return on assets’ is calculated using a measure called ‘Dairy EBIT’, which does not account for stock trading profit and loss (non cash adjustment) or depreciation, therefore ‘Dairy return on assets’ and ‘Dairy EBIT’ have been used as a substitute for true return on assets and EBIT (operating profit).

Visual assessment of scatter plots for the Victorian, Tasmanian and Queensland data sets of a single technical efficiency ratio, such as milk production per cow or per hectare with a whole farm economic efficiency measure, such as return on assets, or operating profit (per cow or per hectare) showed meaningful relationship. As economic theory would predict, any of a wide range of ratios of technical input efficiency can be profitable depending on relative prices. While a trend line could no doubt be fitted to the milk production versus profit data sets, the variation in return on assets around each level of milk production was considerable (Figures 1 and 2). This is observed for all years. For the New Zealand data, milk production per cow or per hectare with operating profit per cow or per hectare, showed a stronger correlation ($R^2 \approx 0.3$), but large variation still existed.
Individually, pasture consumption (grazed plus conserved feed) (t DM/ha), feed conversion efficiency (L energy corrected milk/kg DM feed intake) and purchased supplements (t DM/cow) also showed little correlation with return on assets (e.g. Figures 3 and 4). Studies of dairy businesses in Southland, south Otago and Canterbury present a similar result, with measures such as pasture eaten (t DM/ha), stocking rate (cows/ha), net imported supplements (t DM/cow) and milk production per cow and per hectare in isolation, being poor indicators of operating profit per hectare (R² between 0.02 and 0.1) (Lee 2010; Macdonald and Hedley 2010; South Island Dairy Development Centre 2010).
describe a case study farm which was considering a change in the type of pasture grown to increase water use efficiency in response to increased price of irrigation water and low allocations experienced in preceding years. An analysis of the likely outcome if perennial pasture was replaced with annual pasture (Persian clover and ryegrass), or maize conserved as silage showed that while annual pasture and maize were more water use efficient (in terms of dry matter produced per ML), after accounting for all the costs of conservation, storage and feed out, perennial pasture was the best option based on costs per cent of metabolisable energy consumed. For this farm, higher water use efficiency from a production perspective could be achieved, but most likely at increased cost.

Looking at the same partial efficiency measures (pasture consumption, milk production, feed conversion efficiency) as above, plotted against return on assets, but segmenting farms by system intensity, the results were again mixed. This could be attributed in part to the allocation of farms to different system types. Compared with the farms in the Victorian Dairy Industry Farm Monitor project and Queensland Dairy Accounting Scheme, the farms which participated in the TasMilk60 project could be closely aligned to the Australian five feeding system arrangement. Available information about the farms in the Victorian Dairy Industry Farm Monitor (VDIFM) project meant that farms were grouped by percentage of imported feed which acted as a proxy for farm intensity. The categories were: VDIFM System 1: < 30% imported feed; VDIFM System 2–3: 30% to 50% imported feed; VDIFM System 4: >50% imported feed and <2 t/cow/year and; VDIFM System 5: >50% imported feed and >2 t/cow/year. The Queensland Dairy Accounting Scheme (QDAS) uses three production systems (Murphy and Simpson 2011): QDAS System 1) Grazing – Milk production principally from grazing and grain and concentrates fed in the dairy. There is little or no feeding of silage based feed on a feed pad; QDAS System 2) Partial Mixed Ration (PMR) – Milk production from a combination of grazing, grain, concentrates and silage-based feed on a pad and; QDAS System 3) Total Mixed Ration (TMR) – Milk production principally from a silage-based mixed ration fed on a pad. There is little or no grazing.

Aust. System 1 farms, but with variable economic performance (Figure 5). While it could be concluded that more intensive farms generally have higher milk production per cow and per hectare, and higher feed conversion efficiency, it could not be presumed they will be more profitable. System 1 farms could have similar return on assets, but with lower milk production or feed conversion efficiency (Figure 5). A similar effect can be seen for operating profit per cow with milk production per cow or per hectare in the New Zealand farm data, where nearly all system types could have high or low operating profit (Figure 6). The farms in the Victorian Dairy Industry Farm Monitor data set demonstrated substantial scatter and overlap between system types when return on assets was plotted with milk production (per cow or per hectare) (Figure 7). However, fewer of the less intensive farms (VDIFM System 1) generated a negative return on assets compared to VDIFM Systems 2–3 or System 4 farms. This possibly warrants further scrutiny of the seasonal and operating conditions between 2006/07 and 2010/11. Exploring the milk production of the farms in the Queensland Dairy Accounting Scheme and return on assets or operating profit per cow showed no clear association, but the TMR farms (QDAS System 3) generally had higher milk production (Figure 8). Some of these TMR farms also had high return, but equally there were grazing (QDAS System 1) and PMR (QDAS System 2) farms that gave similar levels of return at lower milk production. Every farm has their own production function – a consequence of individual resources, inputs, skills and preferences, and the implied response function that can be derived from aggregate data does not actually apply to any individual farm. The findings by (Silva-Villacorta et al., 2005) of an analysis of over 600 New Zealand dairy farms also supports this, where different levels of additional feed inputs used to increase milk production per cow and per hectare did not consistently result in higher operating profit per hectare. (Silva-Villacorta et al., 2005) conclude that the efficiency with which farmers were able to convert the additional input to profit varied, and were influenced by individual aspirations and capability. They note that ‘Management skills are required at all levels (of extra feed input use) to generate profit’.
Figure 5: Distribution of feed conversion efficiency (L energy corrected milk/kg DM intake) with ‘Dairy return on assets’ (%) for System 1 (●), System 2 (○) and System 3 (■) type farms between 2006/07 and 2008/09 in Tasmania (Dairy Australia 2011b).

Figure 6: Distribution of milk production (kg protein + fat) per cow and per hectare with operating profit ($) per cow for NZ System 1 (◆), NZ System 2 (○), NZ System 3 (■), NZ System 4 (▲) and NZ System 5 (▼) type farms in 2010/11 in New Zealand (M. Newman unpubl. data).

Figure 7: Distribution of milk production (kg protein + fat) per cow and per hectare with return on assets (%) for System 1 (●), System 2-3 (○) and System 4 (■) type farms between 2006/07 and 2010/11 in Victoria (Department of Primary Industries 2007, 2008, 2009, 2010a, 2011).
In a more formal study of whole farm financial performance and system intensity, Shadbolt (2012) used the DuPont system to examine the key factors for financial success across the five New Zealand farm system types. Information from DairyBase between 2006/07 and 2008/09 was used in the analysis. The DuPont approach is used to assess the factors affecting return on assets and return on equity (net farm income divided by total assets owned) of a business. Profitability in the DuPont system is affected by three factors:

1. Operating profit margin – How efficiently inputs are used to generate profit (earnings)
2. Asset turnover – How well assets are used to generate revenue (turnings)
3. Debt to asset ratio – How well the business uses debt capital (leverage)

As dairy systems moved from low input (NZ System 1) to high input (NZ System 5), stocking rate and milk production (kg protein + fat) per hectare increased (Shadbolt 2012). This was observed for all three years studied. Assessing profitability by return on assets or return on equity across the five systems showed there was no significant difference (P > 0.05) for 2006/07 and 2007/08. While the more intensive systems (NZ Systems 4 and 5) had greater operating profit per hectare, the additional capital needed in these systems produced similar, but not higher return. In 2008/09, the combination of low milk price and relatively high input costs meant that the more intensive NZ System 4 and 5 farms performed worse than NZ System 1 and 2 type farms. Shadbolt (2012) commented that these more intensive systems, ‘while able to continue to produce at higher levels….. are more affected by market risk – both input cost and output prices’. The decline in return on assets in 2008/09 as system intensity increased, was found primarily to be the result of a decline in operating profit margin. While production could be maintained and assets were used reasonably efficiently to generate revenue, the unfavourable input/output prices meant that the efficiency with which inputs could be used to generate profit deteriorated more for the intensive systems. Despite financial performance being related to system intensity for one year analysed, the conclusion reached by Shadbolt (2012) was that in general, farmers across all systems can operate efficiently and return on assets is not related to system type. The most appropriate system for a farmer to operate will depend more on personal preferences and attitudes to risk than on potential economic performance.

**CONSISTENCY OF FARM PERFORMANCE AND RETURN**

In the Darling Downs region of Queensland, farms from each of the three (grazing, PMR and TMR) system types participated in the Queensland Dairy Accounting Scheme. This provided the opportunity to examine farm performance and return with system intensity without some of the regional differences that can occur when considering farms across a whole state of Australia or between regions in New Zealand. Results showed that the TMR farms generally had higher milk production per cow than the grazing or PMR farms, but not always higher return on assets and operating profit per cow. A small number of TMR farms generated very high returns, but there were many other TMR farms that made similar or poorer returns than grazing and PMR farms. Closer inspection of the TMR farms with high return on assets or operating profit per cow revealed that only one farm was in the group of high performing TMR farms each year. Two farms had high returns for two years. This poses the question of whether a top performing farm, say in the top 25% of farm businesses by return on assets in one year,
is likely to be in that group in subsequent years? Evidence suggests that few businesses are able to do this consistently. That is, farm performance is determined in part by random happenings that occur subsequent to the decision-maker making their best bet decisions about inputs and expected outputs.

The Victorian Dairy Industry Farm Monitor, Queensland Dairy Accounting Scheme and TasMilk60 data indicate it is difficult for farms to be in the top 25%, based on return on assets, in successive years (Table 2). Over half the farms in each survey were never in the top 25% for the years examined. Interestingly, in just a relatively short period of time (3 years), 12 farms in the TasMilk60 project and 4 farms in the Queensland Dairy Accounting Scheme managed to make both the top 25% and bottom 25% categories. In the five years of the Victorian Dairy Industry Farm Monitor project, 13 farms across Victoria have appeared in the top 25% and bottom 25% groups. An analysis of over 100 owner-operator farms in the Waikato over three years (2006/07 to 2008/09), found that only 12 farms were consistently in the top quartile for operating profit per hectare and lowest quartile for operating expenses ($/kg protein + fat) (Newman 2010).

<table>
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</tbody>
</table>

The lack of consistency in economic performance is not unusual and has been noted in other surveys and studies (Department of Primary Industries 2010b, Gloy et al. 2002, Langemeier 2010). Factors cited as reasons why farms moved in and out of the top 25% include weather and seasonal conditions, the combination of prices paid and received in a particular year, different sample sizes between years, and being displaced from the top group by other farmers who performed well that year. For the 12 farms in the Waikato, the key difference between these top performing farms compared with average
The two farms that were in the top 25% of performing farms by return on assets for four out of five years in the Victorian Dairy Industry Farm Monitor project differed in production system and size of operation. Both farms had only participated in the four most recent years of the project (2007/08 to 2010/11). The first farm was located in south west Victoria in a lower rainfall area of the region. While rainfall limits pasture growth, pasture consumption was above average for the region, and home grown feed contributed about 65% of metabolisable energy consumed. Grain feeding varied over the four year period between 1 to 2.5 t DM/cow. Total supplements fed were between 3.5 and 4.5 t DM/cow per annum, which comprised forages, by-products and other concentrates in addition to grain, and fed as a partial mixed ration using a mixer wagon and feed pad. The farm had an average herd size of 610 cows for the 4 years, producing 540 kg (protein + fat)/cow. Milk production per cow was above average relative to other south west Victorian farms in the survey. The farm managers closely monitor feed costs and have a strategy of keeping costs low by making use of pasture through grazing and conservation as silage or hay, but also using the mixer wagon and feed pad to feed cheaper purchased feeds and by-products to maintain metabolisable energy and quality of the cows’ diet. The farm managers also have a significant business focus and assess the farm’s financial position on a monthly basis.

The second farm was located in the Macalister Irrigation District of Gippsland and had a seasonal calving pattern. The farm has fertile soils for growing pasture and irrigation water allocations had been relatively high in the four years the farm has participated in the Victoria Dairy Industry Farm Monitor project. Pasture consumption per hectare has been above average during this time, but was not extremely high for the district. Home grown feed made up about 75% of metabolisable energy consumed, with grain and forage supplements contributing approximately 1.0 t DM/cow, and between 0.5 and 1.0 t DM/cow, respectively. Over the 4 years, average milking herd size was 235 cows, producing about 500 kg (protein + fat)/cow. Relative to other herds in Gippsland, milk production per cow was above average, but not exceptionally high. Stocking rate on the farm was not high compared to other farms in the survey for the region, but sufficient to achieve good pasture consumption. The business could be characterised as low input, with relatively moderate use of supplementary feed, fertiliser, machinery and employed labour. These inputs are kept at a level where the managers can be confident of a profitable response in the majority of operating conditions that they are likely to face. The farm managers were also able to combine and manage the available resources and inputs in such a way that good returns were consistently generated without making significant changes to the farm system between years. Similar to the south west Victoria farm, these farm managers have good cost control, and while no single aspect of the farm is technically optimised, very good returns on assets are achieved with limited variability between years.

Manager knowledge and skills, and ability to use resources in the most effective way for a particular set of circumstances is evidently important for the two farms described above. Both farms generated consistently high return on assets, but with different production systems and in different regions of Victoria. Both technically performed above average compared with other farms in the region, but neither achieved exceptionally high performance in any partial efficiency measure, suggesting that attention to detail in many areas is important for good economic performance. It is apparent that businesses with high returns can operate quite differently. The notion that optimising technical efficiency does not always lead to economic efficiency can be further illustrated by looking at the performance of another farm in the Macalister Irrigation District, which also participated in the Victoria Dairy Industry Farm Monitor project. Compared with the Gippsland farm mentioned above, stocking rate, pasture consumption and milk production were all higher and likely to be closer to expectations under best management practices. However, return on assets was generally lower and the farm only made the top 25% group once in the same four year period. While this particular farm could be considered technically

Figure 9: Change in feed conversion efficiency (kg energy corrected milk/kg dry matter intake) over 40 years on an irrigated dairy farm in northern Victoria.
superior, the production system means that input costs are somewhat higher and the business suffers more adversely in years when conditions and/or prices are less favourable. More items are also contracted out on this farm (sowing, silage, repairs, cow health, rearing replacements), leading to higher costs than the Gippsland farm. The labour and land resources, objectives and risk profiles of the two farm businesses in Gippsland are vastly different and both farms are successful in achieving their objectives.

The Dairy Business of the Year award, a competition run in Australia and New Zealand by a private consulting firm and a national bank, provides additional examples of the disconnect between economic performance and farm system. The business performance of the entrants are compared with their peers in the same region and the same type of business, including low, medium and high input, dryland or irrigation, with an overall Australian and NZ winner identified, and ultimately a champion Trans Tasman dairy business recognised. Return on assets is used as the key judging criteria, with weight given to technical indicators of management performance and acknowledgement of herd management, and enlightened and meritorious labour and environmental management. The category, national and supreme winning businesses have come from most dairy regions in both Australia and NZ at different times. In every region and in every year, there are dairy businesses earning returns to capital of 10% p.a. and above. Even with businesses performing well in every region every year, the diversity of locale of finalists and overall winners of each category highlights how the combination of prices and prevailing seasonal conditions will combine to favour some well managed businesses operating in some regions more than other well managed businesses, in any year. That is, there are no 'best systems'; just 'best managers', making their particular systems work best under the specific conditions experienced in a particular production year.

It is difficult to truly gauge and draw enduring conclusions about business performance from a single year, and any number of systems can perform well at various times. As Newman and Savage (2009) correctly point out, every business is unique and strategies and actions that are sound in principle may not work for every business. Activities such as benchmarking or comparative studies can be useful for diagnosing potential areas of improvement within a business; however they tell little about whether the business is performing in a manner that is leading farmers to achieve their goals and they cannot prescribe actions. Performance or return as related to system intensity or complexity means little otherwise.

**HOW DOES RISK CHANGE WITH SYSTEM INTENSITY?**

While there is not necessarily a correlation between technical performance of any single input, whole farm system return, and farm system intensity and complexity, there may be some correlation with risk. The nature of farming means risk is virtually unavoidable. However, risk is not necessarily a negative phenomenon, with profit often being the reward for bearing risk. Risk analysis in agriculture can be difficult and demanding, as farm level questions often need to be examined in a systems context (Hardaker and Lien 2005). The systems view includes biological, technical, financial and human components that all interact (Pannell et al. 2000). There may be numerous uncertain variables to be considered and dependency between variables. In addition, off farm alternatives, and risks associated with these, may need to be included in the decision analysis. Accounting for embedded risk, where some decisions depend on both earlier decisions and on the outcomes of uncertain events, also complicates the analysis. A number of techniques exist that are useful for analysing risky choices, including stochastic simulation where probability distributions of consequences for alternative decisions are determined (Hanoch and Levy 1969; Hadar and Russell 1969). The outcomes of different alternatives are compared using a utility function, the preference of the decision maker, or stochastic dominance tests, and enable the decision maker to make a good and well-informed choice.

In a case study of a dairy farm in south west Victoria, stochastic simulation was used to investigate the return and risk of some alternate futures under a cost-price squeeze (Heard et al. 2012). The farm had 570 milking cows on 233 ha of milking area, plus an additional 338 ha of non-milking area that was leased. Pasture consumption on the milking and non-milking areas were estimated to be 5.8 and 3.9 t DM/ha per annum, respectively, and was lower than expected for the region under best management practices. A number of alternative future options were developed, with the aim of ensuring business viability over the next 10 years. The options included:

1. Increasing the amount of pasture consumed on the milking and non-milking areas, and reducing the non-milking area by 100 ha.
2. Increasing the milking area to 420 ha and herd size to 800 cows, with pasture consumption at the improved levels of option 1.
3. Reducing land area and herd size by relinquishing the lease for the non-milking area and reducing herd size to 370 cows.
The associated costs involved with each option were included, and probability distributions were defined for milk price, supplementary feed prices and pasture consumption. A large number of iterations were run to create a distribution of possible outcomes for measures of interest, including nominal internal rate of return for the business over the 10 year period (the rate of return on the capital invested in the project over the life of the investment), and nominal end owner’s capital.

All options provided a higher nominal internal rate of return (Figure 10) and increased the value of the owner’s capital at the end of 10 years (Figure 11). Options 2 and 3, which were to effectively grow or scale back the business relative to the base farm, both generated similar nominal internal rates of return, but the variability in nominal internal rate of return for option 3 was slightly greater (standard deviation 1.4% versus 1.2%). The median value for the nominal owner’s capital i.e. the money available to the farm owner at the end of the tenth year was significantly greater for option 2 (increasing milking area and herd numbers) compared with option 3 (reducing land area and cow numbers). However, the variability associated with nominal owner’s capital at the end of 10 years for option 2 was considerably higher (standard deviation $1.6 M versus $0.8 M), indicating greater risk associated with this option. (Heard et al. 2012) note that ‘While this option appeared more profitable than the others considered, the risk of adopting such a system should not be ignored. Inherently, the risk with this option is amplified by the sheer scale of operation and consistently achieving high standards of management becomes a challenge.’ Option 3 was relatively less risky, but is not without challenges; good pasture and grazing management is needed. However, the need to source employed labour is somewhat reduced. The findings of this study show that while return in terms of owner’s equity could be considerably increased under a larger farming operation, risk or variability in owner’s equity was also greater. A similar internal rate of return could also be achieved with a smaller sized business, providing farm managers at different stages of career, different risk preferences or family goals with a range of future options that can be profitable.

Figure 10: Nominal internal rate of return (%) for a case study farm in south west Victoria and alternate development options (J. Heard pers. comm. 2012).

Figure 11: Nominal owner’s capital ($) at year 10 for a case study farm in south west Victoria and alternate development options (J. Heard pers. comm. 2012).

Using a similar case study and stochastic simulation approach, the profit and risk of options for a dairy farm in northern Victoria were examined (Myers et al. 2012a). The farm had changed its feeding system to manage the dry seasonal conditions between 2002/03 and 2008/09, however water availability and allocations have increased in recent years prompting a review of the system. The farm had a herd size of 650 cows, approximately 360 ha of milking area, and milk production of 527 kg (protein + fat)/cow. The farm grew annual pasture, lucerne and maize, and had a feedpad where a mixed ration was fed as part of the cows’ diet. Several alternative futures under an environment where water availability was increased relative to the base farm, were developed, two of which were to:

1. Extensify the base farm system: This involved reducing herd size to 500 cows, removing the mixed ration from the diet, and introducing
perennial pasture onto the farm.

2. Intensify the base farm system: This option increased herd size to 1000 cows, while maintaining the same feeding system as the base farm. It was assumed milk production increased, as the mixed ration would comprise a greater proportion of the cows’ diet and the farm could obtain volume incentives from the milk company.

Probability distributions for milk price and supplementary feed prices were used to test the potential impact of fluctuations in these inputs. Distributions for outputs including nominal internal rate of return for the business over the 10 year period and nominal owner’s capital, were constructed. The two alternative futures improved economic performance compared with the base farm, with the median value for nominal internal rate of return and owner’s capital at the end of 10 years greater for both options (Figures 12 and 13). Variability for option 1 (extensify) was smaller for nominal internal rate of return and slightly greater for end owner’s capital than the base farm, whereas variability for option 2 (intensify) was much greater than the base situation for both nominal internal rate of return and end owner’s capital. Similar to the south west Victoria case study, the more intensive option could provide higher net wealth and return at the end of 10 years, but the system would also experience greater variability and risk. Purchased feed made up a larger proportion of the cows’ diet in the intensified system, increasing exposure of the business to fluctuations in the feed market. Option 2 was also particularly sensitive to changes in milk price, and profitability of this system relied on the ability to attract a premium for milk produced. Larger and more intensive operations also face greater risk around labour availability and skills.

Figure 12: Nominal internal rate of return (%) for a case study farm in northern Victoria and alternate development options (B. Myers pers. comm. 2012).

The two examples described suggest that more intensive or complex farm operations may be exposed to increased risk and variability in profit and return relative to less intensive or smaller operations. However, farmers have options to take action, manage, shift or reduce the impact of risks to their businesses, for example through the use of the temporary water market, different financial borrowing strategies, farm insurance, and forward contracts for inputs or outputs. Using such measures means that what appear to be riskier systems can also be very profitable. A farm in the west Gippsland region was used to assess the cost of production and profitability associated with different calving systems (Myers et al. 2012b). The farm had a split calving system where 90% of the herd calved in autumn and the remaining 10% in spring. The base farm generated return on assets of about 6%. The costs, inputs and production of this autumn-dominant calving system were compared to an alternative future which involved operating essentially the same system, but as a spring-dominant calving pattern where 90% of the herd calved in spring and 10% in autumn. Farm performance was analysed over a 10 year period using stochastic simulation and probability distributions for key inputs.

The autumn-dominant calving system had a higher median operating profit, nominal internal rate of return and increase in net worth at the end of the 10 years, relative to the spring-dominant calving system (Table 3). The feed and variable costs in total and per kg protein plus fat were higher for the autumn-dominant calving system compared with the spring-dominant calving system. However, this was offset by the higher income received. The milk production pattern for the autumn-dominant calving herd meant it qualified for a milk payment scheme where incentives are paid.
if a certain proportion of milk is produced in months of traditionally lower milk production (late summer, autumn and early winter). In this case, looking at costs of production would not have revealed the full story on economic and financial performance of this farm.

**Table 3:** Indicators of performance for a farm in west Gippsland with an autumn dominant calving system compared to an alternate system with a spring dominant calving system

<table>
<thead>
<tr>
<th></th>
<th>Base farm (Autumn dominant calving system)</th>
<th>Alternate system (Spring dominant calving system)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Median nominal internal rate of return (%)</td>
<td>8.9%</td>
<td>7.1%</td>
</tr>
<tr>
<td>Milk price ($/kg protein + fat)</td>
<td>$5.20</td>
<td>$4.70</td>
</tr>
<tr>
<td>Total gross income ($)</td>
<td>$1,608,000</td>
<td>$1,415,000</td>
</tr>
<tr>
<td>Variable costs ($)</td>
<td>$774,000</td>
<td>$720,000</td>
</tr>
<tr>
<td>Feed costs ($)</td>
<td>$618,000</td>
<td>$564,000</td>
</tr>
<tr>
<td>Median annual operating profit in Year 4 ($/kg protein + fat)</td>
<td>$315,000</td>
<td>$184,000</td>
</tr>
<tr>
<td>Total gross income ($/kg protein + fat)</td>
<td>$5.90</td>
<td>$5.20</td>
</tr>
<tr>
<td>Variable costs ($/kg protein + fat)</td>
<td>$2.80</td>
<td>$2.60</td>
</tr>
<tr>
<td>Feed costs ($/kg protein + fat)</td>
<td>$2.30</td>
<td>$2.10</td>
</tr>
<tr>
<td>Median annual operating profit in Year 4 ($/kg protein + fat)</td>
<td>$1.15</td>
<td>$0.70</td>
</tr>
</tbody>
</table>

While more intensive systems can generate higher return, but often at greater risk, the timing and quality of decision making can mean the extent of variation in return and profit is less than expected (Gibb 2003). When the impact of the 2002/03 drought in the northern Victorian irrigation region was assessed, higher input systems were predicted to have larger deficits in net cash flow for the drought year and several subsequent years (Armstrong et al. 2005). In practise, some farmers operating such systems had relatively moderate declines in net cash flow. (Armstrong et al. 2005) comment that ‘This does not necessarily mean their systems were lower risk. It appears that more proactive and skilful decision-making reduced the impact of the drought. Conversely, some low input farmers experienced relatively high NCF (net cash flow) deficits’. Again, the importance of farm operator skills and knowledge of their own system is vital and risks can be managed.

**CONCLUSION**

In the last few decades, increased use of supplementary feed, fertiliser, irrigation and other inputs, but also declining farm numbers and increased total and per cow milk production, have contributed to increased farm system intensity in Australia and New Zealand. While both countries classify farms into a system of five feed production types, resource availability, input use, farm family objectives, and operator skills and management ability mean that almost every dairy business is unique. Using a variety of farm surveys, datasets and existing studies, this paper has examined if and how farm performance (considered as production or technical performance), return (return on assets or operating profit), and risk (variations in economic performance over time) change as dairy systems increase in intensity. No single partial technical measure was a strong indicator of return on assets or farm profit. While some positive correlations could be seen with some measures of technical performance and system intensity, significant variability in economic performance was observed. Therefore, profitable businesses are more about the skills of the farm operator and the capability of the management team, and less about the system that is being run. Farms that performed well and generated high return on assets or profit in one year do not necessarily do so year after year. Reasons for this include the combinations of prices paid and received in different years, changes made to the farm system which require a period of time to be incorporated into the existing business, seasonal conditions, and random events that may occur after a decision is made on the best information available at the time. Risk in farming is almost unavoidable. There appears to be some association between increasing farm intensity and risk, however the risk preference of a farm operator is important. A person who is risk averse will be willing to forgo some expected return for a reduction in risk, but increased risk often yields higher return, and strategies can be taken to manage or reduce risk to farm businesses. Farmers contemplating changes to their businesses that alter system intensity may find it valuable to examine the change in return with system intensity, but ultimately looking at farm economic performance is futile without consideration of a farmer’s goals and preferences. Decisions based on maximising profit or
expected outcome will not always lead to the option that is most preferred. Farm operator management skills and ability is critical to successful businesses, and many production systems (low or high intensity) can technically perform well and offer good return and profit.

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Precision dairy farming in Australasia: adoption, risks and opportunities

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SHORT SUMMARY

The use of sensor-derived information and automation to fine tune farm management is increasing. Hypothetically these technologies offer significant gains in labour efficiency and quality of decision making. In practice, variable technical performance, a lack of training and support, and systems that are not integrated frustrate farmers and impede more rapid progress. A co-ordinated and co-operative approach involving farmers, technology developers and industry leadership is required to ensure dairy farmers, and the wider industry, captures the opportunities presented by precision dairy farming.

ABSTRACT

Dairy farm management has historically been based on the experiential learning and intuitive decision-making skills of the owner-operator. Larger herds and increasingly complex farming systems, combined with the availability of new information technologies, are prompting an evolution to an increasingly data-driven ‘precision dairy’ (PD) management approach. Automation, and the collection of fine-scale data on animals and farm resources, via precision technologies can enhance efficiency and decision making on dairy farms. The proportion of dairy farmers using this approach is relatively small (between 10-20 percent of farmers), however industry trends suggest a continual increase. Australasian PD farms have reported both positive and negative stories regarding the approach but to date there has been little industry attention or co-ordination in Australia or New Zealand. A series of workshops was held in late 2011 between industry-good representatives, researchers and farmers, from Australia and New Zealand, to discuss the opportunities and risks associated with PD. To take advantage of the emerging PD opportunity the trans-Tasman workshop group suggested five focus areas including: industry-good co-ordination and leadership in PD; working to define the on- and off-farm value of PD; improving the technology available to farmers; integration of PD within farming systems for improved management; and developing learning and training initiatives for farmers and service providers. Action in these focus areas will enable future dairy farmers to implement the PD approach with enhanced confidence and effectiveness.

Keywords: information technology, farm management, dairy system evolution

PRECISION DAIRY

Origins of the concept and definition

Precision agriculture (PA), and precision farming (PF), are terms representing the use of information and communication technologies (ICT) in managing farm enterprises with the former generally related to arable and horticultural (including viticulture) enterprises, and the latter to livestock industries. The concept of precision farming has been a distinct field in research and farming practice since the 1980s (Bramley 2009) and generally describes a practice initially built on the back of information technology and global positioning systems (GPS) (Pierce and Nowak 1999; Bootle 2002; Blake et al. 2003; Bramley 2009). A form of information-intensive agriculture (Fountas et al. 2006; Schellberg et al. 2008), it involves targeted decision making, and aids farmers in making the ‘correct decision’ while taking into account spatial and temporal variation in their production systems (Bramley 2009). To date, the focus of most research and development has been on the application of precision technologies in arable and horticultural enterprises. However, livestock systems have received increased attention in recent years, for example, pig and poultry (Banhazi and Black 2009), sheep (Atkins et al. 2006) and dairy (Bewley 2010; Eastwood et al. 2012). Most recently, an outcome of the European Union Framework 7 BrightAnimal project on precision livestock farming, has been the suggestion that PF be renamed as ‘Smart Farming’ (Smith 2011).

Precision management of dairy systems has existed in science literature for around a decade, with reference to its use in countries such as Germany (Wendl and Schön 2002; Schulze et al. 2007), Israel (Katz et al. 2007) and New Zealand (Yule et al. 2008). Electronic identification (EID) forms the core feature of precision
dairy (PD), much as GPS acts as the backbone of PF applications (Wendl and Schön 2002). The definition of PD can vary depending on the context in which it is applied, but consistently focuses on the individual animal. For example, Bewley (2010) defines PD as ‘the use of technologies to measure physiological, behavioural, and production indicators on individual animals to improve management strategies and farm performance’. He also states that the objectives are to maximise individual animal potential while facilitating early disease detection and minimising medication use. (Katz et al. 2007) discussed the goal of animal-focused data collection stating that it ‘enables the on-going control of production, animal health and welfare’ particularly with respect to early diagnosis and retrospective analysis of performance. (Uzmay et al. 2010) took a broader approach stating that the aim is to ‘control production processes continuously’ to achieve ‘optimum outcomes in profitability, health, quality and product safety, animal protection, and environmental protection.’ Authors such as Laca (2009) provide a more theoretical view of a future livestock farming system where the positions and behaviours of animals are monitored in the landscape with remote herding and feeding systems combined with health management and traceability. Such a system provides an integrated technology-driven approach, but represents a distant prospect for dairy farmers – with little current consideration for value proposition or co-development.

Historically, PD has been a term used by researchers, rather than farmers (Eastwood 2008) and its adoption has been based on distinct technologies for discrete aspects of farm management (for example, individual feeding) rather than in a coherent farming system and supply chain setting. PD constitutes a shift in management practice, as opposed to a dramatic step change and represents a ‘datafication’ of dairying, where the traditional intuition-driven management styles of farmers (Eastwood and Kenny 2009; Nuthall 2012) merge with decision-making based on data.

The concept of individual management of animals and natural resources is not unique to PD. Farmers of small dairy herds (around 150 cows or fewer) have historically been able to identify differences in production or health and account for them in their management by visual means (Bramley 2009). Precision dairy facilitates this management style for farmers of modern dairy systems which are increasingly larger in herd size and more complex in terms of feeding inputs, resource management, animal health, and human resource management. To apply PD with a sole focus on the animal overlooks other aspects within the farm system, such as labour and the feedbase, both of high importance in Australian and New Zealand dairy systems (García and Fulkerson 2005; Clark et al. 2007). In pasture-based dairy systems where pasture utilisation, pasture quality and costs of production are key profit drivers (Little 2011; DairyNZ 2012) the PD definition needs to be expanded to include the production and management of home-grown feed.

### Precision dairy in an Australasian context

Participants in trans-Tasman workshops (see later section) were asked to describe what constitutes a PD farmer. Some responses that reflect the thoughts from the group are presented in Table 1. The responses provided by participants were aligned to main themes of scale, distinctiveness, management, data, and decision making (Table 2). The consensus amongst the group was that PD relates to activities on-farm (including the networks that exist around farmers) and that it represents an evolution in dairy farming practice – rather than a distinct genre of dairying.

<table>
<thead>
<tr>
<th>Table 1: A selection of statements from participants in a joint DairyNZ and Dairy Australia workshop in 2011 when asked to describe what constitutes precision dairy farming</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Descriptions of a precision dairy farmer</strong></td>
</tr>
<tr>
<td>‘A farmer that makes proactive rather than reactive decisions’ and ‘uses measurement technologies to make informed management decisions and system changes’.</td>
</tr>
<tr>
<td>‘Actively measures pastures and allocates feed based on feed available, growth rate and pasture cover targets; automates herd records and utilises this data for management decisions during milking and other animal health activities’.</td>
</tr>
<tr>
<td>‘Makes decisions at the individual (animal, paddock) level rather than at the herd level, where appropriate. Data are continuously collected but the farmer is alerted on a needs to know basis (e.g. effluent system management) - monitoring then act role. Uses technology to drive business performance through better decision making’.</td>
</tr>
<tr>
<td>‘Uses several technologies in the dairy to assist milking. Has a herd data management software program and uses it effectively to support decisions. Has the capability to individually manage cows e.g. draft them for specific procedures, feed them grain / concentrates to individual milk production’.</td>
</tr>
</tbody>
</table>
Table 2: Aggregated themes from workshop participants on features of precision dairy (PD) farming

<table>
<thead>
<tr>
<th>Theme</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Scale</td>
<td>The focus is on individual animals, fine scale aspects of farm resources, management by exceptions, and covers the whole of the enterprise (i.e. applicable across the farm system)</td>
</tr>
<tr>
<td>Distinctiveness</td>
<td>There was a discussion on PD as a separate farming approach versus part of the ongoing evolution of dairy systems. The general consensus was it represents a part of the evolution.</td>
</tr>
<tr>
<td>Management</td>
<td>PD is based around labour management, optimal production systems and in the end has to be focussed on value on farm.</td>
</tr>
<tr>
<td>Data</td>
<td>PD is based on data which are recent, relevant, and repeatable.</td>
</tr>
<tr>
<td>Decision making</td>
<td>The main benefits are enhanced control, proactive management, timely decision making, informed and improved decision making.</td>
</tr>
</tbody>
</table>

Therefore, the definition for PD farming used in this paper is: ‘the use of ICT for improved control of fine-scale animal and physical resource variability to optimise economic, social, and environmental dairy farm performance’ (Eastwood et al. 2012). Under this definition, a farm using automatic milking technology is not a PD farm because of the robot itself, rather it is through the use of EID, selection/drafting gates, milk sensors and individual feeding capability to tailor management to individual cows which signifies a PD approach.

In the remainder of this paper the trends in adoption of PD farming technologies are described, the risks and opportunities examined. The outcomes from a 2011 trans-Tasman PD workshop series are highlighted, with five areas to focus on to ensure the Australian and New Zealand dairy industries overcome the challenges and capture the opportunities of PD.

**PRECISION DAIRY PRACTICE IN AUSTRALIAN AND NEW ZEALAND FARMING SYSTEMS**

**The use of precision dairy technology in Australia**

The current number of farmers who could be considered PD farmers is difficult to ascertain. However, several surveys in the past five years provide some indication of the extent of use of relevant technologies. A study for the CowTime programme (Watson 2009) asked 300 respondents, approximately 4% of the industry, about their technology use in the dairy shed and compared to a 2004 survey. Of farmers surveyed, 19% routinely used EID in their milking system, up from 13% in 2004, with 46% of these being in rotary systems. Of those using EID, 65% used auto-drafting (same as 2004) and 91% used computer assisted feeding (75% in 2004); 40% also used automatic cup removers, up from 28% in 2004.

(Mackinnon et al. 2010) surveyed 307 dairy farms throughout Australia in 2008/09. They found that where respondents used a computer for their business it was primarily for bookkeeping or financial matters (90%), and also internet/email, recording of milk production and breeding records. Approximately a quarter used EID linked to a computer and almost 20% used a computer for feedbase related records (pasture/crops/irrigation). The use of in-dairy precision technologies by shed type is shown in Figure 1. The adoption of PD technologies was greatest among farmers using rotary dairies. Based on overall numbers, this survey indicated that 11% of herringbone or rotary users also had milk meters, 24% had auto-drafting, 48% auto-teat spray and 43% automated cup removers.

The use of automated milking systems has seen a rise in recent years, with 18 farms operating in 2012. This is expected to rise slowly in the next five years, and currently represents only 0.2% of Australian farms. Based on these numbers, and taking the use of EID and milk meters as a guide, it is likely that the number of PD farmers falls between 10–20% of the Australian dairy industry. No information has been found relating farm size or performance with uptake of these technologies in Australia.

![Figure 1: Automation by shed type, 2008–09 (Mackinnon et al. 2010).](image-url)
The use of precision dairy technology in New Zealand

In 2008 DairyNZ commissioned a phone-based survey of a cross section of New Zealand dairy farmers about their milking practices (Cuthbert 2008). The survey gathered responses from 532 dairy farmers (252 with rotary dairies and 280 with herringbone dairies) from a total dairy farmer population of around 11,000 farms. The responses give some information about the extent of use of PD technologies in the NZ dairy industry.

In a weighted sample across both types of dairies there was moderate use of some basic labour saving technologies such as automated cup removers (18%) and automated teat sprayers (18%). However, only 5% of farmers said that they had electronic identification (EID) tags and 4% stated they had auto-drafting, auto-weighing or used herd management software in the dairy. None of those surveyed used automated heat detection tools and only 2% used electronic milk meters or in-line mastitis detectors. In-bail feeding was relatively popular with 23% using it. However, as indicated by the low use of EID, 85% of respondents used a flat rate feeding system. When examining the results by type of dairy (rotary or herringbone) it was apparent that farmers with rotary dairies had invested in more technologies (Table 3). In particular, the use of automated cup removers, teat sprayers and in-bail feeding was higher, as was the use of auto-drafting. Use of EID, the backbone of PD functionality, was four times higher in rotary dairies and there was six times more use of herd management software in the dairy. Highest on the ‘wish list’ for technologies were: an auto-drafting system (38% of farmers), cup removers (23%), in line mastitis detection (16%), teat sprayers (16%) and EID (14%). In general, this survey highlighted that the use of devices that might be considered PD technologies were more focussed on labour saving than information collection.

<table>
<thead>
<tr>
<th>Technology</th>
<th>Weighted total sample</th>
<th>Herringbone</th>
<th>Rotary</th>
<th>Rotary* (2010 survey)</th>
</tr>
</thead>
<tbody>
<tr>
<td>In-bail feeding</td>
<td>23</td>
<td>18</td>
<td>43</td>
<td>84</td>
</tr>
<tr>
<td>Teat sprayer</td>
<td>18</td>
<td>10</td>
<td>49</td>
<td>97</td>
</tr>
<tr>
<td>Cup removers</td>
<td>18</td>
<td>9</td>
<td>54</td>
<td>100</td>
</tr>
<tr>
<td>Walk-over weigher</td>
<td>4</td>
<td>4</td>
<td>3</td>
<td>45</td>
</tr>
<tr>
<td>EID tags</td>
<td>5</td>
<td>3</td>
<td>13</td>
<td>100</td>
</tr>
<tr>
<td>Auto-drafting</td>
<td>4</td>
<td>2</td>
<td>11</td>
<td>100</td>
</tr>
<tr>
<td>Milk meters</td>
<td>2</td>
<td>1</td>
<td>6</td>
<td>100</td>
</tr>
<tr>
<td>Heat detection</td>
<td>0</td>
<td>0</td>
<td>0.5</td>
<td>30</td>
</tr>
<tr>
<td>In line mastitis</td>
<td>2</td>
<td>2</td>
<td>4</td>
<td>6</td>
</tr>
<tr>
<td>Herd management software in the dairy</td>
<td>4</td>
<td>2</td>
<td>13</td>
<td>100</td>
</tr>
<tr>
<td>Herd management software in the house</td>
<td>74</td>
<td>72</td>
<td>83</td>
<td>55</td>
</tr>
<tr>
<td>PDA or Palm pilot</td>
<td>21</td>
<td>19</td>
<td>28</td>
<td>26</td>
</tr>
</tbody>
</table>

* Results from this 2010 survey are from the rotary benchmarking project described by (Jago et al. 2011). Participants were required to have EID, milk meters and herd management software, therefore these data were from a selected cohort of farmers and cannot be considered representative of all rotary users in the New Zealand dairy industry.
More recently a DairyNZ project on milking management in 80 dairy farms using rotary platforms (Jago et al. 2011) also gathered information regarding technology investment and use. In addition to benchmark data, four workshops were held throughout NZ for farmers in the study, where participants were surveyed specifically about their use of technology. Results with respect to the level of technology used are presented in Table 3. These results need to be taken in context as they represent technology use within a selected group of the dairy industry (larger farms, rotary dairies with EID), but they indicate the importance of automatic cup removers, auto-drafting and auto-spraying for many modern rotary dairies. Also, there was a high degree of in-bail feeding being used and a relatively high use of walk-over weighing. The main reasons participants gave as driving their technology investment were reduction of labour requirements, making milking easier, attracting/retaining staff and efficient feeding. The aspects of precision technology where information is used in decision making (identification of cow health, oestrus, culling) were less important – possibly indicating lower engagement and underutilisation of potential technological benefits in these areas.

There is little quantitative information on the adoption of PD technologies used outside of the farm dairy. Hedley and Yule (2009b) described how variable rate irrigation has been developed with the aid of electromagnetic soil mapping and is now being used to improve water utilisation on dairy farms. Case studies indicated that water savings of between 10 and 20% were feasible (Hedley et al. 2009) and subsequent studies on commercial systems confirmed these levels with water savings of between 8 and 27% achieved through tailoring the irrigation to the soils (Hedley and Yule, 2012). Further savings were made by excluding non-productive areas such as race ways and lanes. Variable rate irrigation has attracted considerable interest from farmers with a significant number of new systems being built as well as kits being retro-fitted to existing irrigation equipment. One such kit was estimated to have paid for itself within the first year through water savings and by allowing the farmer to irrigate a larger area with the same water allocation and equipment (Hedley and Yule 2012).

Automated pasture measurement technologies have been developed over the last ten years. The CDax Pasture Meter™ which measures pasture covers, and is capable of mapping, has been adopted by a considerable number (an estimated 1000 units sold) of dairy farmers (Yule and Eastwood 2011). Pasture quality measurement has been actively researched and the technology now available would indicate that it is feasible to achieve this. Pullanagari (2011) described hyper-spectral sensing techniques capable of determining pasture nutritive value and (Pullanagari et al. 2012a) described multi-spectral techniques capable of the same outcome, although with a lower level of explanation. (Pullanagari et al. 2012b) also investigated the effect of seasonality on multi-spectral sensing’s ability to describe pasture nutritive value and this improved the level of explanation of data collected from commercial dairy farms in New Zealand. Although successful in the research phase this approach has not reached commercial exploitation in a fully commercial environment.

Variable rate application (VRA) of fertiliser is seen as desirable however it is proving very challenging to achieve in New Zealand, due mainly to the small (1 to 2 ha) and often irregular paddock size, the use of large machinery and rotational grazing (Lawrence and Yule, 2007; Yule and Grafton, 2010; Grafton et al. 2011). Other PA technologies however, can be used to improve the accuracy of spread which has a direct economic benefit to the farmer and contractor. For example, guidance and automatic control of the spreader has benefited and these technologies are being adopted by significant numbers of contractors. A modification to VRA, involving soil sampling of individual paddocks and tailoring fertiliser input, has been developed (Lawrence 2012). (Roberts et al. 2010) demonstrated how this can create significant savings for farmers without compromising productivity. The PA technology available on trucks capable of VRA can be utilised for this application, reducing error and improving the accuracy of spread. Most farmers adopting this approach have found it financially beneficial despite the increase in sensing requirements (Yule and Eastwood 2011; Lawrence 2012). By mid-2012 it was estimated that this technology was used by approximately 150 farms (F Calvert and M. White pers. comm.). Using GPS to track applications such as fertiliser, sprays and effluent, has the additional benefit of environmental monitoring, and is being readily adopted on New Zealand farms.

Animal tracking is an area where research as yet has not been adopted by farmers (Betteridge et al. 2009; Draganova et al. 2010); however it can be used to generate management information on cow behaviour, movement and nutrient re-distribution around the farm. Draganova described how GPS collars and sensing equipment such as activity meters and urine sensors could be used to describe the redistribution of nutrient N around the dairy farm in an unbiased way. It was reported that the technologies could be used to formulate detailed...
time budgets of cow activities and their interaction with the farm environment when expressed through GIS analysis (Draganova, 2012). The technology is changing and becoming more affordable and could therefore be adopted to detect changes in behaviour which could indicate health events such as heat detection, however data analysis is still very time consuming and further research efforts are required to streamline these processes before they could be considered suitable for use on commercial farms. Radio telemetry based location systems now cost as little as $20 per cow once infrastructure is in place, as described by Trotter (2012). The farming system value proposition of technologies such as animal tracking remains to be proven, and further co-development research with farmers is required to assess management benefits.

**Factors influencing adoption**

Internationally, the adoption of PD has been slower than expected (Bewley 2010). Similarly, the adoption of on-farm software packages across agriculture as a whole has been much slower than expected (Rosskopf and Wagner 2005). One reason is that the development of technologies has tended to be driven by availability of a technology or transferred from other industries in market expansion efforts, rather than by need (Bewley 2010). This is especially relevant for Australasian farmers as many of the technologies are of international origin and, therefore, designed for European and North American farming operations (Yule and Eastwood 2012).

In detailed case studies of 12 New Zealand farmers using a range of PD technologies and representing a range of farm sizes and farming systems, Yule and Eastwood (2012) uncovered significant challenges limiting adoption of PD in New Zealand. One challenge related to the integration of PD technologies in farm systems leading to difficulties in data exchange and the need to run overlapping systems. There was a lack of learning networks available to farmers and they tended to rely on one-on-one support from the technology provider rather than proactively learning to think about how to use their systems. Compounding this issue was a lack of interaction between farm service providers (e.g. veterinarians and consultants) and PD systems. A third issue was a lack of trust in the technology, in particular, whether the technology would perform as expected when needed and whether the data collected were trustworthy. Finally the link between PD technology and farm workforce was identified as an issue. While many benefits from PD come from labour and skills related areas, some farmers saw PD tools as a double edged sword, in some cases covering a lack of staff skills but in others leading to de-skilling of farm staff. Some farmers have reported having difficulty finding suitably skilled staff to operate these systems.

A two-year longitudinal case study of six PD farmers in Australia found that the tacit knowledge processes of dairy farmers can potentially form a disconnect between farm management practice and use of PF tools (Eastwood 2008). Steep learning curves were observed amongst the case study farmers, and the ability to use PD tools at an advanced level was dependent on the knowledge farmers were able to draw from their networks of practice which included technology suppliers, consultants, and other farmers. The learning costs (in time, lost opportunity, and sometimes reduced farm system performance) associated with PD adoption were often not expected by new users (Eastwood 2008).

In Kentucky, USA, Bewley and Russell (2010) surveyed 229 dairy producers and identified that the most common reasons for modest levels of adoption of PD technologies were not being familiar with technologies that are available (55% of respondents), undesirable cost benefit ratios (42%) and too much information provided without knowing what to do with it (36%). These were followed by not enough time to spend on technology (31%), lack of perceived economic value (30%) and too difficult or complex to use (29%).

(Bewley et al. 2010) identified the difficulty for farmers making investments in PD technologies as uncertainty around factors such as market conditions, technology performance and the impact of technology on the farming system. They used stochastic simulation of a dairy system to assess PD investment decisions. In one example, the potential use of an automated body condition score (BCS) system showed uncertain levels of benefit and was especially dependant on the current herd BCS. While farmer characteristics, market conditions and uncertainty play a role in the decision to adopt PD there are also more complex organisational factors in the PD farming innovation system (Table 4, from Eastwood 2011).
Table 4: Factors influencing uptake of precision dairy technologies (Eastwood, 2011)

<table>
<thead>
<tr>
<th>Factor</th>
<th>Examples</th>
</tr>
</thead>
<tbody>
<tr>
<td>Uncertainty in the investment decision</td>
<td>Market conditions (Bewley et al. 2010)</td>
</tr>
<tr>
<td></td>
<td>Salesman overselling</td>
</tr>
<tr>
<td></td>
<td>Uncertainty over actual benefits, knowledge of opportunities</td>
</tr>
<tr>
<td>Challenges of on-farm implementation</td>
<td>Existence of learning networks (fragmented, under-skilled, lacking knowledge)</td>
</tr>
<tr>
<td></td>
<td>Performance of technology v expectations</td>
</tr>
<tr>
<td></td>
<td>Management adaptation (routine changes, roles of people and technology)</td>
</tr>
<tr>
<td></td>
<td>Data entry, changing structures/processes to incorporate data entry, data analysis, management by exception (de Koning, 2010)</td>
</tr>
<tr>
<td>Organisational factors</td>
<td>Lack of industry RD&amp;E focus on technology integration with farming systems</td>
</tr>
</tbody>
</table>

Opportunities and risks

Potential opportunities from PD arise both inside and beyond the farm gate. Inside the farm gate farmers can achieve benefits in two areas: automation and enhanced decision making ensuring better use of scarce (or costly) resources and leading to more efficient farming (Jago et al. 2007). Outside the farm gate there are also potential benefits of PD systems amongst a variety of stakeholders. The use of automation, alerts, and data recording can contribute to quality assurance and food safety initiatives for milk companies and abattoirs. Farming consultants (nutritionists, agronomists, veterinarians) can interact with the systems by using data to feed into their own analysis, and they can add to their on-farm role by offering services in use of precision technologies and farmer training. This may include remote monitoring of performance, for example, a nutritionist may remotely monitor milk production and live weight data. Herd improvement centres can benefit from accessing daily individual milking data and other stored animal data. These on-farm databases can also be connected to industry level databases to enable benchmarking services and extensive up-to-date information for design of policy. There are also potential benefits for consumers in terms of traceability, animal welfare and knowledge of product history.

Figure 2: The two general areas of precision dairy (PD) benefit linked to examples of associated potential positive and negative implications (Eastwood, 2011).

Success of PD in any given farming system is dependent on a complex interaction of factors and, according to Eastwood (2011) PD can have positive and negative impacts on the farm business (Figure 2). Labour and skills support can lead to labour savings, an overall lower skill requirement in staff and a reduction in the less desirable jobs on farm. However, some unintended consequences can include a negative skill loop where key skills and capability, such as animal husbandry, are degraded. Knowledge silos about how to best use precision technologies can be created, or staff can be intimidated by the learning involved with the new technologies and their application. The area of management enhancement can also have positive and negative features. On the positive side, the use of precision tools can aid management practice that is more efficient, flexible and proactive. Potential negative outcomes can involve poor quality of data, implications of data overload, poor connectivity and
integration, and overconfidence in data leading to use at inappropriate scales of decision making, for example, using milk conductivity measurements as a sole guide of mastitis, or milk yield data to guide highly precise in-shed feeding.

Labour and skills support is often the main driver for investment in precision technologies and provide a good point of entry into these new technologies. As shown previously in Eastwood (2008), the in-shed systems can be in the form of ‘entry-level’ or ‘advanced’ – with entry level systems having less sensor equipment and collecting fewer data and, therefore, being more focused in their functionality. This lower functionality can make the step to PD farming easier for some farmers through fewer data to input or analyse. Management enhancement is where the less tangible, but potentially more valuable, benefits from PD can be achieved. From previous studies, it appears that this functionality is underutilised, partially because it requires more change in farmer routines, mind-set and skills.

Precision dairy technology has significant potential benefits for the New Zealand dairy farm that has experienced growth in farm size, scarce labour and increasing management complexity (Jago et al. 2007; Yule and Eastwood 2011). However, in this emergent phase for PD systems the benefits are being hobbled by issues around technology and management adaptation, ICT skills and engagement, uncertainty of how to unlock benefits, staff-technology interactions and a paucity of capability in the service sector. Future challenges were identified in development of new technologies which align with the needs of farmers in pasture and resource management, and a need for consideration of new policies to protect farmer’s privacy and data ownership (Yule and Eastwood 2011).

In the final section of this paper the outcomes from a series of PD workshops with participants including Dairy Australia and DairyNZ, farmers and researchers are outlined. Five main areas were identified that require focus if the benefits of PD farming are to be realised by a large portion of dairy farmers.

FACING THE CHALLENGES OF PRECISION DAIRY

The increased use of PD in both the Australian and New Zealand dairy industries has heightened the awareness of industry-good organisations such as Dairy Australia and DairyNZ to the potential, as well as the challenges, inherent in this evolving farming practice. In late 2011 and early 2012 a series of workshops and surveys were conducted with a group representing DairyNZ, Dairy Australia, researchers and farmers (Eastwood and Jago 2012). Participants were selected according to their experience in the area of PD either as farmers using some of the technology as well as one choosing not to use PD technologies, researchers in the field, or relevant Dairy Australia/DairyNZ representatives. The process used is outlined as follows:

a) Online survey 1 - Pre workshop survey of PD as defined by workshop participants
b) Workshop 1 – Hamilton, NZ (15 November 2011)
   Specific objectives:
   • Identify issues and opportunities for PD farmers
   • Identify key themes
   • Identify industry good role and response
c) Online survey 2 – Review of key themes from workshop 1
d) Workshop 2 – Melbourne, Australia (8 December 2011)
   Specific objectives:
   • To discuss major research development and extension activities and goals in the PD area
   • Identify research development and extension gaps and gaps in capability
   • Develop a position on whether there is a need for a strategy and collaboration
e) Online survey 3 – Building on key themes from workshop 2 and ranking of priority focus areas
f) Final reporting and phone meeting between DairyNZ and Dairy Australia representatives

The outcome of the workshop discussions identified two high level opportunities of PD within the farm gate (Eastwood and Jago 2012). The first was ‘Good farmers making better decisions’, an area considered to be the significant research challenge. This aspect reflects the potential of PD to support farmers to manage their farming systems more effectively than they could do intuitively. This opportunity particularly applies to resource-use (especially feed, water and fertiliser) and has an approach of making every cow (or paddock or resource input) count. The second opportunity identified was ‘enabling farmers to scale up and/or speed up’ through facilitation of agile farming systems with an ability to adapt and build capability faster. Dairy farmers face pressures which require them to have the ability to change rapidly as system changes occur and the scale of operation changes. PD potentially aids this flexibility; an example given in the workshops was that people working on farms need to perform like a farmer with 30 years’ experience after only three years of practice, which requires improved repeatability and consistency.
This concept of enhanced flexibility and adaptability can be applied within an existing system and/or when shifting system type (e.g. from system 1 to 3 using the DairyNZ farm system definitions, Hedley et al. 2006).

To take advantage of the emerging opportunity of PD, five focus areas were proposed from the workshop process (Figure 3) to help define the potential and practice of PD while ensuring the technology fits with farming needs and developing sufficient industry capability for its effective implementation. The overarching focus area highlights a requirement for better co-ordination and leadership in each of the potential activity areas. Currently, technology developers and retailers are the primary actors in respect to the provision of knowledge and support for PD, however their business models are focussed on technical support, rather than farming systems support (Eastwood and Jago 2012). There is a need to accelerate the learning and training of farmers in adapting to PD systems, and this requires industry-good co-ordination action. A need also exists to ensure technology developers are well informed of industry priorities. This includes leadership on data integration (on-farm and off-farm), matching farmer needs to technology development, integration of technology (via standardisation), testing equipment performance, and development of training programmes.

**1. COORDINATION AND INDUSTRY LEADERSHIP IN PRECISION DAIRY RD&E**

| 2. Define the on and off farm value of precision dairy | 3. Improve the technology | 4. Integrate precision dairy within farming systems for improved management | 5. Develop learning and training for farmers and service providers |

*Figure 3: Proposed focus areas developed through joint workshops in 2011 with DairyNZ and Dairy Australia representatives, farmers and researchers (Eastwood and Jago, 2012).*

**Define the on- and off-farm value of precision dairy for farmers and service providers**

While PD is already being used on many Australasian dairy farms, the value proposition for investment is not yet robust. Issues around trust in technology have also been identified (Yule and Eastwood 2011) which are related to technology performance, user expectations of performance, and understanding of technological capabilities and limitations. Also the impact of farm scale needs to be considered in respect to how it changes approaches to management (i.e. under what conditions would you introduce this technology?). There is a need for independent guidance and information to allow farmers to make informed investment decisions. By understanding key management decisions on farm, and identifying where farmers use information, the areas where information is required for management can be determined and the areas of most value for farmers identified. The potential value proposition for service providers in the PD space, beyond supply of a technology, is also currently unclear.

**Improve the technology**

The area of PD technologies is fast moving and currently involves many products and companies who range from local to multinational. Technology improvements in areas such as performance, compatibility, integration with farming systems, and ability to modularise are required. It is increasingly recognised that a participatory approach is necessary to ensure technologies are fit for purpose and the end-user farmers are involved early in the design phase of the technology development cycle (Ashby and Sperling 2008; Klerkx and Leeuwis 2008; Eastwood et al. 2012).

One area that requires focus is the provision of objective information on technology performance in the field. This information would be useful for farmers to make more informed investment decisions, to establish reasonable expectations and to inform technology developers leading to better products. For example, in the case of mastitis detection technologies there is no agreement on evaluation protocols and a lack of focus on the practical uses of the technologies (Kamphuis et al. 2011). Some comparative data have recently been published for heat detection systems (Kamphuis et al. 2012), however similar issues exist with a lack of agreement on methodology.

**Integrate precision dairy within farming systems for improved management**

Precision dairy does not replace the need for skills in animal husbandry or agronomy, rather it can be viewed as an enabler for enhanced management practice. It can be applied at a micro or macro
management scale and can be used to avoid tasks, automate tasks, or advance management practice. PD provides the opportunity for managers to become ‘exceptional’ managers, for consistent performance and the continuity of that performance even when there is staff turnover. PD also provides the opportunity for greater risk management. Enhanced management can only be possible if the underpinning farm planning structures are already robust, in that the farmer must have defined objectives and know what they need to monitor. Hence, the importance of linking PD with skills in determining the planning, management and review processes on farm. It is critical to identify how good farmers can make better decisions with the assistance of PD technologies and examine moving the focus of PD from just measurement to management using the data.

Develop learning and training for farmers and service providers

Precision dairy presents both specific learning challenges and more general skill requirements. Issues of learning and training relate to ICT skills, staff skills, the capability of technology providers and the wider service sector, in addition to more specialised skills in interpreting/analysing data for farm system management. Questions surround the matching of workforce capability (on- and near-farm) with value proposition across different farming systems. Currently, the use of PD technologies on farm is progressing ahead of the industry skillbase in PD best practice. A long term view is required to build foundation skills in ICT while also building capability in data-driven farm management practice. The role of service providers is vitally important in many agricultural innovation systems, and this is the case with PD. Service provider capability exists in areas such as nutrient management, animal nutrition, grazing management from those who sell products through to agricultural consultants and extension agents. For PD to meet its potential and provide real value to farmers there needs to be an expansion in understanding and capability in the relevant service sector agents.

CONCLUSION

Precision dairy is an emerging opportunity for the dairy industry as a series of tools to address the pressures of human resource management, increasing scale, and heightened consumer awareness of environmental and animal welfare issues. PD has the potential to improve management decisions beyond what is possible through intuition and experiential management processes alone, and to reduce the adaptation period when farmers change systems. The experience of early PD users reveals significant hurdles to overcome if these opportunities are to eventuate across the industry. Currently, technology developments and support of their on-farm use is undertaken by commercial companies, resulting in a relatively disjointed approach to building confidence and understanding amongst farmers of the potential and practical application of PD. There is a clear need for farming systems support. A co-ordinated approach is required to link the efforts at an industry-good level with the needs of farmers and the skills and knowledge of commercial technology suppliers. Co-ordinated action in the five focus areas outlined in this paper will enable dairy farmers to implement the PD approach with enhanced confidence and effectiveness in the future.

ACKNOWLEDGMENTS

The authors would like to thank the participants of a workshop series held to develop a joint Dairy Australia and DairyNZ strategy for PD. These included farmer representatives, investors, extension specialists and researchers from Universities and industry good organisations.

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The evolving extension environment: implications for dairy scientists

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ABSTRACT

This paper provides a case for developing an adaptive extension platform for the dairy sector in Australia and New Zealand that supports evolving dairy farm systems. Drawing on international extension and agricultural innovation system literature and empirical research, significant challenges for agricultural productivity extension were identified that have constrained progress in extension professionalism. These include: the variation in public sector engagement in extension influencing traditional pathways of professional development; the diversity of extension providers away from single organizations with stable visions and ways of acting to multiple organizations and businesses with diverse interests in extension and change; and a relatively uncoordinated approach to define the new extension roles, functions and professional accreditation requirements. Three areas for development are proposed, including: 1. A professional development strategy that incorporates: a) an understanding of the new professional situations extension works within, b) leadership in cross-industry and cross-sector co-ordination concerning the nature of the changing client in RDE&E and, c) clear priorities for extension; 2. A professional development plan that incorporates a workplace learning approach; and 3. For extension specialists to be engaged in defining research priorities, the change agenda and suitable pathways for change alongside other professional groups.

INTRODUCTION

Dairy farm systems continue to evolve in Australia and New Zealand as a consequence of farmer responses to new technologies and changes in their operating environment, including new market requirements and business volatility. These changes in dairy farm systems, including changes in their complexity, diversity and social arrangements require an adaptive and responsive research, development, extension and education (RDE&E) system that supports dairy farmers and those who provide services to them.

At the same time, the extension landscape continues to change and evolve in both countries. In Australia, changes in the institutional environment have seen different public and private organisations modifying their roles and priorities for extension. The pathways in which extension capacity is built has also changed and the professional development of people in the RDE&E system in better understanding whole farm systems is considered an increasing need.

The challenges in delivering extension services to farmers managing changing farm systems have escalated (DPIV, 2008, 2011). At the same time, there are equivalent challenges in achieving the required level of integration between research, development, extension and education in an environment where needs are changing and resources are scarce. The need for an adaptive extension “platform” is essential. A platform can be a structure (e.g. a Memorandum of Understanding, other contractual or structural arrangements) and/or a way of operating (e.g. collaborative, co-ordinated).

This paper aims to present the intellectual basis for an adaptive extension platform for the Australian and New Zealand dairy sector and a discussion of the implications for dairy scientists operating within the dairy RDE&E continuum.

BACKGROUND

Extension is broadly defined as the process of enabling change in individuals, communities and industries involved in the primary industry sector and with natural resource management (Seln, 2006). Moving beyond conceptualisations of extension as “extending knowledge and information”, extension is considered to have a wider role in the whole RDE&E continuum as part of what are increasingly recognised in international literature as “agricultural innovation systems” (AIS) (Hall, 2006; Sorensen, 2011). In AIS, research, extension and education are part of a broader network of actors that include practitioners such as farmers and community members, processing sector groups, agricultural retailers, policymakers, consumers and civic advocacy groups – all potential sources of innovation and change and contributing to it (Jiggins, 2001; Röling, 2009; Nettle et al. 2010; Eastwood et al. 2011, 2012). In AIS, the extension role is considered to perform essential mediating and translating functions in innovation (Klerkx and Leeuwis, 2008, 2009; Howells, 2006).

Given these wider roles for extension as a profession and practice, it is important to consider who is performing extension roles now and how this is changing; the nature of the changes extension seeks
to facilitate; and, the different range of beneficiaries of change (e.g. government & society, the environment, farmers). In the change area of agricultural productivity, the extent of change over the last 20 years in extension strategy and delivery, particularly with respect to private and public contribution and roles, are worthy of particular focus in this paper. Whereas in New Zealand, agricultural productivity related-extension has been fully privatised since the late 1980’s, Australia has seen highly varied institutional and organisational arrangements across different States and at different times in this period. In general, this variation has concerned the extent of public funding for agricultural extension, decreases in academic programs and training in extension, and changing roles across the public, private, collective and vocational education and training (VET) sectors (e.g. accreditation of some extension programs and not others; varying involvement of extension in multi-disciplinary research teams (Kenny and Nettle, 2006).

CHALLENGES TO EXTENSION AS A PROFESSION

In Australia, the decline in State government funding of productivity-related extension delivery, and the focus on natural resource management areas, has resulted in a consequent loss in extension capacity within the publicly funded extension sector and a reduction of skilled extension operatives coming through this development path. (Hunt et al. 2012) identified that this has led to down-grading of professionalism, capacity and skills in many state and territory government agricultural agencies, in turn causing problems with recruitment and lack of career path for staff retained in the public sector.

Traditionally, Government agencies such as Departments of Primary Industries in Australia and the Ministry of Agriculture and Forestry (MAF) in New Zealand had a significant role in training and developing extension staff, especially of new graduates or relatively inexperienced staff. This pipeline of extension capability has ceased or diminished, yet collective or private sector contribution to build extension capability has not developed adequately to fill this void in Australia. In New Zealand, levy-funded extension services through DairyNZ have secured productivity extension capability and some natural resource management (sustainability) capability.

Whilst institutional, academic and funding arrangements have seen a decline in the number of people entering extension as a profession, there have also been challenges in positioning extension as a profession and an equal with the research, development and education professions. (Hunt et al. 2012) identified that some authors have observed that the decline in extension presence and capability has caused a disconnection in the RDE&E feedback loops from farmers to research, extension to research and farmers to extension. The increasing requirements for extension to be performance focused and meeting the challenges of developing and delivering on targets has amplified the need for a more professional approach (PISC, 2012).

The question of whether extension workers are professionals has been asked for at least 30 years or more (Swanson, 1975). Based on the accepted criteria for defining a profession, extension has made some progress during this period but Rivera (2011) identifies a key challenge for extension is to professionalise extension services, across leadership, managerial staff and field agents, with a view to pursuing the continual acquisition and application of knowledge. A pre-requisite for the progression of extension professionalism is the identification of key elements of extension professional practice. A number of international and Australian studies have advanced this knowledge base over the last decade. For instance, different domains for extension practice were identified by Coutts (2001); the way extension works in a learning relationship with farmers to create demand for learning has been described by Kenny (2002); the extension role in understanding and working with a diversity of values and worldviews in the farming population was highlighted by (Waters et al. 2008) and Nettle and Lamb (2010); the development of frameworks for positioning extension responses to different levels of farm decision-making has emerged from the extension profession itself (Markham et al. 2006); and the importance of extension translating farm practice for policy decision-making was described by Paine and Nettle (2009).

Given the nature of professional practice highlighted by the above examples, the ongoing professional development of extension can be understood as needing to evolve within the context of advisory relationships with farmers and other professional groups (Cerf and Hemidy, 2006; Botha, et al. 2008). Of particular note is the observation that extension is continually being faced with new professional situations (Cerf et al. 2011) requiring adjustment to extension knowledge, knowledge of farming systems and change to the nature of the advisory relationship. Recent examples of new professional situation in Australia and New Zealand would include the alignment of farm productivity and environmental outcomes, considering the implications of climate change policies on farm practice, and the increasing management complexity to do with larger farms and staff management. Although these changes apply across the RDE&E system overall, a recognition that extension is
contending with new professional situations is an important aspect for those not directly engaged with extension and funding agencies to consider. A commitment to capacity building of the extension profession requires investment and effort that recognises this context for extension practice. A workplace-research capacity has been suggested as an important feature for capacity building (Nettle and Paine, 2011) alongside cross-sector learning (Nettle, et al. 2010) and professional accreditation.

Professional education is a key criterion for defining a profession, yet at the same time there has been a decline in public extension capability, there has been a decreased number of extension academic staff and programs in universities, and decreasing numbers of extension staff undertaking post-graduate extension-related training. Accreditation and certification are also hallmarks of a profession, yet dairy extension has been slow to make advances in this area. Recent developments in New Zealand with NZIPIM around accreditation represent significant progress in better defining extension and consulting as professional activities in that country. Therefore, an increased focus on the different professional situations for extension as well as the skills and professional development of dairy extension providers is required, as is a robust and well-subscribed professional society to represent dairy extension and extension more broadly. These are important components of a platform for an adaptive extension profession.

**EXTENSION ROLES AND RESPONSIBILITIES ARE CHANGING**

New and emerging priorities are reshaping extension in Australia and New Zealand in response to the shifting strategic directions of organisations and businesses. Nowadays extension is much more diverse and interactive and includes a range of private service providers, diverse intervention methods and improved stakeholder engagement (PISC, 2012). Multiple organisations are now involved in delivering extension across the public, private, industry good (levy-funded) and vocational education and training (VET) sectors. The roles that these key organisations and businesses play in the extension and change process are altering and their relative contributions vary depending on the issue being addressed.

Not only are roles altering, but there is an increasing challenge to ensure integration and coordination across multiple players in the extension landscape. In Australia, no one organization dominates delivery of dairy productivity extension, despite this having been the preserve of State Departments of Primaries Industries over the past two to three decades. As a consequence, the industry has not had an ability to drive a singular agenda for extension - it has had to be a negotiated agenda because no one organization is mandated with this power. The challenge is that this situation slows the pace of change.

The challenge for extension funders and others with a stake in on-farm adoption and change, including researchers and service groups, is understanding the mix of players involved in extension and which ones are the most appropriate to interact with. Even when this can be identified the mode of interaction and who leads the dialogue and interchange between researchers, multiple diverse extension providers, farmers, policy and service groups is often unclear. Usually it is left up to individuals and existing working relationships to establish and progress this interaction.

A further challenge posed by the number and diversity of agencies, organisations and businesses involved in extension is related to building extension capability and professionalism. Historically, in Australia when Departments of Primaries Industries in each State were the significant major extension provider, training, skills development and professional support were the primary responsibility of each of these agencies. They had the scale and critical mass to coordinate and provide the required level of capability building across their respective teams. Their size and the number of staff involved meant that professional development pathways were in place and supported. The challenge in building extension capability has been exacerbated by the decrease in University extension programs and academic staff.

With the fragmentation of extension delivery across a diverse range of providers, building extension capability and professionalism is no longer the responsibility of a small number of government agencies. This responsibility has now become an “industry” responsibility in both Australia and New Zealand. But the challenge remains the bringing together of disparate extension providers into a well coordinated and effective training and development system.

In Australia, the Dairy Moving Forward initiative (2010) and the National Framework for RD&E (PISC, 2012) provide a structural mechanism and potential for leadership for within industry and cross-sector co-ordination of extension professional development. However, three conditions for co-ordination amongst providers will determine the ability for progress to be made: A shared view of the changing “clients” of extension; clear priorities for extension; and, development of a professional development plan that incorporates workplace learning and support.
AGREEMENT ON OUTCOMES IS REQUIRED

Research or extension priorities alone should not lead the focus for innovation and change (Brightling et al. 2010), rather this is best established collaboratively across the RDE&E system. The increasing requirements of RDE&E funders for delivery on clear targets and outcomes, and that all contributors in these changes to have a performance focus, increase the dependencies and need for an increasingly collaborative and professional approach between individual and organisations contributing to improved dairy systems.

There is a national imperative to improve the effectiveness of the RDE&E system in both Australia and New Zealand, and an increasing expectation that RDE&E can demonstrate direct contribution to improved dairy farm performance. This requires the establishment of agreed and shared targets that the range of RDE&E contributors work towards, whilst maintaining their own organisational accountability.

Table 1 outlines some of the risks identified from different approaches to determining activities in RDE&E (adapted from Brightling et al. 2010). Whilst four predominant approaches have been identified, it is still rare to see the approach of multidisciplinary RDE&E program teams developing coordinated approaches to address change in an effective manner. Inherent in this approach is the requirement for agreed and shared targets and a negotiated position on which each member of the project team and their respective organizations will contribute and be accountable for.

<table>
<thead>
<tr>
<th>Model of rural innovation identified</th>
<th>Key processes and strengths</th>
<th>Risks, weaknesses</th>
</tr>
</thead>
<tbody>
<tr>
<td>Research priorities lead the focus for innovation.</td>
<td>Identify knowledge gaps (set research priorities).</td>
<td>Expectation of broad uptake or use of the research or technology without pre-testing.</td>
</tr>
<tr>
<td></td>
<td>Draw on current ‘data’.</td>
<td>There may be many unforeseen consequences when research results are used or applied in a farm system or in new policy.</td>
</tr>
<tr>
<td></td>
<td>Conduct research.</td>
<td>Researchers have to prescribe who is going to use and benefit from the research before it is conducted (i.e. there is lock-in to certain courses of action).</td>
</tr>
<tr>
<td></td>
<td>Extend research to end-users.</td>
<td>The onus of decision-making, learning and adaptation then rests fully on the farmers, service provider intermediaries, communities or policy-makers.</td>
</tr>
<tr>
<td></td>
<td>Strength: Researchers learn about and understand needs of industry, farmers, policy or community.</td>
<td></td>
</tr>
<tr>
<td>Industry issues or “bottom-up” concerns lead the focus for innovation.</td>
<td>Identify sector or industry issues.</td>
<td>Priority setting processes tend to focus on issues of a very general nature, providing limited insight for defining how issues should be addressed or change supported. Priorities tend to be short-term in terms of focus and impact.</td>
</tr>
<tr>
<td></td>
<td>Conduct research or deliver information/extension to address an issue.</td>
<td>Independent investments in research or extension are made and justified as addressing important sector-defined issues without coordinated activity around what was required to collectively advance the issues.</td>
</tr>
<tr>
<td></td>
<td>Strengths: A demand-pull model of rural innovation (Klerkx and Leeuwis, 2008a). Ensures the sector is working on important issues of the commercial environment and not just knowledge gaps. Has broad engagement with the community.</td>
<td>Community-driven action often not recognised as a source of innovation.</td>
</tr>
</tbody>
</table>
Centralised research feeds into local extension processes.

Centralise research to create a critical mass of researchers working together on knowledge gaps.

Extend and translate research to different regional/location needs.

Strengths: Reduces professional isolation of researchers, greater opportunity for co-location of multi-disciplinary research.

This model, similar to approach 1, has the added complexity of requiring researchers to communicate the application of research in entirely different contexts to which the research had been conducted.

The model increases the requirement of local groups to be highly aware of research outside their region and pro-active in translating the importance of research for their regional needs.

Researchers are encouraged to market or promote their research rather than support innovation.

Program teams develop coordinated approaches to address change.

Small groups of researchers, extension people, farmers, policy and service groups are brought together with leadership provided by an area expert or champion.

The group takes responsibility for locating and gathering people together that can contribute to developing agreed positions on a program’s objectives and outcomes and modifying these over time.

The group builds understanding of the commercial environment in which they are trying to innovate.

The group considers the environment that would support change and designs strategies for change (what would make the most difference) and pilots these strategies to inform wider delivery.

The group manages emerging risks and keeps on top of issues’.

The national imperative to improve the effectiveness of the RD&E system provided the institutional impetus for cross-organisation collaboration. Without this, it was up to individuals and existing working relationships to establish and progress teams.

Establishing a large team can mean a more time is required to establish agreed positions.

The risk of developing ‘Group think’ – the antithesis of innovation (Weick, 2002).

The strengths of the coordinated multidisciplinary RD&E team in managing many of the risks associated with a fragmented RD&E pathway is an important development. Ultimately, the combination of RD&E in this way results in far better research questions, based on better knowing the change required and the challenges to achieving it. Equally, there may be many unforeseen and unintended consequences when research results are used or applied in a farm system or in new policy.

IMPLICATIONS FOR DAIRY SCIENTISTS

Despite the challenges facing extension capacity and professionalism, there is a strong incentive for dairy scientists to be receptive to extension input into research and development. Numerous authors including Klerkx and Leeuwis (2008) have advocated for more extensive cooperation between farmers, extension and researchers. The effectiveness of this input and dialogue will be both a function of research’s receptivity to this input (based on demonstration of clear value to improved research project outcomes and uptake by farmers) and extension’s professionalism in brokering this discussion as an equivalent and legitimate participant.

The current disconnection in the RD&E feedback loop indicates that both receptivity and capacity require improvement.

Allied with the above is the requirement for participants across research, development and extension to operate more effectively in multi-disciplinary teams.
In order for a coordinated multidisciplinary RDE&E approach to be effective, changes to current institutional, funding and professional arrangements may need to be considered. The focus on published scientific papers as a basis for performance assessment and promotion of researchers does not easily lend itself to collaboration between RDE&E. Structures or funding that provides an incentive to better define research questions and be more applicable to farmers and extension practitioners may be one option. This will be a significant challenge to the status quo for research agencies, organisations and funders.

Our conclusion is that the current challenges are not only for extension practitioners, organisations and businesses, but extend much more broadly to the overall organisation of the research, development and extension system in both Australia and New Zealand. Looking ahead, and as summarized by (Hunt et al. 2012), innovation in terms of industry-owned R&D&E agencies, government and industry partnerships with universities or a broadening of government partnerships with private sector providers are possible outcomes in the next couple of decades. This raises the importance of renewed governance arrangements for building trust amongst different contributors in the process (van Dijk & van Boekel, 2001). Dairy scientists are a vital part of the RDE&E system, and in the context of an adaptive extension platform, will contribute to the understanding of end-user needs and will be an active partner in improving links between extension and research for the future success of dairy RDE&E. Equally, an adaptive extension platform also requires input from farmers who have a capacity to express their needs of extension and can accommodate thoughts of an ‘industry good’ outcome, not just thinking in terms of their own farm business benefits.

An adaptive extension platform for the dairy sector in Australia and New Zealand that that addresses the issues raised and supports evolving dairy farm systems is required. Further work is needed in both addressing the issues identified and managing any additional future threats that may compromise the development of a more effective RDE&E platform.

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Influence of spring post-grazing height on dairy cow and grass production
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2INRA, AgroCampus Ouest, UMR 1348, Physiologie, Environnement et Génétique pour l’Animal et les Systèmes d’Elevage, F-35590 Saint-Gilles, France

ABSTRACT

The objective of this experiment was to investigate the effect of three early spring post-grazing heights (PGSH; 2.7cm – S, 3.5cm – M or 4.2cm – L), imposed on perennial ryegrass swards for 10 weeks in early lactation, on immediate, carryover and cumulative milk production performance and to quantify grass DM production within each grazing system. Increasing PGSH from 2.7 to 3.5 to 4.2cm linearly decreased \((P<0.001)\) the proportion of grass harvested from 0.94 to 0.82 to 0.74, respectively. Following the entire grazing season cumulative grass DM production was similar between the S and M treatments (14.1 t DM/ha) but the L treatment yielded 1.4 t DM/ha more. There was a linear response \((P<0.001)\) to increasing PGSH in terms of milk yield (22.5, 23.6 and 25.1 kg/cow/day) and milk solids yield (1.75, 1.91 and 2.00 kg/cow/day) for the S, M and L treatments, respectively. End bodyweight and body condition score of the S cows were significantly lower (-20 kg/cow and -0.14, respectively; \(P<0.05)\) than the L cows (469 kg/cow and 2.86, respectively). At the end of lactation cumulative milk and milk solids production was similar for the M and L treatments (5264 and 423 kg/cow, respectively) but there was a tendency for the S treatment to have lower milk production (5017 and 399 kg/cow, respectively).

This study has shown that by grazing to 3.5cm during the early spring period a compromise between high levels of grass utilisation and animal production performance can be achieved. This will have implications on the profitability of pasture based farms as this practice will allow a greater proportion of grazed grass to be utilised in the dairy cow’s diet.

Keywords: dairy cow, post-grazing height, early lactation, carryover

INTRODUCTION

With the abolition of milk quotas in 2015, it is anticipated that dairy enterprises in Ireland will seize the opportunity to expand their grass based production systems and secure their competitive position on the European market (Dillon et al. 2008). Previous recommendations during the early spring period have been to graze perennial ryegrass swards to 4cm during the first two grazing rotations (McEvoy et al. 2008), however, imposing a lower post-grazing height (PGSH) during this time may increase grass availability when grass growth rates are typically low (Brereton et al. 1985). Previous studies have reported a reduction in milk yield with decreased PGSH (Kennedy et al. 2007; McEvoy et al. 2008), however, low PGSH in early spring are also associated with increased grass quality (Stakelum and Dillon, 2007) and are capable of supporting higher levels of milk production (Kennedy et al. 2006) in subsequent grazing rotations. There are contrasting findings with regard to carryover effects of a period of feed restriction in early lactation – the inconsistency between findings may be due to variations in diet (Friggens et al. 1998), timing of restriction or the duration and amplitude of restriction (Grainger and Wilhelms, 1979; Delaby et al. 2009). The objective of this experiment was to i) investigate the effect of PGSH, on immediate, carryover and cumulative milk production performance and ii) quantify grass DM production within each grazing system.

MATERIALS AND METHODS

The experiment was undertaken at the Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland (50° 16’N; 8°25’W). Ninety (27 primiparous and 63 multiparous) spring calving Holstein Friesian dairy cows were balanced on the basis of calving date (February 13; s.d. 17.7 days), lactation number (2.1; s.d. 1.04), dam’s first lactation milk yield and composition (first 37 weeks) for the primiparous cows and previous lactation milk yield for the multiparous cows (4588; s.d. 670.8 kg/cow), milk fat (4.20; s.d. 0.408 g/kg), protein (3.38; s.d. 0.181 g/kg) and lactose (4.63 ; s.d. 0.115 g/kg) concentrations, bodyweight (BW; 482; s.d. 56.6 kg) and body condition score (BCS; 2.92, s.d. 0.139). Animals were randomly allocated to one of three grazing treatments directly post-calving. The treatments were: 2.7cm (severe–S), 3.5cm (moderate–M) or 4.2cm (lax–L) and were imposed during the experimental period from February 14 to April 24, 2011. Following the experimental period similar grazing management regimes were imposed to monitor carryover effects.

An equal area (farmlet) was assigned to each treatment and treatments were managed independently, with an overall stocking rate of 2.73 cows/ha. The difference in PGSH was achieved by allocating a 3 kg DM/cow/day difference in daily herbage allowance
results

During the 10-week experimental period targeted PGS was achieved (2.3, 3.5 and 4.2cm; \( P < 0.001 \)). This was achieved through differences in DHA, which were 7.7, 10.0 and 12.1 kg/cow/day for the S, M and L treatments, respectively. Increasing PGS from 2.3 to 3.5 to 4.2 cm linearly decreased \( P < 0.001 \) the proportion of pasture harvested from 0.94 to 0.82 to 0.74, respectively. The S animals required a lower grazing area per day (-37m²/cow; \( P < 0.001 \)) than the L animals which recorded similar grazed area/cow/day (129m²/cow/day). Mean concentrate input during the experimental period was similar for all treatments (3.4 kg DM/cow/day). Pre-grazing mass and pre-grazing height during the period were higher (+120kg DM/ha and +0.6cm, respectively; \( P < 0.001 \)) for the L treatment than the S and M treatments (956kg DM/ha and 5.8cm, respectively). Following the entire grazing season cumulative grass DM production was similar between the S and M treatments (14.1t DM/ha) but the L treatments yielded 1.4t DM/ha more. All treatments had a similar number of grazing rotations \((n=11)\). There was no effect of PGS treatment on grass quality parameters throughout the experiment.

There was a linear response \((P<0.001)\) to increasing PGS in terms of milk yield (22.5, 23.6 and 25.1kg/cow/day; Table 1) and milk solids yield (1.75, 1.91 and 2.00kg/cow/day) for the S, M and L treatments, respectively. End BW and BCS were similar for the M and L treatments (465kg/cow and 2.83, respectively), however end BW and BCS of the S cows were significantly lower (-20kg/cow and -0.14, respectively; \( P < 0.05 \)) than the L cows (469kg/cow and 2.86, respectively). At the end of the 10-week period, the S animals produced \((P<0.01)\) on average 160kg less milk and 17kg less milk solids than the M and L animals which had similar cumulative milk (1520 and 1577kg/cow) and milk solids production (123 and 126kg/cow). During the 29-weeks subsequent to the 10-week experimental period there was no difference in milk yield, milk composition, BW or BCS between any of the three treatments. At the end of lactation cumulative milk and milk solids production was similar for the M and L treatments (5264 and 423kg/cow, respectively) but the S cows tended to have lower milk production (5017kg/cow) and had lower \((P<0.05)\) total milk solids yield (399kg/cow) than their counterparts.

There was also a linear response in terms of DMI to increasing PGS during the experimental period (13.2, 14.8 and 15.6kg/cow; S, M and L treatments, respectively). During the carryover period there was no difference in DMI between treatments (16.2kg/cow/day).

Discussion and Conclusion

Milk yield and milk solids per hectare were greatest when pasture was grazed to 4.2cm (treatment L) as compared with lower PGS. The greater yield for L was presumably due to a greater allocation of grass per cow and similar grass quality between treatments and the large difference between treatments is also probably reflective of the very restrictive DHA offered to the S cows. Higher pre-grazing yields and heights on the L treatment were a result of cumulative lax grazing as there was no difference in these parameters during the first grazing rotation. Grass quality on the L treatment was similar to the S and M treatments; this emphasises that 4.2cm remains a relatively low PGS in comparison to the lax PGS reported in the literature (>5cm). However, 8% less pastures was utilised above 2.7cm on the L compared to the M treatment. Even though the proportion of grass harvested was greatest on the S treatment, the utilisation of extra grass did not compensate for the reduction in animal performance. Cumulative milk production during the 10-week experimental period was 10% lower than that of the M and L treatments, which were similar. As intake was significantly restricted at a grazing height of 2.7cm, this height may be the minimum PGS that can be achieved by grazing dairy cows. Thus the large restriction in nutrient supply resulted in a reduction in milk production performance. Clearly grazing to 2.7cm for 10-weeks in early lactation is a severe restriction as even following a 29-week period where cows were subsequently well fed they did not compensate in terms of milk production and re-coup the volume lost in early lactation. Although the L cows had a higher daily milk yield than the M cows cumulative milk production at the end of the 10-
week period was not different. When a more in-depth analysis of the data was completed it revealed that for the majority (at least 7 weeks) of the experimental period there was no significant difference between L and M groups, furthermore the GDMI of these two herds was similar.

This study demonstrated that grazing to 3.5cm during the early spring period is a good compromise between achieving high levels of grass utilisation and high animal production performance. This will have positive implications on the profitability of pasture based farms as this practice will allow a greater proportion of grazed grass to be utilised in the dairy cow’s diet.

ACKNOWLEDGEMENTS

This experiment was funded by Teagasc core funding.

REFERENCES


Table 1: Effect of post-grazing height (PGSH) on production performance of spring-calving cows in early lactation (February 14 to April 24)

<table>
<thead>
<tr>
<th>PGSH1</th>
<th>S</th>
<th>M</th>
<th>L</th>
<th>SED</th>
<th>PGSH effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk yield (kg/d)</td>
<td>22.5&lt;sup&gt;a&lt;/sup&gt;</td>
<td>23.6&lt;sup&gt;b&lt;/sup&gt;</td>
<td>25.1&lt;sup&gt;c&lt;/sup&gt;</td>
<td>0.51</td>
<td>0.001</td>
</tr>
<tr>
<td>Milk fat content (g/kg)</td>
<td>43.9&lt;sup&gt;a&lt;/sup&gt;</td>
<td>46.8&lt;sup&gt;b&lt;/sup&gt;</td>
<td>45.9&lt;sup&gt;b&lt;/sup&gt;</td>
<td>0.91</td>
<td>0.015</td>
</tr>
<tr>
<td>Milk protein content (g/kg)</td>
<td>33.1&lt;sup&gt;a&lt;/sup&gt;</td>
<td>34.1&lt;sup&gt;b&lt;/sup&gt;</td>
<td>34.0&lt;sup&gt;b&lt;/sup&gt;</td>
<td>0.35</td>
<td>0.022</td>
</tr>
<tr>
<td>Milk lactose content (g/kg)</td>
<td>46.8</td>
<td>46.9</td>
<td>47.0</td>
<td>0.22</td>
<td>0.636</td>
</tr>
<tr>
<td>Milk solids yield (kg/d)</td>
<td>1.75&lt;sup&gt;a&lt;/sup&gt;</td>
<td>1.91&lt;sup&gt;b&lt;/sup&gt;</td>
<td>2.00&lt;sup&gt;c&lt;/sup&gt;</td>
<td>0.046</td>
<td>0.001</td>
</tr>
<tr>
<td>Mean body weight (kg)</td>
<td>456</td>
<td>463</td>
<td>468</td>
<td>6.6</td>
<td>0.238</td>
</tr>
<tr>
<td>End body weight (kg)</td>
<td>449&lt;sup&gt;a&lt;/sup&gt;</td>
<td>460&lt;sup&gt;b&lt;/sup&gt;</td>
<td>469&lt;sup&gt;b&lt;/sup&gt;</td>
<td>7.3</td>
<td>0.047</td>
</tr>
<tr>
<td>Body weight change (kg/d)</td>
<td>-0.31&lt;sup&gt;a&lt;/sup&gt;</td>
<td>-0.13&lt;sup&gt;b&lt;/sup&gt;</td>
<td>-0.15&lt;sup&gt;b&lt;/sup&gt;</td>
<td>0.079</td>
<td>0.057</td>
</tr>
<tr>
<td>Mean body condition score</td>
<td>2.87</td>
<td>2.91</td>
<td>2.94</td>
<td>0.035</td>
<td>0.211</td>
</tr>
<tr>
<td>End body condition score</td>
<td>2.72&lt;sup&gt;a&lt;/sup&gt;</td>
<td>2.80&lt;sup&gt;b&lt;/sup&gt;</td>
<td>2.86&lt;sup&gt;b&lt;/sup&gt;</td>
<td>0.036</td>
<td>0.003</td>
</tr>
<tr>
<td>Body condition score change&lt;sup&gt;2&lt;/sup&gt;</td>
<td>-0.30&lt;sup&gt;a&lt;/sup&gt;</td>
<td>-0.21&lt;sup&gt;b&lt;/sup&gt;</td>
<td>-0.16&lt;sup&gt;b&lt;/sup&gt;</td>
<td>0.040</td>
<td>0.007</td>
</tr>
<tr>
<td>Mean total dry matter intake (DMI; kg DM/cow/d)</td>
<td>13.3&lt;sup&gt;a&lt;/sup&gt;</td>
<td>14.7&lt;sup&gt;b&lt;/sup&gt;</td>
<td>15.4&lt;sup&gt;b&lt;/sup&gt;</td>
<td>0.35</td>
<td>0.001</td>
</tr>
</tbody>
</table>

<sup>a</sup>-<sup>c</sup>Means within a row with different superscripts differ (P<0.05). SED = SE of the difference. <sup>1</sup>Post-grazing height treatment: S = 2.7 cm; M = 3.5 cm; L = 4.2 cm. <sup>2</sup>Change between the start and the end of PI.
Modelling the effect of increasing dietary proportion of white clover on cow milk production and nitrogen excretion, and profitability of a Waikato dairy farm

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ABSTRACT

The DairyNZ Whole Farm Model was used to evaluate a Waikato dairy farm for productivity, profitability and cow nitrogen (N) excretion based on cows feeding diets with varying proportions of white clover (WC) and perennial ryegrass (PR) over three independent climate years. Diets were: 15% WC (the traditional PR/WC pasture, control) and 40% WC, 60% WC and 80% WC diets derived from monoculture WC and the traditional pasture grown separately. Adjustments were made to increase dry matter intake (DMI) with increased dietary WC. Supplements were fed during treatment diet deficits. Model outputs were DMI, milk solids production, N intake, N in urine and milk, DM production, and operating profit. Relative to the control, the 40% WC increased DMI by 4% while both the 60 and 80% WC diets increased DMI by 5%. Compared with the control the 40, 60 and 80% WC diets increased N intake by 11, 15 and 18%, urinary N by 13, 19 and 22% and per cow and per ha milk solids production by 8, 10 and 12%, respectively. Increasing dietary WC decreased farm-grown DM and increased purchased feed. Income from extra milk solids offset the purchased feed costs resulting in greater profit from ≥40% WC diets compared with the control. Profitability increments were marginal when dietary WC increased beyond 40%. Given the assumptions made, a 40% WC diet can improve milk solids production and farm profitability, but measures to reduce N loss should be considered because this diet resulted in 13% more urinary N excreted compared with the control.

Keywords: white clover; milk solids; nitrogen partitioning; dry matter intake; farm profitability.

INTRODUCTION

Research has demonstrated increased milk production from increased white clover (WC, *Trifolium repens*) proportion of perennial ryegrass (PR, *Lolium perenne*) – WC mixtures (Cosgrove et al. 2006; Marotti et al. 2001). This is attributable to WC's high feeding value, increased intake, digestibility and utilisation (Ulyatt, 1981). Interspecies competition and variable weather conditions limit WC in mixed swards to ≤20% of dry matter (DM) (Chapman et al. 1996). Management practices involving growing WC and PR separately, and controlling cow access to feed allowance, have been used to increase dietary WC in trials (Cosgrove et al. 2006; Marotti et al. 2001). This spatial separation of complementary species provides an opportunity to use WC to increase milk production, but first, WC-rich diets must be tested for their full economic and environmental implications at a farm system level.

One potential limitation of feeding WC-rich diets is increased nitrogen (N) losses to the environment, especially from urine patches. White clover’s crude protein content can be ≥1.5 that of PR (Weller and Cooper, 2001), and increased intake of WC-rich diets often results in excess metabolisable protein. Lactating cows convert approximately 20% of ingested protein into milk and most of the remainder is excreted as urinary N (Castillo et al. 2000). Also, under optimal conditions WC monocultures grow 20% less DM (t/ha) than mixed swards (Brock and Hay, 2001), and increasing the farm area sown as WC monoculture can decrease total farm DM production, increase feed deficits and the cost of supplementary feed, and ultimately reduce farm profit.

The aim of this study was to model a dairy farm system that incorporates spatial separation of WC to increase its proportion in the diet of lactating cows and to quantify the economic and environmental responses (as N excretion).

MATERIALS AND METHODS

Model simulations

The DairyNZ Whole Farm Model (WFM) (Beukes et al. 2008) with the Molly cow model (Hanigan et al. 2009) was used to model a Waikato dairy farm (Friesian cows, age = 2 - 7 years, average live weight = 539 kg, average body condition score = 4.8, stocking rate = 3.0/ha) over three climate years: 1997/1998, 2004/2005 and 2008/2009 representing poor, intermediate and good pasture growth, respectively. The effect of dietary WC content was assessed using four scenarios based on the traditional New Zealand PR/WC pasture estimated to contain 15% WC (control), and this pasture combined with pure WC sown on 0.4, 0.6 and 0.8 of the farm area (with the remainder
sown in traditional pasture) to provide 40, 60 and 80% WC diets, respectively. Pasture growth in the DairyNZ WFM was climate-driven (Ruakura climate data, NIWA) using the (Romera et al. 2009) pasture growth model. Feed quality was user-defined monthly for pasture (mean = 11 MJ ME/kg DM/yr) and annually for WC (12 MJ ME/kg DM/yr). White clover monoculture production was estimated using monthly growth rates for Waikato (G.P. Cosgrove, pers. comm.) and total annual yield adjusted to 80% of the traditional pasture (Brock and Hay, 2001). Treatment diets were fed equally to lactating cows (start of calving = 01 August, mean lactation length = 250 days, dry-off date (all cows) = 30 April). Pasture silage (8.9 MJ ME/kg DM) and maize silage (9.6 MJ ME/kg DM) were fed (loss factor = 0.25, Roche and White, unpublished) during feed deficits. Dry cows were sent to a grazer where they grazed traditional pasture. During periods of surplus WC production, WC allowance was increased and that of traditional pasture reduced to reduce WC wastage (i.e. WC was not ensiled). Surplus traditional pasture was conserved (silage making = September 15 to February 28). Intakes were adjusted to allow 22% extra DMI on the WC component of the 40% and 60% WC treatments (Castle et al. 1983; G.P. Cosgrove pers. comm.). For the 80% WC treatment, the extra DMI on the WC component was 19%, based on findings of the (Harris et al. 1997) study. Model outputs were total herbage production, silage made, purchased supplements, fed supplements, MS production and operating profit (annually) and DMI, N intake, urinary N, milk N (over lactation period). A milk price of NZ$6.10/kg MS was used for all years.

**RESULTS**

**Feed production and consumption**

Compared with the control, the farm grew, on average, 18, 27 and 36% less DM when 40, 60 and 80%, respectively, of the farm was sown in monoculture WC (Table 1). The quantity of silage made corresponded with the annual ranking in pasture production which was greatest in 2008/2009, intermediate in 2004/2005 and least in 1997/1998 (Table 1). No silage was made with the 80% WC treatment (Table 1). Adjusted intakes from the 40, 60 and 80% WC diets increased total lactation DMI by 154, 201 and 211 kg DM/cow, respectively, compared with the control. Supplementary feed was purchased in all milking seasons when ≥60% of the farm was apportioned to WC and only in the 1997/1998 milking season when 40% of the farm was sown in WC. The quantity of purchased feed was greatest in 1997/1998 and lowest in 2008/2009 (Table 1).

**Table 1:** Predicted forage DM production, pasture silage made, supplement purchased* and fed-out, and dry matter intake (DMI) of a dairy farm utilising diets with varying proportions of white clover

<table>
<thead>
<tr>
<th>Season</th>
<th>Clover proportion</th>
<th>Total herbage production (t DM/ha)</th>
<th>Silage made (t DM/ha)</th>
<th>Supplements (t DM/ha)</th>
<th>Total DMI (t/cow/lactation)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Purchased</td>
<td>Fed-out</td>
</tr>
<tr>
<td>1997/1998</td>
<td>0.15</td>
<td>15.0</td>
<td>3.21</td>
<td>-</td>
<td>3.04</td>
</tr>
<tr>
<td></td>
<td>0.40</td>
<td>13.3</td>
<td>1.38</td>
<td>1.67</td>
<td>3.04</td>
</tr>
<tr>
<td></td>
<td>0.60</td>
<td>12.5</td>
<td>0.80</td>
<td>2.46</td>
<td>3.26</td>
</tr>
<tr>
<td></td>
<td>0.80</td>
<td>11.9</td>
<td>-</td>
<td>3.16</td>
<td>3.16</td>
</tr>
<tr>
<td>2004/2005</td>
<td>0.15</td>
<td>16.5</td>
<td>3.37</td>
<td>-</td>
<td>1.76</td>
</tr>
<tr>
<td></td>
<td>0.40</td>
<td>15.2</td>
<td>1.61</td>
<td>-</td>
<td>1.53</td>
</tr>
<tr>
<td></td>
<td>0.60</td>
<td>14.4</td>
<td>1.06</td>
<td>0.66</td>
<td>1.72</td>
</tr>
<tr>
<td></td>
<td>0.80</td>
<td>13.6</td>
<td>-</td>
<td>1.55</td>
<td>1.55</td>
</tr>
<tr>
<td>2008/2009</td>
<td>0.15</td>
<td>18.2</td>
<td>4.75</td>
<td>-</td>
<td>1.21</td>
</tr>
<tr>
<td></td>
<td>0.40</td>
<td>16.2</td>
<td>2.38</td>
<td>-</td>
<td>1.27</td>
</tr>
<tr>
<td></td>
<td>0.60</td>
<td>14.8</td>
<td>1.09</td>
<td>0.18</td>
<td>1.26</td>
</tr>
<tr>
<td></td>
<td>0.80</td>
<td>13.7</td>
<td>-</td>
<td>1.35</td>
<td>1.35</td>
</tr>
</tbody>
</table>

*the remainder of the diet was perennial ryegrass pasture with 15% white clover or supplement feed.
Milk production and farm operating profit

The model predicted curvilinear increases in MS per cow and per ha with increased dietary WC (Figure 1). Relative to the control, the 40, 60 and 80% WC diets increased MS production by 30, 41 and 48 kg/cow and 89, 119, and 141 kg/ha, respectively, corresponding to mean (per cow and per ha) increments of 8%, 10% and 12%.

![Figure 1: Model prediction of MS production per cow (a) and per hectare (b) by cows fed diets with varying proportions and white clover over three seasons. The remainder of the diet was perennial ryegrass pasture with 15% white clover or supplement feed.](image)

Profitability varied with years and treatments, but was higher for the treatment diets than the control (Figure 2). Profitability was highest in 2008/2009 and lowest in 1997/1998. On average, the 40, 60 and 80% WC diets increased profitability (per ha) by 13, 14 and 15%, relative to the control.

![Figure 2: Predicted operating profit of a Waikato dairy farm utilising diets containing varying proportions of white clover over three seasons. The remainder of the diet was perennial ryegrass pasture with 15% white clover or supplement feed.](image)

N intake and excretion

As dietary WC increased, N intake and N excreted in urine and in milk increased (Figure 3). Compared with the control, the 40, 60 and 80% WC diets increased N intake by 11%, 15% and 18%, urinary N by 13%, 19% and 22% and milk N by 8%, 11% and 13%, respectively.

![Figure 3: Predicted N intake and N excreted in urine and milk by lactating cows fed diets with varying proportions of white clover (mean of three seasons). The remainder of the diet was perennial ryegrass pasture with 15% white clover or supplement feed.](image)

DISCUSSION AND CONCLUSION

Milk solids production responses to increased dietary WC were of lower magnitude but consistent with published information from evaluation trials (Castle et al. 1983; Harris et al. 1997; Marotti et al. 2001). The introduction of supplements diluted the adjusted feeding effect applied to WC in treatment rations, and this may partly explain the low response observed in this study. This result indicates that the benefits of WC can be realised at a farm system level but, because of the multiple factor interactions that the farm system is subjected to, the effect is likely to be smaller compared with component study results.
No silage was made when 80% of the farm area was sown in WC, possibly due to increased grazing pressure on the remainder. Farm-grown DM production decreased with increased dietary WC, and the farm relied on purchased supplements in all years when the area sown in WC was ≥60% and in the low total DM production year of 1997/1998 when 40% of the farm area was sown in WC. This indicates the potential of the farm to operate self-sufficiently when up to 40% of its area is sown in WC due to better pasture growth compared to other treatments. Although the amount of purchased feed increased with increased dietary WC, profitability was still greater for treatment diets than for the control. This indicates that increased income from increased MS production more than offset the feed purchase costs. There was little additional effect on profitability when >40% of the farm area was sown in WC, indicating a threshold response around 40% WC. However, approximately 60% of ingested N was partitioned in urine under all diets (Figure 3) and the 40% WC diet increased urinary N excretion by 13% compared with the control.

This study shows that increasing dietary WC by spatial separation of pasture species can increase MS production and profitability of a dairy farm, but mitigation technologies are needed to reduce urinary N excretion. Forage DM production is sensitive to variation in growing conditions, and therefore, increased MS production and profitability from WC-rich diets is likely to differ between regions and milking seasons. There was little additional increase in profitability when dietary WC was increased above 40%, indicating a threshold beyond which there would be diminishing returns. The assumptions made in this study i.e. constant WC quality (12 MJ ME/kg DM) throughout the year and WC DM production = 0.8*traditional pasture DM production, should be taken into account when interpreting these results.

ACKNOWLEDGEMENTS

This work was funded by the Pastoral 21 Research Programme. Pastoral 21 is a collaborative venture between DairyNZ, Fonterra, Dairy Companies Association of New Zealand, Beef + Lamb NZ and the Ministry of Business, Innovation & Employment. Its goal is to provide accessible systems-level solutions for profitably increasing pastoral production while reducing farms’ environmental footprint.

REFERENCES


Economic analysis of options available to irrigated dairy farmers in northern Victoria under increased water availability

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ABSTRACT

Rainfall events in recent years have replenished water storages in Victoria and it is expected that irrigation water allocations in the Northern Irrigation Region will return to 100% high reliability water share for the next few seasons. A whole farm budget was developed to examine how a dairy farm in the Northern Irrigation Region would perform over the next 10 years if it continued to operate in the same way compared to if some systems changes were made. The business examined had a number of different opportunities to capitalise on higher water allocations. Three alternative futures were analysed; 1) introducing perennial ryegrass, 2) extensifying by reducing stocking rate and 3) intensifying by increasing stocking rate on the same land area. It was found that intensifying the system was the most profitable but most variable option and the extensify option was the least profitable and least variable. This work provides a thorough analysis for farmers in northern Victoria who are considering changes to take advantage of increased water availability in the coming years.

Keywords: Irrigation; risk; profitability.

INTRODUCTION

Between 1997 and 2009, rainfall across a large proportion of Victoria was well below average. The decrease in rainfall led to decreased runoff into rivers and catchments, and irrigators in the Northern Victorian Irrigation Region received a series of historically low water allocations. Since 2010, inflows have improved and water allocations on the Goulburn and Murray irrigation systems have returned to 100% of high reliability water share.

The objective of this work was to investigate the options available to dairy farmers who now have more water available compared to the past decade. A case study farm in northern Victoria that had changed its feeding system to manage dry seasonal conditions was chosen to examine the implications on profit, cash flow and wealth of options under increased water availability. We compared results from three alternative futures to the base farm system.

MATERIALS AND METHODS

The approach described in (Ho et al. 2007) and (Heard et al. 2012) was used and comprised several key aspects: namely whole farm biophysical and economic modelling (over a planning period of 10 years), use of a case study farm, and input from an industry steering committee. The analysis of the different systems involved estimating the supply of and demand for metabolisable energy (ME) on a monthly and annual basis (Standing Committee on Agriculture and Resource Management 1990; CSIRO 2007). The whole farm simulation was stochastic, with risky variables such as milk price and end of season water allocation and temporary water price represented as probability distributions (Table 1). Other variables such as supplementary feed prices have been included as being either high, average or low in line with end of season water allocation and are displayed in Table 2. The performance of the alternatives were judged using the criteria of economic efficiency (annual and cumulative profit and nominal internal rate of return), liquidity (annual and cumulative net cash flows) and growth (increase in wealth). Internal rate of return (IRR) can be used to compare investing in one of these systems compared with an alternative investment such as the share market.

Table 1: Key percentiles (P) for each of the probability distributions defined for input variables

<table>
<thead>
<tr>
<th>Input Costs/Yields</th>
<th>Distribution Type</th>
<th>P25</th>
<th>Median P50</th>
<th>P75</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk Price ($/kg milk protein + fat)*</td>
<td>BetaGeneral</td>
<td>4.75</td>
<td>5.09</td>
<td>5.43</td>
</tr>
<tr>
<td>End of Season Water Allocation (%)</td>
<td>Cumulative</td>
<td>72</td>
<td>100</td>
<td>134</td>
</tr>
<tr>
<td>Temporary Water Price $/ML</td>
<td>-</td>
<td>156</td>
<td>108</td>
<td>92</td>
</tr>
</tbody>
</table>

*Milk price is based on a ‘domestic’ payment scheme
Table 2: Decision rules used for purchased supplements as input variables in the model

<table>
<thead>
<tr>
<th>% High Reliability Water Share</th>
<th>&lt;100%</th>
<th>100 – 120%</th>
<th>&gt; 120%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grain ($/t air dry)</td>
<td>370</td>
<td>250</td>
<td>120</td>
</tr>
<tr>
<td>Maize Price ($/t air dry)</td>
<td>320</td>
<td>250</td>
<td>180</td>
</tr>
<tr>
<td>Lucerne Hay ($/t air dry)</td>
<td>400</td>
<td>280</td>
<td>200</td>
</tr>
</tbody>
</table>

BASE FARM AND DEVELOPMENT OPTIONS

The case study farm had adapted its feeding system to include a partial mixed ration (PMR) as a result of several years of low water allocations and dry seasonal conditions. The steering committee believed that there were alternative futures where PMR would remain part of the system. A future without the PMR was also investigated (Extensify 500 cows) where the farm was simplified to a more traditional feeding system of grazed perennial pasture and grain fed in the bail. Some physical details for the base farm and the alternative futures are given in Table 3. The alternative options involved introducing perennial ryegrass (PRG) into the system, extensifying the system by reducing stocking rate, and intensifying by increasing stocking rate compared to the base farm.

Table 3: Basic physical details for the options analysed

<table>
<thead>
<tr>
<th></th>
<th>Base Farm</th>
<th>100% Perennial Ryegrass</th>
<th>Extensify (500 Cows)</th>
<th>Intensify (1000 Cows)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cow Numbers</td>
<td>652</td>
<td>652</td>
<td>500</td>
<td>1000</td>
</tr>
<tr>
<td>Stocking Rate (cows/ha)</td>
<td>1.8</td>
<td>1.8</td>
<td>1.4</td>
<td>2.8</td>
</tr>
<tr>
<td>Milk Production (L/cow)</td>
<td>6,984</td>
<td>6,984</td>
<td>6,984</td>
<td>8,225</td>
</tr>
<tr>
<td>Milk Solids (kg/cow)</td>
<td>527</td>
<td>527</td>
<td>527</td>
<td>620</td>
</tr>
<tr>
<td>Feed Conversion Efficiency</td>
<td>1.1</td>
<td>1.1</td>
<td>1.1</td>
<td>1.2</td>
</tr>
<tr>
<td>Home Area (ha)</td>
<td>373</td>
<td>373</td>
<td>373</td>
<td>373</td>
</tr>
<tr>
<td>Water use (ML)</td>
<td>1,898</td>
<td>2,458</td>
<td>1,623</td>
<td>1,898</td>
</tr>
<tr>
<td>% of diet from purchased feed</td>
<td>28</td>
<td>24</td>
<td>23</td>
<td>42</td>
</tr>
</tbody>
</table>

It was assumed milk production would remain constant at the levels shown in Table 3 for the life of the investment. Also, variable and overhead costs were scaled with cow numbers in both the extensify and intensify systems. Other assumptions specific to the Intensify (1000 cows) option used in the analysis were:

- Partial mixed ration comprised a greater proportion of the cow’s diet, which increased milk production per cow and feed conversion efficiency.
- To reflect productivity incentives that could be obtained, the probability distribution for milk price was modified so that the mean increased by 5%, compared to the price used in the base farm, and standard deviation reduced by 50%.

RESULTS

Each of the alternative systems performed well in terms of nominal IRR. Intensifying the system returned the highest median nominal IRR compared to the base farm and alternate options. However, intensifying the system increased variability in returns (Figure 1).
Intensifying to 1000 cows achieved the highest and most variable cash income of the options analysed (Figure 2). The Base Farm system achieved lowest median annual net cash flow of $236,000. However, intensifying to 1000 cows returned a negative net cash flow for 13% of the time compared with 11% for the base farm, 8% for the 100% PRG option and 4% for the extensify option.

Figure 2: Annual net cash flow for the Base farm and development options.

A key goal of farmers is to increase the net wealth in their farming business. By comparing the nominal owners’ capital at the end of the ten years, the option that best achieves this goal can be assessed. Intensifying the system to 1000 cows returned the owners the most wealth out of the four options, but is also expected to be the most variable (Figure 3). Introducing perennials (100% PRG) back into the system also increased owner’s wealth compared to the base farm. Extensifying the system generated the same nominal owner’s capital to the base farm, although it was more variable.

DISCUSSION AND CONCLUSION

Introducing perennial ryegrass into a Northern Victorian dairy farming system increased the median nominal IRR by 0.8% and nominal owners end capital by $700,000 when compared with the base farm. Variability in returns between these two farm systems was similar, but the exposure of the business to potentially high priced and variable supplementary feed markets was reduced as more feed was grown on the home area, although, exposure to the temporary water market was increased. Net cash flows were on average $50,000 higher than the base farm. It is expected that this option will have negative net cash flows about 8% of the time, meaning the owner would have to borrow additional capital to continue farming. Milk price is the main driver of whole farm profitability for all systems analysed.

Extensifying the dairy farming system to 500 cows was more profitable than the base farm. This system was representative of a traditional grass and grain in the dairy system, but without the costs and complexity of feeding a PMR. Extensifying the system increased the median nominal IRR and net cash flow, though the nominal owners end capital remained similar to the base farm. It also reduced variability for these measures. Net cash flows were expected to be negative in 4% of years compared with 11% in the base farm. This system has a reduced reliance on purchasing temporary water in the market so increased water allocations are not as beneficial as in other options.

Intensifying the system to 1000 cows increased profitability when compared to the base farm. Median IRR increased by 4%, but the variability increased compared to the base farm. The performance of this
option relies on obtaining an increased milk price and increased feed conversion efficiency to achieve the improved return. This option was the most profitable, but also the most risky due to the vastly increased variability. Most of the variability can be explained by an increase the amount of purchased feed. While intensifying the system is considerably more risky on a cash flow basis, this type of system is likely to be able to capitalise better on good seasonal conditions and high milk prices. When water allocations are high, the price of purchased and home grown feed is expected to be lower than average (Table 2), hence, creating a greater margin for the farmer. This system is not likely to be an attractive option for a risk averse operator who would forgo some profit for decreased risk. With an equivalent milk price to the base farm, the intensification option would be less profitable and continue to be more risky compared to the base farm.

There are many different systems that can improve the profitability of a dairy farming system in Northern Victoria. This analysis shows that there is no one best farm system for irrigated dairy under increased water availability in this region. A risk averse operator is most likely to opt for the extensified system. Overall, it performed well. By reducing the proportion of purchased supplements, the system could reduce its exposure to external feed markets. Intensifying the system was the most profitable but also the most risky option. The performance of the intensified system relied on an increase in feed conversion efficiency and receiving an increased milk price. Ultimately there are a range of factors including risk preference that farmers will take into account when deciding what is the best system for them. In a future with higher water availability than the past decade, there are numerous options available to farmers to improve the profitability of their systems and ultimately their wealth.

ACKNOWLEDGEMENTS

This work was supported by funding from Dairy Australia, MurrayDairy and the Department of Primary Industries, Victoria. Thanks to the case study farmer and family for the help to gain an understanding of his farming system. Thanks to the Northern Victorian steering committee and project team for providing insight and understanding into the analysis.

REFERENCES


Nutrient losses from intensive dairy grazing systems in SW Australia

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ABSTRACT

An experiment comprising five farmlets, with dairy cows grazing annual ryegrass pastures, with varying fertiliser nitrogen (N) levels applied, was conducted from 2005 to 2008 in south-western Australia. Farm-gate N and phosphorus (P) budgets were calculated for each farmlet each year, as was N and P leached below the root zone (typically ~0.2 m) and lost in run-off for 2 farmlets. Fertiliser N and total N inputs ranged from 0-387 and 81-563 kg/ha/year respectively, while N outputs in milk and animals ranged from 54-124 kg/ha/year. Corresponding results for P were 0-13, 7-42 and 10-19 kg/ha/year respectively. Mean N and P surpluses (input – output) varied from 46-356 and 0-7 kg/ha/year respectively. Total N and P surpluses were strongly related to total annual N and P inputs respectively. Loss of N in runoff was ~2% of the annual N surplus. Runoff of P exceeded environmental targets even when soil test levels fell to critical levels for pasture growth. Although leaching of N below the root zone was large, all evidence shows that deeper leaching of N and P through the clayey aquicludes common in the area was negligible. This may also apply to other Australian dairy regions with similar hydro-geologies. With modest N losses through runoff and negligible deep leaching, a very large proportion of N was apparently lost in the gaseous form. Some of this is likely to be lost as nitrous oxide, a powerful greenhouse gas. While the adoption of best management practice can reduce N and P losses to the environment, it is likely that productive grazing systems will always contribute N and P to surface runoff at rates above current recommended environmental thresholds.

Keywords: nutrient losses, leaching, runoff, gaseous losses, dairy pasture

INTRODUCTION

Dairy farming systems with increased efficiency of nitrogen (N) use have been the subject of much research in the past 20 years (for example Whitehead 1995; Ledgard et al. 1998, 1999; van der Meer 2001; Barlow et al. 2007). Farmlet studies are particularly useful for determining responses to N fertiliser in pasture-based dairy systems as they take into account N recycling by the animal (Whitehead, 1995). In a New Zealand study, (Ledgard et al. 1998, 1999) used results from a farmlet study to conclude that N fertiliser use in excess of 100-200 kg/ha/year could not be justified on either economic or environmental grounds.

We conducted a dairy farmlet study in south-western Australia to determine the fertiliser N requirements for annual ryegrass-based dairy pastures (Morris et al. these proceedings) and to estimate N and P losses from such dairy production systems (this paper).

MATERIALS AND METHODS

An experiment comprising five farmlets with dairy cows grazing annual ryegrass-based pastures was conducted from 2005 to 2008 in south-western Australia. The experiment was on the typical duplex soil (1-2 m sand to sandy loam over ~20 m thick sequence of clay) with flat topography used for agriculture in the region.

Farmlets, each with 20 Holstein-Friesian cows, varied in fertiliser N level (kg N/ha/day; applied immediately after each rotational grazing) and stocking rate (cows/ha) as follows: 0\1.25; 0.5\1.50; 1.0\1.75; 1.5\2.00; 2.0\2.25.

The N and phosphorus (P) inputs (N or P imported in fertiliser, feeds and stock and N fixed by clover) and outputs (N or P exported in milk, feeds and stock) were estimated for each farmlet annually (after van der Meer 2001).

Detailed descriptions of the methods used to estimate nutrient losses are given in (Staines et al. 2011). Briefly, losses of N and P in surface run-off were measured in representative adjacent paddocks for farmlets N0 and N2.0. Samples of runoff water were collected automatically on a flow-proportional basis (approx. one sample per mm runoff) throughout the study.

Leaching of N and P below the typical ~0.20 m root zone into the surficial aquifer was measured over 4 years with 75 shallow bores, each 1-2 m deep depending on the depth to clay. Bores were monitored monthly to measure and sample water from the entire thickness of the surficial aquifer. The volume of surficial aquifer water was calculated from aquifer thickness and depth-weighted volumetric saturated soil water content. Deep leaching of shallow groundwater (and N and P contained within) into deeper aquifers is negligible in these systems.
Water samples were analysed for a range of N and P compounds at the Chemistry Centre of WA.

Regression analysis was used to examine relationships between nutrient input/output results and runoff/ground water data.

RESULTS

Farm-gate N and P budgets are summarised in Table 1 (means over 4 years). There was a strong relationship between total annual N inputs and N surpluses ($y = 0.91x -58; r^2 0.99; P<0.001$) and between total annual P inputs and P surpluses ($y = 0.95x -14; r^2 0.92; P<0.001$).

Runoff (mm/year) did not differ significantly between farmlets, but varied considerably during the 4 years depending on rainfall. Rainfall/runoff were 883/194, 448/0, 667/74 and 593/23 mm/year from 2005 to 2008 respectively.

The N surplus (kg/ha/year) explained much of the variability in median annual total N concentration ($y = 0.022x + 1.58 r^2 0.98; P<0.01$) and in flow weighted total N concentration in runoff ($y = 0.026x + 1.69; r^2 0.85; P=0.075$). However, the relationship between N surplus and annual total N load in runoff was not significant ($y = 0.015x + 0.76; r^2 0.58; P=0.24$).

The P load and concentration in runoff were not significantly correlated to annual P surplus ($P = 0.10-0.17$). Annual median and flow-weighted total P concentrations were always larger than environmental stream thresholds.

For the surficial aquifer, N surplus explained much of the variability in total N load ($y = 0.88x + 166; r^2 0.74; P=0.002$) and total N concentration ($y= 0.23x + 76; r^2 0.52; P=0.03$). However, leakage into deeper aquifers was found to be negligible (Bennett et al. 2007).

<table>
<thead>
<tr>
<th>Nutrient budget (kg/ha/year)</th>
<th>N0</th>
<th>N0.5</th>
<th>N1.0</th>
<th>N1.5</th>
<th>N2.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nitrogen</td>
<td>86</td>
<td>173</td>
<td>247</td>
<td>327</td>
<td></td>
</tr>
<tr>
<td>Fertiliser inputs</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total inputs</td>
<td>106</td>
<td>180</td>
<td>272</td>
<td>372</td>
<td>458</td>
</tr>
<tr>
<td>Total outputs</td>
<td>61</td>
<td>72</td>
<td>91</td>
<td>98</td>
<td>102</td>
</tr>
<tr>
<td>Surplus (input – output)</td>
<td>46</td>
<td>108</td>
<td>182</td>
<td>274</td>
<td>356</td>
</tr>
<tr>
<td>Efficiency (output/input)</td>
<td>57%</td>
<td>40%</td>
<td>33%</td>
<td>26%</td>
<td>22%</td>
</tr>
</tbody>
</table>

DISCUSSION AND CONCLUSION

Nutrient budgets for the dairy farmlets assessed here indicated mean surpluses of 46-356 kg N/ha/year for rain-fed annual ryegrass-based pastures, depending on N fertiliser input. Mean P surpluses were 0-7 kg/ha/year. For both N and P surpluses were strongly related to total annual inputs. On average, the N surplus represented 71% of total N inputs (range 43-78%). On average, the P surplus represented 21% of total P inputs (range 1-35%).

The N surplus appears to be lost off farm, while the P surplus was either stored in soil and/or lost off farm. Reducing the N surplus through reduced N fertiliser input and/or techniques that allow better N use may represent an opportunity for productivity improvements on commercial dairy farms.

Taken together, the data for runoff indicated that ~2% of the annual N surplus is lost in runoff, which is considerably less than assumed/forecast by previous catchment scale modelling (WQIP, 2010). Nevertheless, even for farmlet N0, the mean annual flow weighted concentrations in runoff exceeded local stream targets (2-5 mg/L vs a stream target of 1 mg/L).

P runoff exceeded environmental targets even when P soil test levels fell to critical levels for pasture
growth (<30 mg/kg Colwell P). It seems likely that most P in surface runoff is not derived directly from applied fertiliser, but that soil P is being released perhaps in response to a concentration gradient between soil water and the water moving across the soil surface.

These observations imply a limit to the ability of productive grazing systems to meet N and P stream runoff targets and may require changes to community expectation and environmental policy.

Leaching of N below the root zone into the surficial aquifer is correlated to farming intensity. The slope of the relationship between N surplus and total N load in the surficial aquifer suggests that, on an annual basis, the amount of N lost by shallow leaching is roughly equivalent to the annual N surplus of a dryland dairy system. However, leaching of N and P from the surficial aquifer into deeper useful aquifers is negligible in dairy regions of south-western Australia, due to the presence of underlying clayey profiles (Bennett et al. 2007). This is in marked contrast to findings in parts of Europe, New Zealand and elsewhere where nitrate leaching into deep aquifers has been shown to be a major mechanism of N loss from dairy farming systems (e.g. Whitehead, 1995; Ledgard et al. 1999).

The large farm-gate N surpluses cannot be accounted for by deep leaching and/or surface runoff. It is likely therefore that most of the unaccounted N is lost in the gaseous form. Part of the N is lost as ammonia gas in summer and autumn (Fillery 2009). The predominant sandy duplex soils in the region are typically waterlogged for much of the growing season. Given the negligible lateral movement of groundwater primarily due to the flat landscape, it is likely that that much of the unaccounted surplus N may be lost by denitrification. This process generates innocuous nitrogen gas and/or the powerful greenhouse gas nitrous oxide, depending on the degree and extent of waterlogging. To what extent fertiliser- and grazing-management can be manipulated on commercial dairy farms to significantly reduce nitrous oxide losses requires further investigation.

While the adoption of best management practices will potentially reduce N and P losses to the environment, in practice, it is likely that productive grazing systems will always contribute N and P to surface runoff at levels above current environmental stream thresholds.

Similar conclusions with regards to the fate of N and P losses may also apply to dairy regions in south-eastern Australia with similar hydro-geologies, but this remains to be investigated.

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REFERENCES


Evaluation and establishment of urinary nitrogen output prediction equations for cows with low and high breeding worth

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ABSTRACT

Urinary nitrogen output is an environmental risk factor in dairy production particularly in pasture-fed grazing cows. Prediction equations offer estimations of urinary nitrogen output and may subsequently help to manage environmental impact. Evaluation of four published prediction equations was performed on a dataset from feeding pasture to low and high breeding worth cows. A new prediction equation was also established to provide better prediction accuracy for cows of different genetic merit. Results showed large variations in prediction accuracy using published equations. A newly established prediction equation achieved high prediction accuracy with 77.3% of the variation in measured urinary nitrogen output being predicted \[
\text{Urinary nitrogen output (g/day)} = -61.1 + 142 \times \text{urinary nitrogen concentration (g/day)} - 19.7 \times \text{urinary creatinine concentration (mm/l)} + 0.28 \times \text{live weight (kg)} - 3.03 \times \text{milk yield (kg/day)} + 13.3 \times \text{milk }^{15}\text{N (‰)}; r^2 = 77.3; P < 0.001.
\]

Keywords: sustainability; breeding worth; pasture; cows.

INTRODUCTION

Quantifying urinary nitrogen output is an important component in sustainable dairying (Pacheco et al. 2007). However, traditional urinary nitrogen output measuring techniques require continuous collection of urine and are subject to errors. In addition, the majority of previously published prediction equations for urinary nitrogen output were developed by manipulating feed components in total mixed ration systems, with limited components reflecting animal variations. As a result, published prediction equations may not be suited for pasture-fed cows with different genetic merit. In New Zealand, breeding worth (BW), a selection index of profit per 4.5 t dry matter of feed; is used as a multi-breed evaluation scale, which combines estimated breeding values for milk volume, yields of fat and protein, live weight, fertility, somatic cell count and residual survival weighted by their relative economic weights. Therefore, the objectives of this study were to evaluate four published equations using pasture-fed cows with high and low BW and also to establish a new prediction equation that can be used to distinguish the urinary nitrogen output of cows with different genetic merit.

MATERIALS AND METHODS

A dataset from cows with high and low BW, housed indoors and fed on cut-and-carry pasture was evaluated. Sixteen individual urinary nitrogen output were measured during the nitrogen balance study. Parameters which required to generate four previously published urinary nitrogen output prediction equations (UN1 to UN4) were measured (Table 1). In addition, a newly identified nitrogen metabolism marker (\(^{15}\text{N}\)) was measured for pasture, milk, urine and plasma samples from each cow. Actual and predicted urinary nitrogen outputs were compared by linear regression analysis using coefficient of determination (\(r^2\)) and probability (p-value) (Genstat 13). In addition, a new prediction equation was also established to provide more precise prediction of urinary nitrogen output from current dataset using linear regression analysis.

RESULTS

The urinary nitrogen output measured through total urine collection ranged between 133 and 191 g N/cow.day, with a mean value of 161 g N/cow.day. Regression analysis showed moderate relationships between urinary nitrogen output and live weight (\(r^2 = 34.8; P < 0.01\)) and urinary creatinine concentration (\(r^2 = 44.0; P < 0.05\)). Prediction accuracy for urinary nitrogen output was generally low using the four published equations, with the highest prediction accuracy achieved using UN4 (Table 1). A newly established prediction equation using this dataset explained 77.3% of the variation in measured urinary nitrogen output \[
\text{Urinary nitrogen output (g/day)} = -61.1 + 142 \times \text{urinary nitrogen concentration (g/day)} - 19.7 \times \text{urinary creatinine concentration (mm/l)} + 0.28 \times \text{live weight (kg)} - 3.03 \times \text{milk yield (kg/day)} + 13.3 \times \text{milk }^{15}\text{N (‰)}; r^2 = 77.3; P < 0.001.
\]
**Table 1: Evaluation of four urinary nitrogen output prediction equations using cows differed in BW**

<table>
<thead>
<tr>
<th>Prediction equation</th>
<th>$r^2$</th>
<th>$P$</th>
<th>Mean g N/day</th>
<th>Range g N/day</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\text{UN}_1 = 0.59 \times nI - 91.4$</td>
<td>-</td>
<td>NS</td>
<td>129</td>
<td>102-156</td>
<td>(Cheng et al. 2011)</td>
</tr>
<tr>
<td>$\text{UN}_2 = 88.8 + 11.6 \times \text{MUN}$</td>
<td>-</td>
<td>NS</td>
<td>170</td>
<td>160-179</td>
<td>(Broderick et al. 2003)</td>
</tr>
<tr>
<td>$\text{UN}_3 = 21.9 \times \text{LWT} / \text{UCcc} \times \text{Uncc}$</td>
<td>25.7</td>
<td>*</td>
<td>204</td>
<td>158-261</td>
<td>(Pacheco et al. 2007)</td>
</tr>
<tr>
<td>$\text{UN}_4 = (3.55 + 0.16 \times \text{DMI} + 6.73 \times \text{CpI} - 0.35 \times \text{my}) \times \text{aU} \times \text{Uncc}$</td>
<td>37.1</td>
<td>**</td>
<td>121</td>
<td>67-148</td>
<td>(Fox et al. 2004)</td>
</tr>
</tbody>
</table>

$^a$ Nitrogen intake (NI); Rumen degradable protein intake (RDPI); Milk yield (MY); Urinary nitrogen output (UN); Urinary nitrogen concentration (UNcc); Urinary creatinine concentration (UCcc); Crude protein intake (CPI); live weight (LWT); Animal unit (AU= LWT / 454).

**DISCUSSION**

The prediction accuracy was low using equation $\text{UN}_1$. The use of nitrogen intake was based on the assumption of cows did not differ in their nitrogen metabolism. This is in contrast to the findings of (Woodward et al. 2011), who provided evidence that high BW cows were able to partition more feed nitrogen to the milk rather than into urine. Although (Bouwman et al. 2010) reported there was a genetic variation in MUN, evaluation of $\text{UN}_2$ using the current data provided little support for this statement. The moderate prediction accuracy using $\text{UN}_3$ ($r^2 = 25.7; P < 0.05$) and $\text{UN}_4$ ($r^2 = 37.1; P < 0.01$) was likely due to the moderate correlation between urinary nitrogen output and live weight. Better prediction accuracy was achieved by adding milk yield and milk $^{15}\text{N}$ based on parameters described in $\text{UN}_3$. We believe this was due to the inclusion of genetic related parameters into the prediction equation. Milk yield is related to the genetic production potential of the cow, as (Davey et al. 1983) showed high BW cows had greater intake and can utilise more of the body reserve to support higher milk production. On the other hand, the basis of using milk $^{15}\text{N}$ in the equation was likely due to the difference in cows’ nitrogen metabolism, namely hepatic transamination (Cheng et al. 2011).

**CONCLUSION**

The results highlighted the complex nature of nitrogen metabolism in cows which differ in genetic merit. Accuracy of using published equations to predict urinary nitrogen output from pasture-fed cows which differ in genetic merit must be validated before applying to large numbers of animals. Ideally, suitable prediction equations should be established using relevant datasets.

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**REFERENCES**


Differentiation of organic from conventionally produced milk

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ABSTRACT

Examining compositional differences between organic and conventionally produced cow’s milk, especially when considering fatty acids, indicate these can be largely explained by the amount of forage in a cow’s diet. Our study was designed to investigate if there was a difference between organic and conventional milk produced in the all-year-round pasture grazing system used in New Zealand. Gas chromatography – mass spectrometry and high performance liquid chromatography were used to examine the fatty acid (FA) and protein composition of bulk milk samples (n = 120), collected throughout the 2010-2011 milking season. The results of the FA analysis showed differences (p < 0.001) for 14 FA, with organic milk containing significantly higher amounts of even-chain FA as well as linoleic acid (LA) and γ-linolenic acid (ALA), while conventional milk samples showed an increase in concentration for odd-chain, branched-chain and unsaturated FA. No significant difference between the two milk varieties could be found for caseins and whey proteins. Differences in FA concentrations between organic and conventional milk on a pasture based dairy system may be due to minor variation in diet composition.

Keywords milk; organic; fatty acids; branched-chain fatty acids; conjugated linolenic acid; pasture grazing.

INTRODUCTION

The presumption that food produced without use of synthetic products (e.g., fertiliser and pesticides) is more nutritious and, therefore, beneficial for human health, has been nurtured for decades by advocates of organic farming. As a consequence of and in response to a loss of consumer confidence in food innocuousness, the organic market has been growing rapidly over the last 20 years. With regard to dairy products, trials conducted predominantly in Europe indicated that milk from organically reared cows, which consumed a high amount of fresh pasture or conserved forage, contained increased amounts of the desirable fatty acids conjugated linoleic acid (CLA) and γ-linolenic acid (ALA). However, recent reviews e.g., (Dangour et al. 2010), which analysed results from various studies comparing organic and conventional products, concluded that research undertaken so far has not provided enough evidence to show a significant difference between both production systems.

The aim of our study was to explore whether compositional differences between organic and conventional milk exist in a low input all-year-round pasture grazing system, typical for the New Zealand (NZ) dairy industry. Our study utilised a side-by-side comparative grassland-based, open grazing dairy trial investigating long-term impact of organic farming on animal health, management, soil conditions and pasture performance.

MATERIALS AND METHODS

Two comparable herds as described by Kelly (et al. 2005) were reared organically (46 cows) or conventionally (53 cows) side by side under the same management at Massey University in Palmerston North, NZ. Both farms were managed according to best practice for organic and conventional dairy farms in similar soil and climate conditions. The pasture grazing was supplemented by a small amount of other forage crops (mainly baleage and turnips with maize silage added for conventional cows). Total amount of supplements for each cow during the milking season was 575 kg/DM for organic and 623 kg/DM for conventional cows, representing 12 and 13% of total DM intake for organic and conventional cows, respectively. During monthly herd testing, milk yield, protein and fat content were measured for each animal. The chemical composition (crude protein, lipids, neutral detergent fibre, and metabolisable energy) of both pastures were analysed seven times throughout the milking season and the plant composition observed twice.

Bulk milk samples for the organic and conventional herd were collected approximately twice weekly between August 2010 and May 2011 (n = 60 samples for each treatment). Samples were analysed for fatty acids (FA) after extraction and methylation based on the method described by (Toledo et al. 2001) using 1, 1, 1 C¹³ Triocanoin as an internal standard (Laroden Fine Chemical AB, Malmo, Sweden). Fatty acid methyl esters (FAME) were separated using GCMS (Shimadzu) with a BTX70 (SGE) column. FAME
where classified via diagnostic marker ions as described by Härtig (2008) and identified via Supelco® F.A.M.E. Mix C4-C24 (Sigma-Aldrich, NZ). Milk samples were also analysed for caseins and whey proteins according to the methods of (Bordin et al. 2001) and (Elgar et al. 2000), respectively. Data has been statistically explored via analysis of variance using a general linear model that included the random effect of date and the fixed effect of treatment. Analysis was carried out with Minitab (version 15, Minitab Inc).

**RESULTS**

Analysis of FA showed differences (P < 0.001) for 14 of 24 FA listed in Table 1. Organic milk contained higher amounts of even-chain FA, while conventional milk samples showed increased concentrations for odd- and branched-chain FA. Individual unsaturated FAs were generally present in greater concentrations in conventional milk apart from linoleic acid (LA) and -linolenic acid (ALA), which were significantly more abundant in organic milk. No differences were observed for poly-unsaturated fatty acids with a chain length longer than C18. Based on the herd testing data, organic and conventional cows had an average seasonal milk yield of 4263 and 4512 kg with a milk fat yield of 233 and 223 kg and total protein of 155 and 161 kg, respectively.

Table 1: Concentration of individual fatty acids (FA) in conventional and organic milk averaged over lactation period

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>Conventional Mean (g/100g FA)</th>
<th>SEM</th>
<th>Organic Mean (g/100g FA)</th>
<th>SEM</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Even-chain saturated FA</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C4:0 Butyric acid</td>
<td>2.81</td>
<td>0.083</td>
<td>2.94</td>
<td>0.084</td>
<td>**</td>
</tr>
<tr>
<td>C10:0 Capric acid</td>
<td>2.91</td>
<td>0.044</td>
<td>3.08</td>
<td>0.048</td>
<td>***</td>
</tr>
<tr>
<td>C12:0 Lauric acid</td>
<td>3.36</td>
<td>0.051</td>
<td>3.47</td>
<td>0.062</td>
<td>*</td>
</tr>
<tr>
<td>C14:0 Myristic acid</td>
<td>11.77</td>
<td>0.113</td>
<td>11.81</td>
<td>0.142</td>
<td>NS</td>
</tr>
<tr>
<td>C16:0 Palmitic acid</td>
<td>30.12</td>
<td>0.309</td>
<td>31.37</td>
<td>0.406</td>
<td>**</td>
</tr>
<tr>
<td>C18:0 Stearic acid</td>
<td>9.96</td>
<td>0.187</td>
<td>11.09</td>
<td>0.276</td>
<td>***</td>
</tr>
<tr>
<td><strong>Odd-chain saturated FA</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C13:0 Tridecanoic acid</td>
<td>0.07</td>
<td>0.002</td>
<td>0.07</td>
<td>0.002</td>
<td>***</td>
</tr>
<tr>
<td>C15:0 Pentadecanoic acid</td>
<td>1.25</td>
<td>0.016</td>
<td>1.15</td>
<td>0.018</td>
<td>***</td>
</tr>
<tr>
<td>C17:0 Heptadecanoic acid</td>
<td>0.54</td>
<td>0.011</td>
<td>0.50</td>
<td>0.014</td>
<td>**</td>
</tr>
<tr>
<td><strong>Branched-chain FA</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C13:0 iso</td>
<td>0.03</td>
<td>0.001</td>
<td>0.03</td>
<td>0.001</td>
<td>***</td>
</tr>
<tr>
<td>C15:0 iso</td>
<td>0.25</td>
<td>0.004</td>
<td>0.23</td>
<td>0.003</td>
<td>***</td>
</tr>
<tr>
<td>C15:0 anteiso</td>
<td>0.42</td>
<td>0.006</td>
<td>0.36</td>
<td>0.006</td>
<td>***</td>
</tr>
<tr>
<td>C17:0 iso</td>
<td>0.34</td>
<td>0.005</td>
<td>0.30</td>
<td>0.004</td>
<td>***</td>
</tr>
<tr>
<td>C17:0 anteiso</td>
<td>0.37</td>
<td>0.004</td>
<td>0.34</td>
<td>0.005</td>
<td>***</td>
</tr>
<tr>
<td><strong>Unsaturated FA</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C16:1 c9 Palmitoleic acid</td>
<td>1.59</td>
<td>0.029</td>
<td>1.52</td>
<td>0.029</td>
<td>**</td>
</tr>
<tr>
<td>C18:1 t9 Elaidic acid</td>
<td>0.21</td>
<td>0.009</td>
<td>0.18</td>
<td>0.007</td>
<td>***</td>
</tr>
<tr>
<td>C18:1 t11 Vaccenic acid</td>
<td>3.47</td>
<td>0.103</td>
<td>2.23</td>
<td>0.072</td>
<td>***</td>
</tr>
<tr>
<td>C18:1 c9 Oleic acid</td>
<td>18.56</td>
<td>0.309</td>
<td>17.83</td>
<td>0.413</td>
<td>**</td>
</tr>
<tr>
<td>C18:2 c9,12 Linoleic acid</td>
<td>0.71</td>
<td>0.016</td>
<td>0.82</td>
<td>0.021</td>
<td>***</td>
</tr>
<tr>
<td>C18:2 c9t11 CLA</td>
<td>1.58</td>
<td>0.068</td>
<td>0.83</td>
<td>0.031</td>
<td>***</td>
</tr>
<tr>
<td>C18:3 c9,12,15 ALA</td>
<td>0.79</td>
<td>0.022</td>
<td>0.96</td>
<td>0.030</td>
<td>***</td>
</tr>
<tr>
<td>C20:5 n3 EPA</td>
<td>0.02</td>
<td>0.002</td>
<td>0.02</td>
<td>0.003</td>
<td>NS</td>
</tr>
<tr>
<td>C22:5 n3 DPA</td>
<td>0.13</td>
<td>0.005</td>
<td>0.14</td>
<td>0.007</td>
<td>NS</td>
</tr>
<tr>
<td>C22:6 n3 DHA</td>
<td>0.01</td>
<td>0.001</td>
<td>0.02</td>
<td>0.001</td>
<td>NS</td>
</tr>
</tbody>
</table>

*** = P < 0.001; ** = P < 0.01; *= P < 0.05
No differences were found for casein (including s1-, s2-, and casein) (27.6 g/kg milk) and whey proteins (including -lactoglobulin, -lactalbumin and BSA) (8.8 g/kg milk) between the two herd (detailed results not shown).

DISCUSSION AND CONCLUSION

Despite similarity in diets, offered in our trial to the conventional and organic herd, in particular when compared to trials conducted in Europe with seasonal indoor housing, many FA were different between the organic and conventional milk samples. It was especially noteworthy that the amounts of generally “desirable” FA (odd, branched and unsaturated FA), were either no different or increased in conventional milk, the exception being ALA which was increased in organic milk. The higher concentrations of odd and branched FA in conventional milk cannot be explained by differences in total milk fat as organic cows had on average a 4 % higher fat yield despite producing 6 % less milk than conventional cows. When considering the literature regarding influence of diet on milk FA composition, it is possible the subtle differences in diets between the two herds explain our results. No difference in chemical composition between both pastures was found, but conventional pasture contained 5% more ryegrass and 7% more dead material, while organic pasture had higher amounts of other grasses (9%), weeds (2%) and herbs (1%). The calculated pasture intake was 4.3 tDM for organic and 4.0 tDM for conventional cows. Further work would be required to determine whether the observed differences in FA composition were the result of the individual cow’s selected (e.g., genetics, and differences in rumen micro biota) minor differences in feed, or the organic regime. Despite the differences between the treatment groups, concentrations observed for both milk varieties fell within the normal range for FA concentrations in milk (Moate et al. 2007). Protein concentration in milk is much less susceptible to changes in diet than FA (Walker et al. 2004). Our results for the protein analysis are therefore in accordance with the literature.

Reasons for the slight differences in composition of organic and conventional milks from cows managed similarly are not known, but may be due to small differences in diet between the two herds. These results have not been evaluated in regard to their nutritional impact on human health.

ACKNOWLEDGEMENTS

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Impact of pre vs. post-milking supplementation on milking interval of cows milked in a pasture-based automatic milking system

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ABSTRACT

Cows milked in pasture-based automatic milking system (AMS) tend to have a lower daily milking frequency (MF) in comparison with cows milked in indoor AMS. Milking with intervals beyond 16-hrs have been reported to have a negative impact on yield and udder health, and therefore it is important to minimise their occurrence. As feed is the main incentive used to encourage cow traffic around the system, a trial was designed to compare pre vs. post-milking feed placement strategies. We hypothesised that pre-feeding would create a stronger incentive for cows to walk from the paddock to the dairy to get milked, due to the reward being more immediate, thereby reducing their milking interval and increasing daily milking frequency and milk yield. Cows in the pre-feeding group returned to the dairy sooner (11:55 vs. 13:24 hh:mm for Pre vs. Post respectively; \( P < 0.001 \)) but had longer milking intervals (15:25 vs. 14:25 hh:mm, respectively; \( P < 0.001 \)). This was due to the time spent in the pre-feeding area (average 56 minutes) combined with a longer average time spent in the pre-milking waiting yard (1:40 vs. 1:20 hh:mm for Pre-fed vs. Post respectively; \( P < 0.001 \)). No difference was observed in daily milk yield/cow (\( P > 0.05 \)). The results of this study demonstrate the potential of manipulating feeding management strategies to influence cow behaviour and traffic in voluntary milking systems.

Keywords: automatic milking system; milking interval; supplementation.

INTRODUCTION

Adoption of automatic milking systems (AMS) has increased in the last 10 years, with over 10,000 farms operating with this technology globally (De Koning, 2011). Due to the voluntary nature of the system, it is not uncommon to have large variation in milking intervals (MI, defined as the time between two consecutive milking events) within and between cows. It is known that MI beyond 16 hours have a reduced milk yield (in kg of milk accumulated per hour of MI) (Delamaire and Guinard-Flament, 2006) and udder health (Hammer et al. 2012). In grazing systems around 30% of all milkings can have intervals above 16 hours (depending on the management practices; N.A. Lyons, unpublished data), which is much higher than the 4.2% reported in indoor systems (Hogeveen et al. 2001). Given that feed is the main incentive encouraging consistent cow flow (Prescott et al. 1998a, Prescott et al. 1998b), management decisions should aim to minimise the incidence of milking intervals extending beyond 16 hours. This does not necessarily mean an increase in overall milking frequency as this should be optimised to meet the farms targets with regard to robot harvesting level and overall farm production.

Previous studies have compared different cow traffic management options (Ketelaar-De Lauwere et al. 1998, Hermans et al. 2003, Bach et al. 2009) and different concentrate allowances (Halachmi et al. 2005, Bach et al. 2007) on cows’ attendance to the milking station and milk production. Yet to date, no data have been published addressing the impact of location of supplementary feed on MI in grazing systems using AMS.

The aim of this study was to compare the impact of supplementary feed available to cows at the dairy either prior to (PRE) or after milking (POST), on cow traffic and milk production, of cows in a grazing system and milked by an AMS. It was hypothesised that cows that were allocated supplementary feed prior to being milked would return to the dairy (from the paddock) after shorter intervals than cows that were offered supplementary feed after milking. In turn this would result in a lower average MI and a reduced incidence of MI’s exceeding 16-hr.

MATERIAL AND METHODS

A field study was conducted between September, 12th and October 10th 2011, at the FutureDairy AMS Research dairy (Elizabeth Macarthur Agricultural Institute, DPI NSW, Camden, Australia). A herd of 175 cows, mixed Holstein and Illawara breed, were milked in a 16-bail prototype robotic rotary (RR; Automatic Milking Rotary AMR™, DeLaval, Sweden) (Kolbach et al. 2012). Cows were randomly allocated to two groups balanced for stage of lactation. Treatments were allocated to each group in a cross over design trial with 2 periods of 13 days each (7 day adaptation period followed by a 6 day measurement period). Cows were managed in one herd throughout the study, and drafted to either PRE or POST milking using automatic drafting gates. Each animal was fitted with a unique electronic transponder, which allowed the electronic log of gate passings to be used to calculate time spent by individual cows in different areas.
Target daily dry matter intake was set at 23 kg DM/cow/day (Table 1). Cows were granted access to 2 allocations of pasture per 24-hr period, referred to as “day” and “night”. Cows presenting at the dairy with no milking permission (based on a minimum milking interval of 4 hours since last milking) or leaving the dairy after milking, were automatically drafted to the day paddock between 9am and 9pm, and to the night paddock between 9pm and 9am. Each paddock had a 12 hour ‘active access period’, followed by a 10 hour ‘voluntary exit’ period, during which cows were expected to voluntarily move to the next pasture allocation. At the end of each voluntary exit period any cows that had not left were fetched and herded to the dairy. Supplements were offered in a feeding area located at the dairy, and consisted of pelleted concentrates supplied through four automatic feed stations (FSC400, DeLaval, Sweden), and a PMR ration on an adjacent feeding area. In addition, and not accounted for in the daily ration, cows received 0.41 ± 0.01 kg concentrate/milking as an enticer, which was offered at the first two bails of the RR.

### Table 1: Daily ration for the herd

<table>
<thead>
<tr>
<th>Type</th>
<th>Allocation</th>
<th>Feed source</th>
<th>Target dry matter intake (kg DM/cow/d)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pasture</td>
<td>Day</td>
<td>Pasture</td>
<td>6.0</td>
</tr>
<tr>
<td></td>
<td>Night</td>
<td>Pasture</td>
<td>8.0</td>
</tr>
<tr>
<td>Supplements</td>
<td>PMR</td>
<td>Cereal Hay</td>
<td>0.7</td>
</tr>
<tr>
<td></td>
<td>PMR</td>
<td>Maize Silage</td>
<td>2.7</td>
</tr>
<tr>
<td></td>
<td>PMR</td>
<td>Concentrate</td>
<td>2.7</td>
</tr>
<tr>
<td>Feed Stations</td>
<td></td>
<td>Concentrate</td>
<td>2.7</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
<td>22.8</td>
</tr>
</tbody>
</table>

Data from measurement periods were analysed using Restricted Maximum Likelihood Procedures (REML) in Genstat 13th Edition (VSN International, UK).

Milking interval was subdivided into 3 main time components: time to return to the dairy (RT = time between exiting the dairy to re-presenting back at the dairy), feeding time either prior to trafficking to pasture or upon return from pasture (FT = time from the entry to exit of feeding area), and waiting time (WT = time from entry to the pre-milking waiting yard to milking start). Milking yield (MY = yield of milk at a particular milking, in kg milk/cow/milking), MF and daily yield (DY = yield of milk harvested per day, in kg milk/cow/day) were also explored.

Models included the main effects of treatment sequence, period, treatment (PRE and POST), stage of lactation (Early ≤ 100 days in milk (DIM); Mid>100 to ≤ 200 DIM and Late > 200 DIM), parity (primiparous or multiparous) and milk yield category (based on pre-trial 7-day average milk yield, cows were allocated into one of three equally sized categories: Low, Mid or High), as well as the interactions treatment x stage of lactation, parity and milk yield. Assumptions were checked using residual plot diagnostic, and, where needed, data were transformed (FT, WT and MF were log-transformed). Significance was determined at \(P<0.05\).

### RESULTS

On average, cows in the PRE feeding group returned ~ 1.5 hr earlier from the paddock to the dairy, than POST cows. However, PRE cows spent more than double the time at the feeding area, and waited 20 more minutes to be milked (Table 2). Overall, cows in the PRE feeding group had a milking interval of 1 hr longer than the POST feeding treatment, and a 5% higher milk yield per milking. Despite PRE cows having a 6% lower MF, no significant difference was observed in DY (mean 20.97 kg/cow/day). Furthermore, pre-fed cows had an extra 9% of milkings with intervals exceeding 16-h (47.5% vs. 38.7% of milkings for PRE and POST-fed cows, respectively).

### Table 2: Predicted means of a REML for return time from the paddock, feeding time, waiting time, milking interval, milking yield, milking frequency and daily yield

<table>
<thead>
<tr>
<th>Outcome</th>
<th>PRE</th>
<th>POST</th>
<th>P - value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Return time (hh:mm)</td>
<td>11:55a</td>
<td>13:24b</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Feeding time (hh:mm)</td>
<td>0:56a</td>
<td>0:23b</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Waiting time (hh:mm)</td>
<td>1:40a</td>
<td>1:20b</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Milking interval (hh:mm)</td>
<td>15:25a</td>
<td>14:25b</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Milking yield (kg/cow/milking)</td>
<td>12.64a</td>
<td>12.07b</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Milking frequency (milkings/cow/day)</td>
<td>1.53a</td>
<td>1.64b</td>
<td>0.001</td>
</tr>
<tr>
<td>Daily yield (kg/cow/day)</td>
<td>20.64a</td>
<td>21.29b</td>
<td>0.627</td>
</tr>
</tbody>
</table>

**Note:** Treatment means with different superscript letters differ statistically \(P<0.005\).
DISCUSSION

Offering supplementary feed before milking appears to be a stronger incentive for cows to walk from the paddock, reducing the return time of PRE fed cows. (Prescott et al. 1998b) suggested that the effort involved in obtaining a reward could affect the willingness to search for it, which could be the case of the POST-fed cows.

The apparent initial advantage of PRE feeding was offset by cows spending more than double the amount of time in the supplementary feeding area. The reasons for spending more time in feeding area cannot be determined with this data, and warrant further investigation.

Cows which had access to feed before milking were also slower to move through the waiting yard. Given that milking is not a strong reward (Prescott et al. 1998b), pre-feeding may have reduced cows’ motivation to move onto the milking platform, because the access to PRE feed may have been sufficient to abate their appetite, or they engaged in other activities (i.e.: ruminating). Research conducted in an indoor system to quantify relationships between facilities, indicated a strong association between milking procedure and feeding in a concentrate station in the exit lane (Halachmi et al. 2000), suggesting that feeding after milking was an effective way of increasing cow traffic through an AMS milking station. However, no comparison was made with feeding before milking in that study.

Although treatment affected return time from the paddock, the proportion of milkings with intervals above 16 hours was not reduced. The lack of a treatment effect on daily milk yield indicates that the impact on milking interval, although significant, was small and not sufficient to affect yield.

CONCLUSION

Pre-feeding cows can reduce the time to return to the dairy of cows milked in a pasture based AMS, although it also increases the time spent in feeding and waiting area, resulting in a higher overall milking interval, but no change in daily milk yield.

ACKNOWLEDGEMENTS

The authors acknowledge the support of Dairy Australia, NSW Department of Primary Industries, University of Sydney, and DeLaval as investors in the FutureDairy project. We also thank the farm staff and technicians for their assistance in preparing and running the trial.


Prescott NB, Mottram TT, Webster AJF (1998a) Effect of food type and location on the attendance to an automatic milking system by dairy cows and the effect of feeding during milking on their behaviour and milking characteristics. Animal Science. 67, 183-193.

Border irrigation in the southern Murray Darling Basin – what is the best inflow rate?

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ABSTRACT

The hydrological performance of border irrigation under various inflow rates has been evaluated. Moira loam soil under perennial pasture exhibited rapid initial crack fill followed by a low final infiltration rate. Consequently, inflow rates from 0.14 to 0.39 ML/d/m caused no substantial difference in infiltrated depth nor deep drainage losses. In determining the best inflow rate on this soil, aspects such as a time saving and ease of management would have greater influence. The more permeable Cobram loam soil under lucerne had relatively high infiltration rates. Irrigation inflow rates of 0.17 ML/d/m provided an average of 76 mm infiltration, compared with 70 mm infiltration for inflow rates of 0.36 ML/d/m. Production data suggest that the higher inflow rate at this site should be implemented with a shorter irrigation interval.

Keywords: Inflow rate; irrigation assessment; infiltration; soil moisture

INTRODUCTION

The dairy industry is a substantial water user in the southern Murray Darling Basin. Over 95% of dairy farms in the region use irrigation, with border (Brouwer et al. 1988) irrigation the dominant irrigation system. This paper reports on preliminary results of measurements and modelling undertaken to compare the effect of increased inflow rate on the hydrological performance of border irrigation system on two soil types.

MATERIALS AND METHODS

Irrigation assessments were made at a perennial pasture site on a dairy farm near Strathmerton, Victoria on Moira loam, a soil with heavy clay subsoil below 20 cm depth (Butler et al. 1942). Bay lengths were 192 m, with slope of 1:1200. Measurements were also made at a lucerne site on a farm supplying dairy fodder near Katunga, Victoria. The site was on Cobram loam, a more permeable soil (Butler et al. 1942) and had bay lengths of 243 m and slope of 1:750.

In this paper inflow refers to the flow at the supply channel outlet to the irrigation bay. At each site, two bays were monitored throughout the 2011/12 irrigation season. For each bay, irrigation inflow, water advance and depth, soil moisture and runoff were measured. Water at both sites was drawn from the regional surface supply. At each site the irrigation inflow data were acquired from an electromagnetic flow (magflow) meter and adjusted for measured transient changes in storage volume in the farm supply channel. Higher inflow rates at the Moira loam site were achieved by supplementing the surface supply with low salinity groundwater, measured with an ultrasonic flow meter attached to the pump outlet. Water advance and depth on the bay was measured using capacitance depth loggers. A calibrated neutron probe and capacitance probes were used to measure soil profile water content. Runoff was measured from the Moira loam bays with logged flumes and from the Cobram loam bays by metered pumping from a small, temporary sump. Lucerne yield was estimated at each harvest by cutting ten quadrats (0.64 x 0.32 m) from each bay to ground level. The dry matter content of each quadrat was determined after drying 1 kg subsample at 100 °C for 48 hrs. The surface irrigation model SISCO (Gillies et al. 2010) was fitted to field measurements by optimising the infiltration and surface roughness parameters.

RESULTS

Average irrigation inflow rates at the Moira loam site were variable between irrigation events, ranging on one bay from 0.14 to 0.26 megalitres per day per metre of bay width (ML/d/m) and from 0.24 to 0.39 ML/d/m on the other. Soil volumetric moisture content below 40 cm depth varied little throughout the irrigation season. The fitted surface irrigation model consistently indicated that the bay cumulative infiltration featured rapid initial crack fill, when most infiltration occurred, followed by a final infiltration rate of less than 1 mm/hr. No substantial differences in infiltrated depth were evident for the range of measured inflow rates.

At the Cobram loam lucerne site, average inflow rates for each irrigation event were consistently 0.17 ML/d/m on one bay and 0.36 ML/d/m on the other. Capacitance probes indicated that irrigation water infiltrated to over 1 m depth and that the lucerne was using water from the soil profile to at least 1 m depth. A surface irrigation model fitted to field measurements indicated a bay average initial infiltration rate of about 90 mm/hr in the first ten
minutes, reducing to approximately 18 mm/hr after 1 hour and 12 mm/hr after 3 hours. At this site, an average of 76 mm was applied with each irrigation of the 0.17 ML/d/m inflow bay, with an average of 70 mm applied to the 0.36 ML/d/m inflow bay. The 0.17 ML/d/m bay grew 27.3 tonnes of dry matter per hectare (t DM/ha), 2.1 t DM/ha more than the 0.36 ML/d/m bay.

**DISCUSSION AND CONCLUSION**

A fitted model used to extrapolate beyond measured inflow rates on the relatively heavy, Moira loam indicated that inflow rate made little difference to infiltrated depth because of the low final infiltration rate and the long duration of surface drainage from bays. Under these conditions deep drainage losses would not be a dominant factor in determining the best inflow rate, and aspects such as time saving and ease of management would be more important.

At the Cobram loam site, lucerne production results indicated that infiltration at the higher inflow rate may not have been fully meeting the crop water requirement at the farmer’s irrigation schedule. A replicated experiment would be required to confirm this.

**REFERENCES**


**ACKNOWLEDGEMENTS**

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Net benefits and risks of changing calving system for a case study farm in West Gippsland

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\textbf{ABSTRACT}

The relative advantages in cost of production and profitability of Autumn and Spring calving for a case study farm in the West Gippsland region of Victoria, south-west of Drouin, has been investigated using simulation modelling over ten years. The performance of the base farm, which was primarily autumn calving, and two alternative spring-dominant calving systems were analysed. The Autumn calving system generated the highest annual net cash flow, highest nominal internal rate of return and greatest growth in owner wealth. Though feed and other variable costs were higher for the Autumn calving system compared to the Spring calving systems, they were more than offset by higher milk price received. This analysis provides a comparison of the costs and benefits of changing from autumn to spring calving, and will assist dairy farmers considering a similar change to their businesses.

\textbf{Keywords:} Dairy, Risk, Economics

\textbf{INTRODUCTION}

A common perception is that dairy businesses with herds calving predominantly in the Autumn in Southern Australia are higher cost operations than Spring calving systems. Milk companies offer incentives to dairy farmers to encourage milk supply in months of traditionally lower milk production (Winter and Autumn). The relative advantages of Autumn and Spring calving for a case study farm in the West Gippsland region of Victoria, south-west of Drouin have been investigated.

\textbf{MATERIALS AND METHODS}

The approach described in (Ho et al. 2007) and (Heard et al. 2012) was used and comprised several key aspects: namely whole farm biophysical and economic modelling, a case study farm, and input from an industry steering committee, over a planning period of 10 years. The analysis of the Autumn and Spring calving systems involved estimating the supply of and demand for metabolisable energy on a monthly and annual basis (Standing Committee on Agriculture and Resource Management 1990; CSIRO 2007). The whole farm simulation was stochastic, with risky variables such as milk price, supplementary feed prices, and pasture yield consumption represented as probability distributions (Table 1). The performance of the alternatives were judged using the criteria of economic efficiency (annual and cumulative profit), liquidity (annual and cumulative net cash flows) and growth (increase in wealth).

\begin{table}[h]
\centering
\begin{tabular}{|l|lll|}
\hline
\textbf{Input Costs/Yields} & \textbf{P25} & \textbf{Median} (P50) & \textbf{P75} \\
\hline
Milk Price ($/kg milk fat + protein) & & & \\
Traditional & $4.30 & $4.78 & $5.15 \\
Domestic & $4.85 & $5.33 & $5.70 \\
Grain ($/t DM) & $234 & $290 & $335 \\
Milk quality hay ($/t DM) & $218 & $255 & $286 \\
Low quality hay ($/t DM) & $198 & $235 & $266 \\
Perennial pasture consumption (t DM/ha) & 10.5 & 11.3 & 12.0 \\
Chicory consumption (t DM/ha) & 15.1 & 15.9 & 16.6 \\
Maize yield (t DM/ha) & 9.9 & 12.3 & 14.4 \\
Annual ryegrass pasture (t DM/ha) & 6.8 & 7.4 & 7.6 \\
Outblock pasture consumption & 9.5 & 10.3 & 11.0 \\
\hline
\end{tabular}
\caption{Key percentiles (P) for each of the probability distributions defined for input variables}
\end{table}

Base farm and development options.

The case study herd was mostly Autumn calving with 90% of the 515 cow herd calving between March and May and the remainder calving in August. This made them eligible for the ‘domestic’ milk price scheme. In the year just past, which formed the base case, production was 538 kg milk protein and fat per cow. On the 206 ha milking area, pasture consumption...
was 11.5 t DM/ha, and 1.2 t DM grain/cow was fed. The system in place on the case study farm when the data was collected was used as the ‘base farm’. The annual Operating Profit (Earnings Before Interest and Tax, EBIT) of the base farm system was $488,000, with 6.6% return to total capital and approximately $6.0 million net worth.

Two potential alternative systems for the case study business, predominantly Spring calving, were defined and analysed. In Spring calving system #1 the same milk production, milking area, pasture consumption, grain fed per cow and stocking rate (2.5 cows/ha) were maintained as for the Base Farm. Spring calving system #2 had a higher stocking rate (3.0 cows/ha) than the base case, and milk production per cow was unchanged. This higher stocking rate opportunity was investigated because the project steering committee argued that it was common for dairy farmers to reduce stocking rate when changing systems from Spring calving to Autumn calving. The additional cows in Spring calving system #2 needed to be fed fully using purchased supplementary feed. Both Spring calving systems #1 and #2 qualified for the ‘traditional’ milk payment scheme.

RESULTS

In the simulations, the Autumn calving base farm consistently generated higher annual and cumulative net cash flow than the Spring calving systems. The high stocking rate Spring calving system #2 had the lowest median and most variable annual net cash flow (ANCF) (Table 2), with negative NCFs 17% of the time. The Spring calving system with the same herd size and production per cow as the base case was substantially more risky than the base farm, with ANCF expected to be negative for 5% of the time, compared with 1% of the time for the base case.

The greater variability of business performance of the Spring calving systems is explained mostly by greater reliance on more expensive and variable cost of purchased feed relative to the base farm. Approximately 37% of the total diet of the high stocking rate Spring calving cows was made up of purchased supplements, compared with 19% in both the base farm and the lower stocking rate Spring calving system. The difference in annual feed cost between the base farm and the low stocking rate Spring calving herd was $54,000, despite having the same cow numbers, the same pasture consumption and feeding the same amount of grain (Table 2). This difference resulted from conserving pasture from the Spring ‘peak’ and feeding out in the following Autumn and winter.

Over the ten year period of analysis of this business, changing from Autumn calving to a Spring-dominant calving system reduced the profitability of the business. The median internal rate of return (IRR), an indicator of economic efficiency measured by the percentage return on all the capital invested in the business, was higher for the base farm than the low stocking rate Spring calving system, but had a similar level of variability. The base farm also had a higher and less variable IRR than the high stocking rate Spring calving system (Table 2). All the systems performed well in terms of economic efficiency, but the base farm was the best.

The Spring calving system with the high stocking rate was less profitable than the other two systems. This could be attributed in part to there being no increase in total pasture consumption with the increase in cow numbers. In practice, increasing stocking rate can be associated with increased pasture consumption. However, in this case, the industry steering committee felt that the farm was already performing well with regard to pasture consumption, and an increase would be difficult to achieve without significantly increasing inputs e.g. fertiliser use. An increase in pasture consumption would reduce the dependence on purchased feed, and the economic performance of the high stocking rate Spring calving system would improve.

Table 2: Summary results for the base farm and development options

<table>
<thead>
<tr>
<th></th>
<th>Base farm (Autumn dominant calving system)</th>
<th>Option 1 (Spring dominant calving system)</th>
<th>Option 2 (High stocking rate Spring dominant calving system)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Median annual net cash flow</td>
<td>$488,000</td>
<td>$363,000</td>
<td>$294,000</td>
</tr>
<tr>
<td>Std Dev</td>
<td>$249,000</td>
<td>$251,000</td>
<td>$338,000</td>
</tr>
<tr>
<td>Median nominal internal rate of return (%)</td>
<td>8.9%</td>
<td>7.1%</td>
<td>5.8%</td>
</tr>
<tr>
<td>Std Dev</td>
<td>1.1%</td>
<td>1.1%</td>
<td>1.4%</td>
</tr>
<tr>
<td>Milk price ($/kg protein + fat)</td>
<td>$5.2</td>
<td>$4.7</td>
<td>$4.7</td>
</tr>
<tr>
<td>Total gross income</td>
<td>$1,608,000</td>
<td>$1,415,000</td>
<td>$1,681,000</td>
</tr>
<tr>
<td>Variable costs</td>
<td>$774,000</td>
<td>$720,000</td>
<td>$992,000</td>
</tr>
<tr>
<td>Feed costs</td>
<td>$618,000</td>
<td>$564,000</td>
<td>$808,000</td>
</tr>
<tr>
<td>Median annual operating profit in Yr 4</td>
<td>$315,000</td>
<td>$184,000</td>
<td>$136,000</td>
</tr>
</tbody>
</table>
A key goal of farmers is to increase their net worth. Owner’s capital at the end of the 10 years indicates which system had the potential to contribute most to owners’ net worth. Nominal owner’s capital at the end of the ten years for the base farm was $1.8 million greater than the best of the alternative systems (Figure 1). The ending net worth with the high stocking rate Spring calving system was the worst of all, with a median value of $11.4 million which was also more variable than the other two systems.

**Figure 1:** Nominal owner’s capital in year 10. This is the capital in nominal terms that would be left if the business was sold at the end of 10 years.

**DISCUSSION**

The results of the analysis indicate that in this region, for this case study, a predominantly Autumn calving system can outperform a Spring calving system. In the case of the farm examined in this analysis, any additional feed costs associated with calving in Autumn were compensated well by the higher price paid for milk in Autumn and Winter. While the Autumn calving system was more profitable than the Spring calving systems, there are ‘non economic’ factors not included in the simulations that warrant consideration. For instance, the industry steering committee identified risks such as a dry Autumn, wet winter, not meeting factory requirements for ‘domestic incentive’ payments and the potential stress on family life. Individual preference for risk will vary with many factors, such as stage of career, age and other personal commitments. Although no economic value was placed on these factors in the analysis, they influence decisions made by farmers.

**ACKNOWLEDGEMENTS**

This work was supported by funding from Dairy Australia, GippsDairy and the Department of Primary Industries, Victoria.

Thanks to the case study farmer and family for the help to gain an understanding of how an Autumn calving system operates. Thanks also to the Dairy Directions Gippsland steering committee for providing insight and understanding into the analysis.

**REFERENCES**


**Water footprint: A new sustainability indicator relevant to the global dairy industry**

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² AgResearch Limited, Ruakura Research Centre, Private Bag 3123, Hamilton 3240, New Zealand

**ABSTRACT**

The water footprint is a new sustainability indicator which can offer strategic insights relevant to reducing environmental impacts related to water use in a product life cycle. There is also interest in its use for environmental reporting and product labelling, with an international standard in development (ISO 14046) and sector guidelines for dairy being prepared by the International Dairy Federation. For case study production systems in the Waikato and Canterbury regions of New Zealand, single score water footprints, integrating consumptive and degradative water use impacts, were 986 and 752 L H₂Oe/kg milk. In both cases, improved nutrient management is highlighted.

**Keywords:** life cycle assessment; water use; water stress; milk; environmental labelling; New Zealand.

**INTRODUCTION**

Freshwater has become a critically scarce and overexploited natural resource in many parts of the world, threatening irreversible damage to ecosystems and the ability to meet the dietary requirements of the expanding world population (Rockström et al. 2009). As such, there exists a clear recognition that the pressure on freshwater systems from the production of goods and services must reduce in intensity (Ridoutt and Pfister 2010). To support this objective, recent years have seen the rapid development of water footprinting, which like carbon footprinting is based on life cycle assessment (LCA). The intent is to quantify potential environmental impacts related to water use across a product life cycle. Impact assessment is critical because the environmental relevance of water use varies, by location and source, due to the local and regional nature of water scarcity (Ridoutt and Huang 2012). Water footprints can help to identify strategically important ways to improve environmental performance. There is also interest internationally in their use for environmental reporting and product labelling. An international standard for water footprinting (ISO 14046) is currently in development and the International Dairy Federation is preparing guidance for application in the dairy sector. The agriculture and food industries are highlighted because globally they account for around 70% of freshwater withdrawals and are a significant contributor to freshwater quality degradation (Ridoutt 2011).

The draft international standard requires that impacts related to both consumptive and degradative water use (pollution) need to be assessed. Initial applications of water footprinting in the dairy sector focussed on consumptive water use alone (Ridoutt et al. 2010) or the reporting of multiple indicators (Zonderland-Thomassen and Ledgard 2012). This study demonstrates a new water footprint calculation method combining consumptive and degradative water use impacts into a single indicator (Ridoutt and Pfister 2012) using two case study dairy systems in New Zealand (NZ).

**MATERIALS AND METHODS**

Typical dairy production systems in the Waikato (North Island; non-irrigated) and Canterbury (South Island; irrigation of 565 mm ha⁻¹ yr⁻¹) regions were studied. Full details of the production systems and data collection are described in Zonderland-Thomassen and Ledgard (2012). Water footprints (cradle to farm gate) were calculated following Ridoutt and Pfister (2012) with results reported in the reference unit of litres of water equivalents (L H₂Oe), where 1 L H₂Oe represents the burden on water systems from 1 L of consumptive water use at the global average Water Stress Index (WSI; Pfister et al. 2009).

**RESULTS**

For fat-and-protein-corrected milk (FPCM) produced in Waikato and Canterbury, the single-indicator water footprints were 986 and 752 L H₂Oe per kg respectively. In both cases, degradative water use made the greatest contribution (Table 1).
**Table 1:** Water footprint results for FPCM produced in Waikato and Canterbury, NZ

<table>
<thead>
<tr>
<th></th>
<th>Waikato (L H₂Oe/kg FPCM)</th>
<th>Canterbury (L H₂Oe/kg FPCM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Consumptive water use</td>
<td>&lt; 1</td>
<td>7</td>
</tr>
<tr>
<td>Degradative water use</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Freshwater</td>
<td>104</td>
<td>80</td>
</tr>
<tr>
<td>Eutrophication</td>
<td>653</td>
<td>492</td>
</tr>
<tr>
<td>Terrestrial ecotoxicity</td>
<td>227</td>
<td>171</td>
</tr>
<tr>
<td>Freshwater ecotoxicity</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td>Marine ecotoxicity</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>986</strong></td>
<td><strong>752</strong></td>
</tr>
</tbody>
</table>

**DISCUSSION AND CONCLUSION**

These results suggest that improved nutrient management is the priority to reduce water footprints in the cases of milk production in Waikato and Canterbury. Further use of LCA-based water footprinting in the dairy sector is encouraged to guide environmental improvement and for reporting to interested stakeholders, which is likely to become increasingly necessary. An important feature of LCA-based water footprinting is that potential tradeoffs with the carbon footprint and other indicators can be quantitatively assessed, as a safeguard against unintended outcomes.

**ACKNOWLEDGEMENTS**

This study was jointly funded by CSIRO Australia and the AgResearch Capability Fund provided by the New Zealand Ministry of Science & Innovation.

**REFERENCES**


Feed nitrogen use efficiency and milk urea nitrogen concentrations on grazing-based dairy farms

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ABSTRACT

We investigated feed nitrogen use efficiency and milk urea N concentrations of lactating herds on 17 commercial dairy farms in Victoria, Australia during two contrasting seasons. The wide range of FNUE and MUN levels between farms and seasons demonstrated opportunities to improve diet management and reduce N intakes on many dairy farms.

Keywords: Feed N use efficiency, milk urea nitrogen

INTRODUCTION

Dairy systems are recognized as significant contributors of excess nitrogen (N) to the environment (Steinfeld et al. 2006). The efficiency with which dairy cows utilise feed N to make milk greatly influences the amount of N excreted in dung and urine. In turn, excreted N results in significant volatilisation and leaching losses in grazing systems. While N intakes and manure N production have received considerable attention in confinement dairy systems, relatively little information is available within grazing systems (Powell et al. 2010). In part this is due to difficulties in determining pasture DM intake, variability in pasture quality and N content between seasons and preferential grazing of pasture species. In this study we investigated the relationships between dietary N intake, feed N use efficiency (FNUE) and milk urea N (MUN) concentrations in contrasting seasons using data from 17 grazing-based commercial dairy farms in Victoria, Australia.

MATERIALS AND METHODS

The dairy farms involved ranged in sized from 57 to 467 ha, herd size ranged from 98 to 680 lactating cows, and milk production ranged from 5,230 to 9,987 l cow⁻¹ year⁻¹ (Gourley et al. 2012). Dairy farms were visited on two occasions; in spring (November 2008) when grazed pasture formed the majority of the dietary intake, and summer (February 2009) when supplementary feeding was higher. Representative samples of all feed components including pasture, and milk, were collected. The amount of pasture consumed by the grazing dairy cows on each farm was calculated based on the energy required by the animals to produce milk, and accounting for additional energy demands such as pregnancy, maintenance, grazing and walking (Heard et al. 2011). The energy provided in all feed components was subtracted from the total energy requirement of the cows to estimate the energy consumed in pasture. The pasture DM consumed was then calculated by dividing the energy required in pasture by the analytical pasture ME. Feed samples were analysed for CP concentrations; milk samples were analysed for protein and MUN concentrations. The average FNUE for the herd was calculated as:

\[ FNUE = \frac{\text{Milk N (g cow}^{-1} \text{ day}^{-1})}{\text{Feed N intake (g cow}^{-1} \text{ day}^{-1})}. \]

RESULTS AND DISCUSSION

Cows consumed between 327 and 792 g N cow⁻¹ day⁻¹, with a median of 513 g N cow⁻¹ day⁻¹. Feed NUE ranged from 0.15 to 0.35, with a median value of 0.23 (Figure 1a). The majority of dairy farms had herd FNUE values well below the optimum target of 0.35. Nevertheless, this range of FNUE values is similar to results from other studies on confinement-based dairy farms (Powell et al. 2010). FNUE was significantly (<0.001) and negatively related to N intake, and there was a significant difference between relationships in spring and summer. This may be explained by differences in pasture availability, amount and type of supplementation and stage of lactation of the herd.

Milk urea N values ranged between 5.3 and 19.8 mg dl⁻¹ with a median of 12.1 mg dl⁻¹ (Figure 1b). There was a significant (P<0.001) positive relationship between N intake and MUN in agreement with previous studies, with no significant difference between seasons (P=0.259). The normal range for MUN concentration is recommended to be between 10 - 14 mg dl⁻¹ with levels above this range indicating excessive, and below, insufficient N intake (Wattiaux, et. al., 2005). The large range of MUN concentrations and the low concentrations measured on many farms in summer, suggests that N intakes are variable and often restricted during summer conditions.

Determining FNUE represents the logical first
step in assessing the efficiency of feed N transformed into milk, N excreted in manure and the proportion of N potentially lost from production within a dairy farm. Improving FNUE may yield multiple benefits, such as reductions in the need to import feeds and fertilizers (Kohn et al. 1997) and decrease the excretion of N. As a way of determining appropriate feed N intakes, MUN may provide a useful indicator, and is commonly used in the USA and Europe on commercial dairy farms (Jonker et al. 1998; Nousiainen et al. 2004).

CONCLUSION

We suggest that simple assessments of FNUE and MUN can be used in grazing-based dairy operations to assess feed N management practices. The FNUE and MUN levels determined in this study demonstrate opportunities to improve diet management and reduce N intake on many dairy farms. Managing seasonal fluctuations in N intake however appears to be a particular challenge in grazing-based systems as MUN levels indicated that excessive CP levels were common on many Victorian dairy farms in spring, while insufficient CP intake was common in summer.

CONCLUSION

We suggest that simple assessments of FNUE and MUN can be used in grazing-based dairy operations to assess feed N management practices. The FNUE and MUN levels determined in this study demonstrate opportunities to improve diet management and reduce N intake on many dairy farms. Managing seasonal fluctuations in N intake however appears to be a particular challenge in grazing-based systems as MUN levels indicated that excessive CP levels were common on many Victorian dairy farms in spring, while insufficient CP intake was common in summer.

![Figure 1:](attachment:image.png) The relationship between feed nitrogen use efficiency (a) and milk Urea nitrogen (b) and nitrogen intake for 17 Victorian dairy farms from samples collected at two separate sampling times.

REFERENCES


Impact of stocking rate and feed use on milksolids production and pasture utilisation in New Zealand pasture based farm systems

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ABSTRACT

Relationships between stocking rate, feed use and milksolids (MS) production were examined using data from 12 individual farmlet trials from 1990 to 2010. Comparative stocking rate (CSR), measured as kg liveweight (LW)/tonne dry matter (t DM) of feed available, was used to examine the effects of feed demand versus availability on pasture utilisation, MS production per cow and per ha, and cow efficiency (MS production/kg LW). A one unit reduction in CSR resulted in 0.47% ($P<0.01$) reduction in pasture utilisation, an increase in MS of 4.5 kg/cow ($P<0.001$) and increased MS production/kg LW of 0.75% ($P<0.001$). There was no significant relationship between CSR and MS/ha. These findings are important for future productivity improvements, particularly when operational challenges (through environmental impact or limited infrastructure) require lower cow numbers. Achieving optimal pasture utilisation, rather than maximum, will create more efficient farm systems.

Keywords: dairy cow; pasture utilisation; comparative stocking rate.

INTRODUCTION

The effects of stocking rate (cows/ha) on farm performance have encouraged increased stocking rate to improve pasture utilisation/ha and MS production/ha in pasture based systems (McCarthy et al. 2011; Macdonald et al. 2008a). Recently the appropriateness of this has been challenged with questions around:

1. The impact of high stocking rates on the environmental footprint of the farm
2. High milk prices relative to supplement price, which have created an opportunity to import feed
3. The need to increase feed allowance per cow to fully realise annual genetic gains in animal performance, either through lower stocking rate or increased imported feed.

Comparative stocking rate (CSR; Macdonald et al. 2008a), can be used to determine the effects of a change in feed demand and supply on farm performance. It is a better descriptor than cows/ha, as it includes cow size and supplements/ha in addition to cow numbers and pasture grown/ha. Farm system modelling has a role in determining when reduced CSR is appropriate, although modelling predictions sometimes assume pasture utilisation is maintained by reducing CSR (Dewes et al. 2010).

The aim of this analysis was to determine the relationships between CSR, production measures and pasture utilisation in pasture based systems.

MATERIALS AND METHODS

Information from 12 multi-year farmlet trials (Macdonald, 1999, Macdonald et al. 2008a, Macdonald et al. 2008b) between 1990 and 2010, representing 98 individual farmlet years, was analysed (see Table 1). Ninety-six per cent of the herds were Holstein –Friesian cows.

Farmlets were managed according to a set of decision rules outlined by Macdonald and Penno (1998), (Macdonald et al. 2005) and measurement procedures are outlined by (Macdonald et al. 2008b). Comparative Stocking Rate was calculated using cow LW at or near the 1st of December and annual net herbage accumulation plus imported supplementary feed. Farmlet multi-year mean data were analysed using a random coefficient regression model in GenStat 14.1 with CSR as a fixed linear effect and trial and CSR within trial as random effects. The trial was deemed to be the set of farmlets which had differing CSR managed under similar decision rules during the same time period. Pasture utilisation was defined as annual pasture disappearance, (estimated from difference between pre and post grazing yield), as a percentage of measured annual net herbage DM accumulation/ha.

RESULTS AND DISCUSSION

This analysis demonstrates significant relationships exist between CSR, and MS/cow, MS production/kg LW and pasture utilisation, (Table 2). This provides a means for predicting the outcomes of changing CSR on key performance parameters and confirms that pasture utilisation will drop by changing to a lower CSR, (Macdonald et al. 2008b). Increasing CSR to maximise pasture utilisation reduces energy intake per cow, increases the proportion of energy consumed being partitioned to maintenance (Baudracco et al. 2010) and reduces...
MS per cow and MS/kg LW. While genetic improvement of cows has occurred during the 20 years of data gathering, the dataset did not allow for the determination of interactions between CSR and genotype. However, one trial (Macdonald et al. 2008b), which contributed 26 of the 98 farmlet years, specifically quantified the effect of genetic change over a range of feed allowances and types. This indicated that the optimum CSR for profit will reduce as genetic merit increases (Glassey and Macdonald, 2007).

Insufficient numbers of farmlets with high levels of supplementary feed (Table 1) prevented the assessment of how relationships between CSR and key performance parameters were altered by supplement input level.

CONCLUSION

Changes in genotype and supplementary feed use over time demands the identification of the appropriate CSR to optimise rather than maximise pasture utilisation. Successful implementation of the chosen CSR is dependent on the skill of the farmer at applying pasture management decision rules making efficient use of supplements and identifying the correct cow genotype for their farm system. Further work is planned to explore the links between CSR, profitability and sustainability.

ACKNOWLEDGEMENTS

Thanks to Barbara Dow (DairyNZ) for statistical analysis and Jim Lancaster, and many others, for farmlet records.

REFERENCES


Table 1: Trial information, supplementary feed type and DairyNZ farm system category for the 98 farmlet years in this study

<table>
<thead>
<tr>
<th>Trial name, duration and grouping</th>
<th>Farmlet years</th>
<th>Farmlet means included in the analysis</th>
<th>DairyNZ farm system category</th>
<th>Farmlets in category</th>
<th>Type of imported supplement used</th>
</tr>
</thead>
<tbody>
<tr>
<td>Jersey-Friesian Stocking rate trial 1991-1993 2 trial groups</td>
<td>8</td>
<td>4</td>
<td>1</td>
<td>4</td>
<td>None</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Grass silage</td>
</tr>
<tr>
<td>1.75 tonnes milksolids trial 1994-1998 2 trial groups</td>
<td>31</td>
<td>15</td>
<td>1</td>
<td>14</td>
<td>None</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Grass silage</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Grass silage, Maize silage, Maize grain</td>
</tr>
<tr>
<td>Stocking Rate Trial 1999-2001 (1 trial group)</td>
<td>20</td>
<td>10</td>
<td>1</td>
<td>11</td>
<td>None</td>
</tr>
<tr>
<td>Holstein-Friesian Strain Trial 2002-2005 (5 trial groups)</td>
<td>26</td>
<td>15</td>
<td>1</td>
<td>12</td>
<td>None</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Grass silage</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Maize silage</td>
</tr>
<tr>
<td>Resource Efficient Dairying trial (RED) 2004-2010 (2 trial groups)</td>
<td>13</td>
<td>5</td>
<td>1</td>
<td>9</td>
<td>None</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Maize silage</td>
</tr>
</tbody>
</table>

Table 2: Relationship between CSR and variables analysed across all farms in dataset

<table>
<thead>
<tr>
<th>Variable</th>
<th>Slope</th>
<th>SE</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>MS/cow</td>
<td>-4.45</td>
<td>0.45</td>
<td>0.001</td>
</tr>
<tr>
<td>MS/ha</td>
<td>-3.30</td>
<td>3.14</td>
<td>0.32</td>
</tr>
<tr>
<td>Pasture Utilisation</td>
<td>0.467</td>
<td>0.091</td>
<td>0.01</td>
</tr>
<tr>
<td>MS as % LW</td>
<td>-0.0075</td>
<td>0.0012</td>
<td>0.001</td>
</tr>
</tbody>
</table>
Grazing cows milked once- or twice-daily have similar milk production responses to energy supplements during early lactation

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2DairynZ, P.O. Box 160, Lincoln University, Lincoln 7647, NZ

ABSTRACT

This experiment compared milk production and body condition score (BCS) responses to energy supplements in grazing cows milked either once- (1X) or twice-daily (2X) for 10 weeks, immediately, post-calving. Regardless of milking frequency, feeding concentrates during the first six weeks post-calving increased energy intakes and tended to increase milk protein production and peak milk and milksolids (fat + protein) yields, but did not alter BCS loss. Milking cows 1X, however, reduced milk and milksolids yields and decreased BCS loss during early lactation compared with 2X. In conclusion, cows milked 1X and 2X had similar milk production and BCS responses to energy supplements during early lactation.

Keywords: once-daily milking; early lactation; concentrate supplements.

INTRODUCTION

In a pasture-based system, milking cows once-daily (1X) provides opportunities for farmers to lower labour requirements, improve animal health and body condition score (BCS), decrease farm costs, and have a more flexible lifestyle (Davis et al. 1999). However, milking 1X decreases milk production per cow relative to milking twice-daily (2X; Davis et al. 1999), and this leads to lower farm revenue. Offering cows supplements when at pasture increases milk production (Bargo et al. 2003); however, it is uncertain whether milk production and BCS responses measured in cows milked 2X are appropriate for cows milked 1X. This study compared the immediate and carry-over effects of feeding energy supplements, during the first six weeks post-calving, on the milk production and BCS of grazing dairy cows milked either 1X or 2X during early lactation.

MATERIALS AND METHODS

Multiparous Holstein-Friesian cows (n=96; 475 kg live weight) were randomly allocated to one of four treatments in a 2x2 factorial arrangement. Cows were milked either 1X or 2X for 10 weeks post-calving; within each milking frequency (MF) treatment, cows were offered a diet of grazed pasture plus lucerne pellets with (CONC) or without (STD) 4.5 kg DM/cow/day of a pelleted concentrate (12.5 MJ metabolisable energy (ME)/kg DM) for the first six weeks post-calving, followed by the STD diet for four weeks.

Concentrate was individually offered to CONC cows twice daily and was gradually introduced into the diet over a seven-day period post-calving, with amounts offered and refused measured to calculate daily intakes. Intakes of pasture (12 MJ ME/kg DM) were estimated from the difference between pre- and post-grazing pasture mass and area grazed. An average of 2.2 kg DM/cow/day of lucerne pellets (9 MJ ME/kg DM) were also fed during Weeks 1-6 due to insufficient pasture.

Milk yields were determined daily for 10 weeks post-calving, while milk composition and BCS (1-10 scale) were determined weekly. Data were analysed using mixed models fitted with REML in GenStat. Data from 17 cows were removed from the analysis as these animals remained on the dietary treatments for more than the proposed six weeks (n = 4, 5, 4, and 4 cows for 1XSTD, 1XCOnC, 2XSTD and 2XCOnC, respectively). Treatment effects were considered significant when \( P<0.05 \) and declared a trend when \( P<0.10 \).

RESULTS

There were no interactions between MF (1X, 2X) and diet (STD, CONC). On average during the first six weeks post-calving, cows offered CONC consumed 3.5 kg DM concentrate/day (43 MJ ME/day) and had greater total estimated energy intakes than cows offered the STD diet (181 vs. 150 MJ ME/day, \( \text{SED} = 2.6 \)), but lower estimated pasture energy intakes (117 vs. 131 MJ ME/day, \( \text{SED} = 2.8 \)) and lucerne intakes (19 vs. 20 MJ ME/day, \( \text{SED} = 0.2 \)). In addition, cows milked 1X had lower total energy intakes than those milked 2X at Week 2 (152 vs. 164 MJ ME/day, \( \text{SED} = 3.3 \)) and Week 3 (160 vs. 172 MJ ME/day, \( \text{SED} = 2.7 \)).

Between Weeks 1-6, cows offered CONC tended to produce more milk protein (Table 1), and tended to have greater peak yields of milk at Week 5 (+2.1 kg/day; +9%) and milksolids (MS; fat + protein) at Weeks 5 and 6 (Figure 1). Cows offered CONC also
tended to have greater daily yields of protein (+0.1 kg; +9%) and MS (Figure 1) at Week 7, one week after concentrate feeding ceased, and cumulative yields of protein and MS between Weeks 7-10 (Table 1). In addition, cows milked 1X had lower yields of milk, fat, protein, and MS during the first 10 weeks post-calving, compared with cows milked 2X (Table 1; Figure 2a).

There was no effect of diet on BCS (results not shown); however, milking cows 1X reduced BCS loss by 0.2 units between Weeks 1-6 (Figure 2b). Cows milked 1X were 0.3 BCS units greater than those milked 2X at Week 6 and this difference remained at Week 10 (Figure 2b).

**DISCUSSION AND CONCLUSION**

Regardless of MF, feeding concentrates to grazing cows during the first six weeks of lactation increased energy intakes, which tended to increase milk protein production, and peak milk and MS yields. For every kg of concentrate DM consumed, cows produced an additional 0.40 kg milk, 5.4 g fat and 19.0 g protein during the supplementation period, with total responses of 0.35 kg milk, 8.0 g fat and 17.4 g protein to Week 10 post-calving; however, greater responses could be expected if cows would have otherwise been underfed (Bargo et al. 2003). In addition, feeding a moderate rate of energy supplements did not alter BCS profiles. Therefore, in early lactation, cows milked 1X or 2X responded similarly to energy supplements by increasing milk protein production, rather than partitioning the extra energy into BCS.

Milking cows 1X during early lactation decreased MS production by 26%, but improved BCS, consistent with other studies (Davis et al. 1999; Phyn et al. 2010). The lack of an interaction between MF and diet indicates that these factors affected milk production and BCS through independent mechanisms, as reported previously (Phyn et al. 2010). Hence, additional high-quality feed could be used to improve milk production in early-lactating cows milked 1X, but purchasing supplements may only be profitable provided pasture is not wasted.

**ACKNOWLEDGEMENTS**

The authors gratefully acknowledge the contributions of staff at the Westpac Taranaki Agricultural Research Station. This study was funded by NZ dairy farmers through DairyNZ Inc.

**REFERENCES**


**Table 1:** Cumulative milk production of cows milked either once-daily (1X) or twice-daily (2X) for 10 weeks post-calving. Cows were offered either a standard diet of grazed pasture plus lucerne pellets (STD) or this diet supplemented with 4.5 kg DM concentrate/day (CONC) for the first six weeks post-calving followed by the STD diet thereafter. There were no interactions (P<0.05) between milking frequency (MF) and diet. Mean values with the standard error of the difference between means (SED) for the main effects of diet and MF are presented.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Week</th>
<th>CONC</th>
<th>STD</th>
<th>1X</th>
<th>2X</th>
<th>SED</th>
<th>Diet</th>
<th>MF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk, kg</td>
<td>1 to 6</td>
<td>1019</td>
<td>961</td>
<td>834</td>
<td>1146</td>
<td>40.9</td>
<td>0.23</td>
<td>&lt;0.01</td>
</tr>
<tr>
<td></td>
<td>7 to 10</td>
<td>636</td>
<td>608</td>
<td>503</td>
<td>742</td>
<td>21.9</td>
<td>0.29</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Fat, kg</td>
<td>1 to 6</td>
<td>47.2</td>
<td>46.4</td>
<td>41.2</td>
<td>52.5</td>
<td>2.84</td>
<td>0.80</td>
<td>&lt;0.05</td>
</tr>
<tr>
<td></td>
<td>7 to 10</td>
<td>29.8</td>
<td>28.6</td>
<td>24.3</td>
<td>34.1</td>
<td>0.64</td>
<td>0.15</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Protein, kg</td>
<td>1 to 6</td>
<td>37.2</td>
<td>34.4</td>
<td>30.2</td>
<td>41.5</td>
<td>1.10</td>
<td>0.07</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td></td>
<td>7 to 10</td>
<td>23.4</td>
<td>21.9</td>
<td>18.7</td>
<td>26.5</td>
<td>0.60</td>
<td>0.08</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Milksolids, kg</td>
<td>1 to 6</td>
<td>84.5</td>
<td>80.8</td>
<td>71.3</td>
<td>94.0</td>
<td>3.80</td>
<td>0.40</td>
<td>&lt;0.01</td>
</tr>
<tr>
<td></td>
<td>7 to 10</td>
<td>53.1</td>
<td>50.5</td>
<td>43.0</td>
<td>60.6</td>
<td>1.16</td>
<td>0.09</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>
Figure 1: Milksolids (fat + protein) yield (kg/cow/d) of cows offered either a standard diet of grazed pasture plus lucerne pellets (STD) or this diet supplemented with 4.5 kg DM concentrate/day (CONC) for the first six weeks post-calving followed by the STD diet for four weeks thereafter. Mean values with the standard error of the difference between means (SED) are presented. *(P<0.10).

Figure 2: a) Milksolids (fat + protein) yield (kg/cow/d) and b) body condition score of cows milked either once-daily (1X) or twice-daily (2X) for 10 weeks post-calving. Mean values with the standard error of the difference between means (SED) are presented. *(P<0.10), **(P<0.05), ****(P<0.01), ****(P<0.001).
Generating saleable carbon offsets from dairy farm systems
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ABSTRACT
A case study approach was used to investigate the economic impact, risks and opportunities for Victorian dairy farmers under the Federal Government’s Carbon Farming Initiative (CFI). The emissions of methane and nitrous oxide from three case study farms were estimated using the Dairy Greenhouse Gas Abatement Strategy calculator. The three farms had milking areas ranging from 129 to 177 ha and outblock areas of up to 411 ha. The number of milking cows on each farm ranged from 288 to 390. Two abatement strategies were then applied to each farm to quantify the possible reduction in emissions, as tonnes of carbon dioxide equivalents (t CO2-e), and the potential value of offsets generated under a range of carbon prices. The abatement strategies tested were feeding cows oils to reduce methane emissions and applying nitrification inhibitors to pastures to reduce nitrous oxide emissions. On the 3 farms examined, total annual methane and nitrous oxide emissions ranged from 1493 to 2215 t CO2-e, with methane accounting for 75-78% of this total. It was found that the application of nitrification inhibitors reduced annual nitrous oxide emissions on the case study farms by up to 19%, whilst feeding cows an oil supplement reduced farm methane emissions by up to 3%. Even if the carbon price was $25/t CO2-e, the income from the sale of offsets in either strategy would be at best $2125/year per farm. It is concluded that the likelihood of farmers adopting these strategies on the basis of generating carbon offsets alone is unlikely.

Keywords: carbon offsets; emissions; Carbon Farming Initiative; greenhouse gases

INTRODUCTION
The Australian Government has committed to a reduction in greenhouse gas emissions, with a carbon pricing scheme introduced in July 2012. Agriculture has been excluded from the scheme, however dairy farmers will be affected through rising input costs and possible “pass-back” from milk factories as processing costs increase (Whittle et al. 2011). One option available to farmers to potentially recoup these costs is to consider participating in the Carbon Farming Initiative (CFI). This scheme is a voluntary carbon offsets scheme whereby farmers generate carbon credits by reducing their farm’s emissions or sequestering carbon which they can then sell to other sectors.

One strategy to reduce methane emissions on a dairy farm is through increasing the amounts of fats and oils in the diet of cows. Using results from their study, together with data from the literature, Moate (et al. 2011) found that for every 1% increase in fat in the diet, enteric methane is reduced by 3.5% irrespective of the type of supplementation. An effective strategy to reduce nitrous oxide emissions is through the application of nitrification inhibitors (de Klein and Eckard 2008). In northern Victoria, these have been shown to reduce nitrous oxide emissions in urine patches on pastures by 47% for 50 days in spring and by 27% for 25 days in January (Kelly et al. 2008). Recent research in south-west Victoria has shown a 35-45% reduction in nitrous oxide emissions, with the period of effectiveness lasting approximately 70 days when applied in September and 100 days when applied in May (Kelly et al. 2012).

Whilst these strategies technically achieve reductions in emissions, there is a need to quantify these at a farm level and assess the viability of the CFI for dairy farmers. A case study approach was used to investigate the economic impact, risks and opportunities for Victorian dairy farmers participating in the scheme.

MATERIALS AND METHODS
A case study farm from each of the 3 key dairying regions in Victoria was used in the analysis (Table 1). All farms were pasture-based systems.
### Table 1: Key details of case study farms used

<table>
<thead>
<tr>
<th>Farm</th>
<th>Farm area (ha)</th>
<th>Milking cows</th>
<th>Farm milk solids</th>
<th>Nitrogen applied (t/annum/farm)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Milking area</td>
<td>Outblock area</td>
<td>No.</td>
</tr>
<tr>
<td>Nth Vic</td>
<td>129</td>
<td>411</td>
<td></td>
<td>390</td>
</tr>
<tr>
<td>Gippsland</td>
<td>140</td>
<td>105</td>
<td></td>
<td>380</td>
</tr>
<tr>
<td>SW Vic</td>
<td>177</td>
<td>-</td>
<td></td>
<td>288</td>
</tr>
</tbody>
</table>

Methane and nitrous oxide emissions from the farms were estimated using version 1.4 of the ‘Dairy Greenhouse Gas Abatement calculator’ (DGas) (Christie et al. 2011), with results reported in carbon dioxide equivalents (CO₂-e). The key assumptions used in the analysis of the two abatement strategies are given in Table 2.

### Table 2: Key assumptions for the two abatement strategies tested

<table>
<thead>
<tr>
<th>Strategy 1: Feeding milking cows oil supplements to reduce methane emissions</th>
<th>Strategy 2: Spraying nitrification inhibitors onto pasture to reduce nitrous oxide emissions</th>
</tr>
</thead>
<tbody>
<tr>
<td>A 1% increase in dietary oil will reduce enteric methane by 3.5%¹</td>
<td>Inhibitor sprayed on milking area only</td>
</tr>
<tr>
<td>Up to 7% of total oil can be fed in the diet</td>
<td>Cows were grazing areas where inhibitor was applied during the period of its effectiveness</td>
</tr>
<tr>
<td>Oil supplement will replace existing supplement (kg for kg DM)</td>
<td>Nitrous oxide emissions were reduced by 45% for 100 days when inhibitor applied in May and 35% for 70 days when applied in September in SW Victoria² and Gippsland</td>
</tr>
<tr>
<td>Cows’ diet already contains 3% oil</td>
<td>N fertiliser was applied at the time the inhibitor was effective</td>
</tr>
<tr>
<td>Oil supplements fed in summer for 90 days</td>
<td>Inhibitor was applied twice per year at a total cost of $165/ha/year</td>
</tr>
<tr>
<td>Extra energy from the oil supplement can be partitioned into milk where 5.5 MJ ME can produce 1 litre of milk of the same composition as the case study farm</td>
<td>Additional DM was valued in terms of ME on a comparative c/MJ basis with purchased supplementary feed</td>
</tr>
<tr>
<td>The cost of the oil supplement was the same as the grain supplement it replaced</td>
<td>Dry matter yield increases used baseline pasture consumption data from each farm to calculate the amount of extra feed produced at DM yield increases of 5, 10, 15 or 20%</td>
</tr>
<tr>
<td>No change to feed delivery system in the dairy was needed</td>
<td></td>
</tr>
<tr>
<td>Oil supplement had an estimated ME of 13.8 MJ/kg DM, with the ME values for the existing grain supplements 12.6, 12.5 and 13.2 for the Nth Vic, Gippsland and SW Vic case study farms, respectively</td>
<td></td>
</tr>
</tbody>
</table>

¹Moate et al. 2011; ²Kelly et al. 2012; ³Kelly et al. 2008

### Results

Across the case study farms, methane emissions were reduced by 29-39 t CO₂-e/farm if the feeding oils strategy was applied (Table 3). Decreases in nitrous oxide emissions from the use of nitrification inhibitors were 50-85 t CO₂-e (Table 3). At a carbon price of $25/t CO₂-e, this would mean income from the strategies applied would be up to $975/farm/year for feeding oils and $2125/farm/year for the use of nitrification inhibitors on the case study farms.
Table 3: Estimated changes in farm methane (CH$_4$) and nitrous oxide (N$_2$O) emissions when two different abatement strategies are applied

<table>
<thead>
<tr>
<th>Farm</th>
<th>Baseline CH$_4$ emissions (t CO$_2$-e/year)</th>
<th>CH$_4$ emissions (t CO$_2$-e/year) when feeding oils strategy applied</th>
<th>Baseline N$_2$O emissions (t CO$_2$-e/year)</th>
<th>N$_2$O emissions (t CO$_2$-e/year) when nitrification inhibitors strategy applied</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nth Vic</td>
<td>1734</td>
<td>1700</td>
<td>481</td>
<td>431</td>
</tr>
<tr>
<td>Gippsland</td>
<td>1443</td>
<td>1404</td>
<td>470</td>
<td>385</td>
</tr>
<tr>
<td>SW Vic</td>
<td>1139</td>
<td>1110</td>
<td>355</td>
<td>286</td>
</tr>
</tbody>
</table>

Table 4 estimates the magnitude of production benefits according to assumptions in Table 2, including some sensitivity analysis around yield increases for the nitrification inhibitors strategy.

Table 4: Possible net production benefits from implementing the 2 abatement strategies

<table>
<thead>
<tr>
<th>Nth Vic</th>
<th>Gippsland</th>
<th>SW Vic</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Strategy 1: Feeding oils</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Estimated increase* in average milk income if additional ME converted to milk ($/farm/year)</td>
<td>7956</td>
<td>9251</td>
</tr>
<tr>
<td><strong>Strategy 2: Applying nitrification inhibitors</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Estimated net value of additional feed ($/farm/year) at yield increases of:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>5%</td>
<td>-16652</td>
<td>-15648</td>
</tr>
<tr>
<td>10%</td>
<td>-12019</td>
<td>-8197</td>
</tr>
<tr>
<td>15%</td>
<td>-7387</td>
<td>-745</td>
</tr>
<tr>
<td>20%</td>
<td>-2754</td>
<td>6706</td>
</tr>
</tbody>
</table>

* Assuming a price of $4.77/kg protein and fat

**DISCUSSION AND CONCLUSION**

The likelihood of farmers adopting the strategies described on the basis of the sale of carbon offsets alone is remote, particularly when the annual costs of participating in the CFI are estimated to be in the order of $2500/farm (Australian Farm Institute, 2011). Assuming a long-term average milk price of $4.77/kg protein and fat, the range in annual milk income from the case study farms is approximately $600,000 to $1,200,000. This further suggests that farmers are unlikely to pursue the small amount of income from the sale of offsets under the CFI.

If net production benefits from applying the strategies described are possible, farmers may consider participating in the CFI. However the potential to achieve a production benefit will vary widely between farms. Variable responses to oil and fat supplementation have been reported in the literature, with milk yield responses influenced by a number of factors including basal diet, stage of lactation, energy balance, fat composition and amount of supplemental fat (NRC 2001). In the study reported here, the estimate of production benefit is at the upper limit of what is possible. There is a chance that no production benefit will be observed in practice and there may even be negative effects on concentrations of milk protein and fat (Moate et al. 2011). In the case of nitrification inhibitors, pasture DM yield increases may be possible under certain conditions. In the study reported here, a range of DM yield increases were tested within the range of what has been achieved in New Zealand. In New Zealand, pasture DM yield benefits of up to 36% from nitrification inhibitors applied to urine patches have been observed, with an estimated 21% increase in annual dry matter yield at the paddock scale (Moir et al. 2007). As the cost of applying the inhibitor was $20,000-$30,000 per farm per year in this study, DM yield benefits in the order of what’s been observed in New Zealand would be necessary to achieve a net production benefit on these farms. However, DM yield benefits of this magnitude have been not observed to date in Victoria. For example, in SW Victoria, DM yield benefits between 0 and 15% have been found when the inhibitors are applied to urine patches, but are considered unlikely to be significant at the paddock scale (Kelly, 2011).
As there will be costs for participating in the CFI and the income received from the sale of carbon offsets is estimated to be relatively small, a continued focus on the core business of producing milk in the most efficient way possible is recommended for most dairy farms, rather than implementing the strategies examined here for the purpose of generating carbon offsets.

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The influence of farm size on income, costs and profitability: results from the Dairy Industry Farm Monitor Project 2006-07 to 2010-11

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ABSTRACT

The topic of farm size and the question “is bigger always better?” continues to be hotly debated by farmers, agricultural economists and farm management consultants around the world. This analysis, using the Dairy Industry Farm Monitor Project historical dataset from 2006/07 to 2010/11, was made to investigate the influence that farm size, defined by the number of cows milked, had on income, costs and profitability. The results indicate that in general larger farms generated higher returns on asset over the five year period analysed. When the total range of returns for individual farms within each category was analysed it was revealed that well managed medium and large farms can perform equally as well as extra large farms. Small farms stand out clearly as having lower mean return on assets, mainly due to the much higher imputed labour costs these farms incur.

Keywords: Dairy, Farm size, Dairy Industry Farm Monitor Project

INTRODUCTION

“Get big or get out!” Sound familiar? The topic of farm size and the question “is bigger always better?” continues to be hotly debated by farmers, agricultural economists and farm management consultants around the world. In general the arguments for increasing size stem from the belief that by increasing the size of businesses farmers will be able to take advantage of economies of size. That is, they will be able to produce more with lower input costs per unit of production. The reduction in costs comes predominantly from spreading total overhead costs over a greater level of production. The aim of this analysis was to investigate the differences in income, costs and profitability of dairy farms of different size, defined by the number of cows milked, using the Dairy Industry Farm Monitor Project historical dataset from 2006/07 to 2010/11 to determine if farm size was a key determinant of profitability.

MATERIALS AND METHODS

The Dairy Industry Farm Monitor Project was established in 2006/07. Annually, it produces a report on the financial and physical performance of dairy farms from the three regions of Victoria; Northern Victoria, South West Victoria and Gippsland. The methods used for farm management economic assessments are described in (Malcolm et al. 2005). The project provides information on individual farms and uses analyses of profit and wealth to assess and compare farm performance focusing on the key measures earnings before interest and tax, net farm income, return on assets and return on equity.

Using the DIFMP historical dataset from 2006/07 to 2010/11 the farms were grouped by size, in terms of the number of cows milked, according to the definitions used by Dairy Australia in the National Dairy Farmer Survey. Thus, less than 151 cows are milked in a small farm, between 151 and 300 cows are milked in a medium farm, between 301 and 500 cows are milked in a large farm, while extra large farms are those where more than 500 cows are milked.

Initially whole farm performance was assessed using the whole farm measures of return on assets and return on equity. In addition, the return on assets of farms of different sizes was analysed and the median, quartile one (Q1) and three (Q3), and complete range of results within each category were assessed.

In order to make comparisons between the different sized farms, income and costs were broken down and presented per kilogram of milk solids sold. All figures displayed are the mean for each group for each year and are expressed in nominal terms. This analysis enabled better interrogation of the data to assess how income and costs vary across farms of differing size and how these variations contribute to differences in whole farm performance.

RESULTS

The results indicated that in general larger farms have generated higher returns on asset over the five year period analysed (figure 1). The exception to this was in 2007-08 when medium farms recorded a mean return on asset of 10.3 percent compared to 9.2 percent recorded by large farms. Over the period mean return on assets has been -0.6 percent for small farms, 4.9 percent for medium farms, 5.0 percent for large farms and 7.1 percent for extra large farms.
While this data indicates that the larger the farm the higher the annual return on assets, when the distribution of returns over the total period is examined, we observe slightly different results (Figure 2). In the box plots in Figure 2, the middle horizontal bar indicates the median for the data set, while the top and bottom horizontal bars of the ‘box’ represent the first (25th percentile) and third (75th percentile) quartile ranges respectively. Finally the long vertical ‘whiskers’ at each end of the boxes represent the total range for all data. While extra large farms achieve the highest mean and median return on assets, medium and large farms performed similarly and had a greater range of returns than extra large farms. Large farms recorded a similar minimum return on assets, while the minimum recorded by medium size farms was much lower.

These results indicate that while the mean return on assets for extra large farms was higher, well managed medium and large farms can perform equally as well as extra large farms. Small farms stand out clearly as having lower mean return on assets and the median value for small farms indicates that approximately half the farms made a profit while half did not. The main impact on the return on assets of small farms was the cost for imputed labour which rose significantly as farms decreased in size with small farms reporting imputed people costs up to four times higher than those reported on extra large farms in some years.

Across the three larger farm size groups it can be seen that the median is toward the lower half of the Q1 to Q3 range indicating that the data is not evenly distributed and that there is a skew toward lower returns.

**DISCUSSION AND CONCLUSION**

The analyses presented here details farm size specific comparisons of key farm profitability indicators over the period 2006/07 to 2010/11. The overall results of the analysis indicate that extra large farms have recorded the highest mean return on assets and highest mean return on equity over the past five years. These returns have been produced primarily by the high gross farm income earned by extra large farms. Total costs including variable and overhead costs for medium, large and extra large farms were very similar over the period. The mean gross farm income and milk price received on small farms was lower than all other sized farms. Variable costs on small farms were similar to those on farms of other sizes however overhead costs were much higher caused mainly by higher imputed costs for labour and management and depreciation. As a result, total costs were higher. Earnings before interest and tax and net farm income were similar for medium, large and extra large farms. The high costs incurred on small farms meant earnings before interest and tax and net farm income were well below the levels reported on the larger farms.

Despite these higher mean returns reported by the extra large farms, individual farms across all categories have performed strongly across the years. This was reflected in the number of farms from all categories ranked in the top 25 percent on an annual basis. These results indicate that as opposed to ‘get big’ the axiom to which dairy farmers should adhere in the twenty first century is ‘get smart’. While farm size had an influence over income, costs and profitability, farms of all sizes had the ability to generate strong business returns and smart farm managers are already making this happen.

**ACKNOWLEDGEMENTS**

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Thanks to the participants of the Dairy Industry Farm Monitor Project who have willingly submitted their farm information over the past five years.


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Using metabolomics to identify important processes and compounds in dairy factory processing waters

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ABSTRACT

Metabolomics, a combination of advanced analytical chemistry and associated bioinformatics, has been extensively used to study plants, animals and human health. Many diagnostic marker compounds used to monitor cancers have been discovered using these techniques. We used Dairy factory wastewater as a model system for developing the use of metabolomic techniques for investigating phosphorus (P) and nitrogen (N) transformations in dairy soils.

Over two years, wastewater from Burra Foods was sampled and analysed using GC-MS. Using multivariate statistical techniques we determined that para-nitrophenol was closely associated with the P and ammonia concentrations within the bioreactor and could potentially be used to monitor anaerobicity. In 2012 DPI commenced metabolomic analyses of dairy soils.

Keywords: Metabolomics, GC-MS, LC-MS, bioinformatics, dairy pasture.

INTRODUCTION

Metabolomics, a combination of advanced analytical chemistry and associated bioinformatics, has been extensively used to study plants, animals and human health. Many diagnostic marker compounds used to monitor cancers have been discovered using these techniques. Metabolites are short-chain carbon compounds that are most often analysed using gas or liquid chromatography combined with a mass spectral detection (GC-MS or LC-MS). Bioinformatics is the use of statistical analyses to mine the large data sets derived from these analyses and identify associations that are indicative of the underlying processes. The Department of Primary Industries has been using dairy processing wastewaters as model system to develop the use of metabolomic techniques for investigating soil processes, including phosphorus (P) and nitrogen (N) transformations.

MATERIALS AND METHODS

Wastewater from an aerobic bioreactor treating dairy factory wastewater at a dairy processing facility in Korumburra, Victoria was used in the study. Two year’s of dairy factory In-feed, Processing (i.e. Mixed Liquor) and Effluent wastewaters were sampled 11 times and analysed for physicochemical properties (i.e. pH, EC, TN, TP, NH₄-N, NO₃-N, DRP, TDP) and trace organic species. Details of the experimental protocols can be found elsewhere (Heaven et al. 2012). Data were analysed using: (a) Genstat Thirteenth Edition (www.vsni.co.uk) for descriptive statistics and mixed model analyses; (b) The R Statistical Computing Package (http://www.r-project.org/) for the Wilcoxon rank sum test; and (c) Unscrambler (CAMO Software, St. Peters, NSW, Australia) for Principal Component Analysis (PCA) and Partial Least Squares-Discriminant Analysis (PLS-DA).

RESULTS AND DISCUSSION

From the GC-MS data forty-nine compounds were tentatively identified which could be grouped into different classes depending on functional group. Most compounds were attributable to milk (i.e. fatty acids) or milk derivatives (e.g. indoles are formed from microbial breakdown of proteins and amino acids). Dicarboxylic acid compounds found primarily in the bioreactor were likely to be from materials used to upgrade the bioreactor in 2008 or lubricants and greases used to maintain the wastewater treatment system (Heaven et al. 2011). Two USEPA priority pollutants (Santana et al. 2009) were identified. Para-cresol, was found in all the wastewater samples and is produced from biodegradation of amino acids. 4-nitrophenol, was intermittently detected in Infeed and Mixed Liquor samples and present in all Supernatant samples.

Multivariate analyses were performed on the combined GC-MS analyses and physicochemical measurements, a data matrix consisting of over 5000 elements. PCA showed no clear separation between wastewater types and explained just over half the variation. The DRP/TP ratio was opposed to the OP/DRP on the loading plot suggesting a possible inverse
relationship between inorganic P and total P, which is consistent with DRP being incorporated into the microbial biomass. There were similar observations for N. For PLS-DA (Figure 1) most P analyses (with the exceptions of DRP, DRP/TP and TDP) were found to cluster around the Mixed Liquor predictor. The most important predictors of Infeed wastewater were NO₃, NO₂/TN, TDN, and pH analyses reflecting denitrification in the bioreactor.

Besides p-cresol, compounds that correlated with the Infeed wastewater were either fatty or benzoic acids. The fatty acids included nonanoic and octanoic acid. Nonanoic acid is a minor component of milk fatty acids and forms when cheeses are made via bacterial processes. Hydroxylated fatty acids, 3-hydroxyoctanoic acid, 2-hydroxyhexanoic acid and 2-hydroxyheptanoic acid, were also correlated with the Infeed wastewater. This suggests that some oxidation of milk fatty acids may have occurred prior to wastewater entering the bioreactor.

**CONCLUDING COMMENTS**

The learnings from this study have been incorporated into a new study investigating N and P transformations in soil and soil-water, and the microbiological (i.e. biochemical) processes affecting them. We are hopeful that through using such tools we will provide the foundation science that will underpin a “Step” farm efficiency and soil management (e.g. reduce fertilizer use on dairy farms).

**REFERENCES**


Milksolids concentration of Holstein-Friesian cows does not affect the milk production response to once-daily milking

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ABSTRACT

Jersey cows have a lower milksolids (MS; fat + protein) production loss when milked once-daily (1X) compared with Holstein-Friesian (HF) cows, and this response is commonly attributed to their greater MS concentration. This study investigated the effect of MS concentration in HF cows on the MS response to whole- and part-season 1X milking. Data indicate there was no difference in the MS response to 1X milking in HF cows selected for either high or low MS concentration. Therefore, alternative characteristics (i.e. mammary cell regulation) may be responsible for the different response to 1X milking between Jersey and HF cows.

Keywords: once-daily milking; milksolids concentration; breed.

INTRODUCTION

Once-daily (1X) milking has many benefits (improved lifestyle, animal reproduction and body condition score; BCS); however, on average, milksolids (MS; fat + protein) production is reduced by approximately 25% (Clark et al. 2006). Research results indicate that Jersey cows have a smaller MS production loss compared with Holstein-Friesian (HF) cows when milked 1X for the whole lactation (20 and 30%, respectively; Clark et al. 2006). Additionally, Jersey cows selected for high milk protein concentration (4.1%) had a lower relative reduction in MS yield compared with HF cows (3.3% milk protein) when milked 1X for 12 weeks in peak lactation (Carruthers et al. 1993). Based on these data, the greater apparent tolerance of Jersey cows to 1X milking may be due to their greater MS concentration. This study investigated whether phenotypic selection for greater MS concentration in HF cows would reduce the MS loss with 1X milking.

MATERIALS AND METHODS

Multiparous HF cows (n = 114) were allocated to either high MS (>8.5%) or low MS (<7.5%) based on the previous seasons’ MS concentration. Primiparous HF cows (heifers; n = 30) were also allocated to high or low MS based on once-a-day production values (Livestock Improvement Corporation, NZ). At calving, (Aug 10th ± 21 days; mean ± standard deviation) cows within each MS group were allocated to either 1X milking for the whole lactation or twice-daily (2X) milking until January 21st and 1X milking thereafter (2X/1X). This resulted in 4 treatments: 1) High MS milked 1X (Hi1X; 8.9% MS), 2) Low MS milked 1X (Lo1X; 8.0% MS), 3) High MS milked 2X/1X (Hi2X/1X; 8.7% MS), and 4) Low MS milked 2X/1X (Lo2X/1X; 7.9% MS). Treatments 1 and 2 were managed as separate herds stocked at 3.5 cows/ha, and treatments 3 and 4 were managed together stocked at 3.3 cows/ha. Each treatment contained 20% heifers and the experiment was conducted over two lactations.

Individual milk yield was measured daily, and milk composition and BCS (1 to 10 scale) were determined fortnightly. Udder capacity was measured at three time points during the first year (November, January and April) as described by (Carruthers et al. 1993). Each year, cows were dried-off on May 13th, or earlier if milk production fell below 5 kg milk/day for two consecutive weeks.

Data were analysed using mixed models fitted with REML in GenStat (VSI International 2011). Treatment effects were considered significant when P<0.05 and declared a trend when P<0.10.

RESULTS

There were no interactions between MS concentration and milking frequency (Table 1). On average, HF cows milked 1X for the entire season produced 23% less MS (kg/cow/day) than those milked 2X/1X (Table 1). From January onwards, cows milked 1X from calving continued to produce less MS than those switched to 1X milking in January (20 and 18% for Hi1X and Lo1X, respectively) and there was no effect of MS concentration on production during this period (data not presented). There was no effect of MS concentration or milking frequency on lactation length. At dry-off, BCS was greater in cows milked 1X for the whole lactation; but was not altered by MS concentration (Table 1).

Udder capacity during November and January tended to be less in cows selected for high MS (P = 0.07 and 0.10, respectively) and in cows milked 1X (P = 0.05 and 0.07, respectively; Table 2). These differences were not evident in April.
Table 1: Cow numbers, milk production, days in milk (DIM), and body condition score (BCS; 1 to 10 scale) for Holstein-Friesian cows with high (Hi) or low (Lo) milksolids (MS; fat + protein) concentration, milked at two different milking frequencies (MF); once-daily for the whole season (1X), or twice-daily until January 21st and then 1X until dry-off (2X/1X) for two years. Stocking rates were 3.5 and 3.3 cows/ha for 1X and 2X/1X herds, respectively.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Lo1X</th>
<th>Hi1X</th>
<th>Lo2X/1X</th>
<th>Hi2X/1X</th>
<th>SED</th>
<th>MS</th>
<th>MF</th>
<th>MSxMF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cow nos</td>
<td>49</td>
<td>49</td>
<td>23</td>
<td>23</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fat (%)</td>
<td>3.6</td>
<td>3.9</td>
<td>3.5</td>
<td>3.7</td>
<td>0.06</td>
<td>&lt;0.001</td>
<td>0.61</td>
<td>0.68</td>
</tr>
<tr>
<td>Protein (%)</td>
<td>4.4</td>
<td>5.0</td>
<td>4.4</td>
<td>5.0</td>
<td>0.11</td>
<td>&lt;0.001</td>
<td>0.04</td>
<td>0.68</td>
</tr>
<tr>
<td>MS (%)</td>
<td>8.0</td>
<td>8.9</td>
<td>7.9</td>
<td>8.7</td>
<td>0.14</td>
<td>&lt;0.001</td>
<td>0.24</td>
<td>0.68</td>
</tr>
<tr>
<td>Kg milk/cow</td>
<td>3,444</td>
<td>3,007</td>
<td>4,270</td>
<td>4,106</td>
<td>273.0</td>
<td>0.13</td>
<td>&lt;0.01</td>
<td>0.44</td>
</tr>
<tr>
<td>Kg MS/cow</td>
<td>274</td>
<td>267</td>
<td>338</td>
<td>357</td>
<td>22.0</td>
<td>0.69</td>
<td>&lt;0.01</td>
<td>0.37</td>
</tr>
<tr>
<td>Kg MS/ha</td>
<td>959</td>
<td>935</td>
<td>1,115</td>
<td>1,178</td>
<td>21.9</td>
<td>0.71</td>
<td>&lt;0.001</td>
<td>0.42</td>
</tr>
<tr>
<td>DIM</td>
<td>250</td>
<td>245</td>
<td>252</td>
<td>257</td>
<td>10.7</td>
<td>0.87</td>
<td>0.30</td>
<td>0.41</td>
</tr>
<tr>
<td>BCS at dry-off</td>
<td>5.1</td>
<td>4.9</td>
<td>4.7</td>
<td>4.8</td>
<td>0.14</td>
<td>0.19</td>
<td>&lt;0.01</td>
<td>0.19</td>
</tr>
</tbody>
</table>

Table 2: Total udder capacity (kg milk/cow) for Holstein-Friesian cows with high (Hi) or low (Lo) MS (fat + protein) concentration, milked at two different milking frequencies (MF); once-daily for the whole season (1X), or twice-daily until January 21st and then 1X until dry-off (2X/1X) for two years. Stocking rates were 3.5 and 3.3 cows/ha for 1X and 2X/1X herds, respectively.

<table>
<thead>
<tr>
<th></th>
<th>Lo1X</th>
<th>Hi1X</th>
<th>Lo2X/1X</th>
<th>Hi2X/1X</th>
<th>SED</th>
<th>MS</th>
<th>MF</th>
<th>MSxMF</th>
</tr>
</thead>
<tbody>
<tr>
<td>November</td>
<td>20.4</td>
<td>18.3</td>
<td>21.9</td>
<td>20.8</td>
<td>1.1</td>
<td>0.07</td>
<td>0.05</td>
<td>0.61</td>
</tr>
<tr>
<td>January</td>
<td>17.6</td>
<td>15.2</td>
<td>18.2</td>
<td>18.0</td>
<td>1.0</td>
<td>0.10</td>
<td>0.07</td>
<td>0.28</td>
</tr>
<tr>
<td>April</td>
<td>10.1</td>
<td>10.6</td>
<td>12.0</td>
<td>9.8</td>
<td>0.9</td>
<td>0.63</td>
<td>0.65</td>
<td>0.17</td>
</tr>
</tbody>
</table>

DISCUSSION AND CONCLUSION

There was no effect of MS concentration on the MS production loss when HF cows were milked 1X for the whole or part season. The lack of an effect may be due to the smaller difference in MS concentration (1% unit) between high and low MS cows in the present study, compared with the 2% difference between Jersey and HF cows (10 and 8% MS, respectively; Clark et al. 2006). Cows with a high MS concentration tended to have a smaller udder capacity during peak (November) and mid (January) lactation, which is probably due to these cows storing smaller volumes of a more concentrated milk, as there was no difference in MS yield between the high and low MS treatments. In conclusion, phenotypic selection for greater MS concentration in HF cows does not alter the daily or total MS response to whole- or part-season 1X milking. Therefore, alternative characteristics (i.e. mammary cell regulation) are likely to be responsible for the different response to 1X milking in Jersey and HF cows.

ACKNOWLEDGEMENTS

Authors gratefully acknowledge the farm staff and technical team at the Westpac Taranaki Agricultural Research Station. This study was funded by NZ dairy farmers through DairyNZ Inc.

REFERENCES


Climate change influences on the seasonality of pasture supply in NW Tasmania

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ABSTRACT

Modelling future climate scenarios for North West Tasmania has shown that the mean number of days/annum that the moving 10 day mean daily pasture growth rate (PGR; kg DM/ha.day) is less than 15 kg DM/ha.day is predicted to decline from 190 days/annum in the baseline period of years (1971 to 2000) to 167 days/annum during the years 2031 to 2060. In addition, the mean number of days/annum that the moving 10 day mean PGR is greater than 30 kg DM/ha.day is predicted to increase from 118 days/annum in the baseline period of years to 138 days/annum during the years 2031 to 2060. However, the seasonal and inter-annual variations in pasture supply experienced in the baseline period of years will remain into the future.

Keywords: Climate change, pasture growth rate, North West Tasmania, modelling.

INTRODUCTION

Climate is an important driver of pasture production and variability in climate results in differing patterns of pasture supply both within and between years. Pasture growth and high utilisation efficiency are key drivers of profitability for grazing systems and the strong seasonality (>50% of total annual growth in spring) and high inter-annual variability in pasture production makes this goal more difficult to achieve (Chapman et al. 2009). This study aimed to explore how future climate scenarios are likely to influence both the seasonality and inter-annual variability in pasture production for the dairy region of North West Tasmania.

MATERIALS AND METHODS

Daily climate data developed from the Climate Futures of Tasmania project was accessed for Flowerdale (41.0°S, 145.6°E). Six down-scaled A2 (i.e. higher end worst case scenario) global circulation files (GCMs; CSIRO3.5, ECHAM5, GFDL2.0, GFDL2.1, MIROC3.2 and UKHad) were used, in conjunction with the biophysical pasture model DairyMod (Johnson et al. 2008), to simulate daily pasture growth rates (PGR; kg dry matter (DM)/ha.day) for a rain-fed perennial ryegrass pasture sward. Moving 10-day mean PGRs were calculated for each GCM and categorised into one of three levels: deficit pasture supply (i.e. ~ < 1 cow/ha; PGR < 15 kg DM/ha.day), sufficient pasture supply (i.e. ~ 1-2 cows/ha; PGR between 15 to 30 kg DM/ha.day) and surplus pasture supply (i.e. ~ > 2 cows/ha; PGR > 30 kg DM/ha.day). The mean annual count of each category of PGR for each GCM was then determined for three 30-year periods: baseline years of 1971 to 2000 and two future climate period of years: 2001 to 2030 and 2031 to 2060.

RESULTS

The frequency of pasture deficit supply was predicted to decline in the two future climate periods of years across all GCMs when compared to the baseline period of years 1971 to 2000, with the exception of the CSIRO3.5 model in years 2031 to 2060 (Table 1). In contrast, the frequency of pasture surplus was predicted to increase in the two future climate periods of years across all GCMs when compared to the baseline period of years 1971 to 2000 (Table 1).

**Table 1:** Mean number of deficit, sufficient and surplus pasture days per annum for North West Tasmania using six global circulation models for a baseline period of years (1971 to 2000) and change in mean number of deficit, sufficient and surplus pasture days for two future climate periods (2001 to 2030 and 2031 to 2060) compared to the baseline period of years (1971 to 2000)

<table>
<thead>
<tr>
<th>Pasture supply</th>
<th>Period</th>
<th>CSIRO3.5</th>
<th>ECHAM5</th>
<th>GFDL2.0</th>
<th>GFDL2.1</th>
<th>MIROC</th>
<th>UKHad</th>
<th>Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>Deficit (PGR &lt; 15 kg DM/ha.day)</td>
<td>Baseline</td>
<td>182.5</td>
<td>189.7</td>
<td>189.1</td>
<td>190.1</td>
<td>189.5</td>
<td>201.6</td>
<td>190.4</td>
</tr>
<tr>
<td></td>
<td>2001-2030</td>
<td>-8.6</td>
<td>-20.7</td>
<td>-11.6</td>
<td>-19.2</td>
<td>-17.5</td>
<td>-29.2</td>
<td>-17.8</td>
</tr>
<tr>
<td></td>
<td>2031-2060</td>
<td>+1.1</td>
<td>-27.1</td>
<td>-20.1</td>
<td>-22.7</td>
<td>-25.6</td>
<td>-49.1</td>
<td>-23.9</td>
</tr>
<tr>
<td>Sufficient (PGR 15 to 30 kg DM/ha.day)</td>
<td>Baseline</td>
<td>63.6</td>
<td>56.6</td>
<td>56.9</td>
<td>54.7</td>
<td>54.7</td>
<td>55.8</td>
<td>57.1</td>
</tr>
<tr>
<td></td>
<td>2001-2030</td>
<td>-0.6</td>
<td>+4.0</td>
<td>+4.9</td>
<td>+10.9</td>
<td>+7.9</td>
<td>+1.4</td>
<td>+4.7</td>
</tr>
<tr>
<td></td>
<td>2031-2060</td>
<td>-12.1</td>
<td>+3.3</td>
<td>+10.5</td>
<td>+5.7</td>
<td>+6.3</td>
<td>+10.3</td>
<td>+4.0</td>
</tr>
<tr>
<td>Surplus (PGR &gt; 30 kg DM/ha.day)</td>
<td>Baseline</td>
<td>119.2</td>
<td>119.0</td>
<td>119.2</td>
<td>120.4</td>
<td>121.0</td>
<td>107.8</td>
<td>117.8</td>
</tr>
<tr>
<td></td>
<td>2001-2030</td>
<td>+9.1</td>
<td>+16.7</td>
<td>+6.6</td>
<td>+8.3</td>
<td>+9.6</td>
<td>+27.8</td>
<td>+13.0</td>
</tr>
<tr>
<td></td>
<td>2031-2060</td>
<td>+11.0</td>
<td>+23.8</td>
<td>+9.6</td>
<td>+16.9</td>
<td>+193</td>
<td>+38.7</td>
<td>+19.9</td>
</tr>
</tbody>
</table>

Detail of GCM selection and downscaling of CFT data can be found at www.dpac.tas.gov.au/divisions/climatechange/adapting/climate_futures.
DISCUSSION AND CONCLUSION

The results of this study have indicated that although annual pasture production is likely to increase in North West Tasmania due to increasing daily temperatures and atmospheric carbon dioxide concentrations and relative small changes in precipitation, the seasonality of feed supply is likely to become more pronounced. Changes to farm management will be required to most effectively capture the additional pasture production (e.g. altered calving dates) and alleviate the seasonal influences and inter-annual variations in pasture supply (e.g. increased reliance on irrigation or pasture species with deeper rooting systems and/or improved drought tolerance).

ACKNOWLEDGEMENTS

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REFERENCES


Microbial community response to nitrogen use in dairy soils

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2Department of Primary Industries, Victorian AgriBiosciences Centre, 1 Park Drive, Bundoora, Victoria, 3083, Australia

ABSTRACT

High-resolution molecular assays were used to determine the extent to which the microbial community structure was associated with chemical and physical characteristics of soil and/or with pasture plant species dominance in dairy soils. Seasonal changes were observed in soil microbial (bacteria, archaea and fungi) community structure in dairy pastures for a range of management practices in Victoria and south-western Australia (Margaret River region). Management practices included intensity of grazing, nitrogen application, irrigation and effluent disposal. The dominance of genes associated with nitrogen cycling varied with management practice and with associated changes in soil chemical characteristics. Considerable natural heterogeneity in estimates of microbial dominance in the dairy pasture soils was observed. Therefore, additional soil sampling approaches were adopted to minimise effects of soil type or climate.

Keywords: dairy soil, molecular assays, nitrogen, phosphorus, microbial communities

INTRODUCTION

The Australian dairy industry relies on significant fertiliser inputs to increase or maintain milk production (Bolland and Guthridge 2007a; Bolland and Guthridge 2007b; Gourley et al. 2007; Dairy Australia 2012). Investigation of effects of fertiliser management on soil biological processes provides information complementary to knowledge of soil chemical and physical fertility (Abbott and Murphy 2003; Eckard et al. 2007; Jenkins et al. 2009). Microbial processes are essential for cycling nutrients from organic matter in soil (Johnson et al. 2008) and have potential to increase efficiency of nitrogen and phosphorus fertiliser use (Mele and Crowley 2008; Johnson et al. 2008).

MATERIALS AND METHODS

Management practices sampled included intensity of grazing, nitrogen application, irrigation and effluent disposal. The molecular assays used included Terminal Restriction Fragment Length Polymorphism (T-RFLP) and Polymerase Chain Reaction Denaturing Gradient Gel Electrophoresis (PCR-DGGE) of 16S rDNA genes. The intention was to identify management practices that either limited or enhanced the functional capacity of soil microbial processes as shown using similar techniques by Supaphol et al. (2011).

RESULTS AND DISCUSSION

Microbial community profiling illustrated seasonal changes in soil bacterial community structure in dairy pastures in Victoria (Figure 1). The dominance of species based on detection of 16S genes associated with nitrogen cycling varied with management practice. There was also a marked seasonal influence.

Figure 1: CCA ordination of 120 soil samples from 12 dairy pastures with different management histories and significant environmental variables based on 240 terminal restriction fragments generated from the 16s region of bacterial rDNA. Sample treatments are: low input N (green shades); effluent N input (blue shades); medium input N (pink shades); and high input N (orange shades). Victorian Department of Primary Industries.

There were few distinctive relationships between soil chemical characteristics and the presence of dominant bacterial groups. In soils collected from south-western Australian dairy pastures (Figure 2),
there was a weak correlation between the occurrence of denitrifiers and level of soil nitrogen. In the same soils, both soil nitrogen and soil phosphorus were weakly correlated with the presence of acidobacteria. While microbial communities in dairy pasture soils were influenced by management practices, bacteria, archaea and fungi did not all respond in the same way to soil chemical fertility.

Considerable heterogeneity in estimates of microbial dominance in dairy pasture soils was observed. Therefore, additional soil sampling approaches were adopted to minimise effects of soil type or climatic variables. This included sampling experimental plots with a range of management practices at a single field location (Victoria) and the establishment of simulated pasture swards in dairy pasture soils under controlled environmental (glasshouse) conditions which differed in pasture species dominance and fertiliser application (southwest Western Australia).

**CONCLUSION**

Soil microbial communities in a range of dairy pasture soils demonstrated marked seasonal shifts illustrating the dynamics of nutrient cycling processes in soil. While microbial communities in dairy pasture soils were influenced by management practices, bacteria, archaea and fungi did not all respond in the same way to soil chemical fertility. High-resolution molecular assays were used to identify dominant microbial pathways for the nitrogen cycle in dairy pasture soils but relationships between microbial pathways, soil chemistry and fertiliser use efficiency are complex. There is a need to understand soil biological as well as soil chemical processes for a more complete evaluation of the long-term impacts of dairy pasture management practices on soil fertility.

**ACKNOWLEDGEMENTS**

This research was supported by Dairy Australia. The Department of Primary Industries Victoria (DPI-Victoria) and The Department of Agriculture and Food Western Australia (DAFWA) both assisted by locating dairy sites for study. Dairy producers in WA kindly provided access to field sites.

**REFERENCES**


Maintaining milk production in the presence of clover root weevil on an intensive pasture based dairy system

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ABSTRACT

Clover root weevil (CRW) (Sitona lepidus) is an exotic pest that attacks white clover. The weevil was first detected on the Lincoln University Dairy Farm (LUDF), an intensive, Canterbury (South Island), pasture based demonstration dairy farm, in December 2008. Ongoing monitoring observed a buildup of root-feeding larval populations reaching a mean peak of 300 larvae/m² in the spring of 2010, contributing to a subsequent and significant decline in white clover content in the pasture. The impact of reduced clover on the LUDF is likely to have contributed to reduced cow intake, milk production and cow body condition. LUDF has since implemented management changes to negate the impact of CRW. Responses included substituting clover fixed N with N fertilizer and modified grazing practice, with clover re-establishment a priority. Biocontrol of CRW should also assist in mitigating the recurrence of damaging larval populations.

Keywords: white clover; dairy; pastoral farming; pest impacts; sitona lepidus; microctonus aethiopoides; biocontrol

INTRODUCTION

The Lincoln University Dairy Farm (LUDF) is an intensive, pasture based demonstration dairy farm. LUDF has 630-670 cows (4 - 4.25 cows/ha) on 160 ha effective and is in the top 2 - 5% of NZ dairy farms in terms of profitability. The dairy platform has several aims including maximising sustainable profit, and in 2011-2012 added a specific emphasis of productivity, without increasing the farm’s overall environmental footprint. Maximising energy yield (animal intake) from white clover/ryegrass is the basis of the farm’s production system. White clover is a critical part of New Zealand’s advantage in pastoral livestock farming, providing nitrogen fixation and enhanced animal intake and feed quality when part of a ryegrass / clover sward. An exotic pest, clover root weevil (CRW) (Sitona lepidus) was first found in the North Island of New Zealand in 1996. The larvae attack the clover roots including the nitrogen-fixing nodules while adults feed on the foliage. CRW can have significant impacts on clover productivity and persistence. It was first detected in the South Island in 2006. As part of the effort to reduce the impacts of CRW, the biological control agent Microctonus aethiopoides (an Irish strain of parasitoid wasp) has been released in New Zealand (Gerard et al. 2006).

MATERIALS AND METHODS

On the LUDF, irregular monitoring for pasture pests has been conducted since 2004. This included sampling for above ground insects using a modified blower vac and soil cores (10 cm x 10 cm deep) for below ground insect pests. A wide range of pasture and animal production parameters are collected on the LUDF including daily milk production, weekly pasture quality analysis (NIRS) and weekly assessments of growth rate [rising plate meter, winter formula using Pasture Coach software]. This information was critical to measuring the impacts of pastoral pests on the dairy production system. White clover seed counts were carried out on three paddocks, with 50 x 25mm x 100mm soil cores per paddock taken on 15 June 2011. White clover seed was extracted from the soil and white clover seed kg/ha calculated.

RESULTS

In December 2008, adult CRW was first detected in very low densities (<1 adult m⁻²) on the LUDF. In response, more regular monitoring of larval densities on the farm was initiated to understand the phenology and potential impacts of CRW under irrigation in Canterbury. On a monitor paddock, larval densities were observed to reach levels of 300 larvae/m² by mid-October 2010, a threshold value deemed to cause significant damage in earlier North Island research (Gerard et al. 2007). During the 2010/11 season, a significant change in pasture composition was observed with substantial clover loss, attributed to destruction of the root system by CRW larvae. The loss of white clover was very clear in the 2010/11 season with almost no clover visible in the pasture, compared to previous seasons where
clover had been estimated at around 25% of the sward. Milk production suffered markedly (Table 1). The immediate response was an increase in applied N of 75 kg/ha in 2010/11 followed by a number of management changes including a further 90 kg N/ha in 2011/12 (10 split applications/yr; Table 1).

Table 1: Selected production and inputs at LUDF 2008/09 to 2011/12

<table>
<thead>
<tr>
<th>Parameters</th>
<th>08/09</th>
<th>09/10</th>
<th>10/11</th>
<th>11/12</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kg MS production per ha</td>
<td>1634</td>
<td>1710</td>
<td>1683</td>
<td>1861</td>
</tr>
<tr>
<td>Kg MS production per cow</td>
<td>384</td>
<td>415</td>
<td>396</td>
<td>471</td>
</tr>
<tr>
<td>Tonnes DM of supplementary feed</td>
<td>234</td>
<td>171</td>
<td>210</td>
<td>227</td>
</tr>
<tr>
<td>purchased for lactation</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fertiliser N (kg N/ha)</td>
<td>200</td>
<td>185</td>
<td>260</td>
<td>350</td>
</tr>
</tbody>
</table>

The additional N was applied through the October - March period (an extra 20 kg N/ha/application every 3 weeks) when pasture was actively growing and nitrogen fixation from clover would normally have contributed substantial N. It also coincided with the period where CRW larval populations are near their peak (October-November). In the 2011/12 season, modified herd and grazing management practices were implemented to aid intake, including splitting of herds to assist younger and thinner cows, marginally increasing the allowable grazing residual and using a mower to achieve these residuals. In many paddocks it was observed that the recovery of white clover in the pasture was still poor. This was compounded by a low clover seed bank (0-0.75 kg white clover seed/ha), a level deemed insufficient to support re-establishment of clover. Consequently 42 ha of pasture was oversown with 4 kg/ha white clover seed. Recovery will be aided by the presence of Microctonus aethiopoides where it is anticipated that biocontrol will lead to a reduction in damaging larval populations, thereby allowing white clover to be sustained in the pasture.

**DISCUSSION**

The loss of white clover observed during the 2010/11 season and attributed to CRW larvae was perhaps a combination of below ground herbivory compounded by the presence of root diseases during a wet winter. When combined with grazing pressure from cows, it created the ‘perfect storm’ leading to the loss of white clover from the sward.

In response to CRW, LUDF implemented management changes to negate the impact of this pest. The combination of substituting clover fixed N with N fertilizer and modified grazing management practices appeared to support cow intake in a less favourable environment and negate much of the impact of CRW. The importance of clover is not to be underestimated with re-establishment now being a high priority. Subsequent reports of transitory white clover decline on farms across Canterbury, as CRW has spread and built up in the absence of the biocontrol agent, indicates that the experience on the LUDF will not be unique. The lessons learnt at LUDF become increasingly relevant as the clover root weevil spreads further across Canterbury.

**ACKNOWLEDGEMENTS**

The authors thank John Proffitt for technical assistance in collection of insect data and LUDF staff for their support of the research carried out on the farm. Seed count analysis was carried out by New Zealand Seedlab, Christchurch.

**REFERENCES**


Relationships between concentrate intake, milk income and costs for Tasmanian dairy herds

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ABSTRACT

The Tasmilk60 study collected whole farm data from pasture based dairy farms over three years (2006/07, 07/08, 08/09) and found; when farms were grouped according to the level of concentrate fed per cow, there were only small differences in profit between farms. Further analysis of the Tasmilk60 data indicates one reason larger differences in profit were not found is that operating costs excluding concentrates, that is, costs for non concentrate feeds, pastures, irrigation, labour, animals and overheads, tend to increase as concentrate intake per cow increases. Farmers and their advisors need to be aware of the relationships between concentrate feeding and per cow production and consider these in the context of the whole farm system when deciding on concentrate feeding strategies for dairy herds.

Keywords: Tasmilk60; concentrate; milk; margin; costs; profit.

INTRODUCTION

The Tasmilk60 study collected farm production and financial data from Tasmanian dairy farms over three consecutive years and found differences in profit between farms “...using low, moderate and high concentrate feeding levels are small compared with the variability between farms in profit within each concentrate feeding level.” (Dairy Australia, 2011, p26). The data from the Tasmilk60 study was analysed further in this study to shed more light on the relationships between concentrate feeding, milk income and farm operating costs.

MATERIALS AND METHODS

The Tasmilk60 study was an observational study conducted to better understand the interaction between concentrate input, risk, management and profit in a pasture based dairying system. It involved the collection of data across a spectrum of farms using different concentrate feeding rates in the same climatic and market context. The study enrolled 21 farms with low concentrate feeding (<1t/cow/year), 27 farms with medium concentrate feeding (1 to 2t/cow/year) and 21 farms with high concentrate feeding (≥2t/cow/year). Milk prices for participating farms averaged $4.41, $6.52 and $5.38/ kg MS for 2006/07, 07/08 and 08/09 respectively.

RESULTS

The effect of concentrate intake on per cow milk income, concentrate costs and all other cash operating costs (non concentrate costs) across the participating herds is shown in Figures 1 and 2 for 2006/07 and 07/08. In 06/07 the milk income increased by $673/t concentrate DM fed and the concentrate purchase price was $375/tDM. Cash operating expenses per cow excluding concentrates, that is, pasture, irrigation, feed, labour, management, animal and overheads costs also appear to increase as concentrate intake per cow increases. In 06/07 non concentrate costs increased by $409/cow for each one tonne increase in concentrate DM/cow and this cost was greater than the margin over concentrate cost. The high milk price in 07/08 caused the marginal milk income to increase compared to the previous year and concentrate costs also increased to $539/tDM. In 07/08 the margin over concentrate cost was offset by the $350/cow increase in non concentrate costs as concentrate intake increased. Analysis of the three years data found the primary sources of the non concentrate cost increases were the result of increases in per cow costs of non concentrate feed, pasture, irrigation, labour and management.

Figure 1: The relationships between the level of concentrate fed (t DM/cow) in 2006/07, 07/08 and 08/09 and milk income, ($/cow), concentrate cost, ($/cow) and non concentrate costs, ($/cow).
**DISCUSSION**

Over 75% of the variation between farms in milk income per cow was explained by concentrate intake per cow and a margin over the concentrate cost was achieved. The margin over concentrate cost was not reflected in higher farm profit because of the tendency for farm operating costs, excluding concentrate costs, to increase as concentrate intake increases. The analysis demonstrates that the reason concentrate intake was not found to be strongly linked with profit in the Tasmilk60 study was that farm costs other than concentrates tend to increase as concentrate intake increases.

**CONCLUSION**

Decisions about concentrate feeding should include an assessment of both the marginal income and marginal cost of the feed and an assessment of the impact of concentrate feeding on non-concentrate costs. Calculation of margin over feed costs on commercial dairy farms is not a useful indicator of relative profitability between farms.

**ACKNOWLEDGEMENTS**

Steve Little, Feed2milk program leader for Dairy Australia provided access to TasMilk60 data.

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Dairy Australia 2011: Performance, Profit and Risk in Pasture Based Dairy Feeding Systems. Findings from the TasMilk60 study, pp. 1-58.
Nitrogen fertiliser responses in intensive dairy grazing systems in SW Australia

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ABSTRACT

An experiment to determine responses to nitrogen (N) fertiliser (0-2 kg/ha/day) was conducted over 4 years in south-western Australia with five dairy farmlets using annual ryegrass-based pastures. Average monthly variation in grazed pasture N response efficiency ranged from 6 to 34 kg pasture DM per kg fertiliser N applied and was close to linear over the range employed. In contrast the response of silage yield to applied N was strongly curvilinear, with a peak at approximately 60 kg N per ha and a mean silage N response efficiency of 20 kg dry matter (DM) per kg fertiliser N. As N response efficiencies in dairy pastures are multifactorial and complex, we have commenced the development of a decision support tool to help with more profitable N fertiliser advice for dairy pastures.

Keywords: nitrogen fertiliser; nitrogen response; dairy pasture

INTRODUCTION

Pasture responses to applied nitrogen (N) fertiliser have been determined for pasture grown either in pots, mown plots or grazed field plots using a common herd across all N application levels (Whitehead 1995). In his review of such studies Whitehead (1995) recommended to use individual herds for each N fertiliser application level as this is the only methodology that properly takes into account N recycling by the animal. Three such previous studies have been conducted to determine the fertiliser N requirements for dairy production in Australasia. Two Australian studies used tropical grasses (Davison et al. 1985; Cowan et al. 1995), while a New Zealand study used perennial ryegrass (Penno et al. 1996; Clark 1997). With the benefit of lessons learnt from these studies, we conducted a dairy farmlet study to determine the fertiliser N requirements for annual ryegrass pastures.

MATERIALS AND METHODS

An experiment made up of five dairy farmlets with annual ryegrass-based pastures was conducted from 2005 to 2008 in south-western Australia (annual growing season May-November). Farmlets, each with 20 Holstein-Friesian cows, varied in fertiliser N level (kg N/ha/day) and stocking rate (cows/ha) as follows: 0.125, 0.5, 1.5, 1.01, 1.52, 2.02, 2.25. Pastures were rotationally grazed when ryegrass reached the 2.5-3 leaf stage. The experiment quantified responses of grazed pasture, silage yield and milk production. Grazed pasture use was estimated by using rising plate meters and was also back-calculated based on metabolisable energy requirements of each farmlet each year. The relationship between the two methods was robust ($r^2 = 0.97$).

Analyses of variance were used to compare treatment means. Farmlet-year was considered the experimental unit. Data were analysed for the main effects of farmlet (fertiliser N level and associated stocking rate) (4 d.f.) and year (3 d.f.). Least significant differences ($P < 0.05$) were used in multiple comparisons, if the main effect of farmlet and/or year were significant ($P < 0.05$).

RESULTS

Consumption of supplementary feed per cow (concentrate, silage, hay), and production of milk and milk components per cow were unaffected by farmlet treatments. Therefore, the higher stocking rate associated with increasing fertiliser N levels applied was responsible for proportional increases in milk and milk components production per ha. Milk responses per ha to applied fertiliser N each year were about linear. Averaged over the 4 years, N response efficiency for milk protein plus fat production (kg/ha increase per kg N/ha applied) was 1.28 (range 0.94-2.23).

In grazed pasture the N response efficiency varied considerably from month to month and year to year (Table 1). The marginal N responses efficiency for each of the four N fertiliser increments from 0 to 2 kg N/ha/day was 7.6, 9.8, 9.5 and 6.8 kg pasture DM per kg N fertiliser applied respectively ($P > 0.05$).

Table 1: Monthly N response efficiency for grazed annual ryegrass pastures (mean and range for 2005-2008)

<table>
<thead>
<tr>
<th>Month</th>
<th>Mean (kg pasture dry matter per kg N fertiliser applied)</th>
</tr>
</thead>
<tbody>
<tr>
<td>May</td>
<td>5.6</td>
</tr>
<tr>
<td>Jun</td>
<td>8.0</td>
</tr>
<tr>
<td>Jul</td>
<td>11.6</td>
</tr>
<tr>
<td>Aug</td>
<td>13.3</td>
</tr>
<tr>
<td>Sep</td>
<td>14.0</td>
</tr>
<tr>
<td>Oct</td>
<td>27.0</td>
</tr>
<tr>
<td>Nov</td>
<td>34.0</td>
</tr>
</tbody>
</table>

Range not applicable. Data for one year only as other three years were too dry for N fertiliser application.
The response of silage yield to applied fertiliser N was strongly curvilinear. Fertiliser N levels required to achieve 95% of maximum silage yield ranged from 48-87 kg N/ha (mean 60). The N response efficiency at 60 kg/ha fertiliser N applied varied from 9 to 29 kg DM (mean 20) per kg fertiliser N.

DISCUSSION AND CONCLUSION

The marginal N response efficiency did not differ statistically between the four N increments employed. However, in a separate 6-year plot study with annual ryegrass, we employed a wider range of N fertiliser (0 to 4 kg N/ha/day). This study, which used a common herd to graze all treatments, showed that the response of grazed pasture to applied N was strongly curvilinear and peaked at approximately 1.5 kg N/ha/day (Bolland, unpublished data). It is therefore likely that no significant increases in grazed pasture use would have been obtained beyond 2 kg N/ha/day in our farmlet study and that the marginal cost of any additional pasture grown would have increased to very high levels.

In both grazed pasture and silage, there was a trend towards lower N response efficiencies in wet years compared to drier or normal years.

Our study showed that N response efficiencies in dairy pastures are multifactorial and complex. As a result, we have commenced the development of a decision support tool to help with more profitable N fertiliser advice for dairy pastures.

ACKNOWLEDGEMENTS

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REFERENCES


Replacing wheat with canola in mixed rations fed to grazing cows increases milk production

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ABSTRACT

A 28-d experiment was conducted in spring to measure milk production from grazing cows offered different supplements in different ways. There was no difference between milk yields of cows offered cereal grain and pasture silage in the paddock and those consuming the same amount of estimated metabolisable energy (ME) as a partial mixed ration (PMR) containing wheat grain, maize grain, maize silage and lucerne hay. However, when some wheat grain was replaced with canola meal, energy-corrected milk yield was increased at the higher rates of supplement intake. Further research is needed to elucidate the mechanism responsible for this response.

Keywords: partial mixed rations; pasture; protein; milk production; canola meal

INTRODUCTION

In southeast Australia, grazed pasture is the main source of nutrients for dairy cows, but it is commonly supplemented with grain or concentrates fed in the dairy and/or conserved forage fed in the paddock. Highly variable rainfall over the last decade has increased the reliance on bought-in supplements to meet the nutritional requirements of milking herds. Using traditional feeding systems, reductions in marginal milk production responses have been reported when more than 5 to 9 kg DM of grain/cow/d is consumed (Beever and Doyle, 2007), however, there is little information on the benefits and costs of alternative supplements and the manner in which they are fed. This experiment was conducted to determine whether feeding cows supplements as a partial mixed ration (PMR) on a feedpad was more productive than feeding supplements separately as grain in the dairy and forage in the paddock. A second aim was to quantify the effect on milk production of replacing some wheat in the PMR with canola meal and thus altering the crude protein content.

MATERIALS AND METHODS

In spring 2010, 160 cows were allocated to 20 groups of eight. Each group was then randomly assigned to one of three dietary treatments, Control (8 groups), PMR (8 groups) and PMR+Canola (4 groups). All cows grazed a pasture allowance of 14 kg DM/cow/d of perennial ryegrass (Lolium perenne L.) pasture plus supplements at different amounts. Control cows were supplemented with rolled wheat grain fed twice daily in the dairy and pasture silage fed in the paddock, with two groups each offered 8, 10, 12 or 14 kg DM total supplement/cow/d. The ratio of wheat:silage was 75:25 (DM basis). The PMR cows were offered a PMR comprising (DM basis) 39% rolled wheat grain, 20% maize grain, 32% maize silage and 9% lucerne hay. The PMR was offered on a feedpad after each milking (8, 10, 12 or 14 kg DM total supplement/cow per d; two groups per amount) and was estimated to provide the same metabolisable energy (ME) as the Control cows obtained from wheat and silage. The PMR+Canola cows were fed in the same way as the PMR cows at 12 or 14 kg DM total supplement/cow per d, except the ration comprised (DM basis) 23% rolled wheat grain, 20% maize grain, 32% maize silage, 9% lucerne hay and 16% canola meal. This ration was estimated to provide the same ME as the PMR, but with a higher crude protein content.

The experiment consisted of a 14-d adaptation period followed by a 14-d measurement period. Yield of energy-corrected milk (ECM) was measured three times per week during the measurement period and exact supplement dry matter intake (DMI) was calculated by weighing feed offered and refused. This information was used to graph predicted ECM against supplement DMI (Figure 1).

RESULTS

For both the Control and PMR cows, energy corrected milk (ECM) yield increased linearly \( (P<0.05) \) with increasing amounts of supplement offered, but there was no difference between the two diets at any level of intake. Predicted ECM yield, however, was greater \( (P<0.05) \) for the PMR+Canola cows than for cows on the other two diets at a supplement intake of 13 kg DM/cow/d. Predicted concentrations and yields of milk fat were also greater \( (P<0.05) \) for the PMR+Canola cows than for cow on the other two diets at supplement intakes of 13 and 15 kg DM/cow/d.
DISCUSSION AND CONCLUSION

This experiment provides the first Australian data showing that replacing cereal grain with canola meal in PMRs fed to grazing dairy cows can increase ECM production when high amounts of supplement are offered. This response was driven in part by higher concentrations and yields of milk fat, but further experiments are required to determine the exact mechanism by which these gains occurred. Under the conditions of this experiment, insufficient supplement was fed to reach the point of negative milk production response in either the Control or PMR diets. It is concluded that the form and composition of supplements offered to grazing cows receiving very high levels of supplementation can have an important influence on the efficiency of use of those supplements.

ACKNOWLEDGEMENTS

This research was funded by DPI and Dairy Australia.

REFERENCE


Figure 1: Yields of energy-corrected milk from cows fed increasing amounts of supplement as the Control diet ( ), the partial mixed ration (PMR; ) and the PMR including canola (PMR+Canola; ). For each diet, each data point is the mean of two groups per level of intake, calculated from the 14-d measurement period. Lines are fitted curves for each diet.
Phosphorus changes in soil and soil water from a dairy farm after cultivation

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ABSTRACT

Tilled dairy pasture has the potential to conserve nutrients that would otherwise move into surface waters, contributing to eutrophication of waterways. We report the first year’s results from a study comparing the effects of cultivation, phosphorus (P) fertiliser and vegetation in a randomised complete block design. Nutrients were analysed in soil and soil water samples. Generally, nutrient concentrations in soil water declined with ploughing, particularly at the soil surface. Fertiliser and pasture treatment effects were inconclusive. Data suggests that ploughing retains more phosphorus on dairy farms.

Keywords: mouldboard ploughing; phosphorus; stratification; dairy; pasture.

INTRODUCTION

Conserving nutrients on-farm is desirable. In dairy farms, phosphorus (P) and nitrogen (N) are often deposited on the soil surface when fertilisers are applied and plant material and wastes decompose. Nutrients near the soil surface may be mobilised into surface water and be transported to freshwater ecosystems leading to eutrophication and cyanobacterial blooms (Grace et al. 2010). Cultivation is one way of lessening excessive nutrient concentrations at the soil surface and potentially lowering nutrients exports without necessarily affecting the agronomic potential (i.e. 0-100 mm Olsen P) of the soil. A study on a dairy farm in the Gippsland region of Victoria has shown that three years after laser grading, an extreme form of cultivation, total dissolved P in soil water from irrigation bays (0-20 mm) was lower than from ungraded bays (1.49 vs. 4.55 mg P/L, P < 0.05). These observations were not reflected in the dissolved reactive P concentrations (graded: 1.01 mg P/L vs. ungraded 1.47 mg P/L, P > 0.05, 0-20 mm) or soil test P (0-100 mm) (Nash et al. 2007). Following this study, more economically viable methods of cultivation have been tested. Here we report a study investigating the changes in P and N in soil following mould-board ploughing (Watkins et al. 2012).

MATERIALS AND METHODS

The experimental site (c. 0.5 ha) was located near Poowong, West Gippsland, Victoria, Australia on a mainly Grey Dermosol soil. A randomised complete block design (3 blocks, 12 × 6 m plots, 36 plots total) consisting of two types of cultivation (mouldboard ploughed or unploughed) and vegetation (ryegrass (Lolium spp.) or a mixed sward of white clover (Trifolium repens) and ryegrass), and three rates of P fertiliser(10, 35, and 100 kg P/ha) was established. In November 2009, each plot was sampled at 0-20 mm and 0-100 mm after cultivation but before P fertiliser treatments were applied. Fertiliser treatments were applied in March 2010. Sampling at 0-20 mm and 0-100 mm then occurred in May, July, October and November 2010. Soil samples were analysed for soil moisture, Olsen P, Colwell P, CaCl2 P, TP, TN, P Buffer Index, Skene K, Available S, TC, Oxidisable Organic Carbon and Organic P using standard methods. Soil water extracts were analysed for DRP, TDP, TP, TN, NO3-N, NH4-N using standard methods with DUP, PP, PN, DIN and DON calculated subsequently. Pastures were analysed for protein, carbohydrate, fibre, fat and energy.

RESULTS AND DISCUSSION

Prior to ploughing, the 0-20 mm soil and soil water samples had higher N and P concentrations relative to the 0-100 mm samples. An exception was the soil water analyses for NO3 (0-20 mm: 5.4 mg/kg vs. 0-100 mm 7.3 mg/kg), possibly due to a combination of denitrification and a high spring rainfall leaching N to lower depths.

Following ploughing but prior to P treatments being applied, soil water (0-20 mm) P concentrations were higher and N concentrations lower in the unploughed plots (both P< 0.001). Similar trends were found for 0-100 mm soil and soil water analyses. The results probably reflect inversion of the topsoil, and for P, increased adsorption on clay brought to the surface, and for N, disturbance of organic matter and aeration stimulating the microbial population and increasing ammonification and nitrification.

Generally, P fertilisation increased P concentrations in soil water (P< 0.001) and soil. Following P application, the 0-20 mm soil water tests for ploughed and unploughed plots had average DRP concentrations of 0.25 and 0.80 mg P/L, and average TDP concentrations of 0.51 and 1.52 mg P/L respectively (P< 0.001, Figure 1). N concentrations in soil water during this period were higher in
unploughed versus ploughed plots, and generally decreased over time before increasing. For the soil samples (0-20 mm), ploughing lessened Olsen P, Colwell P, Organic P and CaCl₂ P concentrations ($P < 0.001$) although the agronomic importance of these changes is questionable. Vegetation type had no significant effect except for NH₄⁺ concentrations (mixed sward plots: 11.0 mg/kg N; monoculture plots: 8.5 mg/kg N, $P = 0.003$) and pasture quality with the mixed sward pasture having a higher yield and feed quality than the monoculture plots.


**Figure 1:** Mean Dissolved Reactive P (DRP) and Total Dissolved P (TDP) concentrations in soil water for ploughed and unploughed treatments at different P fertiliser levels. Week represents the number of weeks since fertiliser treatments began. Error bars $P > 0.05$.

**CONCLUDING DISCUSSION**

Destratification by ploughing could be incorporated into farm management practice without a loss of productivity when pasture requires renovation, a summer forage crop is to be planted, or if soil P concentrations have increased in surface soils. However, the advantage of ploughing to conserve nutrients and decrease nutrient exports must be measured against disadvantages of cultivation. For example, increased soil erosion and consequent export of particulate P can occur on steeper slopes (>5%) after cultivation. For optimum effectiveness, cultivating machinery would need to mix or invert the soil in a vertical plane.

**REFERENCES**


Prediction of urinary nitrogen output from pasture-fed dairy cows

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ABSTRACT

Prediction equations using easily acquired measurements could offer an estimate of urinary nitrogen output (UNO), therein helping to refine nutrient management on dairy farms. However, there is little evidence regarding the validity of currently used equations for pasture-based diets. Using a dataset derived from a pasture-fed cow study, five published equations were evaluated for their usefulness in predicting UNO. Results indicated large variability in prediction accuracy ($r^2 = 36.8 - 77.5$). A new prediction equation that achieved higher prediction accuracy was established ($r^2 = 85.4$).

Keywords: sustainability; pasture; cows; urea.

INTRODUCTION

Urinary nitrogen output (UNO) is an environmental risk factor in dairy production systems, particularly in grazing cows. Traditional UNO measuring techniques require continuous collection of urine and are subject to errors. Because of this, there is considerable interest in being able to predict UNO from easily measured parameters. However, the majority of prediction equations for UNO were developed for cows fed total mixed rations and may not be suited for grazing dairy cows. The objective of this study was to evaluate the validity of five published equations for estimating UNO in pasture-fed cows. The collected data were further used to develop an equation based on a metabolism marker ($^{15}$N).

MATERIALS AND METHODS

A dataset obtained from 15 mid-lactation rumen-fistulated cows fed fresh pasture (13.1-20.1 kg DM intake: DMI) and supplemented with various levels of urea (0-336 g/d/cow) in a metabolism stall experiment was used. Measurements were DMI, feed nitrogen concentration, rumen degradable protein intake (RDPI), milk yield, milk nitrogen concentration, urine output (UO), urinary creatinine concentration, faecal output, faecal nitrogen concentration, body weight, and plasma and feed $^{15}$N. Individual cow UNO was calculated as the difference between N intake and N output in milk and faeces: UNO = nitrogen intake - faecal nitrogen output - milk nitrogen output. Urinary nitrogen concentration (UNcc) was calculated as UNcc = UNO/UO. Calculated UNO was compared with five published UNO prediction equations (Table 1), using coefficient of determination ($r^2$) and probability (p-value) as a measure of the effectiveness of the equation in representing actual UNO. A new prediction equation was also established using linear regression analysis with all measured parameters (Genstat 13).

RESULT

There were large variations in the accuracy with which published equations predicted UNO ($r^2 = 36.8 - 77.5$; Table 1). Urinary nitrogen output could be more accurately predicted by including the difference between plasma and feed $^{15}$N with RDPI (UNO (g/d) = 0.13 × RDPI (g/d) + 46.9 × plasma $^{15}$N - feed $^{15}$N (%o) - 194.4; $r^2 = 85.4$; $P < 0.001$).

Table 1: Evaluation of validity of published equations in determining the urinary nitrogen output (UNO; g/day) of dairy cows fed on freshly cut pasture

<table>
<thead>
<tr>
<th>Prediction equation</th>
<th>$r^2$</th>
<th>P</th>
<th>Mean</th>
<th>Range</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>UNO$_1 = \text{RDPI} \times 0.0628 + 55.6$</td>
<td>77.5</td>
<td>***</td>
<td>218.5</td>
<td>174.6-244.1</td>
<td>Nennich et al. 2006</td>
</tr>
<tr>
<td>UNO$_2 = 0.59 \times \text{NI} - 91.4$</td>
<td>53.7</td>
<td>**</td>
<td>236.2</td>
<td>162.8-282.2</td>
<td>Cheng et al. 2011</td>
</tr>
<tr>
<td>UNO$_3 = 88.8 + 11.6 \times \text{MUN}$</td>
<td>50.7</td>
<td>**</td>
<td>259.7</td>
<td>209.6-313.5</td>
<td>Broderick et al. 2003</td>
</tr>
<tr>
<td>UNO$_4 = 21.9 \times \text{BW} / \text{UCcc} \times \text{UNcc}$</td>
<td>36.8</td>
<td>*</td>
<td>453.5</td>
<td>292.8-580.1</td>
<td>Pacheco et al. 2007</td>
</tr>
<tr>
<td>UNO$_5 = (3.55 + 0.16 \times \text{DMI} + 6.73 \times \text{CPI} - 0.35 \times \text{MY}) \times \text{AU} \times \text{UNcc}$</td>
<td>67.2</td>
<td>***</td>
<td>213.6</td>
<td>107.2-288.7</td>
<td>Fox et al. 2004</td>
</tr>
</tbody>
</table>

* Nitrogen intake (NI); Rumen degradable protein intake (RDPI); Milk yield (MY); Urinary nitrogen output (UNO); Urinary nitrogen concentration (UNcc); Urinary creatinine concentration (UCcc); Crude protein intake (CPI); Body weight (BW); Animal unit (AU; AU= BW/ 454)
DISCUSSION AND CONCLUSION

There were large variations in predictability using five published equations, with those of Nennich (et al. 2006) and (Fox et al. 2004) providing the most reasonable estimates of UNO. The best prediction involved an understanding of the rumen degradability of the crude protein fraction, with poor correlations between UNO and MUN, NI, and UCc. The basis for the newly established equation is isotopic fractionation of nitrogen during hepatic transamination (Cheng et al. 2011). This resulted in an improvement in accuracy relative to just RDPI alone (Nennich et al. 2006), but requires a blood sample. The results indicate an ability to determine UNO with reasonable accuracy with knowledge of RDPI. However, caution is required in extrapolating predictive equations across systems.

ACKNOWLEDGMENT

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Increased productivity and reduced environmental footprint - Are high production, low GHG emission dairy farms in New Zealand possible?

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ABSTRACT

Considerable efforts continue in the search for management options and opportunities for mitigation of greenhouse gas (GHG) emissions and nutrient losses from New Zealand (NZ) dairy farms. An extensive search was undertaken to identify high production, low GHG emission dairy farm systems according to the whole-farm system models Farmax® and Overseer®; two farms in the Waikato (farms A and B) and two in Southland (farms C and D) were identified. Annual GHG emissions from the selected farms (A through D) were estimated to be 9.5, 12.0, 10.4, and 9.5 tonnes CO2-e/ha and 8.6, 9.9, 8.6, and 8.5 kg CO2-e/kg milksolids (MS), respectively, well below the average NZ farm range (11 – 13 kg CO2-e/kg MS). Lower emissions intensity (kg CO2-e/kg MS) farms tended to be more profitable, achieved greater feed conversion efficiencies (i.e. less dry matter consumed per kg MS) and achieved an almost 1:1 ratio of MS production per kg liveweight (LW), compared with farms in a larger nationwide dataset. The current modelling exercise provided examples of the opportunities for highly profitable, greenhouse gas efficient commercial dairy farms.

Keywords: dairy; greenhouse gases; stocking rate; wintering policies; profitability.

INTRODUCTION

Farmer focus groups have been involved in whole-farm system modelling exercises and mitigation-scenario testing to develop a better understanding of on-farm repercussions of GHG and climate change (Dynes et al. 2011). These modelling exercises were compiled to examine the relationships between nutritional, productive, reproductive and financial variables and GHG emissions and N losses to the environment (Duchemin, 2011). The objective of the current study was to identify and examine actual dairy farms that were highly productive and profitable while maintaining reduced GHG emissions. A further objective was to compare the environmental outcomes from these farms with those of a larger, nationwide modelling dataset obtained from NZ dairy farms (Duchemin, 2011).

MATERIALS AND METHODS

Criteria for the selection of farms included a) seasonal milk suppliers with predominantly pasture-based systems and low levels of imported feed and nitrogen (N) fertiliser use (selected farms were within System 2, DairyNZ), b) high MS production per animal and per ha, c) high 6-week in-calf rate, low empty rate and high Breeding Worth, and d) competitive farm operating profit. Expectedly, these criteria would aid in identifying profitable dairy farms with emissions intensity ≤ 9.5 kg CO2-e/kg MS while maintaining sensible emissions per ha. DairyNZ’s extension team and the DairyNZ-operated DairyBase data collection system (www.dairybase.co.nz) were used to identify potential dairy farms. Once identified, comprehensive on-farm interviews were conducted.

The whole-farm system model Farmax® Dairy Pro (herein Farmax; v. 6.4.0.12) was used to examine feed flow, key physical indicators, and financial outputs from the selected dairy farms. The farms modelled were assumed to be in steady state, both in terms of opening and closing numbers of cows and corresponding body weights. Opening and closing dates were June 1, 2010 and May 30, 2011, respectively. The farm-scale nutrient budget model Overseer® (herein Overseer, version 5.4.10) was used to examine some of the environmental impacts and nutrient losses of these farms.

RESULTS

Identifying suitable farms that fitted the criteria of high production, low emission proved to be a difficult task; less than 5% of the farms within the database used held potential for further review. Two farms in the Waikato (North Island; farms A and B) and two in Southland (South Island; farms C and D) were selected. Although differing in size, all farms tended to be reliant on home grown feeds for most of their needs; imported feed ranged from 2 to 10% of feed consumed (Table 1). Farm B relied on more supplements and imported feed than did the other 3 farms. The amount of feed required to produce a unit
of MS was greatest for farm B, with the least FCE (i.e. the greatest amount of dry matter consumed per kg MS).

Annual GHG emissions from the selected farms (A through D) were estimated to be 9.5, 12.0, 10.4, and 9.5 t CO$_2$-e/ha; corresponding emissions intensity values were 8.6, 9.9, 8.6, and 8.5 kg CO$_2$-e/kg MS (Table 2). Because wintering policies were different among farms, estimated emissions from farms C and D are shown as adjusted (Adj); by keeping dry cows on farm, emissions intensity values were increased by 9.3 and 9.4% for farms C-adj and D-adj, respectively. Methane emissions accounted for 57 (farms B) to 63% (farm A) of total emissions.

**DISCUSSION**

A reduction in SR (i.e. the number of lactating cows relative to the grazing area used to support them) per se may lead to responsible environmental stewardship, but may also lead to a sizeable reduction in profits. Losses of pasture quality along with losses in cow performance are a consequence of inferior pasture management. Alternatively, the farms selected opted for nutritional diets with a high intake potential, capable of producing almost 1 kg MS per kg LW (Figure 1a) without compromising profitability. Although low stocked dairying often requires a high level of managerial skill to be successful, these systems were associated with low emission levels and highly competitive farm operating profits (Duchemin, 2011). Interestingly, MS per unit LW exhibited no relationship with GHG emissions per ha (Figure 1b), suggesting that improvements in individual animal production were not at the expense of increased total emissions. Emissions intensity ranged from 8.4 to 9.6 kg CO$_2$-e/kg MS, well below the average NZ farm range (11 - 13 kg CO$_2$-e/kg MS; Overseer).

**CONCLUSION**

The selected farms achieved high quality pastures with a high intake potential, despite the complexities of reducing SR on pasture quality. Although low stocked dairying often requires a high level of managerial skill to be successful, these systems were associated with low GHG emission levels and high farm operating profits. The short-termed, small scale nature of this modelling exercise implies certain caution when extrapolating these results to longer periods of time. Notwithstanding this limitation, the current modelling exercise provided examples of the opportunities for highly profitable, GHG efficient commercial farms.

**ACKNOWLEDGEMENTS**

The authors gratefully acknowledge the cooperation of the dairy farmers that participated in this modelling exercise. This work was supported by MPI through the Sustainable Land Management and Climate Change fund (Cont. 20482-SLMACC, Farm management and GHG for the pastoral sector).

**REFERENCES**


### Table 1: Key descriptive, productive and financial indicators of four dairy farms identified as high production, low emission systems in New Zealand; output from Farmax

<table>
<thead>
<tr>
<th>Farm</th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
</tr>
</thead>
<tbody>
<tr>
<td>Location</td>
<td>Waikato</td>
<td>Waikato</td>
<td>Southland</td>
<td>Southland</td>
</tr>
<tr>
<td>Effective area, ha</td>
<td>93</td>
<td>72</td>
<td>185</td>
<td>299</td>
</tr>
<tr>
<td>N applied, kg/ha</td>
<td>58</td>
<td>178</td>
<td>119</td>
<td>129</td>
</tr>
<tr>
<td>Pasture produced, t DM/ha/yr</td>
<td>14.9</td>
<td>15.1</td>
<td>13.9</td>
<td>13.1</td>
</tr>
<tr>
<td>Pasture consumed, t DM/ha/yr</td>
<td>12.5</td>
<td>13.5</td>
<td>12.1</td>
<td>10.3</td>
</tr>
<tr>
<td>Imported feed consumed, t DM/ha/yr</td>
<td>0.64</td>
<td>1.55</td>
<td>0.32</td>
<td>0.27</td>
</tr>
<tr>
<td>Total feed consumed, t DM/ha</td>
<td>13.9</td>
<td>15.9</td>
<td>13.1</td>
<td>11.9</td>
</tr>
<tr>
<td>Crops grown, ha</td>
<td>-</td>
<td>3.5</td>
<td>5.0</td>
<td>23.0</td>
</tr>
<tr>
<td>SR (^1), cows/ha</td>
<td>2.80</td>
<td>3.21</td>
<td>2.76</td>
<td>2.44</td>
</tr>
<tr>
<td>Lactation length, d</td>
<td>268</td>
<td>262</td>
<td>265</td>
<td>266</td>
</tr>
<tr>
<td>BCS (^2) at calving</td>
<td>4.7</td>
<td>4.9</td>
<td>4.9</td>
<td>5.0</td>
</tr>
<tr>
<td>Liveweight (LW), kg/ha</td>
<td>1203</td>
<td>1386</td>
<td>1286</td>
<td>1132</td>
</tr>
<tr>
<td>Milksolids, kg/cow</td>
<td>408</td>
<td>377</td>
<td>446</td>
<td>463</td>
</tr>
<tr>
<td>Milksolids (^3), kg/ha</td>
<td>1117</td>
<td>1212</td>
<td>1232</td>
<td>1124</td>
</tr>
<tr>
<td>Milksolids, kg/kg LW</td>
<td>0.93</td>
<td>0.87</td>
<td>0.96</td>
<td>0.99</td>
</tr>
<tr>
<td>Feed conversion efficiency (^4)</td>
<td>12.8</td>
<td>13.6</td>
<td>11.1</td>
<td>11.1</td>
</tr>
<tr>
<td>Operating profit (^5), NZ$</td>
<td>175,941</td>
<td>116,947</td>
<td>434,391</td>
<td>523,276</td>
</tr>
<tr>
<td>Operating profit (^5), NZ$/ha</td>
<td>1,892</td>
<td>1,624</td>
<td>2,348</td>
<td>1,750</td>
</tr>
</tbody>
</table>

\(^1\)Stocking rate at peak lactation. \(^2\)Body condition score (New Zealand 1-10 scale), mean value. \(^3\)Supplied to factory. \(^4\)kg dry matter consumed/kg MS. \(^5\)Calculated at a milksolids price of $5.20/kg MS.

### Table 2: Annual nitrogen (N) losses and greenhouse gas (GHG) emissions of four dairy farms identified as high production, low emission systems; output from Overiser

<table>
<thead>
<tr>
<th>Farm</th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>C-adj (^1)</th>
<th>D-adj (^1)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nitrogen, kg N/ha</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Applied</td>
<td>58</td>
<td>178</td>
<td>119</td>
<td>129</td>
<td>119</td>
<td>129</td>
</tr>
<tr>
<td>Leached</td>
<td>22</td>
<td>52</td>
<td>27</td>
<td>26</td>
<td>33</td>
<td>31</td>
</tr>
<tr>
<td>N(_2)O emissions</td>
<td>5.9</td>
<td>7.6</td>
<td>6.7</td>
<td>5.8</td>
<td>7.2</td>
<td>6.3</td>
</tr>
<tr>
<td>Farm surplus N (^2)</td>
<td>113</td>
<td>198</td>
<td>134</td>
<td>127</td>
<td>148</td>
<td>144</td>
</tr>
<tr>
<td>NCE (^3)</td>
<td>41</td>
<td>29</td>
<td>38</td>
<td>36</td>
<td>35</td>
<td>33</td>
</tr>
<tr>
<td>GHG emissions, t CO(_2)-e/ha</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Methane (CH(_4))</td>
<td>6.00</td>
<td>6.85</td>
<td>6.19</td>
<td>5.61</td>
<td>6.86</td>
<td>6.2</td>
</tr>
<tr>
<td>Nitrous oxide (N(_2)O) emissions</td>
<td>2.95</td>
<td>4.02</td>
<td>3.45</td>
<td>3.14</td>
<td>3.72</td>
<td>3.4</td>
</tr>
<tr>
<td>Carbon dioxide (CO(_2))</td>
<td>0.60</td>
<td>1.14</td>
<td>0.73</td>
<td>0.75</td>
<td>0.84</td>
<td>0.8</td>
</tr>
<tr>
<td>Total emissions</td>
<td>9.55</td>
<td>12.01</td>
<td>10.37</td>
<td>9.51</td>
<td>11.3</td>
<td>10.4</td>
</tr>
<tr>
<td>GHG emissions intensity, kg CO(_2)-e/kg milksolids (MS)</td>
<td>8.6</td>
<td>9.9</td>
<td>8.6</td>
<td>8.5</td>
<td>9.4</td>
<td>9.3</td>
</tr>
</tbody>
</table>

\(^1\)Farms C-adj and D-adj represent farms C and D but with dry cows on the milking area during the dry period. \(^2\)Farm surplus N = N in the system as a potential contributor to losses. \(^3\)Nitrogen conversion efficiency, N in product relative to N inputs (i.e. N from fertiliser, fixation and supplemental feeds).
Figure 1: Milksolids (MS) productivity (X; kg MS/kg cow LW) and a) greenhouse gas (GHG) emissions intensity [kg CO₂-e/kg MS = 15.61 (1.16) – 7.40 (1.41)X; \( P < 0.001 \) for intercept and slope; \( R^2 = 0.61, CV = 6.2 \)] and b) GHG emissions [kg CO₂-e/ha = 10.31 (3.84) + 0.62 (4.66)X; \( P = 0.02 \) for intercept and \( P = 0.90 \) for slope; \( R^2 = -0.06, CV = 18.0\% \)]. Data from selected dairy farms are in closed circles (●), whereas data in open circles (○) belong to a larger dataset (Duchemin, 2011).
Cost of growing alternative fodder crops on an out-block in northern Victoria

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332 Lincoln Square North, Carlton, Victoria, 3053

ABSTRACT

A spreadsheet partial budget (discounted net cash flow) over 10 years was used to investigate the cost of purchasing an out-block to grow irrigated fodder in northern Victoria under medium and severe (run of dry years) climate scenarios on a representative farm. Random water allocation sequences over the 10 year timeframe were based on climate projections from the Northern Region Sustainable Water Strategy (Department of Sustainability and Environment 2008).

The out-block was used to grow cereal and maize conserved as silage, lucerne and annual pasture (ryegrass/shaftal-clover mix) conserved as hay. Assumptions on crop water use, expected dry matter yields (DM) and metabolisable energy yields (ME; MJ/kg DM) were key determinants of the cost of producing fodder and therefore profit under the two climate scenarios. Plant water use and estimated DM yields and ME content were varied depending on allocation and to account for the potential effects of higher temperatures (such as the run of dry years scenario).

Under a medium climate scenario, the total cost of ME was less than $0.025/MJ kg DM in 95% of years. If DM yields declined under a run of dry years climate scenario, then the number of years where cost was less than $0.025/MJ kg DM decreased to 0%.

Cereal crops and lucerne perform better under drier conditions due to a smaller reduction in yields compared with the other crops. Cereals also have a lower water cost component as a percentage of total cost. This research has illustrated the importance of understanding the possible impacts of increasing temperatures on the ME content of pastures and crops. Home-grown feed has a number of benefits including lower transaction and transport costs. These benefits may place some farmers who can consistently produce quality feed at a comparative advantage.

Keywords: Fodder; out-block; climate change; irrigation; dry matter; metabolisable energy.

INtRODUCTION

Climate change and continuing water reform that includes the Northern Victoria Irrigation Renewal Project and water buybacks are likely to increase the number of properties shifting from intensive irrigation to opportunistic irrigation.

Climate change in particular could alter the proportion of grazed pasture in the diet of dairy cows, increasing the reliance on purchased supplements (concentrates and fodder) or the production of conserved fodder on out-blocks.

This study investigated the cost of growing fodder on an out-block under moderate and severe (run of dry years) climate scenarios. The out-block was used to grow cereal and maize conserved as silage, lucerne and annual pasture (ryegrass/shaftal-clover mix) conserved as hay.

MATERIALS AND METHODS

A partial budget (discounted net cash flow) over 10 years was used to investigate the cost of purchasing an out-block to grow fodder. The two measures considered were variable costs per ha which has cash flow and risk implications and net cost of estimated ME produced and conserved over the 10 years. The crops grown were cereal for silage (20%), lucerne for hay (50%), maize for silage (10%), annual pasture for hay -ryegrass/shaftal-clover mix (20%). Data on costs for each of the crops was taken from DPI (2009).

To test the potential impact of fluctuations in water allocations and ME yields on profitability under the two climates, probability distributions were developed and included in the budgets instead of single values. Cumulative probability distributions were taken from the Northern Region Sustainable Water Strategy (Department of Sustainability and Environment 2008) and used to describe water reliability profiles under the two climates. For the moderate climate scenario the profiles are formulated by applying a percentage reduction, determined by CSIRO predictions, to the entire historic inflow record. For the run of dry years scenario, the average reduction of July 1997 – June 2007 (from the long term average) was applied to the entire historic record of inflows in the Goulburn system. Program Evaluation and Review Technique or PERT distributions, were applied for ME yields across the two climate scenarios. A PERT distribution is similar
to a triangular distribution, in that it has the same set of three parameters (minimum, mean and maximum). A range of expected ME yields was established for each of the irrigated crops based on earlier work undertaken by DPI (2011) and (Bell et al. 2011). The add-in package to Microsoft Excel @Risk was used to select random sequences of both water allocations and ME yields for the ten year period across the two climates.

It was assumed that in the case of a crop water shortfall due to low allocations, water was purchased on the temporary tradeable water market. Temporary water price was calculated by adding the opportunity cost of owning a megalitre (ML) of high reliability water share (HRWS) to the base water price ($50/ML). Opportunity cost is the net benefit forgone by choosing one alternative (e.g owning HRWS) over another (e.g investing capital elsewhere) and is valued at 6 per cent return per annum. It also attempts to take into account the new carryover policy by allocating half the price to be influenced by the previous year’s allocation and the other half to the current year allocation.

RESULTS

Maize had the highest variable cost per ha (Figure 1); ensiling, fertiliser, seed and water are the major inputs for maize. Given its high DM and ME yield, it was actually the second least expensive source of ME compared with the alternatives tested. Average variable cost for each of the crops is shown in Figure 1 for the medium climate scenario (there is no change in the ranking under the severe climate scenario). High variable costs for some crops can lead to cash flow problems and therefore have risk implications which should be considered.

The economic ranking of crops changes considerably when ME yields are considered. An important finding from the research was that home-grown lucerne is likely to provide a cheaper alternative compared to purchasing lucerne hay whilst pasture hay appears to be more expensive to grow and conserve compared to purchasing. Under a drier climate, lucerne appears to be cheaper than other forage crops due to a smaller reduction in DM yield. Maize silage and annual pasture hay is more variable (standard deviation) due to the wider range in estimated ME yields under the severe (run of dry years) climate scenario and increased water requirement (Figure 2).

Cereals perform better under drier conditions as ME yields are maintained compared to other crops and cereals have a relatively lower water cost component as a percentage of total cost. Water use rises under drier conditions to maintain production.

Metabolisable energy and crop sensitivity to water use were key determinants of the cost of producing fodder and therefore profit. When assessed across the 10 year analysis period for all crops under a moderate climate scenario, the total cost of ME was less than $0.025/MJ kg DM in 95% of years. If DM yields were assumed to decline with ME yields under a drier climate scenario, then the number of years where cost was less than $0.025/MJ kg DM significantly decreased to 0% (Figure 3). This is due to the combined effect of reduced DM yields, decreased ME yield and higher costs under the drier climate situation. It highlights the importance of management expertise under drier climates to minimise DM yield reductions.
Figure 3: Net cost per MJ/kg DM under a moderate climate scenario (red distribution) and minimum yields under drier climate scenario (blue) where DM yields reduce.

DISCUSSION AND CONCLUSION

This research has improved the understanding of the costs of growing a range of irrigated fodder crops under varying climatic conditions in northern Victoria. Because the market for feed is well informed and is a close substitute for irrigation water it is not reasonable to assume that on the whole growing feed is better than purchasing feed. A properly functioning market should adequately reflect the cost of growing feed in a given year as it factors in the price of inputs such as water. Home-grown feed, however, has a number of benefits including lower transaction and transport costs. These benefits may place some farmers who can consistently produce quality feed at a competitive advantage.

For those dairy farmers with a comparative advantage, fodder production should encompass what the business specialises in. This concept is known as the boundary of the firm and is used to define the things businesses can do better than other firms such as growing their own feed inputs. As pointed out by Malcolm (2011), as the dairy economy in Australia has developed and evolved, the boundaries of the dairy farm firm too have evolved. Many farmers recognise this and where there is no comparative advantage farmers have established vertical relationships backwards along the production and marketing chain to their feed input suppliers.

Growing as opposed to purchasing fodder can provide greater certainty in regard to quality and result in a cheaper feed source. However, by choosing to grow fodder, farmers are more exposed to climate variability albeit this can be reduced by the type of crop grown (i.e. more cereals).

It is important to note that the analysis has not accounted for tactical or operational actions that a farm manager can take to improve profitability of the enterprise in a year with either poor/good prices or seasonal conditions.

REFERENCES


ANIMALS
Dairy cow welfare- the role of research and development in addressing increasing scrutiny

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2AgResearch Ltd., Ruakura Research Centre, East Street, Private Bag 3123, Hamilton 3240, New Zealand.

SUMMARY

Pasture-based dairying in New Zealand and Australia is coming under increasing animal welfare scrutiny as farms become larger and more intensive. Over the past decade, animal welfare research has helped identify the risks for animal welfare in these dairy systems, and management opportunities for ensuring good welfare. Continued research, extension and industry adoption will enable dairy producers to address changing community expectations.

ABSTRACT

Pasture-based dairying in New Zealand and Australia has come under increasing animal welfare scrutiny as a result of changing public expectations for farm animal management. Concurrently, efficiency-driven changes in dairy management practices, and a broadening of the feedbase beyond traditionally grazed pasture have resulted in increased intensification of the dairy industries. This intensification has included a higher proportion of grain concentrates in the diet (particularly in Australia), and the greater management of cows off pasture and even in housing (particularly in New Zealand). Research to assess the animal welfare implications of these changes, and to recommend good practice management has concentrated on issues of cow environments and cow feeding, including body condition. Research has shown that cows may be managed for a few hours per day on concrete surfaces without compromising their lying behaviour and other indicators of welfare, but that longer periods off pasture require the provision of a well drained and comfortable lying surface. Other research has defined the extremes of hot and cold/wet conditions beyond which cows benefit from provision of adequate shade and shelter. Research on cow body condition has indicated that welfare responses are aligned with measures of health and productivity in supporting the need to maintain a minimum body condition prior to calving and during the subsequent weight loss period of early lactation. Continued research, extension and industry adoption will enable dairy producers to address community expectations as they continue to change their farming practices.

Keywords: dairy cows, animal welfare, intensification, body condition

INTRODUCTION

Dairy cattle farming in New Zealand and Australia has traditionally been pasture-based. In common with trends in other regions such as North America, dairy farming in Australasia has undergone consolidation in recent years, resulting in larger farm and herd sizes. Developments in management aimed at maintaining economic sustainability and overcoming the production limitations and inherent variability in production associated with a reliance on pasture have also resulted in a broadening of the feedbase, with a greater use of conserved forage and grain-based concentrates (Doyle et al. 2001). Increased regulations around nutrient loss and soil damage have also put pressure on traditional pasture management. Concurrently, there has been an increased use of off-pasture areas for cow management, such as feedpads and stand-off areas (Moran and McDonald 2010).

The standards of husbandry and welfare practised during the farming of livestock are becoming increasingly important factors influencing customer perceptions of product quality in many markets. Those practices that are of concern to the consumer and that cannot be adequately addressed, may damage the image and marketability of livestock products, and adversely affect sustainability of the industry.

The increasing herd size and intensification of dairy production in Australia and New Zealand has occurred against a background of a heightened public interest in animal welfare. As a consequence dairy industry practices and performance have come under increasing scrutiny (Stafford and Gregory 2008). Concerns include the prevalence of lameness, the distances walked by cows on large farms, low body condition, reduced ability to supervise individual animals, and the potential for alterations in cow time budgets for comfort behaviours (Tucker et al. 2005; Stafford and Gregory 2008). Furthermore, the development of new practices will bring additional requirements for animal welfare assurance.

Research in dairy systems examining animal welfare issues can contribute to three important
areas. These are 1) providing the basis for recommendations for farm management practice change that enhances animal welfare; 2) providing the evidence base for animal welfare minimum regulatory standards and guidelines; and 3) providing information on welfare performance and intended standards to markets, regulatory authorities and the general public. Together, the research in these areas can assist producers to maximize the potential of their animals by improving animal performance and meeting market expectations. The objective of this paper is to review animal welfare research that has been conducted over the past decade in Australian and New Zealand dairy systems, and to consider the impacts and benefits of this and future research in the area.

**HUMAN-ANIMAL INTERACTIONS**

It can be argued that the quality of management within a farming system is as important to the animals’ welfare as the type of system itself. Consequently, while a number of studies have rightly examined various management practices and animal environments (reviewed later in this paper), a valuable theme of research has examined the nature and impacts of stockperson attitudes and behaviour in Australasian dairying systems. This is particularly important given that there is less opportunity for positive interactions associated with feeding, due to the pasture-based nature of the system. (Breuer et al. 2000) undertook detailed measurements of stockperson attitudes and behaviour, and cow behaviour and productivity, across 31 dairy farms in south-eastern Australia. Although the study was not designed to demonstrate causality, a number of informative associations between these variables were identified. Stockperson attitudes towards their cows, identified through questionnaires about talking to cows and patting the animals, were correlated with positive behaviours observed in interacting with the herd. Furthermore, positive stockperson behaviours were correlated with increased milk yield, whereas milk production was negatively correlated with fearfulness of the cows in a standard fear test using an unfamiliar person.

Other studies have examined the importance of human-animal interactions during the rearing process. An experimental study by (Schütz et al. 2012) examined the effects and persistence of the type of early handling of dairy calves on their subsequent responses to humans. Calves that were positively handled in the first month of life (by encouraging interaction and providing pats and scratches) showed reduced avoidance of an unfamiliar person when tested at 3 months of age, compared with negatively handled calves. When these calves were examined again at 1 year of age it was found that flight distance of both positive and negatively handled calves was less than control calves. (Schütz et al. 2012) suggested that the amount of human contact during rearing has a greater effect on subsequent responses than the nature of that handling.

A similar effect to the results of (Schütz et al. 2012) was recorded in dairy heifers by (Breuer et al. 2003). In this study, heifers up to 14 months of age were allocated to either positive or negative handling treatments. Negative handling consisted of interaction incorporating the use of slaps from the human, as well as hits (not forceful) with a plastic pipe. The researchers found that positively handled heifers showed a greater propensity to approach a person and had a reduced flight distance. This effect was accompanied by reduced cortisol responses to handling in positively handled heifers (Breuer et al. 2003).

**FEEDING AND NUTRITIONAL MANAGEMENT**

One of the challenges of managing a predominantly pasture-based feeding system is vulnerability to climate-induced feed shortages, particularly if these coincide with key periods such as peak lactation or mating. Even with the capacity to buy in feed, there are periods when cows can lose weight and body condition, particularly in early lactation, and this may be independent of feeding level (Roche et al. 2009). In recent years, animal welfare researchers have attempted to assess the mental state of cows in reduced body condition, aiming to quantify the levels of cow hunger. For a comprehensive review of the physiological and health effects of variations in cow condition, the paper by (Roche et al. 2009) is recommended.

(Schütz et al. 2006) measured feeding motivation in both lactating and pregnant non-lactating cows in response to various levels of short-term feed restriction. The researchers found that lactating cows were willing to walk longer distances as the duration of feed deprivation was increased to a maximum of 9 hours. The pregnant, non-lactating cows did not show the same increase in motivation. It is likely that the difference reflects the increased energy demands in the lactating cow. A subsequent study (Matthews et al. 2012) examined the effects of differing cow body condition score on a number of behaviours indicating welfare at pasture. The lactating Holstein-Friesian cows had condition scores ranging from 2.5 to 8.5 on a 10-point scale. The study found that BCS was negatively correlated with time spent grazing and standing, and less conditioned cows spent less...
time resting than cows with more body condition. However, the resting time of the thinnest cows used in the study was still approximately 9.4 hours per day, and thus within the normal range for grazing dairy cows (Wales et al. 1999). Further research is currently being undertaken to quantify the health status, feeding motivation and potential hunger of cows in reduced body condition under New Zealand conditions.

**HUSBANDRY PROCEDURES**

Most of the husbandry procedures conducted on Australian and New Zealand dairy farms are similar to those conducted in other dairying regions. Examples of such procedures include disbudding of calves, vaccination and health treatments, use of foot baths, and feet trimming – which is less common than in North American or European dairy systems due to increased walking lessening the risk of hoof overgrowth.

In common with other dairying regions, the majority of dairy cattle in Australia and New Zealand are naturally horned. Research in beef cattle conducted by the Australian Beef CRC has worked to identify alleles responsible for polled, horned and intermediate status in cattle, and in the future this could reduce the need for disbudding in dairy cattle (Prayaga, 2007). In the meantime, research has focused on ways to alleviate pain. A number of papers have provided clear evidence that treatment with both local anaesthetic and a non-steroidal anti-inflammatory (NSAID) is best practice for alleviating pain (Stewart et al. 2009), however practical methods of administering this regime are still required (Stafford and Mellor 2005).

Induction of calving is a husbandry procedure with welfare implications that is relatively unique to Australasian dairying. Declining cow fertility (in common with other dairying regions), combined with a need to match peak lactation with spring grass growth in seasonal pasture-based systems led to the practice of bringing forward late-calving cows by several weeks through hormonal induction of parturition (MacDiarmid, 1983). Because of concerns with the sustainability of the practice, including animal welfare concerns for the cow and calf, research has examined the impact of the procedure, and also the effectiveness of alternatives to calving induction. A prospective cohort study across 62 herds in Gippsland, Victoria examined the effects of calving induction on calf survival and cow health and productivity (Mansell et al. 2006). The researchers found that the percentage of calves born alive and surviving until sale declined from close to 100% for cows induced at 8.5 months of pregnancy to 70% for cows induced at 8 months of pregnancy. Induced cows also had significantly greater occurrence of retained foetal membranes (16.4 vs. 4.6%), and of other health problems (8.0 vs. 5.35%). Guidelines for calving induction (regulated in New Zealand), now include measures to minimise risks to cow and calf welfare, although induction remains a contentious issue.

These concerns over the consequences of calving induction have led to its use becoming much more limited, and research has focused on alternative means of ensuring that calving patterns and cow fertility can appropriately match feed supply (Beukes et al. 2005). These strategies may include hormonal treatments to aid the resumption of cyclicity, synchronization programs for heifers, extended lactations and the adoption of split-herd calving systems (Pyman and Macmillan 2010; Macmillan 2010; Auldist et al. 2011).

**LAMENESS**

Although lameness in dairy cows is rightly viewed as a health problem, the potential impact on ability to access resources such as food, shade and water, and the pain suffered by lame cows mean that it is also a significant welfare issue. Most research in New Zealand and Australia has focused on the effects of management practices and external environmental conditions such as track conditions on cow foot health. For example, Gregory and Taylor (2002) examined cow preferences for walking on different track surfaces and identified a strong preference for walking on a softer surface than a hard-packed track. This supports earlier research on the relationships between track surface and clinical lameness by (Chesterton et al. 1989). The types of lesions causing lameness in New Zealand dairy herds have been identified as mainly white line disease and sole injury (Chesterton et al. 2008). Further research has identified that the aetiology of these conditions may vary, and that a ‘one size fits all’ management approach to lameness prevention may not be optimal (Lawrence et al. 2011).

The impacts of lameness on cow welfare have been well documented for Australasian dairying conditions. Lameness in dairy cows generally is known to potentiate nociception, reducing the animal’s thresholds for the perception of and sensitivity to pain (Whay et al. 1998). (Laven et al. 2008) measured changes in the nociceptive threshold of cows treated for lameness in New Zealand and found such changes persisted for at least 28 days after treatment, but were improved at 100 days. These results emphasized the importance of lameness prevention for improving cow welfare. The
long term impacts of lameness were also highlighted by the results of (Alawneh et al. 2012), who found that when analysed retrospectively, reductions in cow body weight were identifiable for up to 3 weeks after lameness was first detected, and were measurable for up to 4 weeks after treatment. Lame cows lost an average of 61 kg (95% confidence interval 47 to 74 kg). Similarly, the ability of lame cows to conceive within a pasture-based seasonal calving system is reduced (Alawneh et al. 2011), leading to an increased risk of culling. The most recent estimate of lameness prevalence in Australian dairy cows was 28% (Lean et al. 2008), suggesting that there is considerable scope to improve cow welfare through improved lameness prevention, detection and treatment.

**THERMAL CHALLENGE – HEAT AND COLD**

Although pasture-based dairying may be viewed as having potential welfare benefits in terms of animal freedom of movement and provision of a ‘natural’ environment, the corollary is that cows have a greater risk of exposure to adverse weather conditions. Grazed dairy cattle in most regions of Australia and New Zealand may be subject to either cold and wet, or hot and humid conditions, or both, depending on location and time of the year.

(Tucker et al. 2007) investigated the effects of shelter and animal body condition in cows exposed to winter conditions incorporating artificial wind and rain. Over 6 weeks, outdoor cows experienced an average temperature of 4.9°C, and cows in a semi-enclosed barn experienced 5.6°C. The minimum wind chill values were -9.9°C and -3.1°C, for outdoor and sheltered cows respectively. Importantly, there was an interaction between body condition and shelter, with the adverse effects of exposure to wet and cold conditions (reduced lying, eating and body temperature) being exacerbated in cows in lower body condition. In a subsequent study, (Webster et al. 2008) exposed cows outdoors to a week of wind and rain resulting in a mean environmental temperature of 3.4 °C and a wind chill of -0.3 °C. Although the air movement and wet conditions were artificially supplemented for experimental purposes, the resulting conditions were not dissimilar to what may occur at times during winter in New Zealand or southern Victoria and Tasmania. In comparison with cows under a barn shelter, the exposed animals exhibited increases in plasma cortisol and thyroxine, and a greater amplitude in the diurnal pattern of body temperature. However, mean body temperature was 0.07°C higher in the exposed cows, and there were no substantive differences in immune response to vaccination. The greatest physiological changes occurred during the initial period of exposure. It should be noted that the cows in the study were non-pregnant, non-lactating and in good body condition. The results of (Webster et al. 2008) suggest that dairy cows exposed to periods of cold and wet conditions may undergo a challenge to their welfare, but these effects are most likely in response to a sudden weather change for cows that are otherwise in robust health and condition.

A study by (Schütz et al. 2010) aimed to quantify cows’ motivation to access shelter when exposed to either dry, wet, windy or wet and windy conditions. In contrast to the researchers’ expectations cows did not seek overhead shelter more in response to rain and/or wind, although wet conditions induced more standing behaviour. In common with the findings of other studies, wet conditions reduced overall lying and feed intake.

Research on cow welfare in response to warm weather has quantified the benefits of providing shade under varying heat conditions, and mitigation strategies for reducing heat stress when cows are held in yards for milking. (Fisher et al. 2008) examined the effects of shade on the welfare of grazed, lactating dairy cows during summer in the Waikato region of New Zealand (latitude 37°47’ S). Groups of cows were grazed over 10-day periods either with or without shade in a crossover design. Cows started to use shade when the ambient temperature reached 25°C and shade use increased exponentially with increasing temperature. On days when the temperature was above this threshold, cows spent a mean of 80 min per day in the shade, but there were no differences between shaded and unshaded cows in grazing time per 24 hours, indicating that cows adjusted their behavioural patterns. Shaded cows had lower peak and mean body temperatures during the day than unshaded cows, but there was no difference in mean 24-hour body temperature. Interestingly, despite the relatively small physiological and behavioural changes induced by shade access, milk production was 3% greater for shaded cows than for unshaded cows. These findings supported the results obtained by (Kendall et al. 2006), who found that lactating dairy cows in the same region produced 3% more milk when given access to shade at the height of summer. Although cows with access to shade grazed less during the day, there were no overall differences in grazing times. One feature of the body temperature data recorded using vaginal loggers by (Kendall et al. 2006) was that both groups of cows exhibited a rise in temperature associated with walking and yarding for afternoon milking. This effect has prompted research into cooling strategies during the afternoon
milking period. (Kendall et al. 2007) measured body temperature and behaviour of cows in response to shade, water sprinklers, shade and sprinklers, or no treatment during yarding prior to afternoon milking. The study found that whereas both shade alone and sprinklers alone reduced cow respiration rates, sprinklers were more effective at reducing cow body temperature, and this effect persisted for longer than when shade only was provided. The combination of shade and sprinklers was also beneficial, with effects becoming apparent when the temperature-humidity index (THI) exceeded 69. This THI value equates to a temperature of 25°C and a relative humidity of 0.77, suggesting that there may be welfare benefits in providing cooling during afternoon yarding in dairy cows at lower thermal conditions than previously assumed (Kendall et al. 2007). Despite sprinklers being more effective at reducing body temperature, and reducing insect annoyance, a recent study demonstrated that cows prefer shade (Schütz et al. 2011).

Holstein-Friesian cows may have a higher proportion of dark coloured coat, and this may render the animals more susceptible to the heat stress inducing effects of solar radiation than would be measured from a simple combination of ambient temperature and humidity. Accordingly, (Tucker et al. 2008) examined the effects of solar radiation on the behaviour and physiology of lactating cows with and without access to shade during summer. Shade provision was provided by structures that provided 25, 50 or 99% effective shading. In contrast to the authors’ hypothesis, cows with a predominantly black coat used the 99% shade less than cows with either predominantly white or mixed coats. However, overall there was a strong positive relationship between the level of solar radiation and the use of shade by almost all the cows, and cows with greater access to shade had lower body temperatures.

**MANAGEMENT ENVIRONMENTS**

Although New Zealand and Australian dairying systems largely still have a dependence on grazed pasture, changes in farm management practices over the past 10 to 15 years have resulted in periods of time when many cows do not have a grass-covered field underfoot. Initially, these management changes were focused on the winter period when cows were pregnant and not lactating. A combination of factors including the reduced feed intake of cows at this time, increasing stocking rates over time, and the risk of treading damage to waterlogged pastures resulted in cows being removed from pasture for periods of time and either fed elsewhere or allowed to graze for a short period at pasture before removal each day. Because alternative areas to pasture are generally only used temporarily, farmers and researchers examined various low cost solutions, rather than building full housing. (Stewart et al. 2002) recorded the behaviour of cows on commercial New Zealand dairy farms during these ‘stand-off’ periods on various surfaces. Pregnant non-lactating cows managed on woodchip surfaces lay down for an average of 11.3 hours per day, significantly longer than cows on concrete (2.4 hours) and gravel laneways (4.1 hours). Lying times for cows of less than approximately 6 hours per day are considered undesirable, and result in stress-induced perturbations of the hypothalamic-pituitary-adrenal axis (Fisher et al. 2002).

Further evidence on the effects of stand-off environments on cow behaviour were provided by an experimental study conducted by (Fisher et al. 2003). In a replicated latin square design, non-lactating cows were allocated to either a wood chip pad, a concrete yard, a gravel-surfaced farm laneway or a small paddock. The cows were held on the stand-off areas for 4 days at a time, apart from a 3-hour period each day spent grazing at pasture. The total time spent lying per day was greater for cows on the woodchip pad (11.9 hours), than for cows on the concrete yard (7.0 hours), farm laneway (5.7 hours), or small paddock (6.9 hours). Cows on stand-off treatments where lying was reduced attempted to compensate by lying down to a greater extent during the 3-hour grazing period at pasture. Cows on the concrete yard had lower bodyweights and higher faecal glucocorticoid metabolite concentrations at the end of the 4-day stand-off period than cows on the wood chip pad and the small paddock. These results highlight the importance of providing a well-drained and comfortable surface for cows to rest upon during periodic removal from pasture.

Further developments in cow management have resulted in lactating cows being managed off pasture for periods of time on some farms. In New Zealand, this may be influenced by environmental considerations, including nutrient management and avoidance of treading damage (Laven and Holmes 2008). In order to examine the effects of these management strategies, (McLeod et al. 2009) allocated lactating cows to one of three replicated treatments. These were access to pasture for 4 hours twice a day after milking (total 8 hours), access to pasture for 8 hours in a single bloc between milking, or access to pasture throughout the day apart from milking (control). Cows in the first two treatments were maintained on a woodchip pad between grazing periods, with access to water but not feed. The results showed that cow feed intakes were reduced from 13.6 kg DM per cow daily in the control treatment.
Welfare Measures

Although research aimed at developing improved measures of animal welfare may not contribute directly to farm management practices, welfare methodology studies enhance researchers’ ability to objectively assess welfare and identify good practice in cow management environments and husbandry procedures.

The capacity to assess animal stress responses through minimally invasive techniques has been the main focus of research in this area. (Morrow et al. 2000) used ACTH stimulation tests in lactating cows to validate the measurement of corticosteroids in urine as a measure of activation of the stress-responsive hypothalamic-pituitary-adrenal axis. In a subsequent study (Morrow et al. 2002), the researchers identified faecal glucocorticoid metabolites that could be used to measure hypothalamic-pituitary-adrenal axis activation in dairy cows during the preceding 8 to 15 hours. This technique has been used in a number of later applied welfare research studies (e.g. Fisher et al. 2003; Webster et al. 2008).

Another approach for non-invasive welfare measurement has examined the use of infrared thermography to quantify stress responses in dairy cattle (Stewart et al. 2005). In a study using Friesian calves, an adrenalin challenge resulted in a decrease in eye temperature as measured 0.5 m away using infrared thermography. This technology has showed promise in early detection of a number of health and welfare issues (Schaefer et al. 2011), and may help fill the gap in animal surveillance in systems with a low number of labour units per cow.

IMPACT OF WELFARE RESEARCH AND CONCLUSIONS

The two key areas in which dairy cow welfare research in Australia and New Zealand has contributed to farm management practices are in reinforcing the importance of maintaining suitable cow body condition, and in evaluating the impact of increasing intensification of the pasture-based system and recommending improved management strategies as a result. The research on the animal welfare impacts of body condition has supported management strategies derived from nutritional and fertility research on the need to maintain cow body condition above minimum levels in order to optimize the chances of cyclicity and conception following mating, to maintain milk production and to avoid health and welfare problems. Animal welfare research has also contributed to recommendations and farmer adoption of good practices during the move from purely pasture-based system to a range of systems with an overall greater intensity. Where cows are maintained off pasture for periods of time, this is less frequently done in ad hoc facilities, such as milking shed yards, and more in purpose built areas that are designed to provide comfortable, dry lying areas. As some dairy systems in Europe move towards greater extensification, and the trend towards intensification and even housing occurs in New Zealand, existing animal welfare research in each region should become more relevant.
to the other. In this case it is likely that moving from one type of management system to another does not in itself make the welfare of the animals inherently better or worse, it essentially means that there are a new set of challenges that have to be evaluated and managed.

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J. J. Loo – Functional Welfare

**ABSTRACT**

Animal welfare is an important social construct showing that humans recognise the sentient nature of animals and manage them accordingly; however, because the concept differs depending on individual perceptions of the acceptability of different practices and appropriate endpoint measurements, objective evaluation of an animal’s welfare state is challenging. A good level of welfare, however, is not achieved merely by the absence of difficulties (e.g. pain, injury, disease, distress) but by the animal’s capacity to overcome them. Production oriented (utilitarian) opinions contend that high production indicates good welfare, as an animal must be healthy and well-nourished to achieve it. Although there is truth in this premise, high production can, in itself, result in stresses with no obvious signs that potentially predispose animals to ill health. Advances in high-throughput metabolite (“metabolomics”) and gene expression (“transcriptomics”) analysis techniques have enabled the rapid identification of multiple biomarkers that, in combination, reflect the metabolic and immunocompetence functional capacity of the animal. With this knowledge, the effects of management, nutrition, physiological state, and their interactions can be evaluated for their effect on functional capacity. As the links between metabolism, immunology (“immunometabolism”) and mental state are elucidated, these techniques also offer a means to assess if the animal also experiences feelings of malaise. Collectively, these measurements, therefore, can indicate “functional welfare”, which encompasses biological function/physical state, and some components of mental state as part of animal welfare.

**BACKGROUND**

The welfare state of domesticated animals is the responsibility of humans because animals are under their “custodianship”. Animal welfare is a social construct (Fisher 2009), making an objective evaluation of an animal’s welfare state challenging. The problem is that the concept differs depending on people perceptions of acceptable practices and acceptable endpoint measurements. In accordance with Fraser and Broom (1990), the welfare state depends upon the “degree of success achieved in coping with difficult conditions”. This definition recognises the importance of both affective and functional states, but, more importantly, it facilitates the objective measurement of factors that contribute to animal welfare. Namely, a proper level of welfare is not achieved merely by the absence of difficulties (e.g. pain, injury, disease, distress), but by the animal’s capacity to overcome them (i.e. the animal is functionally competent) and the herdsman’s ability to manage them (i.e. human responsibility for the animals in their charge) (Bertoni and Calamari 2006).

A current challenge in livestock production is how to evaluate the negative sensations of animals that are regarded as suffering (Duncan 2004). Perceptions motivate the animal to react to needs (e.g. a need for food and water is associated with hunger and thirst, loneliness with a lack of social contact). This aspect of animal welfare involves subjective measurements of how an animal “feels” (affective state), determined either through motivation tests (e.g. what will an animal give up or what effort will it undergo to perform a necessary act) or through inferences drawn from animal behavioural traits (Matthews et al. 2012).

In comparison, within the latter class of measures, some authors (Sørensen et al. 2001; Winckler 2006) suggest three directly-measurable parameter types: physiological, behavioural and pathological. Others include a performance index (Bertoni et al. 1999; Veissier et al. 2000). The difference is small, but not irrelevant, as only animals living in proper conditions and in good health can perform properly according to their genetic background within the context of the management system. A clear example is the fact that in pasture-based systems, cows of high-genetic merit may produce below their genetic capacity but are not functionally or behaviourally compromised. Performance is, thus, a considerable indicator of the animal’s functional welfare state. The inclusion of performance as an indicator of welfare state was also suggested by Broom (1997), Rushen and de Passillé (1998) and Nielsen (1999), but has been strongly opposed by proponents of strict animal “welfare” measures (Rollin 2004; Winckler 2006) as well as in the final
recommendation of the project “Welfare Quality” funded by the EU.

As a compromise, Calamari and Bertoni (2009) proposed a composite evaluation model [“Integrated Diagnostic System Welfare” (IDSW)] based on two types of parameters:

- indirect parameters: characterisation of the life environment according to ideal conditions (housing, management, feeding, microclimate, and hygiene), which can guarantee desirable (possible) comfort;
- direct or animal-based parameters: evaluation of the animal’s response to the life environment (physiological, behavioural, performance and health indices), because their adaptation capacity can be affected by many factors and cannot be fully foreseen.

The IDSW weighs each parameter according to its relevance for welfare and groups them into three clusters: life conditions (30% of the final score), feeds and feeding (30%), and animal response (40%), including performance (including fertility), metabolic conditions, behaviour, and health. This proposal recognises that it is important for animals to exhibit behaviour within “normal” ranges, but underscores that objective measures of the effect of management, nutrition, and the environment on the cow’s ability to function normally, withstand challenges to the immune system, and to live a relatively long life must be provided at least equal weighting to affective state in any welfare debate. In this scenario, welfare would be reduced by disease, injury, psychological difficulties, or malnutrition. Modern experimental techniques have improved the ability to measure this concept of “functional welfare” and the application of these techniques will be discussed here.

**NUTRITION AND WELFARE**

One of the most comprehensive definitions of animal welfare is that proposed by Webster: “the welfare of an animal is determined by its capacity to avoid suffering and sustain fitness”; this implies that for a proper evaluation of an animal’s welfare state the negative effectors (and their avoidance) and positive effectors of welfare need to be taken into account. Nutrition is a key factor that can alter the welfare state of an animal. An in-depth discussion of nutritional management and metabolism in periparturient cows is available in a companion paper (Roche et al. 2012). There are at least four main considerations when evaluating the link between nutrition and welfare:

- appetite satisfaction (satiety): ensuring enough feed and water availability and their intake.
- malnutrition:
  - deficiencies or excesses of specific nutrients: particularly essential nutrients, which, if limiting, can enhance susceptibility of tissues to damage (e.g. parakeratosis with zinc deficiency) or result in impairment of the immune system, thereby increasing the risk of infectious diseases (e.g. mastitis with vitamin E deficiency).
  - diet formulation: examples include diets with excessive non-structural carbohydrates leading to greater risk of acidosis, diets that lead to prolonged negative or positive energy balance, increasing the risk of production-related diseases (e.g. ketosis), or diets that result in over-conditioning, increasing the risk of developing “fat cow syndrome”.
  - poisoning effects: toxic plants, naturally occurring alkaloids, chemical contamination, spoilage effects of bacterial-mould, which release metabolites like mycotoxins, or endogenous metabolites produced by animal tissues (e.g. reactive oxygen metabolites in the case of oxidative stress).

Optimal nutrient intake is more likely to ensure animal fitness. Except for the physical and psychological effects of hunger and thirst and the clinical pathology of poor nutrition-induced disorders, it is difficult to assess the adverse effects of poor nutritional management. Evaluating the effects of malnutrition on functional welfare requires that examination of the potential effects on tissue damage (i.e. those induced directly by biochemical abnormalities or indirectly by toxic compounds and diseases that impair health status).

Behavioural signs occurring during infection and inflammation include fever, weakness, malaise, listlessness, and inability to concentrate. Sick individuals become depressed and lethargic, show little interest in their surroundings and stop eating and drinking (Dantzer 2001). These types of responses are of special interest for two reasons:

- the link between health disorders and poor welfare are clearly evident (i.e. links between physical and mind effects). Furthermore, the pro-inflammatory cytokines (PIC: IL-1 and TNF) negatively affect brain function [e.g. depression, irritability and cognitive disorders (Dantzer et al. 2008)] and also cause an exaggerated pain response, which is more evident at the whole-animal level (Watkins and Maier 2000).

as suggested by Fleck (1989) the effects of PIC at clinical and sub-clinical level can be assessed fairly objectively through changes in circulating...
concentrations of acute-phase proteins [APP; positive (posAPP) and negative (negAPP)]. The reduction in concentration of the negAPP (e.g. albumin, lipoproteins), in particular, is a better indicator of a systemic PIC effect because the response is longer-lasting. Thus, the posAPP are less robust than negAPP in the evaluation of sub-clinical conditions, which also contribute to the well-being of cows.

The use of PIC and APP as biomarkers of functional welfare is of great interest because sub-clinical conditions are relatively frequent in intensive animal production systems (both confinement and pasture-based) and likely reduce welfare, as reported in swine (Fossum 1998). For example, (Burke et al. 2010) reported lower circulating concentrations of albumin, a negative APP, before calving and through early lactation in dairy cows that had no evident malaise but had subclinical endomatisis at 28-42 days post-calving. Singling out PIC as the sole cause of poor functional welfare might seem naïve and certainly difficult to demonstrate, but (Dantzer et al. 2008) reported convincing evidence in humans (and laboratory animals) that depression (i.e. mental malaise) is more frequent in individuals with coronary heart disease, obesity, obstructive sleep apnoea and psoriasis, all of which are characterised by a low-grade inflammatory condition (i.e. elevated concentrations of PIC).

This review proposes that these factors might also be important in detecting malaise in animals; the possible link between welfare, health and nutrition could, in fact, be far more extensive than just infections, parasitism, metabolic diseases, digestive upsets, and toxicoses. It could extend to any situation characterised by a significant release of PIC (with or without clinical signs). For instance, in the post-partum period, cows can be without obvious signs of disease, but clearly seem apathetic, depressed, and have reduced appetite. More importantly, these seemingly “problem-free” cows may be in poor nutritional status because they eat less (Trevisi et al. 2010a) and have lower energy efficiency (Trevisi et al. 2007; Trevisi et al. 2010a) Consequently, these animals suffer from a more severe state of negative energy balance (NEB) and are more susceptible to developing other diseases, further loss of body condition score (BCS), and are likely to be less fertile (Trevisi et al. 2007; Bertoni et al. 2008; Trevisi et al. 2009) and culled prematurely.

CRITICAL ORGANS THAT DETERMINE THE FUNCTIONAL STATE OF THE DAIRY COW

Genetically-imposed nutrient prioritisation: consequences for key organs as it relates to functional state and productivity

Over the past 40 years, the focus of the dairy industry in most countries has been on maximising milk yield/cow, thereby creating a “nutrient highway” from the daily ration and mobilization of body reserves [-0.6 kg fat/day, -0.04 kg protein/day, and ~0.15 kg water/day during the first 8-weeks of lactation (Tammenga et al. 1997) directly to the udder to sustain milk production. As discussed in more detail (Roche et al. 2012), in the early postpartum dairy cow a series of biological mechanisms bring about the prioritization of milk production at the cost of body reserves (Bauman and Currie 1980; Ingvartsen 2006); for example, insulin concentrations are drastically reduced and the response of hormone-sensitive lipase in adipose tissue to lipolytic stimuli in high-yielding dairy cows (e.g. low insulin, high growth hormone and catecholamines, or high glucocorticoid concentrations; (Vernon 2005) is greater, thus, facilitating lipid mobilisation and its preferential partitioning to the udder. An increase in messenger RNA (mRNA) expression of lipolytic genes (e.g. -adrenergic receptors, hormone-sensitive lipase) is part of the multifaceted regulation of lipolysis (Sumner and McNamara 2007). Non-esterified fatty acids (NEFA) released from adipose depots travel primarily to liver where they are fully oxidised to $CO_2$, partly metabolized to ketone bodies, or esterified into triglyceride (TAG) and released into the bloodstream as very-low density lipoprotein (VLDL); if NEFA are excessive, or lipoprotein synthesis inadequate, or there is insufficient ruminal propionate produced for the synthesis of adequate oxaloacetate, a portion is converted to ketone bodies and TAG stored as cytosolic lipid droplets (Drackley 1999). Elevated NEFA concentrations have been negatively correlated with pancreatic function in early postpartum cows (Bossaert et al. 2008).

In addition to facilitating lipolysis, hypoinsulinaemia promotes gluconeogenesis (up to 4 kg glucose per day; (Drackley et al. 2001; Reynolds et al. 2003) and facilitates the uncoupling of the somatotropic axis (i.e. the growth hormone (GH)–insulin like growth factor 1 (IGF-I) axis) in liver due to a decrease in mRNA expression of the GH1A receptor (Lucy 2007). As IGF-I production in liver is suppressed, the negative feedback of IGF-I is removed at the level of the hypothalamus/pituitary gland, and GH concentrations increase. High GH
concentrations not only stimulate milk production but also enhance and sustain gluconeogenesis in liver and lipolysis in adipocytes (Etherton and Bauman 1998). The resulting high blood NEFA and GH concentrations antagonise insulin actions, place additional stress on liver function, and contribute to a persistent state of peripheral insulin resistance (Lucy 2007; Pires et al. 2007). Under these scenarios, even more glucose is spared and made available to the mammary gland for lactose synthesis.

Because ruminants have inherently low rates of VLDL synthesis and secretion (Pullen et al. 1990), accumulation of TAG in liver cells as well as extensive output of ketone bodies, such as -hydroxybutyrate (BHBa), into the circulation likely occurs in all dairy cows (Reynolds et al. 2003). The metabolic load placed on the periparturient cow’s liver is exacerbated by the decrease in dry matter intake (DMI) and negative energy balance (NEB), which often occurs as early as 10 days prior to parturition (Allen et al. 2005). Failure of cows to adjust their metabolism adequately to support increased nutrient requirements postpartum often leads to their early removal from the herd.

The concept of “immunometabolism” as it relates to functional welfare in transition dairy cows

“Immunometabolism” was defined recently as “an emerging field of investigation at the interface between the historically distinct disciplines of immunology and metabolism”, explicitly recognising the link in humans between obesity and the immune system, and the fact that obesity-induced inflammation promotes the onset of chronic diseases (Mathis and Shoelson 2011). At the core of this concept is the recognition that there are “multilevel interactions between the metabolic and immune systems”, implying “cross-talk” or “communication” between key cells and organs, which are probably orchestrated by unique mechanisms that are largely responsible for the complications that characterise the “metabolic syndrome” (e.g. understanding such complex intra-tissue mechanisms might lead to the discovery of preventative or therapeutics; Mathis and Shoelson 2011).

Research during the last decade has underscored the complex interrelationships between the immune system and metabolic, and physiological adaptations occurring in key tissues (e.g. liver, mammary, adipose, immune cells) during the transition from the late-pregnant, non-lactating period to lactation (i.e. the transition period). Some of these have been discussed in detail in another review in this issue (Roche et al. 2012). Many different aspects of the bovine immune system change during the periparturient period, but excessive inflammation is a dominant feature in several economically-important disorders such as metritis and mastitis (Bertoni et al. 2009; Sordillo et al. 2009). In addition to undergoing a period of reduced immunological capacity (i.e. immunosuppression), periparturient cows also are faced with a tremendous augmentation in the production of reactive oxygen metabolites (ROM) and PIC, particularly after parturition (Bertoni et al. 2009; Sordillo et al. 2009; Trevisi et al. 2009). The consequence of reduced periparturient immunological capacity is that cows are less responsive to invading pathogens and become more susceptible to infectious diseases, particularly mastitis (Overton and Waldron 2004).

Increased oxygen use by the liver soon after parturition (Reynolds et al. 2003), reflecting a doubling of metabolic rate, means that this organ is a prime site where a proper balance of ROM production and availability of antioxidant defences must be achieved. The liver is also a key responder to PIC signals arising from metabolism and/or disease (Bionaz et al. 2007; Bertoni et al. 2008; Bertoni et al. 2009; Trevisi et al. 2012). Because prepartal management can affect metabolism (Bernabucci et al. 2005; Roche et al. 2005; Dann et al. 2006; Roche 2007; Sordillo and Aitken 2009; Roche et al. 2012), inflammation status (Bertoni et al. 2009; Burke et al. 2010), and immune system responses (Rontved et al. 2005; Graugnard et al. 2012) in key tissues such as liver and mammary, a more holistic approach (i.e. systems physiology) must be used to study these complex interrelationships. It has been argued previously (Loor 2010) that a systems approach should encompass molecular mechanisms as well as whole-animal functional information (e.g. production variables and blood profiles of metabolites, hormones, and “biomarkers” of inflammation and immune function).

In the subsequent sections a brief description is provided of the use of “biomarkers” to evaluate functional welfare as it relates to metabolism and inflammation, with examples of their application in periparturient cows. The applicability of molecular techniques and “bioinformatics” concepts to expand our systems understanding in the context of functional welfare is also discussed.

**BIOLOGICAL MEASURES IN BLOOD AND TISSUES USED IN EVALUATING FUNCTIONAL STATE**

Evaluating the functional state of animals, and particularly those in production systems, has been facilitated by the use of “biomarkers” (i.e. a biological molecule in blood or tissues). Table 1 provides an example of the most-studied biomarkers during the periparturient period, along with the “normal” temporal response observed post-partum. In
theory, a biomarker can be objectively and routinely measured and, thus, can serve to determine or predict a functional state, including normal biologic or pathogenic processes. In addition, these biomarkers should be useful for monitoring the functional state of an animal in response to therapeutic interventions (i.e. serve as pharmacologic markers) or management changes (e.g. stocking rate, nutrition), variations in behaviour (e.g. eating, drinking), and their potential interactions (Dann et al. 2005; Weary et al. 2009; Graugnard et al. 2012; Huzzey et al. 2012).

Table 1: Changes in some inflammatory, metabolic, homeorhetic and homeostatic biomarkers during the periparturient period. When available the relative changes over time post-partum are indicated. Arrows denote decrease (⇓) or increase (⇑) in concentration. Data were from Ingvartsen (2006); (Bertoni et al. 2008, 2009); (Bionaz et al. 2007); Relling and Reynolds (2007), (Trevisi et al. 2009, 2011, 2012); (Schoenberg et al. 2011a).

<table>
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<tr>
<th>Biomarker</th>
<th>Relative change between late-pregnancy and early lactation</th>
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</thead>
<tbody>
<tr>
<td><strong>Inflammation and liver function</strong></td>
<td></td>
</tr>
<tr>
<td>Ceruloplasmin</td>
<td>⇑ to -4 d, then ⇑ by 14 d</td>
</tr>
<tr>
<td>Haptoglobin</td>
<td>⇑ to 4-7 d, then ⇑ by -14-18 d through 28 d</td>
</tr>
<tr>
<td>IL-6</td>
<td>⇑ to 0 d, then ⇑ by 4 d and ⇑ by 9 d</td>
</tr>
<tr>
<td>TNF-</td>
<td>⇑ to 0 d, then ⇑ to 8 d, then ⇑ by 30 d</td>
</tr>
<tr>
<td>Albumin</td>
<td>⇑ to 7 d, then ⇑ by 28 d</td>
</tr>
<tr>
<td>Bilirubin</td>
<td>⇑ to 4 d ⇑ 21 d</td>
</tr>
<tr>
<td>Globulin</td>
<td>⇑ to 0 d ⇑ 63 d</td>
</tr>
<tr>
<td>ROM¹</td>
<td>⇑ to 7 d ⇑ 28 d</td>
</tr>
<tr>
<td>PON</td>
<td>⇒ to 0 d, then ⇒ to 0-7 d ⇑ 63 d</td>
</tr>
<tr>
<td>Cholesterol</td>
<td>⇒ to 0 d, then ⇒ to 0-7 d ⇑ 28 d</td>
</tr>
<tr>
<td>Globulin</td>
<td>⇒ to 0 d, then ⇒ to ~30 d, and changes little</td>
</tr>
<tr>
<td>Vitamin A</td>
<td>⇒ to 0 d, then ⇒ to ~30 d, and changes little</td>
</tr>
<tr>
<td>Alkaline phosphatase</td>
<td>⇒ to 0-28 d</td>
</tr>
<tr>
<td>Lactate dehydrogenase</td>
<td>⇑ to 0-28 d</td>
</tr>
<tr>
<td>Gamma-glutamyl transferase</td>
<td>⇑ to 0-28 d</td>
</tr>
<tr>
<td>Glutamic oxaloacetic acid transferase</td>
<td>⇑ to 0-28 d</td>
</tr>
<tr>
<td><strong>Metabolism</strong></td>
<td></td>
</tr>
<tr>
<td>NEFA</td>
<td>⇑ to -14 d, then ⇒ ~14-40 d</td>
</tr>
<tr>
<td>Glucose</td>
<td>⇒ at 0 d ⇒ 7 d ⇑ 63 d</td>
</tr>
<tr>
<td>BHBA</td>
<td>⇑ to 7 d ⇒ -14-35 d</td>
</tr>
<tr>
<td>Urea</td>
<td>⇒ at 0 d ⇒ 7 d ⇒ - 14 d ⇑ 63 d</td>
</tr>
<tr>
<td>Fibroblast growth factor-21</td>
<td>⇑ to 0 d ⇒ 7 d</td>
</tr>
<tr>
<td><strong>Homeorhesis</strong></td>
<td></td>
</tr>
<tr>
<td>Progesterone</td>
<td>β</td>
</tr>
<tr>
<td>Placental lactogen</td>
<td>β</td>
</tr>
<tr>
<td>Estrogens</td>
<td>β</td>
</tr>
<tr>
<td>Prolactin</td>
<td>Ý</td>
</tr>
<tr>
<td>Somatotropin</td>
<td>Ý</td>
</tr>
<tr>
<td>Leptin</td>
<td>β</td>
</tr>
<tr>
<td>Ghrelin</td>
<td>⇒ to 29 d</td>
</tr>
<tr>
<td>Glucocorticoids (cortisol)</td>
<td>⇑ around 0 d, then decreases</td>
</tr>
<tr>
<td><strong>Homeostasis</strong></td>
<td></td>
</tr>
<tr>
<td>Insulin</td>
<td>⇒ to 14-20 d, then ⇑ to 63 d</td>
</tr>
<tr>
<td>Glucagon</td>
<td>⇑ to 40 d, then remains unchanged</td>
</tr>
<tr>
<td>Parathyroid hormone</td>
<td>Ý</td>
</tr>
<tr>
<td>1,25-dihydroxyvitamin D3</td>
<td>Ý</td>
</tr>
<tr>
<td>Calcitonin</td>
<td>β</td>
</tr>
<tr>
<td>GIP</td>
<td>⇑ to 29 d</td>
</tr>
<tr>
<td>GLP-1</td>
<td>⇑ to 29 d</td>
</tr>
<tr>
<td>OXM</td>
<td>⇑ to 29 d</td>
</tr>
<tr>
<td>CCK</td>
<td>⇑ to 20 d</td>
</tr>
</tbody>
</table>

¹Abbreviations: reactive oxygen metabolites (ROM), paraoxonase (PON), glucose-dependent insulinotropic polypeptide (GIP), glucagon-like peptide 1amide (GLP-1), oxyntomodulin (OXM), cholecystokinin (CCK).
By far the most-commonly used biomarkers of functional state in periparturient dairy cows are NEFA and BHBA (LeBlanc 2010), which can reflect the energy balance status of the animal. However, they are blunt tools. There is current interest in the scientific community to identify a more complete set of biomarkers that can be routinely used in the field for monitoring energy balance status, liver function (Bionaz et al. 2007; Bertoni et al. 2008; Trevisi et al. 2009), inflammation status (Bossaert et al. 2012; Trevisi et al. 2012), and “physiological imbalance” (Bjerré-Harpoth et al. 2012). The latter concept is an attempt to aggregate several biomarkers that reflect the function of the digestive tract, and the metabolic and immune state of the animal (i.e. a variation of these biomarkers from normal should help identify animals that are at a greater risk of developing clinical or subclinical production conditions (Bjerré-Harpoth et al. 2012).

From a practical standpoint, biomarkers of functional state should be measurable in blood and other biological fluids including urine (e.g. ketone bodies; (LeBlanc 2010) and milk (e.g. citrate; (Bjerré-Harpoth et al. 2012). They should be relevant beyond the periparturient period, when most of the clinical and subclinical conditions occur, enabling the identification of management problems during lactation, such as over- and under-nutrition, overstocking, and their potential interactions. In the context of studying the link between the immune system and metabolism, both of which are central to assess the overall functional state of animals, we first must understand the process of inflammation along with its causes and effects on the animal must be understood.

**CYTOKINES AND INFLAMMATION: KEY PLAYERS DETERMINING FUNCTIONAL WELFARE**

Cytokines are proteins (i.e. a type of biomarker) secreted by white blood cells and a variety of other cells in the body (Turnbull and Rivier 1999), including Kupffer cells in the liver (Moshage 1997; Ceciliani et al. 2012), white adipocytes, and adipose tissue-resident immune cells (e.g. macrophages); they are produced mainly during inflammation as a response to tissue irritation and injury caused by infection or other damage, including oxidative stressors (Goddeeris 2010). Cytokines exert pleiotropic actions in a large number of tissues and cells. In particular, they are part of a counter-regulatory system that plays a crucial role during immune system activation and suppression favouring mechanisms of defense and repair, but also helping to control an excessive defense response by the host (Kapcala 1999), which would be dangerous for the body.

The various cytokines can be classified as being PIC (e.g. IL-1, IL-6 and TNF), which promote a local and a systemic response to help the defense system (Cousins 1985; Elsasser et al. 1997), and anti-inflammatory cytokines (AIC, e.g. IL-4, IL-10), which dampen the activity of the former to prevent detrimental effects (Grimble 2001). As a whole, the clinical effects of cytokines are part of “sickness behaviour” (Broussard et al. 2001; Dantzer et al. 2008). They are responsible for a sequence of events defined as the acute-phase response, which involves several organs and tissues including the hypothalamus, liver, adipose, and reproductive tract (Elsasser et al. 1997).

In the liver, PIC promote the synthesis of posAPP (Powanda 1980; Petersen et al. 2004), e.g. haptoglobin, serum amyloid A, ceruloplasmin, C-reactive protein, 1-antitrypsin, whose concentrations in blood increase very rapidly after a challenge (i.e. within few hours). As the posAPP increase, other blood proteins such as albumin, transferrin, retinol-binding protein decrease and are referred to as negAPP. Their quick reduction is a consequence of altered vascular permeability that promotes the loss of proteins from blood (Fleck 1989) or that increases their renal clearance. The negAPP continue to decrease at a slower rate, and this is followed by a gradual increase to pre-event concentrations; the latter response is a consequence of the down-regulation of the synthesis of negAPP in the liver (Powanda 1980), likely as a counter-regulatory mechanism facilitating the synthesis of posAPP. Thus, pro- and anti-inflammatory responses in tissues such as liver are closely regulated at the level of gene transcription and these mechanisms can be studied en masse using high throughput molecular technologies discussed later.

**The relevance of inflammation to liver function**

The peculiarity of the liver that produces more posAPP and reduces the synthesis of negAPP becomes particularly dangerous in the transition period. In this physiological stage, two of the most important functions of the liver are gluconeogenesis from amino acids and long-chain fatty acid metabolism (Drackley 1999), which PIC tend to counteract. Negative responses of PIC on liver metabolism have been well-described in non-ruminants (Khovidhunkit et al. 2004), and recent data from gene expression work (Loor et al. 2005; Bradford et al. 2009; Vels et al. 2009) have provided some evidence that this mechanism might also be functioning in the periparturient bovine liver. Additional work in this area is urgently needed, and should lead to identification of management and nutritional strategies to alleviate the systemic state...
of inflammation in the cow (also in clinically-healthy ones; Bertoni et al. 2008) around calving.

Upon a pro-inflammatory challenge, fatty acid oxidation in non-ruminant liver is reduced partly due to the lower expression/activity of several nuclear receptors coordinating lipid metabolism (e.g. peroxisome proliferator-activated receptor (PPAR); (Chinetti et al. 2000)]. There is evidence that the expression of PPAR-alpha (PPAR) increases after calving (Loor et al. 2005), at least in part, due to the increased influx of NEFA arising from adipose tissue lipolysis. Dairy cows overfed energy diets prepartum had lower rates of palmitate oxidation and greater esterification in liver tissue after calving (Litherland et al. 2011), a period that is characterized by inflammatory-like conditions (Bionaz et al. 2007; Bertoni et al. 2008). As a consequence of these conditions and of the possible reduction in liver function, the post-partum period is characterized by a reduction of several essential proteins (e.g. albumins, some enzymes, “carriers” of vitamins and hormones, and lipoproteins). For instance, the increase in blood bilirubin concentration is likely a consequence of the down-regulation of key liver enzymes involved in its clearance from the body (e.g. UDP-glucuronosyltransferase; (Kamisako et al. 2000; Bertoni et al. 2008). In addition, the synthesis of apoprotein B100 decreases markedly soon after parturition (Gruffat et al. 1997; Bernabucci et al. 2004), leading to reduced hepatic VLDL synthesis and export, coupled with TAG accumulation in the liver (Katoh 2002; Bertoni et al. 2006).

**Links between inflammation and metabolism, nutrition, and energy balance**

In non-ruminants the evidence is compelling that PIC have a strong effect on metabolism and nutrition. Their increase in blood acts on the brain through several mechanisms (Johnson and Finck 2001), with a subsequent increase in catabolic processes (lipolysis and proteolysis) and a reduction in feed intake. Thus, the increase in concentration of PIC due to “disease” or “malaise” is responsible for depressed nutrient intake, and a concurrent increase in mobilization of body reserves. The consequence is a decrease in animal performance, rendering the animal more susceptible to develop new diseases related to the nutrient shortage. Overall, these adaptations lead to a vicious loop: diseases or malnutrition cause PIC release which reduce feed intake and this contributes to new diseases (Koutsos and Klasing 2001).

In the context of the periparturient cow, it is evident that negative effects of PIC (i.e. inflammation) may also occur via the worsening NEB, particularly at calving, and by suboptimal (excess or inadequate) nutritional management (again a vicious cycle). There is strong evidence that onset of disease, severe NEB, and the release of PIC all contribute to poor functional welfare in transition dairy cows. This topic has been discussed in more depth by (Roche et al. 2012). Figure 1 provides a schematic overview of the molecular mechanisms between nutrition and inflammation. Briefly, the main intracellular mechanisms encompass:

- an inflammatory stimulus activates the transcription regulator (i.e. a protein that regulates transcription of mRNA → protein) NF-κB, causing an up-regulation of the expression of several inflammatory genes [e.g. TNFα, IL-1β, and IL-6, MCP-1, the inducible isoform of cyclooxygenase (COX2), and the inducible form of nitric oxide synthase (NOS2); (Elewaut et al. 1999)].
- PIC can exert a feed-forward up-regulation of their synthesis (i.e. help sustain inflammation).
- NF-κB activation can be stopped by several mechanisms that act as anti-inflammatory agents (e.g. cortisol, AIC, antioxidant systems). Both PPARα and PPARγ can respond to some long-chain fatty acids and potentially serve as anti-inflammatory agents, interfering with the activity of NF-κB and increasing the expression of IkB, which is an NF-κB inhibitor (Moraes et al. 2006); in bovine cells, 16:0, 18:0, and 20:5n-3 fatty acids seem most potent (Bionaz et al. 2012c).
- some drugs, such as aspirin (Barnes 1997), exert an anti-inflammatory activity at the cellular level and systemic level.
- some nutrients (e.g. antioxidants) can have an anti-inflammatory function (Conner and Grisham 1996) and stop the activation of NF-κB promoted by the increase of reactive oxygen metabolites (ROM).
- other nutrients, such as methionine, can indirectly increase the production of glutathione, a potent antioxidant, and there is evidence that rumen by-pass methionine supplementation during the periparturient period might provide a source of this antioxidant to dairy cows (Osorio et al. 2012).
Figure 1: Regulation of nuclear factor kappa B (NF-kB) activity. TNF-, tumor necrosis factor; IL, interleukin; M-CSF, G-CSF, macrophage and granulocyte colony-stimulating factor respectively; MCP-1, monocyte chemoattractant protein-1; ICAM-1, intracellular and vascular cell adhesion molecule-1 respectively; TRX, thioredoxin; I-kB, inhibitory unit of NF-kB; ROM, reactive oxygen metabolites; COX-2, induced cyclooxygenase; NOS, induced nitric oxide synthase.; PPAR, peroxisome proliferator-activated receptor. Adapted and modified from selected papers (Barnes 1997; Calder 2002; Rimbach et al. 2002).

Besides the factors mentioned, a wide number of macro and micronutrients can have an inflammation-modulating function (Suchner et al. 2000; Sordillo and Aitken 2009). Among the former, examples include other amino acids (glutamine, arginine, cysteine, branched amino acids, taurine) and mono and polyunsaturated fatty acids. Among the micronutrients, examples include vitamins (A, D, E and C) and trace minerals (Zn, Cu and Se; Maggini et al. 2007). Clearly, there is need for more research in this area in transition dairy cows.

The link between inflammation, dry matter intake control, nutrition, and welfare in the periparturient period

As discussed in a previous section of this review, the release of PIC contributes to a reduction of functional welfare in dairy cows. Ingvaltsen and Andersen (2000) recognised the strong antagonistic effects of the immune system response on DMI around parturition, and Johnson and Finck (2001) presented convincing evidence for a role of cytokines in causing anorexia in sick animals. They also suggested a functional link between adipose tissue function via leptin release and control of food intake. Such an effect may be more relevant in monogastric animals or cows at later stages of lactation (in more positive energy balance) because the concentrations of leptin from late-pregnancy through early lactation decrease gradually regardless of pre-partum energy intake level (Janovick et al. 2011; Schoenberg et al. 2011b). Whether long-term elevation of blood leptin in energy-overfed cows or those with greater BCS pre-partum (Schoenberg et al. 2011b) is mechanistically associated with satiety post-partum remains to be established. What seems evident is that inflammatory conditions around calving (Bionaz et al. 2007; Bertoni et al. 2008) are related to a slower rise in DMI (Trevisi et al. 2002), which in turn leads to a longer period of NEB and greater likelihood that PIC would have a negative effect on functional welfare.

The relationship between nutrition and functional welfare in the periparturient period is complex, and cannot be limited to the severity of the unavoidable NEB or to pro-inflammatory effects of metabolic and infectious diseases that cause PIC release. In fact, as reported by (Van den Top et al. 1996), ad libitum-fed cows (regardless of BCS) during the dry period were more likely to develop fatty liver post-partum. Similar results have been reported consistently in recent years (Dann et al. 2005; Douglas et al. 2006; Janovick and Drackley 2010; Ji et al. 2012). Thus, dry period nutritional management is important in determining the functional welfare of cows.

The trigger of the inflammatory signals in overfed animals, particularly when animals are not sick, remains unknown. In humans, it is now well-accepted that obesity and type 2 diabetes can be considered as states of low-grade chronic inflammation with roots in the metabolic alterations that characterise these conditions. If the trigger factor is the surplus of nutrients per se, the causative molecules and
underlying signalling pathways are the same as in classical inflammation (i.e. PIC, APP, and related mediators; (Hotamisligil 2006). Simply, the para-inflammatory response may occur "with conditions that were not present during the early evolution of humans, including the continuous availability of high-calorie nutrients, a low level of physical activity, exposure to toxic compounds, and "old age" (Medzhitov 2008). As herbivores, ruminants clearly did not evolve to consume "high-energy"/low-fibre feedstuffs; thus, it is not unexpected that an energy-overfed or high BCS pregnant cow could behave metabolically as an obese non-ruminant. The direct link between high-energy diets and inflammation needs to be evaluated more closely, but the data from (Janovick-Guretzky et al. 2007) seems to support such a relationship and the potential for those cows to have lower welfare.

Summary

The periparturient period is characterized by inflammatory-like conditions, which can have adverse effects on the animal including a reduction in voluntary feed intake and performance, an induction of pain and discomfort, and an alteration from proper liver function, including a greater risk of developing fatty liver. If these inflammatory-like conditions persist over the short-term, a vicious cycle ensues whereby inflammation can severely compromise the animal’s welfare (e.g. increase body tissue catabolism as a result of reduced feed intake and lower feed efficiency). Both the physiological state and the inflammatory status of cows can be assessed by measuring specific biomarkers. These are biological molecules measured in fluids or tissue (e.g. TAG) that can be successfully used to monitor, for example, the state of energy balance of a cow (e.g. NEFA) but also the inflammatory status of the animal. Several macro and micronutrients may potentially help alleviate inflammation and the oxidative stress that characterizes the transition period, but more work in this area is needed. In combination, the different types of biomarkers provide a more holistic (systems) view of the functional state of the cow.

THE “LIVER ACTIVITY INDEX” AND THE “LIVER FUNCTIONALITY INDEX” CONCEPTS TO EVALUATE FUNCTIONAL WELFARE

There is compelling evidence that the periparturient period is characterized by systemic inflammatory-like conditions which, if severe, can compromise the ability of the cow to achieve optimal milk production (Bionaz et al. 2007; Bertoni et al. 2008). This state of inflammation, regardless of the cause (e.g. infection, poor nutrition, stress), increases the risk of severe pain and suffering as suggested by (Dantzer et al. 2008) (hence poor welfare) due at least in part to PIC release. Tools to diagnose inflammatory events (including subclinical) are of great interest to objectively evaluate the welfare status of cows and/or herds.

Previous work has indicated that negAPP are more appropriate as indices of long-lasting systemic consequences of inflammation (Bionaz et al. 2007; Bertoni et al. 2008); the association between posAPP response after calving and acute inflammatory phenomena is not always clear cut or readily apparent (Trevisi et al. 2011) because of the short duration of elevation. However, the reason for the variation in each negAPP is not always clear. Thus, composite indices that include three or more negAPP are better as diagnostic tools (i.e. in a similar fashion to the “physiological imbalance” concept).

Bertoni and co-workers proposed two composite indices based on the blood concentrations of some negAPP measured in the first month of lactation (Bertoni et al. 2006; Trevisi et al. 2011): the Liver Activity Index (LAI) and the Liver Functionality Index (LFI). With both indices, the initial aim was to evaluate the relationship between current and future performance (fertility) with inflammation status during the first month of lactation. The inflammation status of the cow is better assessed using the concentrations of the negAPP as biomarkers, and these are included in the LAI and LFI evaluation. Both indices have been recently described in detail by (Trevisi et al. 2011).

Liver Activity Index (LAI)

The LAI includes the average blood level at 7, 14 and 28 days in milk (DIM) of albumin, lipoproteins (indirectly measured as total cholesterol), and Retinol Binding Protein (RBP, measured as retinol whose level in blood is strictly related to RBP synthesised by the liver). Data from these blood parameters are transformed into units of standard deviation for each cow as follows:

• the mean value of the herd population of each plasma parameter (albumin, total cholesterol, and RBP) is subtracted from each cow value at 7, 14, and 28 DIM and divided by the corresponding standard deviation.

• the final LAI score for each cow is the arithmetical mean of the three partial values obtained from the three selected blood indices from the three blood samples.

• the LAI values represent an estimation of the consequences of an inflammation which occurs at or around calving time in each cow checked within a defined herd.
Liver Functionality Index (LFI)
The LFI includes concentrations of albumin, lipoproteins (indirectly measured as total cholesterol) and bilirubin (as indirect measure of the enzymes synthesized by the liver, which also coordinate bilirubin clearance) (Trevisi et al. 2011). This index measures the relevant changes in concentrations between 3 and 28 DIM, standardised with the optimal pattern of change for the three parameters obtained from healthy cows at the same stage of lactation (Bertoni et al. 2008). As with LAI, the LFI allows the evaluation of the consequences of an inflammation occurring at or around calving time. In addition, because it represents an absolute value the LFI can be used to compare cows from different herds.

Can LAI and LFI be applied on farm?
The two indices are well correlated (Trevisi et al. 2010a), but the determination of LFI is easier and cheaper than LAI. Thus, considering that the LFI allows for a comparison between herds, it appears a more reliable index to measure the success or failure of the adaptation of cows during the transition period. Interestingly these indices provide a biological measure of the extent of inflammatory consequences also in cows without clinical signs. Despite the fact that LAI and LFI were originally developed to assess the influence of inflammation on performance, both can be useful from a practical point of view. Indeed, the monitoring of these indices allows the identification of cows that require closer scrutiny and/or might benefit from suitable therapeutic measures for a quicker recovery still at 30 days of lactation, particularly in cows showing signs of severe inflammation, with apparently normal health. Low values of LAI and LFI at the end of the first month of lactation can identify two different types of “problem” animals:

• cows that continue to suffer from inflammatory phenomena (e.g. sustained elevated concentration of haptoglobin at the end of the * month post-calving), and that require an accurate diagnosis concerning uterine or mammary gland health, and foot/hoof integrity.

• cows that have resolved the inflammatory events occurring around calving, but that exhibit inadequate liver function (e.g. low levels of negAPP), which would demand some additional treatment to accelerate recovery not only of liver but other organs as well.

• in either of the above situations cows might be at risk of impaired reproductive function and, thus, could be treated appropriately.

The usefulness of the aforementioned therapeutic interventions requires further investigation.

Perspectives on the utilisation of inflammatory parameters around calving
The use of LAI or LFI indices requires substantial amount of work, several blood samples and do not permit a timely detection of cow problems immediately after calving; therefore, new indices are needed. In recent studies, the ranking of cows in accordance with values of LAI or LFI allowed the detection of important changes in blood markers for each cow before calving (i.e. might be useful in terms of detecting cows more prone to developing inflammatory response). For instance, (Trevisi et al. 2010b) found that cows with low LAI measured in the first month of lactation, even without showing signs, were characterized in the last month of pregnancy by slightly lower plasma levels of some negAPP (e.g. RBP, lipoprotein, albumin) and haemolytic complement, as well as higher levels of syalic acid and ROM. In other studies (Trevisi et al. 2010a; 2012) reported that cows with lower LFI had higher concentrations of IL-6, ceruloplasmin, bilirubin, NEFA, ROM and lower concentrations of RBP and lysozyme before calving. Despite the fact that the latter results were obtained in cows with extremely low LFI values, they confirmed that cows that previously suffered from an inflammatory event are more responsive to a new inflammation. These preliminary results are promising (e.g. some negAPP and related parameters could be detected before calving to identify cows more susceptible to higher inflammatory response in the transition period), but further mechanistic studies are required.

Is there a link between LAI and nutritional management prepartum?
The link between overfeeding energy and susceptibility to developing fatty liver (and related disorders) postpartum is unequivocal. When the LAI was calculated for cows in the study of (Janovick et al. 2011), published in part (Janovick-Guretzky et al. 2007), it was observed that almost 50% of cows receiving ad libitum access to a moderate-energy diet during the dry period fell into the quartile with low LAI (i.e. had signs of inflammation). In contrast, only 17% of cows in the control group (fed to meet energy requirements) fell into the low LAI quartile. Not surprisingly, cows in the low LAI had lower milk yield, but despite this, had greater BCS loss and lower fertility (Janovick-Guretzky et al. 2007). There seems to be no doubt that the dry period may be
pivotal as a cause of health (inflammation) problems, and consequently of a decline in cow welfare due to PIC release.

**MOLECULAR TECHNOLOGIES TO STUDY FUNCTIONAL WELFARE**

*mRNA expression “profiling”*

The study of the transcriptome (i.e. transcriptomics) is referred to as “expression profiling” and is aimed at examining the expression level of the mRNAs in a given cell or tissue. The use of “microarrays” as a method for studying large portions of an organism’s mRNAs was first described in 1995 by researchers at Stanford University (USA) and revolutionised the way in which experimental biology could be performed. Initial studies in bovine using this technique date back to the early 2000s (Yao et al. 2001), with their first use in periparturient cows in 2005 (Loo et al. 2005). Currently there are several commercially-available microarrays (e.g. Affymetrix Bovine GeneChip, Agilent Bovine Gene Expression Microarray) that provide complete coverage of the bovine transcriptome (~23,000 transcripts).

The techniques that are most commonly-used for transcriptomics and data analysis include:

- reverse transcription (RT) polymerase-chain reaction (PCR): it is commonly used to accurately quantify the absolute or relative amounts of target mRNA but on a “small” scale (e.g. from a single mRNA to 40-50 transcripts). The goal with this tool is to focus specifically on the mRNA (genes) that make-up a pathway of interest for the proposed hypothesis (e.g. fatty acid oxidation, gluconeogenesis, milk fat synthesis, or the acute-phase response).

- “high-throughput” techniques: these are commonly used to quantify the relative amounts of hundreds of mRNAs simultaneously, either via the use of DNA microarrays (Loo 2010) or “next-generation sequencing technology” (RNAseq; Wang et al. 2009; Liu 2011). Microarrays can be constructed using genome sequencing information for the species of interest by chemical “spotting” of DNA products on a solid support, such as glass. Thus, the amount of information generated with this technique is dependent on the number of DNA products “spotted” on the platform, but could include the entire transcriptome (e.g. ~23,000 mRNAs in the case of bovine). The advantage of RNAseq technology is that it allows to measure all mRNAs (and other types of RNAs) present in a biological sample (Wang et al. 2009).

- “clustering analysis”: this is one type of transcriptomics data analysis that can be used to “distil” the resulting data, which can encompass multiple tissues and/or time-points (Bionaz and Loo 2012) to a more comprehensible outcome; this approach subdivides the groups of genes that change in an experiment into a smaller number of categories, which then allows the user to analyse them in a more focused fashion (D’Haeseleer 2005a). Application of clustering analysis to gene lists from a given experiment leads to grouping of genes according to common patterns of expression (e.g. genes that are up-regulated, down-regulated, or do not change during the periparturient period). Within these clusters there could be hundreds of genes associated with related (e.g. Glycolysis and TCA cycle) or unrelated biological pathways. Furthermore, depending on the expression pattern (e.g. slight down-regulation or marked down-regulation) two different clusters could contain different genes that belong to the same biological pathway. Gene expression clustering allows an open-ended exploration of the data, without getting lost among the thousands of individual genes (D’Haeseleer 2005c). An example of a clustering approach to examine the functional state of liver during the transition period in cows fed to meet or exceed dietary energy requirements during the dry period is presented in Figure 2. Data are from (Loo et al. 2005, 2006) and were re-analysed by Bionaz and Loo (2012).

- “bioinformatics”: this field of research has provided the conceptual framework for communicating biological knowledge generated from transcriptomics studies in a more biologically-relevant fashion (Shaiazad and Loo 2012). Bioinformatics is generally defined as a field that relies on computational resources to analyse biological data (e.g., genome, transcriptome, metabolome) on a large scale (Luscombe et al. 2001). One of the goals of bioinformatics is to accelerate the interpretation of large amounts of ‘omics’ data. For instance, (Bionaz et al. 2012a) used transcriptomics and bioinformatics to explore bovine mammary function at several time points during the dry period and lactation. Another recent study also used the same approach on bovine liver transcriptome data throughout the periparturient period (Bionaz and Loo 2012). Bioinformatics tools consist of freely-accessible or licensed software packages that have been developed to store, retrieve and analyse biological data such as DNA, mRNA and protein sequence, structure,
function, biological pathways and genetic interactions. Examples include:

- Ingenuity Pathway Analysis® (IPA; www.ingenuity.com): this is a widely-used bioinformatics tool that performs pathway and network analyses of transcriptomics data. A drawback is the high-cost of the yearly license fee. Figure 3 depicts results from IPA analysis of clusters 4 and 8 in Figure 2. Table 2 also provides examples of studies that relied on IPA for evaluation of tissue functional state.

- Freely-accessible tools: examples include the Kyoto Encyclopaedia of Genes and Genomes (KEGG) (http://www.genome.jp/kegg/pathway.html) and DAVID Bioinformatics Resources Database (http://david.abcc.ncifcrf.gov/). KEGG is a manually-curated bioinformatics resource containing information on more than 200 biological pathways. DAVID provides a variety of tools for generating biological meaning from transcriptomics studies. Recently, another freely-available tool (Dynamic Impact Analysis, DIA) for bioinformatics analysis that uses KEGG and DAVID was developed and validated with bovine mammary transcriptome data (Bionaz et al. 2012b).

Figure 2: k-means clustering results from affected genes in liver of cows fed ad-libitum to exceed net energy requirements (Ad-lib.; ~140% of requirements) or cows fed to meet but not greatly exceed (Control; ~100%) requirements during the dry period. Data pertain to -65 (dry-off, i.e. with a value of 0 in the Y-axis), -30, -14, 1, and 14 days relative to parturition. On the X-axis days are represented by a line for Control and ad-libitum-fed cows. The colour line visible in some panels represents the average expression pattern over time.
Figure 3: Bioinformatics analysis of genes in cluster 4 (top panel) and cluster 8 (bottom panel) from Figure 2 that were affected by overfeeding dietary energy during the period (i.e. genes showing down-regulation during the periparturient period). The analysis was performed using IPA software, and the pathway names are those assigned by IPA. The $-\log$ (P value) and size of the bar denote the likelihood that the specific pathway was affected by overfeeding energy. Threshold (orange line) was set at $P \leq 0.05$ (i.e., 1.30 log-scale). The ratio value is calculated as the number of affected genes that belong to a pathway over the total number of genes that IPA assigns to a pathway. This value provides an idea of the coverage of a particular pathway within a list of genes supplied by the user. The analysis revealed that overfeeding energy during the dry period led to down-regulation (denoted by down arrows) of immune- (complement system, acute-phase response signalling), metabolic- (fatty acid metabolism), and transcriptionally-regulated functions (LXR and FXR activation) associated with bile acid synthesis and other aspects of lipid metabolism. Such responses provide evidence of potentially negative effects of this nutritional management on the liver’s ability to contribute to the immune response of the organ besides potentially impairing basic tissue functions.

Summary

Transcriptome changes exert a major influence on physiological function and adaptation to nutrition, disease, and/or physiological state. Thus, application of high-throughput technologies (microarrays, RNaseq) can help capture those adaptations by generating massive amounts of biological data. One approach to help process these massive datasets is to use gene clustering as a way of segregating groups of genes with similar expression profiles or interacting functions. The use of bioinformatics software packages can then provide a way of discerning the actual biological effects to a particular treatment (e.g. over-feeding vs. under-feeding), drug (e.g. non-steroidal anti-inflammatory drugs), physiological state (e.g. periparturient period), or disease state (e.g. ketosis). More importantly, however, these high-throughput approaches are of utmost importance to achieving a more holistic understanding of the functional state of livestock (systems physiology) because genes rarely function alone or have a single function (Wittkopp 2007). In fact, the functional outcome in a tissue depends on complex interactions among genes as well as regulatory proteins (i.e. transcription regulators) that could, in turn, be regulated by nutrients or metabolites.
Table 2: Use of transcriptomics and bioinformatics in bovine to evaluate the functional state of tissues in response to ketosis, mild or severe NEB, subacute ruminal acidosis, or sub-fertile genotype. Up-regulation, ▲; Down-regulation, ▼. All studies used IPA for bioinformatics.

<table>
<thead>
<tr>
<th>Most-affected pathways/functions</th>
<th>Phenotype/ tissue</th>
<th>Most-affected biological processes</th>
<th>Functional outcome¹</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Estrogen receptor signalling, protein ubiquitination pathway, chemokine signalling, ERK/ MAPK signalling, and apoptosis signalling</td>
<td>Ketosis/liver</td>
<td>Oxidative phosphorylation▼; protein ubiquitination▼; ubiquinone biosynthesis▼; cytokine signalling▲; fatty acid uptake/transport▲; fatty acid oxidation▲; cholesterol synthesis▼; growth hormone signaling▼; fatty acid desaturation▼</td>
<td>Increased fatty acid catabolism; overall reduction in energy metabolism</td>
<td>(Loor et al. 2007)</td>
</tr>
<tr>
<td>Immune response to pregnancy, luteolysis, and support of embryo growth and development; regulation of histotroph composition</td>
<td>Sub-fertile genotype/ endometrium</td>
<td>▲: PKA signalling, Leptin signalling via PI3K-dependent pathway, A2A receptor signalling▼; IL-22 signalling pathway, Antiviral actions of interferons, Angiotensin signalling via STATs, IFN-γ signalling pathway</td>
<td>Impaired immune response and tissue development</td>
<td>(Walker et al. 2012)</td>
</tr>
<tr>
<td>Immunological and inflammatory disease</td>
<td>Severe NEB/ endometrium</td>
<td>Inflammatory response genes ▲; matrix metalloproteinases▲; chemokines▲; cytokines▲; calgranulins▲; interferon-inducible genes▲</td>
<td>Increased uterine inflammation and impaired immune response</td>
<td>(Wathes et al. 2009)</td>
</tr>
<tr>
<td>Oxidative stress, mitochondrial dysfunction, endoplasmic reticulum stress, natural killer cell signalling, p53 signalling</td>
<td>Severe NEB/ spleen</td>
<td>Oxidative stress response ▲; Mitochondrial dysfunction ▲; Endoplasmic reticulum stress pathway ▲; Natural killer cell signalling ▲; p53 signalling ▲</td>
<td>Decreased innate adaptive immunity; increase in apoptosis and oxidative stress</td>
<td>(Morris et al. 2009)</td>
</tr>
<tr>
<td>Lipid metabolism, connective tissue development and function, cell signalling, cell cycle, and metabolic diseases</td>
<td>Severe NEB/ liver</td>
<td>LXR/RXR activation▼; Fatty acid transport and oxidation▲; Amino acid metabolism▲</td>
<td>Increased fatty acid catabolism; inhibition of cell growth and tissue repair; increased oxidative stress</td>
<td>(McCarthy et al. 2010)</td>
</tr>
<tr>
<td>Biosynthesis of steroids, lipid metabolism, and vitamin and mineral metabolism</td>
<td>Subacute ruminal acidosis/ rumen epithelium</td>
<td>Biosynthesis of steroids and cholesterol ▼; LXR/RXR activation▼</td>
<td>Increased rumen epithelial short-chain fatty acid metabolism; decreased cholesterol biosynthesis</td>
<td>(Steele et al. 2011)</td>
</tr>
</tbody>
</table>

¹Use of IPA does not fully allow for a thorough evaluation of the functional impact (importance of a pathway) and the net direction (activation, inhibition, or no change) of the change in a particular pathway or function. See Bionaz et al. for an in-depth discussion.
FUNCTIONAL STATE AND WELFARE OF PERIPARTURIENT DAIRY COWS ASSESSED WITH TRANSCRIPTOMICS AND BIOINFORMATICS

The level of nutrient intake during the dry period alters functional and welfare state

As discussed above the acute phase response (APR) is a complex, systemic, early defense system activated by trauma, infection, or stress. Inflammation is a dominant factor in several economically-important disorders, such as metritis and mastitis (Sordillo et al. 2009). The liver is a central organ during the APR, which normally occurs after parturition (Bertoni et al. 2009) or in the early-phase following an infection (Jiang et al. 2008). (Bertoni et al. 2009) concluded in their review that clinical or sub-clinical inflammation and related PIC are the common linkage between health disorders and low welfare in early post-partum cows.

The onset of NEB per se around parturition is not the cause of PIC release but stronger and more prolonged NEB could lead to a greater risk of metabolic diseases and particularly ketosis and fatty liver (Bertoni et al. 2009; Roche et al. 2012). From a molecular standpoint, a characteristic of under-nutrition-induced ketosis in the early post-partum period is the up-regulation of genes and transcription regulators (e.g. PPAR) associated with cytokine signalling and particularly IL-6 (Loor et al. 2007), which is elevated in blood of periparturient cows that have low LFI values (Trevisi et al. 2012). Excess dietary energy prepartum leading to increasing adipose tissue deposition can contribute directly to increased and prolonged NEB post-partum and, thus, the amount of NEFA released into blood, which, in turn, can compromise immune function (Roche et al. 2005; Loor et al. 2006; Bertoni et al. 2009; Sordillo et al. 2009).

In two recent studies, a microarray consisting of 7,872 annotated cattle genes was used to evaluate liver transcriptional adaptations to prepartal level of energy and change in physiological state (Loor et al. 2005; Loor et al. 2006). Diets were fed ad libitum to exceed net energy requirements (~140% of requirements), were restricted to provide less than estimated requirements (~80%), or were fed to meet but not greatly exceed (~100%) calculated energy requirements during the dry period. When the individual data sets (Loor et al. 2005; Loor et al. 2006) were combined and re-analysed statistically (Bionaz and Loor, 2012), a total of 4,970 genes were affected due to the interaction of treatment × time (Figure 4). This dataset was analysed using the Dynamic Impact Approach (DIA) developed by (Bionaz et al. 2012b).

![Figure 4](image-url): Expression patterns of 4,970 genes affected by the interaction of diet and time relative to parturition in cows fed ad-libitum to exceed net energy requirements (~140% of requirements), cows restricted to consume less than estimated requirements (~80%), or cows fed to meet but not greatly exceed (~100%) calculated energy requirements during the dry period. Adapted from Bionaz and Loor (2012).

An in-depth discussion of the results from the bioinformatics analysis was reported by Bionaz and Loor (2012). Here the potential for this approach to evaluate the functional state and welfare of the cow as it relates to nutritional management during the dry period is outlined. Visual appraisal of the patterns of expression of the 4,970 genes from dry-off (65 days from calving) through 49 days post-partum in Figure 4 clearly indicates that both over-feeding and under-feeding energy cause alterations in mRNA expression over the dry period and early lactation with most-dramatic changes occurring primarily during the periparturient period (i.e. -30 through 28 days around calving). Those responses are visually striking and demonstrate that nutritional management per se can substantially alter the molecular mechanisms in the liver during the transition from pregnancy into lactation. Clearly, nutrition cannot only elicit direct effects on liver but also indirect effects through changes in hormonal profiles and/or peripheral signals. Thus, the molecular analyses should be complementary to measures of biomarkers in blood and animal behaviour observations, as discussed above.

The use of the DIA to study changes in biological pathways among the 4,970 affected genes also revealed novel features of the liver’s adaptations to nutritional management and its physiological state (Figure 5). The following are key points discussed in depth by Bionaz and Loor (2012):
Figure 5: Selected biological pathways resulting from bioinformatics analysis of the 4,970 affected genes (Figure 4). Bioinformatics analysis was performed using DIA, which allows for a relative ranking of the top impacted pathways (Y-axis) and the direction of the impact (red bars = activation, green bars = inhibition). Adapted from Bionaz and Loor (2012).

- Fatty acid metabolism and PPAR signalling were among the most-inhibited pathways during the transition period, particularly in energy-overfed cows. It is striking that both biological processes were inhibited well-ahead of calving. Cows in the restricted-energy group had an apparent activation of both processes particularly at 14 and 28 days post-partum. From a functional perspective these data agree with the observation that over-feeding led to greater lipid accumulation in liver post-partum (Loor et al. 2006).

- The cows overfed prepartum had a more pronounced increase in ketone body metabolism after parturition, suggesting a greater degree of ketogenesis relative to the other groups. Those data are supported by the greater blood BHBA in the overfed vs. under-fed cows (Loor et al. 2006).

- Another novel finding was the marked activation of steroid biosynthesis in the liver of overfed
cows well-ahead of parturition. The reason for this response prepartum is not readily apparent. However, the post-partum activation of this pathway might be related with synthesis of cholesterol, as a way of removing excess TAG (Loor et al. 2006) in VLDL. Alternatively, this activation might simply be associated with synthesis of steroids such as oestrogens or their receptors [i.e. liver expresses oestrogen receptors and their blockade in rodents results in decreased lipid transport and fatty liver among other effects (Barros and Gustafsson 2011)], which may contribute to the peripartum reduction in DMI (Roche et al. 2012).

**Biomarkers of functional state and welfare in undernutrition-induced ketosis**

The first evaluation of the liver transcriptome in cows with clinical ketosis during the first two-weeks postpartum was reported by (Loor et al. 2007). Several novel adaptations to ketosis were uncovered in that study which relied on microarrays and bioinformatics analysis. The set of affected genes (~2,000) was reanalysed using the DIA approach to gain additional insights into the functional state of the tissue (Figure 6). The DIA approach confirmed the original observation using IPA that intracellular energy production shuts down during clinical ketosis (Loor et al. 2007). ‘Energy metabolism’ was the most-affected metabolic pathway (Figure 6) followed by ‘carbohydrate metabolism’, ‘metabolism of other amino acids’, ‘metabolism of cofactors and vitamins’, and ‘lipid metabolism’.

In a recent microarray study, marked inhibition of carbohydrate and lipid metabolism were observed, with a lesser inhibition of energy metabolism in liver from mid-lactation cows that were feed-restricted for 5 days (Akbar et al. 2012). The liver of feed-restricted mid-lactation cows also had an activation of ‘metabolism of other amino acids’ but no change in the impact (or activation/inhibition) on other pathways such as ‘translation’ and ‘folding, sorting, and degradation’. The latter were markedly inhibited in the ketotic liver (Figure 6). From a mechanistic standpoint these responses suggest common and distinct biological adaptations of the bovine liver to undernutrition depending on physiological state.

Obviously, the endocrine, immune, metabolic, and behavioural state of cows differs in early than in mid lactation and probably have an indirect effect on the measured molecular responses. The intent in providing these examples of the application of transcriptomics and bioinformatics to study functional welfare was not to discuss the data extensively, but rather underscore their utility in learning more about the system (i.e. the transition cow, in this instance) and the impact of management on functional welfare.

**Figure 6:** Bioinformatics analysis of microarray data from cows affected by under-nutrition-induced ketosis. Data from (Loor et al. 2007) were analysed using DIA. The direction of the bar denotes activation (above 0) or inhibition (below 0) of the specific biological pathway from the KEGG database. The circle above each bar denotes the impact (i.e. importance) of each biological pathway (e.g. energy metabolism was highly-impacted and inhibited due to the onset of clinical ketosis).

**CONCLUSIONS AND FUTURE RESEARCH**

Progress over the last several decades in the fields of dairy cattle physiology, biochemistry, genetics, and immunology has provided the means to develop objective measures to assess the ability of the cow to function “normally”, withstand challenges to the immune system, and live a relatively long life in response to changes in management, nutrition, and the environment. This concept is defined as functional welfare and can complement other measures of welfare which may encompass affective state and natural behaviour. The use of classical biomarkers (e.g. NEFA) and, more recently, composite indices of molecules that can provide an evaluation of the functional state of tissues and the whole animal have improved tremendously opportunities to evaluate the concept of functional welfare in periparturient cows. Inflammation clearly plays a role in determining the welfare state of dairy cattle during the transition period, with far reaching effects induced by PIC, including decreasing DMI and, potentially, contributing to metabolic disease (e.g. fatty liver). While the triggers of hepatic inflammation around
calving are still not well-understood, but over-nutrition clearly appears to be a factor. Further research in this area would be beneficial from a farm systems standpoint. The application of genome-enabled experimental techniques and bioinformatics tools for data interpretation, has enhanced understanding of the functional state of tissues in a more holistic fashion. The ability to generate massive datasets on the entire set of mRNAs in a given tissue or tissues, and several examples from studies with dairy cattle underscores the usefulness of the approach for enhancing knowledge of functional state as it relates to management, nutrition, and cattle genotype. Further research in periparturient dairy cattle using these modern tools can complement measures of biomarkers in biological fluids. Those efforts can also lead, potentially, to the discovery of novel biomarkers with important attributes such as the control of particular biological functions.

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Katoh N (2002) Relevance of apolipoproteins in the metabolism and lipoprotein metabolism: mechanisms and effects of infection and inflammation on lipid and lipoprotein metabolism: mechanisms and


The effect of feed trough space and feed barriers on heart rate responses in partial mixed ration fed cows on a feed pad

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ABSTRACT

Inadequate feed trough space is a potential stressor at group feeding of dairy cows due to the competition. This may be particularly apparent when feed accessibility is limited, as is the case with feeding cows on a feed pad in a Partial Mixed Ration (PMR) feeding system. A feed barrier that provides physical separation between cows reduces competition at the feed trough. The objective of this study was to examine how space allowance at the feed trough and the provision of feed barriers interact to affect the stress caused by the competition among PMR fed cows on a feed pad. 144 Holstein Friesian cows were provided with 0.6m, 0.75m, and 1m of feeding space with or without feed barriers. Treatments were replicated twice while crossing over the treatments spatially as well as for the groups weekly over 3 weeks. The percentage increase in mean heart rate was reduced significantly \((P<0.001)\) with increasing space allowance and dominant cows showed a less increase \((P<0.05)\) compared to submissive cows. Furthermore, it was significantly affected \((P<0.05)\) by the interaction between space allowance and the feed barrier provision. These results indicate that increased feeding space from 0.6m to 0.75m to 1.0m per cow reduced the stress caused by overcrowding on the feed pad within a PMR feeding system. At higher space allowances, feed barriers can be used to further reduce the stress caused by competition. Furthermore, subordinate cows were more prone to the stress caused by the competition on the feed pad.

Keywords: partial mixed ration; feed pad; competition; dominant; submissive; heart rate.

INTRODUCTION

Group feeding of cattle results in competition for feed (Olofsson, 1999). When feeding space is inadequate, the low ranking, subordinate cows are the most limited in their access to the feed bunk during the times of peak feeding activity (DeVries et al. 2004). Due to the aggressive behaviour of dominant cows, submissive cows may experience fear and stress resulting in frequent withdrawal from the feeder and lower intake of feed (DeVries et al. 2004). This may be particularly apparent when access to feed is limited, as is the case with feeding cows mixed rations on a feed pad for part of the day as they don’t get the chance to shift their feeding times. When the feed is missed out on the feed pad, subordinate cows are less likely to compensate in the paddocks at reduced pasture allowances due to the variable climate. Most studies have examined the effects of space allowance on general biological defensive responses with intensively housed cows with unlimited access to a total mixed ration (Fisher et al. 1997, Olofsson, 1999, DeVries et al. 2004, Huzzey et al. 2006). Given that inadequate feed trough space is a potential stressor during group feeding of dairy cows, change in heart rate may be a suitable and non-invasive biological response to measure the stress. Hence, it is important to establish if similar effects of feed trough space on physiological indicators of stress occur in PMR fed dairy cows on a feed pad. In this study, cows were given limited access to mixed rations on a feed pad after each milking with reduced grazed pasture. We hypothesized that reducing the feed trough space from 1.0m to 0.75m to 0.6m per cow on a feed pad would increase competition, resulting in increased heart rates between treatments, particularly in subordinate cows. A feed barrier that provides physical separation between cows reduces competition at the feed trough (Endres, 2005, Huzzey et al. 2006). Therefore, we further hypothesized that the feed barriers may reduce the negative effects of crowding at a given space allowance on a feed pad.

MATERIALS AND METHODS

This experiment was conducted at the Department of Primary Industries (DPI) - Victoria, Ellinbank Centre (38°14’S, 145°56’E) during April and May 2012 with the approval from the DPI Agricultural Research and Extension Animal Ethics Committee, Hamilton, Victoria.

a. Pre-experimental phase

A total of 144 multiparous, late lactating Holstein Friesian cows were used in this study. They were managed as two herds of 72 and kept on pasture for about 18 -20 hours a day. Grazed perennial rye grass contributed approximately one third of their
daily dry matter intake (6 kg DM/cow/day) and the remainders were made up of 73% DM cereal grain and 27% DM forage supplements fed as a mixed ration (12 kg DM/cow/day) on a feed pad twice a day after each milking. Each herd of 72 were divided into 6 groups of 12 cows, which were balanced for age (5.76±1.867 yrs), annual milk production (7299±1328 L), days in lactation (179.7±19.08), body weight (585.5±46.51 kg), body width (74.8±3.28 cm) and body condition score (4.4±0.22). During the 1st week of acclimatization, cows were fed in their assigned subgroups at a feeding space of 0.75m per cow. During this adaptation period, the social hierarchy within each group was determined using the individual Index of Success (IS) at an experimentally reduced space allowance of 0.2 m per cow over 3 feeding sessions using video records (Mendl et al. 1992, DeVries et al. 2004).

\[
\text{IS} = \frac{\text{number of cows that an individual is able to displace}}{\text{number of cows that an individual is able to displace + number of cows that are able to displace the individual}} \times 100\% 
\]

Depending on the calculated IS, the three most submissive cows as well as the three most dominant cows were randomly assigned to 3 pairs (one dominant and one submissive) within each subgroup and were fitted with heart rate monitors (Polar RS800CX™, Finland) to monitor the heart rate responses during subsequent feed pad feedings. The experimental design was fully factorial by space (3 levels: 0.6, 0.75, 1.0m) and barriers (2 levels: with and without barriers). All 6 treatments were replicated twice at a time while crossing over the treatments spatially as well as for the groups weekly over the experimental phase of 3 weeks.

b. Experimental phase

Following the 1st week of social adaptation, 12 subgroups were assigned to their treatments in the 2nd week. At each week, animals were given 4 days of adjustment followed by 3 days of data collection. During the data collection, one random selected pair was monitored on the first day for both morning and afternoon feeding sessions. The monitors were swapped to the second and third pairs of cows from the same subgroup on the second and third days during that week. After this was completed, the treatments were switched between the subgroups and the same procedure was then repeated over the remaining 2 weeks.

c. Data collection

Heart rate was recorded at 5 s intervals in beats per minute (bpm) and recorded data was initially divided into 3 phases. They were; i) mean minute heart rate 2 mins before feeding, ii) heart rate data 1 min. before feeding session, iii) mean heart rate during the feeding session. The mean minute heart rate calculated 2 mins before feeding session was used as the baseline level as the cow was standing in the holding yard after the application of the monitor. The heart rate data during 1 min before feeding was discarded as the cow was walking from the holding yard to the feed pad. In order to reduce any effects of individual differences in the baseline levels, mean heart rate during feeding at different treatments was expressed as percentage change from the individual baseline levels. Data was analyzed using a mixed effects model with Restricted Maximum Likelihood (REML) method in GenStat 13 software. Residuals were examined graphically for normality of distribution and constant variance using histograms and residuals versus fitted values and normal quantile plots.

RESULTS

Table 1 summaries the mean comparison of IS and the feeding behaviours between the three most dominant and the three most submissive cows within the pre-determined subgroups. There was a clear hierarchy established within each subgroup of 12 cows at the feeding space of 0.2m per cow and those determined social orders facilitated the application of limited heart rate monitors during the experimental phase. As demonstrated in table 2, percentage increase in mean heart rate was reduced significantly (P<0.001) with increasing space allowance and dominant cows showed significantly less increase (P<0.05) in heart rate compared to submissive cows. There was a significant interaction (P<0.05) between space allowance and the feed barrier provision on percentage increase in mean heart rate. That increase in mean heart rate was reduced by the provision of head barriers at each space allowance except at 0.6m (see Table 3 - a, b, c).
Table 1: Mean comparison between dominant and submissive cows in terms of IS and feeding behaviours at a feeding space of 0.2 m/cow on the feed pad over 3 feeding sessions.

<table>
<thead>
<tr>
<th>IS and other feeding behaviours</th>
<th>Social status of cows</th>
<th>p-value</th>
<th>S.E.D.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Dominant (n=36)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Mean</td>
<td>S.D.</td>
<td>Mean</td>
</tr>
<tr>
<td>Index of Success</td>
<td>92.81</td>
<td>12.61</td>
<td>12.40</td>
</tr>
<tr>
<td>Feeding time (mins.)</td>
<td>19.13</td>
<td>1.03</td>
<td>2.98</td>
</tr>
<tr>
<td>Number of feeding bouts</td>
<td>1.06</td>
<td>0.13</td>
<td>0.67</td>
</tr>
<tr>
<td>Inactively standing time (mins.)</td>
<td>1.20</td>
<td>1.03</td>
<td>17.35</td>
</tr>
<tr>
<td>Individual feeding time x 100</td>
<td>94.08</td>
<td>5.12</td>
<td>14.66</td>
</tr>
</tbody>
</table>

Table 2: Main effects from REML variance components analysis for on percentage changes in mean heart rate from the baseline levels.

<table>
<thead>
<tr>
<th>Main effects</th>
<th>Mean</th>
<th>P value</th>
<th>S.E.D.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Space allowance</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.60 m</td>
<td>11.03</td>
<td>&lt; 0.001</td>
<td>0.72</td>
</tr>
<tr>
<td>0.75 m</td>
<td>10.88</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1.00 m</td>
<td>8.34</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Barrier provision</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>10.16</td>
<td>0.698</td>
<td>0.55</td>
</tr>
<tr>
<td>No</td>
<td>10.02</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Social status</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dominant</td>
<td>9.36</td>
<td>0.037</td>
<td>0.74</td>
</tr>
<tr>
<td>Submissive</td>
<td>10.81</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Time of feeding</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AM feeding</td>
<td>10.52</td>
<td>0.123</td>
<td>0.68</td>
</tr>
<tr>
<td>PM feeding</td>
<td>9.66</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 3: Interaction effects from REML variance components analysis for on percentage changes in mean heart rate from the baseline levels.

(a) Means for Space allowance x Barrier provision effect

<table>
<thead>
<tr>
<th>Space allowance</th>
<th>Barrier provision</th>
<th>Social status</th>
<th>Mean</th>
<th>P value</th>
<th>S.E.D.</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.60 m</td>
<td>Yes</td>
<td>Dominant</td>
<td>12.43</td>
<td>0.018</td>
<td>(0.96 – 1.06)</td>
</tr>
<tr>
<td></td>
<td>No</td>
<td>Dominant</td>
<td>11.13</td>
<td>0.230</td>
<td>(1.08 – 1.29)</td>
</tr>
<tr>
<td>0.75 m</td>
<td>Yes</td>
<td>Dominant</td>
<td>10.15</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>No</td>
<td>Dominant</td>
<td>9.46</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1.0 m</td>
<td>Yes</td>
<td>Dominant</td>
<td>7.89</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>No</td>
<td>Dominant</td>
<td>7.48</td>
<td></td>
<td></td>
</tr>
<tr>
<td>P value</td>
<td></td>
<td></td>
<td>0.917</td>
<td></td>
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</tr>
<tr>
<td>S.E.D.</td>
<td></td>
<td></td>
<td>(1.48 -1.84)</td>
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</tbody>
</table>

(b) Means for Barrier provision x Social status effect

<table>
<thead>
<tr>
<th>Barrier provision</th>
<th>Social status</th>
<th>Mean</th>
<th>P value</th>
<th>S.E.D.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yes</td>
<td>Dominant</td>
<td>9.22</td>
<td>0.542</td>
<td>(0.91 – 1.06)</td>
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<tr>
<td>No</td>
<td>Dominant</td>
<td>9.46</td>
<td>10.54</td>
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<tr>
<td>P value</td>
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<tr>
<td>S.E.D.</td>
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(c) Means for Space allowance x Barrier provision x Social status effect

<table>
<thead>
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<th>Space allowance</th>
<th>Barrier provision</th>
<th>Social status</th>
<th>Mean</th>
<th>P value</th>
<th>S.E.D.</th>
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</thead>
<tbody>
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<td>Yes</td>
<td>Dominant</td>
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<tr>
<td></td>
<td>No</td>
<td>Dominant</td>
<td>9.86</td>
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<tr>
<td>0.75 m</td>
<td>Yes</td>
<td>Dominant</td>
<td>8.30</td>
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<tr>
<td></td>
<td>No</td>
<td>Dominant</td>
<td>10.61</td>
<td></td>
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<tr>
<td>1.0 m</td>
<td>Yes</td>
<td>Dominant</td>
<td>6.96</td>
<td></td>
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<tr>
<td></td>
<td>No</td>
<td>Dominant</td>
<td>8.01</td>
<td></td>
<td></td>
</tr>
<tr>
<td>P value</td>
<td></td>
<td></td>
<td>0.917</td>
<td></td>
<td></td>
</tr>
<tr>
<td>S.E.D.</td>
<td></td>
<td></td>
<td>(1.48 -1.84)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

DISCUSSION AND CONCLUSION

This is the first study to examine how space allowance at the feed trough and the provision of feed barriers interact to affect the stress caused...
by the competition among PMR fed cows on a feed pad. When the space allowance at the feeder increased, the percentage increase in heart rate reduced as the cows experienced less stress caused by the competition. This finding is in agreement with (DeVries et al. 2004), as they demonstrated that increasing the feeding space up to 1.0 m per cow allowed indoor cows to space themselves further apart while feeding and reduced the frequency of aggressive interactions. At 0.6m, feed barriers increased the percentage increase in heart rate in both dominant and submissive cows showing that provision of feed barriers was overridden by the space allowance, particularly at lower levels. This may be due to the competition only among dominant cows at lower space allowances as subordinate cows were more likely to withdraw themselves from the feeder and standing at the back when there was no physical separation among individuals. This finding is underpinned by (DeVries et al. 2004) and (Huzzey et al. 2006) as they demonstrated that subordinate cows were displaced most often at lower feeding space allowances. However, having feed barriers at 0.6m encouraged all the cows to fit in at the feeder while aggravating the competition as the individuals were too close to each other. Therefore we conclude that increased feeding space from 0.6m to 0.75m to 1.0m per cow reduced the stress caused by overcrowding on the feed pad within a PMR feeding system. Furthermore, subordinate cows were more prone to the stress caused by the competition on the feed pad. At higher space allowances, feed barriers can be used to further reduce the stress caused by competition, but not significantly when it comes to feeding mixed rations for part of the day. These findings will be further fortified by the analysis of visual observations for feeding and social behaviours and heart rate variability data in future.

ACKNOWLEDGEMENTS

This experiment was co-funded by Department of Primary Industries (DPI) - Victoria, University of Melbourne and Dairy Australia. The authors are grateful to the technical and farm staff at the DPI, Ellinbank Centre and the Werribee Centre for cow husbandry, sampling and technical assistance and Murray Hannah for statistical advice.

REFERENCES


Impact of wintering system in the southern South Island of New Zealand on the lying behaviour of dairy cows

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2DairynZ, Private Bag 3221, Hamilton, 3240
3DairynZ, c/- Federated Farmers Building, 70 Forth Street, Invercargill, 9810

ABSTRACT

In the southern regions of the South Island of New Zealand winter is a critical period in the set up of the farm and cows for the following lactation. Climate and soil conditions limit the extent to which pasture can be used to feed cows fully through June and July resulting in wintering systems reliant on forage crops and conserved pasture. Under current wintering systems, many cows fail to achieve pre-calving body condition score targets. In an attempt to address this poor performance, farmers are looking at alternative wintering systems involving off-pasture methods for their dairy cows. The animal welfare implications of off-pasture wintering systems are not well understood, although it is known that they differ from pasture-grazing systems. The stocking density and lying surface are likely to affect cows’ lying behaviour. Six farms representing a range of wintering systems were included in this study during winter 2011. On each farm IceTags® were attached to the lower leg of at least 10 cows in each wintering group, for 7 days, once during the winter period. Lying times in the barn systems were generally less than grazing systems and wintering pads. In all systems cows averaged 8 hours per day lying, however there was considerable variability between systems in the proportion of cows not achieving this target. The results are discussed in relation to stocking density and lying surface type.

Keywords: Wintering system; dairy; animal welfare; lying behaviour.

INTRODUCTION

During winter, dairy cows are often required to gain at least 0.5 body condition score units in preparation for the next calving and the subsequent lactation; however, the challenging environmental conditions during winter in the southern regions of the South Island of New Zealand result in an inability to grow sufficient pasture (Dalley, 2011) to meet the energy requirements to achieve the recommended body condition score targets (Roche et al. 2009). Consequently, farmers are looking for alternative wintering systems such as housing systems, wintering pads or grazing crops. Although wintering pads and housed systems allow more control over feed inputs and minimise treading damage (Stewart et al. 2002), they may have associated risks for animal welfare as there is generally less space available per cow compared with outdoor systems. The amount of time a dairy cow spends lying each day affects their comfort and welfare (Fisher et al. 2003). This may be influenced by the nature of the lying surface, with reduced lying times being reported on exposed concrete (Haley, 2001) and under wet (Tucker et al. 2007) and muddy conditions (Muller, 1996). Dairy cows typically spend 9-12 hours per day lying (cited in Fisher et al. 2003), and a preference to lie for at least 8 hours/day. Insufficient time spent lying results in physiological stress and behavioural signs of frustration such that maximising lying times is an important objective in dairy management systems (Hristov et al. 2008). Reduced cow comfort leading to increased time spent standing on hard surfaces will also increase the prevalence of lameness (Cook and Nordlund, 2009).

There is little documented information on the effects of different wintering systems on cow behaviour on commercial New Zealand dairy farms. Due to a significant proportion (20%) of New Zealand’s dairy cows being farmed in the southern South Island (DairynZ, 2011) and its challenging environmental conditions, the use of off-pasture wintering systems is increasingly common. Consequently, the behaviour and welfare of dairy cows in these systems needs to be better understood. The objective of this study was to assess the impact of a range of wintering systems in Southland and South Otago on the lying behaviour of dairy cows.

MATERIALS AND METHODS

Farm Details

This study, conducted during winter 2011, utilised six commercial dairy farms across Southland and South Otago which had been monitored since 2010. The key criteria for selecting the farms and wintering systems to be studied were determined from farmer group meetings and interviews as part of a farmer networking project in winter 2010 (Tarbotton et al. 2012). The six farms represented a range of wintering systems, the main characteristics of which are reported in Table 1.
Table 1: Characteristics of the monitored farms. Hectares: MP = effective milking platform; SB = support block. Cows: peak number of cows milked in the 2009-2010 season (M) and wintered in 2010 (W). Milksolids: kg milksolids produced in the 2009-2010 season per cow and per hectare.

<table>
<thead>
<tr>
<th>Wintering system</th>
<th>Location</th>
<th>Hectares</th>
<th>Cows</th>
<th>Milksolids</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Herd Home™</td>
<td>Tapanui</td>
<td>95 (MP)</td>
<td>275 (M)</td>
<td>478 kg/cow</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>300 (W)</td>
<td>1383 kg/ha</td>
</tr>
<tr>
<td>Self-feed wintering pad</td>
<td>Edendale</td>
<td>110 (MP)</td>
<td>335 (M)</td>
<td>430 kg/cow</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>387 (W)</td>
<td>1309 kg/ha</td>
</tr>
<tr>
<td>Free stall barn &amp; crop (swedes)</td>
<td>Drummond</td>
<td>120 (MP)</td>
<td>308 (M)</td>
<td>422 kg/cow</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>310 (W)</td>
<td>1083 kg/ha</td>
</tr>
<tr>
<td>Loose house barn &amp; crop (kale)</td>
<td>Gore</td>
<td>270 (MP)</td>
<td>780 (M)</td>
<td>449 kg/cow</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>850 (W)</td>
<td>1297 kg/ha</td>
</tr>
<tr>
<td>Pasture</td>
<td>Mabel Bush</td>
<td>229 (MP)</td>
<td>800 (M)</td>
<td>403 kg/cow</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>825 (W)</td>
<td>1407 kg/ha</td>
</tr>
<tr>
<td>Crop (swedes and fodder beet)</td>
<td>Wallacetown</td>
<td>262 (MP, incl. crops)</td>
<td>730 (M)</td>
<td>388 kg/cow</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>803 (W)</td>
<td>1081 kg/ha</td>
</tr>
</tbody>
</table>

**MEASUREMENTS**

Animal welfare was assessed during the experiment on the basis of the area available per cow (stocking density) and lying times. The stocking density was calculated by dividing the total area available by the number of cows. Lying times were assessed using IceTags® (IceRobotics, Scotland; (McGowan et al. 2007)) on at least ten cows, selected randomly within the group, for a 7-day period on each farm. Measurements were made over three 7-day periods, with two farms being monitored in each period. For farms with a combination of wintering systems, IceTags® were applied to cows in each system, in the same period. The total lying time per cow per day was calculated, to determine whether cows achieved recommended daily lying targets (Verkerk et al. 2006). The number of short-duration (< 4 minutes) lying bouts per day was used as an indicator of cow restlessness and discomfort (Hill et al. 2009) and the farm mean and standard deviation of these were then calculated. Weather data (temperature, wind speed and rainfall) was collected from the Invercargill and Dunedin airports as well as a private weather station at Ryal Bush, although only the Invercargill airport data is presented (Table 2).

Table 2: Invercargill airport weather data for the three periods of behaviour monitoring on six farms in Southland and South Otago during winter 2011

<table>
<thead>
<tr>
<th>Wintering system</th>
<th>Period (week)</th>
<th>Mean temperature (°C) (range)</th>
<th>Mean wind-speed (km/h) (max gust)</th>
<th>Total rainfall in period (mm) (day range)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Free stall barn/crop</td>
<td>21/06 to 28/06</td>
<td>6.1 (-0.2 – 12.9)</td>
<td>10.7 (20.6)</td>
<td>4.06 (0 - 0.5)</td>
</tr>
<tr>
<td>Crop</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pasture</td>
<td>29/06 to 06/07</td>
<td>6.0 (-1.9 – 13.3)</td>
<td>8.9 (20.6)</td>
<td>1.77 (0 - 1.3)</td>
</tr>
<tr>
<td>Self-feed wintering pad</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Herd Home™</td>
<td>07/07 to 14/07</td>
<td>4.1 (1.1 – 9.2)</td>
<td>25.2 (59.1)</td>
<td>102.7 (14.5 – 27.7)</td>
</tr>
<tr>
<td>Loose house barn/crop</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**RESULTS**

Weather data for the monitoring periods are reported in Table 2. Monitoring in the Herd Home™ and loose house barn/crop system occurred during the period with lowest average temperature, highest mean wind speed and greatest total rainfall.

Area per cow and lying times in the barn systems were generally less than those on the crops, pasture and the wintering pad (Table 3). In all systems, the herd average lying target of 8 hours was achieved, although the systems varied in the proportion of cows not achieving the target. The cows in the pasture-based system achieved the highest lying time and all cows lay for at least 8 hours. Those in the Herd Home™ spent the least time lying, and had the largest percentage of cows that failed to reach the 8 hour minimum lying target. Cows in the loose house barn had the highest number of short-duration bouts (Table 3) but cows on crop also had consistently more short duration lying bouts and more variability within the monitored groups.
Table 3: Lying surface, area per cow and lying behaviour of cows on six dairy farms in Southland and South Otago during winter 2011

<table>
<thead>
<tr>
<th>Indicator</th>
<th>Off-grazing:</th>
<th>Grazing:</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wintering system</td>
<td>Lying surface type</td>
<td>Area per cow (m²/cow)</td>
</tr>
<tr>
<td>Off-grazing:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Herd Home™</td>
<td>Slatted concrete</td>
<td>3.7</td>
</tr>
<tr>
<td>Loose house barn</td>
<td>Sawdust</td>
<td>5.2</td>
</tr>
<tr>
<td>Free stall barn</td>
<td>Rubber matting</td>
<td>8.0</td>
</tr>
<tr>
<td>Wintering pad</td>
<td>Bark chips</td>
<td>12.0</td>
</tr>
<tr>
<td>Grazing:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Crop (kale)</td>
<td>Soil</td>
<td></td>
</tr>
<tr>
<td>Crop (swedes 1)</td>
<td>Soil</td>
<td></td>
</tr>
<tr>
<td>Crop (fodderbeet)</td>
<td>Soil</td>
<td></td>
</tr>
<tr>
<td>Crop (swedes 2)</td>
<td>Soil</td>
<td></td>
</tr>
<tr>
<td>Pasture</td>
<td>Pasture</td>
<td></td>
</tr>
</tbody>
</table>

**DISCUSSION**

The current study utilised both grazing (pasture and crop) and off-grazing wintering systems (wintering pads and barns). The animal welfare implications differ between these two types of systems and variations in cow behaviour are largely due to stocking density and lying surface type and condition.

Cows housed in either the Herd Home™ or barn systems had less area per cow compared with grazing and wintering-pad cows, which may have contributed to the lower lying times and fewer cows achieving 8 hours of lying time. While all wintering systems met the industry recommended average of 8 hours per day, it was only on the wintering pad, and pasture and swede grazing systems that all individual cows achieved the industry target. Considerable variation in weather conditions during the monitoring periods on individual farms may have contributed to these differences. The farms (Herd Home™, loose housed barn and kale crop) with more animals not achieving 8 hours per day lying were monitored during the period of lowest mean temperature, highest wind speed and greatest rainfall (Table 2). Snow also fell during this period. Analysis of average daily lying times during this period (data not presented) showed a reduction in lying time for both barn and crop cows, however the effect on the crop cows was much greater than those indoors.

Evidence in the literature on the effect of stocking density on lying behaviour of cows in New Zealand wintering systems is limited. The results from the current experiment support those of (Fisher et al. 1997) and suggest a clear relationship in off grazing systems - as the area per cow increased so too did the lying times (Table 3).

Lying surface has been shown to have a significant impact on the willingness of cows to lie down (Fisher et al. 2003) with concrete being the least preferred surface. The slatted floor in the Herd Home™ is concrete, which may also have contributed to the lower lying times in this system (Haley, 2001). In addition air movement under the slats may have created draughts, reducing the warmth around the cows when lying. Soil and sawdust/bark chips provide a softer surface for lying, however their condition, i.e. wetness and temperature, may impact on the lying duration of individual cows (Tucker et al. 2007; Muller, 1996). This may explain the higher number of short duration lying bouts and increased variability in the loose house and crop cows in the current study. This monitoring period coincided with a stormy period and weather factors are likely to have led to greater discomfort and disrupted lying patterns in the crop cows. As a consequence of the severe weather conditions, cows in the loose barn were provided with an extra feed which also disrupted lying behaviour. Both the sawdust and soil were wet during the period of monitoring. Although there are heat-saving benefits to lying (Tucker et al. 2007), the heat loss associated with lying on these surfaces may have decreased the lying times.
CONCLUSION

This study evaluated the lying behaviour of dairy cows in a range of wintering systems during a Southland/South Otago winter in New Zealand. The results indicate that cows wintered in the Herd Home™, free stall barn and loose house barn spent less time lying than those wintered outdoors. Furthermore, more severe weather and wintering systems where the lying surface became wet and/or muddy were associated with increased short-duration lying bouts. Both stocking density and lying surface are important factors influencing cow comfort and, therefore, animal welfare in a range of wintering systems.

ACKNOWLEDGEMENTS

We thank the participating farmers for their willingness to share their farm performance details and Barbara Dow (DairynZ) for summarising the behaviour data. We also acknowledge the MPI Sustainable Farming Fund and Environment Southland for their co-funding of this DairynZ-led Southern Wintering Systems Initiative. The monitoring was also supported by Ministry of Business, Innovation and Employment project C10X0813.

REFERENCES


Use of indwelling rumen pH meters to compare the rumen pH of grazing dairy cows fed supplement either in the dairy or as a partial mixed ration on a feedpad


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ABSTRACT

The aim of this experiment was to investigate indicators of sub acute ruminal acidosis in grazing cows during the critical period of transition to a diet of supplementary grain twice daily in the dairy at milking (Control group), or a partial mixed ration (PMR group) on a feedpad. Indwelling rumen pH meters, set to record every 10 min were deployed in 20 rumen fistulated cows (12 PMR and 8 Control group cows). The data for the first 7d of the feeding period were analysed, using a Student t-test (PMR vs Control). There was no difference in the daily mean pH between PMR (6.17) and Control (6.14) cows (+0.03 pH units; 95%CI -0.09 to 0.16; \( P = 0.58 \)). The percentage of time (per d) that the rumen pH was less than 5.6 for PMR cows was 11.6% compared with 15.7% for Control cows (-4.2%; 95%CI -8.9 to 0.6%; \( P = 0.08 \)). The percentage of time (per d) that the rumen pH was less than 6 for PMR cows was 33.4% compared with 37.2% for Control cows (-3.9%; 95%CI -14.5 to 6.7%; \( P = 0.45 \)). Similarly, there were no effects of treatment for time*pH units under 5.6 or 6.0. It was concluded that for the initial 7-d transition period to the PMR and Control diets used in this study there were no significant differences in rumen pH parameters.

Keywords: dairy cow; rumen pH; SARA; indwelling pH meter.

INTRODUCTION

One of the health risks for grazing dairy cows fed supplementary grain is sub acute ruminal acidosis (SARA), particularly when fed their supplement in the dairy as a ‘slug’ of several kilograms of grain. The fermentation of this grain can lead to a drop in rumen pH below the threshold level for SARA, considered to be somewhere between pH 5.5 – 5.8, depending on the reference (Garrett et al. 1999; Beauchemin and Penner 2009). Having fistulated cows in a study group allows regular collection of rumen samples and monitoring of the rumen pH, but removing cows from pasture to manually sample their ruminal fluid could lead to a change in their grazing behaviour. Recently there have been technological advances in the development of indwelling, wireless pH meters. This is advantageous in research involving cows living at pasture, where the number of manual samples that can be taken is limited.

The objective of this study was to investigate whether the parameters of rumen pH indicative of SARA in grazing cows were different during the 7d adaptation period to a supplement fed as a partial mixed ration (PMR group) on a feedpad or fed as grain in the dairy at milking (Control group).

MATERIALS AND METHODS

Twenty multiparous Holstein-Friesian cows (18 to 66 DIM) grazed perennial ryegrass, with an allowance of approximately 14 kg DM/cow/d. Control cows were fed crushed wheat grain twice daily in the bail at milking, and pasture silage in the paddock. Partial mixed ration (PMR) cows were fed their supplement as a mixed ration of rolled wheat grain, maize grain, maize silage and lucerne after milking on a feedpad. For both groups, the ratio of grain:forage was 0.75:0.25 (DM basis) and the offered supplements were isoenergetic, with a level of total supplement/cow/d of approximately 10kg DM. A pH measurement bolus (KB5, Kahne Limited, New Zealand) was inserted into the rumen of 20 rumen fistulated cows (8 from the Control group and 12 from the PMR group) at the commencement of the 28-d feeding period. Rumen pH was logged every 10 min and the data stored. Boluses were temporarily removed 2 weeks after deployment and the data downloaded.

Statistical analyses. The data for the first 7d of adaptation period were summarised using MATLAB software to elicit daily mean pH, percentage of time (per d) that the rumen pH was less than 5.6, percentage of time (per d) that the rumen pH was less than 6, time in min*pH units under 5.6 and time in min*pH units less than 6.0. The data were then analysed using a Student t-test (PMR vs Control). The proportion of cows with pH <5.6 for ≥3 h/d was compared using Fisher’s exact test. A \( P \) value of <0.05 was used for statistical significance.

RESULTS

An example of the rumen pH recorded for 24h by one of the pH measurement boluses in a PMR cow is presented in Figure 1.
The results of the rumen parameters recorded in the first 7 d of the adaptation period are presented in Table 1. There was no effect of treatment (P=0.36) on the time rumen pH was <5.6 (33% of PMR cows and 62% of Control cows).

**Table 1:** Rumen parameters (mean ± SD) recorded during 7-d adaptation period to diet

<table>
<thead>
<tr>
<th>Rumen pH parameter</th>
<th>PMR (n=12)</th>
<th>Control (n=8)</th>
<th>p value</th>
<th>95% CI (PMR – control)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Daily mean pH</td>
<td>6.17 ± 0.12</td>
<td>6.14 ± 0.15</td>
<td>0.58</td>
<td>-0.09 to 0.16</td>
</tr>
<tr>
<td>% time under pH 5.6 (per d)</td>
<td>11.6 ± 4.4</td>
<td>15.7 ± 5.7</td>
<td>0.082</td>
<td>-8.9 to 0.6</td>
</tr>
<tr>
<td>% time under pH 6.0 (per d)</td>
<td>33.4 ± 9.2</td>
<td>37.2 ± 13.6</td>
<td>0.45</td>
<td>-14.5 to 6.7</td>
</tr>
<tr>
<td>Time in min * pH units under 5.6</td>
<td>896 ± 364</td>
<td>1238 ± 497</td>
<td>0.092</td>
<td>-746 to 62</td>
</tr>
<tr>
<td>Time in min * pH units under 6.0</td>
<td>2672 ± 700</td>
<td>3027 ± 1230</td>
<td>0.42</td>
<td>-1259 to 548</td>
</tr>
</tbody>
</table>

**DISCUSSION**

The aim of this study was to assess if there was an effect of supplementary feeding method on rumen pH parameters that may be indicators of rumen function or SARA. Daily mean pH is one parameter that can be assessed, but this may vary from cow to cow, and even from day to day, and what may be considered a low mean pH for optimal digestion may not necessarily result in the changes associated with SARA (Bramley et al. 2008). While many of the studies of rumen pH have focused on cows fed a total mixed ration, there have also been studies of rumen pH in cows grazing pasture and fed supplements; 23 of these were reviewed by Kolver and de Veth (2002) who reported a mean pH across the studies of 6.2, with a range between 5.6 and 6.7. This was similar to the mean pH of 6.17 for PMR and 6.14 for Control cows in the experiment reported here.

Per cent of time that the pH is below 6.0 and 5.6 are reportedly relevant for assessment of optimal rumen function and the threshold for SARA respectively (Mould et al. 1983; Nocek, 1997; Olsen, 1997). (Gozho et al. 2005) defined SARA as a rumen pH <5.6 for >3h/d. This is 12.5% of the day and, by this definition, some cows in this study had SARA during the 7 day period, but there was no difference between treatments. It was not surprising that transition dairy cows undergo fluctuations in their rumen pH, with this period acknowledged to be when the rumen is most susceptible to acidosis as a result of microbial adaptation (Mackie and Gilchrist, 1979; Fernando et al. 2010) and changes to the absorptive surface of the ruminal papillae (Liebich et al. 1987; Steele et al. 2011). There was no significant difference between PMR and Control in the time spent below the defined rumen pH thresholds.

**CONCLUSION**

It was concluded that there was no significant effect of diet (i.e. slug feeding vs PMR) on rumen pH parameters commonly associated with SARA.


Automated assessment of animal health and welfare using infrared thermography: early detection of disease

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ABSTRACT

In the changing face of dairy farming there is an increasing need for automated technologies, including those capable of regular monitoring of health and welfare states in animals. Infrared thermography (IRT) has been used successfully as an early detection tool for diseases such as bovine viral diarrhoea (BVD) and bovine respiratory disease (BRV) in beef feedlots and to detect mastitis, oestrus and lameness in dairy cows. IRT has potential to detect a number of health issues; however, the efficacy of implementing automated IRT technologies under extensive New Zealand and Australian farming conditions is unknown. We discuss the use of IRT in an automated early detection system for disease and consider the implications for this technology to be used to detect health and welfare issues in the New Zealand and Australian dairy industries.

Keywords: Infrared thermography; early disease detection; bovine respiratory disease; non-invasive detection

INTRODUCTION

The average dairy herd size (376 in New Zealand and 230 in Australia in 2011) has tripled in the last 30 years, and NZ Dairy Statistics (2010/11) report that 9% of New Zealand herds have 750 or more cows. This has led to an increasing reliance on automated in-shed systems to reduce labour costs and a decrease in experienced human contact on an individual cow basis. This less ‘hands on’ approach poses potential risks to animal health and welfare and there is an urgent need for automated systems that are capable of filling this gap in surveillance. Further to the above, diseases which are not diagnosed early cause a significant economic cost to the dairy industry. For example, it has been estimated that bovine viral diarrhoea (BVD) costs NZ $30 million annually and mastitis may cost the industry up to $200 million. The impact on the industry is not only in monetary terms, through decreased herd milk production, milk quality and reproductive performance, increased treatment costs and culling rates; there are also negative effects in terms of public perception with respect to animal welfare. Increasing public awareness of animal health and welfare and how livestock are managed on-farm has led to an increase in consumer demand for ‘welfare friendly’ products, which in turn has placed pressure on our animal-based agricultural industries to provide such products. The aim of this paper is to outline our research investigating the use of infrared thermography (IRT) in an automated system for disease detection in dairy cattle using technology that has been developed for detecting disease in Canadian beef feedlots and discuss the implications for the New Zealand and Australian dairy industries.

USES OF INFRARED THERMOGRAPHY

IRT is the measurement of radiated electromagnetic energy. In the electromagnetic spectrum, broad range infrared radiation wavelengths (3–12 μm) are longer than visible light and in animals 40–60% of heat loss is within this range. IRT has been used for many years in human and veterinary medicine. More recently, we have demonstrated that IRT technology is effective in detecting small changes in eye temperature associated with changes in blood flow due to stress and pain in cattle (e.g., Stewart et al. 2009; Stewart et al. 2010). The advantage of the technology over invasive procedures, such as blood sampling, is that infrared images can be collected non-invasively without interference or restraining the animal and thereby reducing the confounding effect of handling stress.

In Canada, researchers have been using IRT to non-invasively diagnose animals with BVD and bovine respiratory disease (BRV). The industry’s standard practice to identify calves with disease is the observation of clinical symptoms by farm staff, at which point intervention measures are taken. Unfortunately, the appearance of clinical symptoms is usually several days or more into the course of the disease and by then the animal often requires considerable medical attention, including the use of antibiotics, in order to recover. In a BVD virus induction model, (Schaefer et al. 2004) used infrared thermography (IRT) as an early detection method for identifying calves with BVD. They found significant increases in eye temperatures several days to one week before clinical signs of infection. The use of IRT to diagnose animals with BRD has also been established (Schaefer et al. 2007; Schaefer et al. 2012).
Recent developments have demonstrated the use of a fully automated system using RFID readers by which IRT data can be collected when an animal visits a water or feed trough (Schaefer et al. 2012). The advantage of the automated system is that from an animal behavioural perspective, animals can attend the water station voluntarily and data can be collected non-invasively without restriction or capture. Hence, both thermal radiated values from the eye, as well as watering frequency and other behaviours can be obtained non-invasively. Data can be downloaded wirelessly via the internet. Hence, data and animal responses can be monitored remotely at will to make crucial management and treatment decisions. Using this system, (Schaefer et al. 2012) demonstrated that true positive animals for BRD, based on clinical scores, core body temperature and haematology, had higher IRT temperatures compared to true negative animals (35.7±0.35 °C vs. 34.9±0.22°C positive vs. negative respectively). Figure 1 illustrates a typical IRT profile of eye temperature for a true positive and a true negative calf over several days.

![Figure 1: Example of a true positive animal displaying rising peak values for orbital maximum temperatures for several days and a comparatively stable orbital maximum temperature for the same several days for a true negative calf from (Schaefer et al. 2012).](image)

Proof of concept studies, using mastitis induction models, have shown that infrared thermography can be used to early detect mastitis (e.g., Colak et al. 2008; Hovinen et al. 2008; Polat 2010). Currently, the dairy industry’s standard practices for detecting mastitis in milking cows include visual examination and palpation of quarters, stripping quarters and examining milk for flakes, clots etc., electrical conductivity and milk somatic cell counts (SCC). However, these changes are often detected late in the timescale of an udder infection and do not identify all classes of infection, subclinical infections, or those that take some time to display clinical signs. Furthermore, general clinical symptoms, such as changes in core or rectal temperature, also develop late in the course of an infection.

(Hovinen et al. 2008) experimentally induced mastitis in 6 cows with 10 μg of Escherichia coli lipopolysaccharide infused into the left fore quarter of each udder, and the right fore quarter served as a control. The IRT temperature of the udder increased both in experimental and control quarters. The first systemic and local signs of clinical mastitis were noted in all cows 2 h after the induction, whereas it took 4 h for rectal temperature, milk SCC, and electric conductivity to increase post-induction. In addition to mastitis, the uses of IRT in the dairy industry include early detection of oestrus (Hurnik et al. 1985) and lameness (Nikkhah et al. 2005).

**IMPLICATIONS FOR NEW ZEALAND AND AUSTRALIAN DAIRY INDUSTRIES**

The efficacy of implementing these automated IRT technologies under New Zealand and Australian conditions is unknown. Therefore, the current focus of our research is to investigate the use of IRT as an automated system for early disease detection in dairy cattle based on the technology that has been developed for detecting disease in Canadian beef feedlots. We are currently testing the efficacy by which this thermal biometric technology can be adapted to New Zealand and Australian dairy systems for detection of several health issues.

A trial has integrated an IRT scanning system into an automated calf feeding station. The existing production and behavioural information (e.g., number of visits, feed intake, milk removal velocity) that the system currently gathers in combination with thermal changes may be a useful early predictive index for common diseases in dairy calves, such as rotavirus.

The technology also lends itself to positioning in the milking shed for detection of health issues such as mastitis, lameness and oestrus. We are investigating how the technology could be combined with other shed technologies such as automated drafting. The final goal is a system that alerts farmers, from prediction indexes, if an animal shows signs of disease at a much earlier stage than is currently possible. Action such as drafting for treatment and/or isolation from pen mates at risk of contamination can then be taken, markedly reducing the suffering and debilitation associated with disease states as well as losses in production. Automated information such as this, integrated into existing systems and monitored on a daily individual animal basis, has potential to facilitate a major advance in decision-making abilities for the farmer and improvements in animal productivity, health, welfare and economics.
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Reproductive technologies for the future – a role for epigenetics

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ABSTRACT

Epigenetic mechanisms, such as DNA methylation, regulate gene expression and, subsequently, phenotype, without changing the underlying DNA sequence. It is well established that the environment and nutrition can regulate methylation and, therefore, modify phenotype. In this review, regulation of DNA methylation and in particular, the influence of B-vitamins on one-carbon metabolism is outlined, and how deficiency or supplementation with B-vitamins, such as folate, can influence disease. Evidence is provided for the roles of B-vitamins in regulating reproduction and how deficiency of B-vitamins may be impacting dairy cattle fertility. Results from our laboratory provide evidence for an association between DNA methylation and gene expression in the endometrium during early pregnancy. It is, therefore, hypothesised that DNA methylation may regulate the uterine response to the embryo during early pregnancy and that aberrant DNA methylation during this time may jeopardise pregnancy success. Further research is required to establish if B-vitamin supplementation can improve reproductive success and if this effect is via changes to DNA methylation and gene expression in the endometrium, or via positive effects on oocyte and embryo development.

Additional keywords: DNA methylation, one-carbon metabolism, fertility, endometrium, dairy cows

BACKGROUND

Until recently, genetic selection in dairy cows has focused primarily on milk production traits, with very few countries including functional traits such as fertility in selection indices (Miglior et al. 2005). As a result, milk production capacity of the modern dairy cow has increased dramatically, but fertility has steadily declined (Garnsworthy et al. 2008). Reduced fertility results in longer inter-calving intervals, lower voluntary culling, and higher replacement rates (Royal et al. 2000), particularly in seasonal pasture-based systems. Consequently, it is estimated that 50% of the improved profitability from genetic selection for milk production was lost due to lost productivity associated with reduced fertility (Evans et al. 2006). There is also the environmental cost of poor fertility, as more cows are required to sustain a given replacement rate, increasing methane production (Garnsworthy 2004; Evans et al. 2006).

Fertilisation rates in cattle are relatively high, at around 90% and are not affected by milk production or age, given the same quality of semen and correct timing of artificial insemination relative to oestrus (Diskin et al. 2006). The discrepancy in bovine reproductive performance comes in calving rate. Calving rate for heifers or low to moderate-producing lactating cows is estimated to be around 55%, with an embryonic and foetal mortality rate of 40%. In contrast, calving rate in high producing cows is less than 40% and foetal mortality is closer to 60%. It is estimated that 70-80% of these losses occur during the pre-implantation period of embryonic growth, between days 8 and 16. The causes of embryonic loss during this period include chromosomal abnormalities, inheritance of embryonic lethal alleles, poor embryo quality or development, asynchrony between the developing embryo and maternal endometrium, lack of sufficient maternal-embryonic signalling, an adverse uterine environment, or poor receptivity of the endometrium to the embryo (Binelli et al. 2001b; Thatcher et al. 2001; Peterson and Lee 2003; VanRaden and Miller 2006; Garnsworthy et al. 2008). Epigenetic factors that potentially regulate some of these functions will be the focus of this review.

EPIGENETICS

Epigenetics is defined as heritable changes in gene expression unrelated to altered DNA sequences (Waddington 1939; Holliday 1987). These epigenetic modifications include remodelling of chromatin through modification of DNA methylation, or post-translational modification of histone tails (Dolinoy et al. 2007). The fundamental unit of chromatin is the nucleosome. The nucleosome is an octamer composed of four core histone proteins (H2A, H2B, H3, H4) around which 147 base pairs of DNA are wrapped. Histone modifications include acetylation, methylation, ubiquitylation, phosphorylation, and sumoylation. The most commonly studied histone modifications are acetylation, methylation and phosphorylation (Kouzarides 2007). DNA methylation involves the covalent modification of DNA through the addition of a methyl group to the cytosine ring of the DNA strand. This addition
converts cytosine to 5-methylcytosine and is catalysed by DNA methyltransferases (DNMTs). Four DNMTs have been identified in mammals: DNMT1, DNMT2, DNMT3a and DNMT3b.

- DNMT1 maintains DNA methylation during replication, by copying DNA methylation of the old DNA strand to the newly synthesised strand.
- DNMT2 is characterised as having weak DNMT activity in vitro and has been reported to methylate transfer RNA (Jurkowski et al. 2008).
- DNMT3a and DNMT3b are responsible for de novo methylation, as they are able to target unmethylated CpG sites (Brero et al. 2006).

In mammals, DNA methylation occurs most commonly at the cytosine residue of a CpG dinucleotide. DNA methylation is generally associated with inhibition of promoter activity, as it can prevent the binding of transcription factors and is associated with an indirect repression of chromatin state through recruitment of methyl-CpG-binding proteins (MBPs).

**NUTRITIONAL INFLUENCES ON EPIGENETICS**

The methyl groups required for DNA methylation are generated via one-carbon metabolism. This is a cyclic process that involves the transfer of one-carbon groups such as methyl groups between compounds and requires dietary micronutrients, or in the case of ruminants, microbial derived micronutrients. Folate, Choline, B-vitamins 2,6 and 12 all feed into the one-carbon metabolism cycle to produce cellular S-adenosylmethionine (SAM), the molecule that donates the methyl group to a cytosine residue in the process of DNA methylation (Fox and Stover 2008, Figure 1).

Folate is firstly reduced to dihydrofolate (DHF) and then to tetrahydrofolate (THF) by dihydrofolate reductase. THF is then incorporated into the one-carbon metabolism cycle as a carbon donor. The next step involves the degradation of Glycine or Serine to yield a methylene group on THF (5,10-methylene THF), which can then be reduced by methylenetetrahydrofolate reductase (MTHFR) to 5-methyl THF (Sumner and Matthews 1992). Vitamin B-6 is required for synthesis of 5,10-methylene THF, and vitamin B-2 (riboflavin) is a co-factor of MTHFR function (Ma et al. 2009). 5-methyl THF is then used as a co-substrate for re-methylation of homocysteine to methionine by the enzyme methionine synthase. Methionine synthase requires vitamin B-12 as a co-factor for this reaction (Ma et al. 2009).

Methionine can also be produced via the transfer of a methyl group from betaine to homocysteine to produce dimethylglycine (DMG) and methionine. An alternative source of methionine comes in the form of dietary choline. Choline is oxidised to betaine, which acts as a methyl donor for conversion of homocysteine to methionine (Ueland et al. 2005).

S-adenosylmethionine can be synthesised from methionine and ATP by the enzyme methionine adenosyltransferase. The methyl group (CH₃) in SAM can then be donated to an acceptor substrate such as DNA (DNA methylation) by SAM-dependent methylases or DNA methyltransferases (DNMTs). This reaction produces S-adenosyl homocysteine, which is hydrolysed to homocysteine and adenosine by S-adenosylhomocysteine hydrolase (Selhub 1999).

**Figure 1:** One-carbon metabolism cycle. Dietary or microbial folate, choline and vitamins B-2, -6 and -12 all feed into the one carbon metabolism cycle to produce SAM, the methyl donor for DNA methylation of CpG dinucleotides. DHF: dihydrofolate; THF: tetrahydrofolate; MTHFR: methylenetetrahydrofolate reductase; MS: methionine synthase; BHMT: betaine homocysteine methyltransferase; DMG: dimethylglycine; MAT: methionine adenosyltransferase; SAM: S-adenosylmethionine; DNMT: DNA methyltransferase; SAH: S-adenosyl homocysteine.

Micronutrients and vitamins can influence the availability of the methyl donor SAM for DNA methylation, thereby affecting the degree of DNA methylation that occurs at specific sites in the genome. Deficiency of any of the three B-vitamins involved in one-carbon metabolism can result in reduced activity of their co-factor enzymes. For example, vitamin B-12 deficiency in rats reduces activity of methionine synthase (Yamada et al. 2000). In addition, deficiency of these vitamins results in increased homocysteine, which can have negative effects, such as increased risk of occlusive vascular disease (Boushey et al. 1995).

Several groups have reported the effects of folate and choline supplementation or deficiency on DNA methylation: Folic acid supplementation
during the rat juvenile-pubertal period resulted in increased methylation of several gene promoters (insulin receptor, peroxisome proliferator-activated receptor alpha, and the glucocorticoid receptor) (Burdge et al. 2009) and adult rats fed a diet high in folate had increased promoter CpG methylation of the NAT2 gene (Wakefield et al. 2010). In contrast, folate deficiency in rats results in DNA strand breaks and hypomethylation of the p53 tumour suppressor gene (Kim et al. 1997). Dietary choline supplementation can reverse some of the negative effects of folate deficiency in mice (Craciunescu et al. 2010). Offspring of rodents fed a choline deficient diet during pregnancy have decreased neurogenesis and diminished neural function (Craciunescu et al. 2003; Mehedint et al. 2010). Maternal choline deficiency is associated with hypomethylation of promoter regions in genes that regulate angiogenesis in the brain (Mehedint et al. 2010). In contrast, hypermethylation of CpG islands in the promoter regions of tumour suppressor genes is a major cause of cancer (Esteller 2002), and high doses of folic acid have been associated with increased risk of colorectal cancer in some but not all studies (Williams 2012). Additionally, polymorphisms in folate-metabolism genes has also been associated with a greater risk of cancer (Shrubsole et al. 2004; Larsson et al. 2006; Murtaugh et al. 2007; Xu et al. 2007; Suzuki et al. 2008; Mostowska et al. 2011; Pawlik et al. 2012). Deficiency in micronutrients can negatively influence DNA methylation and gene expression and micronutrient supplementation can improve phenotype. However, excessive supplementation may negatively impact DNA methylation, therefore, further research is required to establish the optimum amount of supplementation with micronutrients such as folate and choline.

ENVIRONMENTAL INFLUENCES ON EPIGENETICS

Exposure to an adverse environment during foetal development has been linked to disease susceptibility later in life (Barker 2004; Gluckman et al. 2008). Changes to the foetal epigenome have provided a link between the environment and differences in gene expression linked with disease (Jirtle and Skinner 2007). The Agouti gene in mice is an elegant example of how the environment, and in particular nutrition, influences the epigenome, and, therefore, the phenotype. The wild-type Agouti gene codes for a paracrine signalling molecule that produces either a black (eumelanin (a)) or yellow (phaeomelanin (A)) pigment (Dolinoy 2008). There are several dominant mutations of the Agouti gene, including the viable yellow allele (A\(^{vy}\)). This is a dominant pleiotropic mutation, resulting in varying degrees of yellow fur, adult-onset obesity, diabetes and tumorigenesis (Duhl et al. 1994; Miltenberger et al. 1997). The activity of the A\(^{vy}\) Agouti allele is dependent on its epigenetic state. Methylation correlates inversely with Agouti expression. Therefore, depending on the epigenetic state of regulatory regions in the promoter, mice appear either brown or yellow or a mosaic of yellow and brown (Figure 2) (Dolinoy et al. 2007). The A\(^{vy}\) mouse model has been used to characterise the effects of nutritional and environmental factors on epigenetic regulation of gene expression and the adult phenotype. It has been reported that maternal exposure to the xenobiotic chemical bisphenol A (BPA) leads to alteration of the foetal epigenome, and in particular, a modified expression of the agouti allele via changes to DNA methylation. BPA in the maternal system caused demethylation of the agouti gene, resulting in the gene being turned on. Maternal exposure to BPA caused a shift in the coat colour distribution towards yellow. Interestingly, this phenotype was rescued through nutritional intervention. The addition of folic acid as a methyl donor, or the phytoestrogen genistein, counteracted the negative effects of exposure to BPA. Offspring from supplemented mothers had a reduction in BPA-associated DNA demethylation in the promoter region, which controls expression of the A\(^{vy}\) allele (Dolinoy 2008).

Figure 2: Agouti gene regulated by DNA methylation. The degree of methylation in the promoter of the agouti gene determines its expression levels and subsequent phenotype. Bees provide another example of how nutrition influences DNA methylation and subsequent phenotype. Future queen bees are raised on a diet...
of royal jelly. This substance modifies methylation patterns in the genome, altering the transcriptome. Consequently, queen bees are fertile and much larger than worker bees that did not receive royal jelly (Kucharski et al. 2008; Foret et al. 2009). In addition, queen bees emit pheromones that suppress ovarian activation in worker bees. The suppression of ovarian activity is also achieved through a mechanism involving modification of DNA methylation patterns in the worker bee (Hoover et al. 2003).

These examples provide evidence of how nutrition and the environment can affect DNA methylation patterns to have major phenotypic consequences. Similar examples are likely in cattle and, if elucidated, may provide a mechanism for favourably manipulating the chances of pregnancy success.

**DEDEMETHYLATING AGENTS AND ARTIFICIAL TRANSCRIPTION FACTORS**

Epigenetic markers, such as DNA methylation, can be reversibly modified by the environment and nutrients. In cancer characterised with aberrant DNA methylation of tumour suppressor genes, it is possible to use demethylating agents and rescue gene function (Momparler 2005; Hagemann et al. 2011). However, demethylating agents such as azacitidine are not specific and, therefore, demethylation occurs globally (Hagemann et al. 2011). Another approach involves the use of artificial transcription factors in combination with demethylating agents. Artificial transcription factors can be designed to target specific regulatory regions within a gene’s promoter, thereby regulating transcription. In this way, disease-related aberrant gene expression can be modulated. This approach has been utilised, in combination with a demethylating agent, to reactivate the transcription of an epigenetically silenced gene (mammary serine protease inhibitor: MASPIN) in tumour cells (Beltran et al. 2008).

**TOOLS FOR STUDYING DNA METHYLATION**

The effects of the environment and nutrition on DNA methylation can be investigated in a relatively high-throughput manner. Genome-wide DNA methylation can be quantified using methylated DNA immuno-precipitation (MeDIP) combined with microarrays or next-generation sequencing (Weber et al. 2005). In MeDIP, a DNA sample is divided into two aliquots and one sample is immuno-precipitated with an antibody that binds methylated cytosine. This binding results in an enriched sample containing only methylated DNA. The sample can then either be sequenced or hybridised to a microarray. For microarray hybridisation, the methylated DNA enriched sample and non-enriched sample are labelled with different dyes, and the intensities quantified to determine methylation state (Figure 3). Bisulphite sequencing is required to identify the specific sites of DNA methylation and, therefore, the differences in methylation between the samples. Treatment with bisulphite results in conversion of un-methylated cytosine residues to uracil. Bisulphite treated and untreated DNA samples can then be sequenced to determine if and where the DNA was methylated. There are several other approaches utilised for quantification of DNA methylation; these have been reviewed previously (Hurd and Nelson 2009; Bock et al. 2010; Harris et al. 2010; Hirst and Marra 2010; Laird 2010) and will not be discussed in this review.

**DNA METHYLATION AND UTERINE FUNCTION**

The uterus is a dynamic tissue that undergoes extensive periods of remodelling. The uterus undergoes cyclical changes in response to the ovarian steroids oestrogen and progesterone throughout the reproductive cycle as well as changes in response to the embryo that are necessary to establish and maintain pregnancy. Even more extensive remodelling occurs following parturition, when the uterus of the dairy cow undergoes involution. Involution involves physical shrinkage of the uterus, necrosis and sloughing of the caruncules,
and regeneration of the endometrium. The process of involution is usually complete within 6-8 weeks following calving (Sheldon et al. 2008). Many transcriptional changes occur during these times and are potentially regulated by DNA methylation.

**Embryo implantation**

Synchronous development of the embryo and a receptive endometrium is critical to the establishment and maintenance of pregnancy (Achache and Revel 2006). At least 30% of human pregnancies are lost prior to implantation (Macklon et al. 2002) and it is estimated that up to 80% of pregnancy losses in dairy cattle occur during the pre-implantation period (Diskin et al. 2006).

There are many transcriptional changes that occur in response to pregnancy (Robinson et al. 2000; Spencer et al. 2004; Baurersachs et al. 2006; Klein et al. 2006; Forde et al. 2010; Klein et al. 2010; Merkl et al. 2010; Walker et al. 2010) and these changes differ among animals with divergent fertility phenotypes (Walker et al. 2012). Differences are also reported among animals that became pregnant to artificial insemination (Walker et al. 2010; Merkl et al. 2010; Klein 2010; Bauersachs et al. 2006; Klein et al. 2004; Bauersachs et al. 2006). Gene expression was from samples that had been previously assessed for DNA methylation at 415,000 sites in the genome (Wu et al. 2007; Wu et al. 2009). It has been hypothesised, therefore, that aberrant DNA methylation in the endometrium may contribute to reproductive disorders and/or infertility (Shiozawa et al. 2002; Wu et al. 2005; Xue et al. 2007; Logan et al. 2010; Fürst et al. 2012).

Methylation has been highlighted as a potential regulatory mechanism in uterine receptivity to the embryo and aberrant methylation may contribute to poor fertility in cattle. For example, E-cadherin is a glycoprotein with reported roles in uterine receptivity to embryo implantation (Li et al. 2002; Jha et al. 2006; Liu et al. 2006). E-cadherin is down-regulated in some infertile women and is down-regulated in a non-receptive endometrial cell line (Rahnama et al. 2009; Matsuzaki et al. 2010). Inhibiting methylation of E-cadherin in a non-receptive endometrial cell line results in up-regulation of E-cadherin and the cell line becoming receptive. Another gene regulated by methylation, HOXA10, is expressed in the endometrium and is also involved in regulating endometrial receptivity. Down-regulation of HOXA10 in women with endometriosis has recently been associated with aberrant methylation (Wu et al. 2005).

Preliminary data from our laboratory suggests a correlation between DNA methylation and gene expression in the endometrium. We quantified DNA methylation at 415,000 sites in the genome from samples that had been previously assessed for genome-wide gene expression profiles (Walker et al. 2010; Walker et al. 2012). Gene expression was then tested for correlation with DNA methylation to identify transcriptional differences potentially regulated by DNA methylation. Forty two per cent of the correlated genes were differentially expressed between pregnant and non-pregnant, cycling animals, and 11% were differentially expressed between fertile and sub-fertile dairy cow genetic strains. Several pathways enriched in transcriptional studies were identified as containing genes potentially regulated by DNA methylation. For example, interferon signalling pathways were enriched in pregnant and fertile animals (Walker et al. 2010; Walker et al. 2012). During early pregnancy, the embryo signals its presence to the mother to prevent luteal regression and establish pregnancy. The primary signalling molecule used by the embryo is interferon-tau (IFNτ) (Hansen et al. 1999). Secreted IFN binds to receptors on the endometrium, activating the JAK-STAT pathway (Binelli et al. 2001a). Stat 1 homodimers (GAF), or Stat 1-stat 2 heterodimers, and IRF9 (ISGF3) then bind to the promoters of IFN-stimulated genes, activating their transcription (Hansen et al. 1999).

Several genes in this pathway were up-regulated in pregnant cows and were also down-regulated in sub-fertile cows. Interestingly, IFR9, which is up-regulated in pregnant cows and down-regulated in sub-fertile cows, had a negative correlation between DNA methylation and gene expression; this indicates that methylation may have a role in transcriptional regulation of the IFR9 gene. This gene is stimulated by interferons and is also part of the ISGF3 complex that hyper-activates the transcription of several IFN-stimulated genes (Figure 4). These data imply that DNA methylation could be regulating some of the unexplained differences in the response to IFN in fertile and sub-fertile phenotypes. DNA methylation was also correlated with gene expression of several genes in other pathways predicted to be important in critical events during early pregnancy. These events included cell adhesion, cytoskeleton remodelling and cell proliferation pathways. The relevance of these pathways in early pregnancy has been previously reported (Walker et al. 2010; Walker et al. 2012).

Correlation of DNA methylation and gene expression in these pathways provides additional support for a role of DNA methylation in early pregnancy responses. Genes that contribute to the enrichment of these pathways demonstrated a negative correlation between DNA methylation and gene expression. Although, the correlation among DNA methylation and gene expression does not confirm that DNA methylation is regulating gene expression in the uterus in response to the embryo, it is a critical step in establishing likely causative relationships between DNA methylation and gene expression.
Figure 4: Interferon signalling pathway. Stat1-stat2 heterodimers and IRF9 (ISGF3) bind to the interferon stimulated response element (ISRE) in the promoter region of interferon stimulated genes (ISGs), activating their transcription. Genes of the interferon signalling pathway that were differentially expressed in the comparison of pregnant vs. cycling (pvsC) and sub-fertile vs. fertile (SFvsF) dairy cows at day 17 of pregnancy. The shading refers to genes that were up-regulated in pregnant and/or down-regulated in sub-fertile cows.

Post-partum uterine infection

A uterine infection or inflammation in the early post-partum cow is common, and can remain unresolved for 10 to 20% of cows (Borsberry and Dobson 1989; McDougall et al. 2007; Sheldon et al. 2009). Infection results from micro-organisms ascending into the uterus from the vagina following parturition, but the inflammation may be associated with the infection, systemic metabolic perturbations during the transition period, or a combination. Uterine infection is associated with reduced reproductive function, including suppression of gonadotropin secretion, perturbation of follicular growth and function, disruption to ovulation, as well as reduced submission, and conception and pregnancy rates (Bell and Roberts 2007). Structural and functional effects of bacterial infection on the endometrium likely contribute to reduced fertility. Furthermore, infection is associated with reduced fertility at both the time of infection as well as after the infection is resolved (LeBlanc et al. 2002b, 2002a).

The postpartum uterus has a disrupted epithelial surface, coupled with fluid and tissue debris that support bacterial growth (Konigsson et al. 2002). It is estimated that 90% of cows have bacterial contamination in the uterus within the first two weeks post-calving. However, the presence of bacterial contamination does not necessarily result in infection; this is dependent on the bacterial population and species present, as well as the ability of the cow to mount an immune response to the bacterial contamination (Azawi 2008). Defence against pathogens in the uterus is three-fold:

• Anatomical:; the epithelium of the endometrium provides a barrier against microorganisms; while the vulva, vestibule and cervix hinder bacterial migration to the uterus,
• Functional:; endometrial gland secretions provide a chemical defence, and
• Immunological:; the action of inflammatory cells and humoral antibodies help prevent infection (Azawi 2008).

Uterine disease is most prevalent following parturition, when animals are in negative energy balance, although there is no causal link between negative energy balance and uterine disease. There is, however, some evidence that severe negative energy balance is associated with a reduction in immune function and increased inflammation in the uterus (Wathes et al. 2009). Furthermore, uterine disease has been associated with high blood non-esterified fatty acid concentrations, an indicator of negative energy balance and associated with reduced pre-partum neutrophil function (Hammon et al. 2006).

Preliminary data from our laboratory has identified transcriptional differences between animals with and without a post-partum uterine infection, with some genes also demonstrating promoter DNA methylation and gene expression correlations. We hypothesise that aberrant DNA methylation may be involved in the sub-fertility associated with post-partum uterine infection. Current work is focussing on identifying candidate genes and epigenetic markers associated with sub-clinical uterine infection.

ON-FARM APPLICABILITY

Methylation of DNA is a key regulatory mechanism for the control of normal gene expression. DNA methylation relies on the availability of methyl groups from SAM synthesis provided through the one-carbon metabolism pathway. This process relies on an adequate supply of B-vitamins, such as folate, in the diet, or through production by microbes in the rumen in dairy cows.
B-vitamin supplementation can influence DNA methylation, resulting in alterations to gene expression and phenotype. B-vitamin status has been associated with the probability of conception and risk of pregnancy loss in women (Reznikoff-Etiévant et al. 2002; Ronnenberg et al. 2007).

It has been reported that rumen microbial production of folate, and other B-vitamins, may be insufficient in high producing dairy cows (National Research Council. 2001). Subsequently, several studies have examined the effects of folate, vitamin B-12, and methionine supplementation on milk production and energy metabolism (Girard and Matte 2005; Graulet et al. 2007; Preynat et al. 2009b, 2009a; Preynat et al. 2010). Supplementation with B-vitamins appears to improve energy metabolism and likely influences the methylation cycle. In addition, it has been reported that supplementation with a rumen-protected B-vitamin complex results in an increase in conception to first service rate, providing a possible link between methylation and reproduction in dairy cows (Juchem et al. 2012).

Supplementation with B-vitamins may improve conception rate to first service through positive effects on oocyte quality and embryo development. Deficiency in folate, or higher than normal levels of homocysteine in the follicular fluid, have been associated with poor ovarian function including, reduced folliculogenesis, oocyte quality, fertilisation rate and poorer early embryo development (Haggarty et al. 2006; Boxmeer et al. 2008a; Boxmeer et al. 2008b; Altmae et al. 2010; Kwong et al. 2010). The effects of folate-mediated one-carbon metabolism on fertility have recently been reviewed (Laanpere et al. 2010).

Further research is required to establish if B-vitamin supplementation has a direct effect on DNA methylation in the endometrium or an indirect effect via the oocyte and embryo.

CONCLUSIONS AND FUTURE RESEARCH

The environment and in particular nutrition can regulate DNA methylation, thereby, modifying phenotype. Micronutrients and vitamins can influence the availability of the methyl donor SAM for DNA methylation, affecting site-specific DNA methylation and gene expression. Gene expression in the uterus is intricately controlled during the oestrous cycle, pregnancy and during post-partum involution. Methylation has been highlighted as a potential regulatory mechanism in uterine receptivity to the embryo and in disease aetiology. Given the association between DNA methylation changes and gene expression in the endometrium during early pregnancy, and the positive association between B-vitamin concentrations and fertility, we hypothesise that B-vitamin supplementation could be used to positively influence DNA methylation in the endometrium, thereby improving reproductive outcome through enhanced endometrial function. Future research should focus on the implementation of high-throughput techniques to quantify DNA methylation in the uterus and establish if gene expression is associated with DNA methylation during different stages of the oestrous cycle, pregnancy and during uterine involution and disease. The potential to positively influence uterine gene expression and therefore reproductive performance through nutritional intervention provides a promising avenue for future research.

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Amelioration of thermal stress impacts in dairy cows

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ABSTRACT

Heat stress negatively impacts on a variety of animal production parameters. Advances in management strategies have alleviated some of the negative impact of thermal stress on farm animals, but production continues to markedly decrease during heat events in summer, particularly in dairy cattle. In this paper we introduce a Dairy Risk Assessment Program (DRAP) which has been resulted in the development and refinement of mathematical algorithms using scientific literature to produce a user friendly software package designed to assist users in predicting heat loads in dairy cow herds. This software package is designed to be used by the dairy industry to better manage cows during times of elevated environmental temperatures by equipping producers, managers, and dairy industry personnel with Heat Load Index (HLI) values calculated based upon site information, stock characteristics, management practices, and mitigation variables specific to their dairy production unit. When a heat event is imminent producers can then introduce management strategies such as providing shade or additional water troughs or implementation of nutritional strategies. Some of these nutritional strategies include dietary CrPct, betaine and antioxidant supplementation or altering the rate of starch fermentation. These nutritional strategies are discussed at some length in this paper.

INTRODUCTION

By 2030 it is likely average temperatures will increase by 0.5 to 1.5°C across southern Australia. Rainfall patterns are expected to change with south and south-eastern Australia likely to receive less and as a consequence there is likely to be an increase in the incidence of heat stress in livestock in Southern Australia with impact on the dairy and sheep industries. Heat stress negatively impacts on a variety of animal production parameters (eg. milk yield and quality, wool growth, tissue growth, feed intake) and therefore is a significant financial burden already that will only get worse if predictions about effects of climate change on southern Australia are true. Advances in management strategies (i.e. cooling systems, provision of shade, adequate provision of water) have alleviated some of the negative impact of thermal stress on farm animals, but production continues to markedly decrease during heat events in summer, particularly in dairy cattle. A dramatic reduction in feed intake is an obvious sign of heat stress and is thought to be primarily responsible for many of the negative effects of heat stress on animal production. Another easily recognized heat stress factor is reduced milk yield, which generally is reduced to a greater extent than predicted by the reduced feed intake alone. Even on well-cooled dairies or in temperate areas, heat stress typically decreases milk yield by 10-15% and on non-cooled management systems or during extreme heat events milk yield can decrease by 40-50% during severe conditions. What is needed then is information on how to predict the onset of heat events, an understanding of the physiology and biology of heat stress, knowledge of some of the predisposing conditions (other than ambient or radiant temperature), and some means to mitigate or alleviate acute and chronic heat stress to ensure animal productivity and welfare. This paper will briefly address these issues, describe a predictive model designed to assess the likelihood of a heat event occurring and identify some dietary means to mitigate heat stress.

MEASUREMENT OF HEAT LOAD

The Temperature Humidity Index (THI), which is calculated from air temperature and relative humidity, is one measure that has been used to evaluate heat stress in cattle. The principle of THI is that as it increases, with higher environmental temperature and/or relative humidity, it becomes progressively more difficult for cattle to cool themselves, and body comfort decreases. Since the early 1990’s, the THI has been commonly used in the feedlot beef and dairy industries as a means of estimating ‘heat load’ and the likely effects on cattle productivity and welfare. In dairy cattle, a THI greater than 72 is traditionally considered mild heat stress. At a THI greater than 78,
cows experience moderate heat stress and markedly reduced milk production and other physiological effects are generally observed.

The THI was originally developed by Thom (1958) and extended to cattle by (Berry et al. 1964). However, the THI is based on a retrospective analysis of studies carried out at The University of Missouri in the 1950’s and early 1960’s on a total of 56 cows averaging 15.5 kg milk per day. In contrast, average production per cow in Australia and elsewhere is presently over 25 kg/d with many cows producing above 35 kg/d at peak lactation. It is clear that the sensitivity of cattle to thermal stress is increased when milk production is increased thereby reducing the “threshold temperature” when milk loss begins to occur (Berman, 2005). For example, within the herd located at the Dookie campus of The University of Melbourne we identified the high (27 to 37 litres milk/day) and low yielding (>22 litres milk/day) and measured their susceptibility to heat stress based on panting scores. In total, 34 (25%) cows were identified as very susceptible to heat stress with 17 of these cows being categorized in the top 40 milk producers, with only 1 featuring in the bottom 20 cows that were producing less than 22 litres milk/day. Furthermore, we identified 30 of the least susceptible cows to heat stress and repeated the cross referencing and found only 4 of these cows to be in the top 40 milk producers, and none in the bottom 20. Quite clearly, higher milk yields are associated with increased risk for heat stress. Consequently, as genetic, management and nutritional improvements have been made resulting in increased milk yields some have questioned the validity of using the THI alone as a measure of the likelihood of heat stress occurring (Collier et al. 2012).

As an indirect measure of heat stress in cattle, THI has two major limitations. Firstly, heat load in cattle is determined by four factors: 1) air temperature, 2) relative humidity, 3) air speed and 4) solar radiation; however, THI only accounts for 1 and 2. Secondly, THI does not enable the measurement of the accumulation of heat load over time (eg. after several days/ nights). In dairy cattle, there is also now concern that the THI threshold of 72 may underestimate heat load in modern, high yielding Friesian-Holstein cows, because increasing milk yield increases sensitivity of cattle to heat stress. Recent research has shown that increasing milk production from 35 to 45 kg/day reduced the threshold temperature for heat stress by 5°C. Since 2002, an improved heat stress measure has been developed for the Australian beef feedlot industry with funding by MLA which addresses the first limitation. The Heat Load Index (HLI), developed based on data collected at Australian feedlots (Gaughan et al. 2008), uses a black globe temperature rather than ambient temperature, and takes into account air temperature, air movement and solar radiation effects. The HLI of a ‘reference animal’ is described, and a table of adjustment factors provided which can be used to estimate the upper HLI threshold under different feedlot circumstances (breed, coat colour, days on feed, shade, temperature of water in troughs, manure management etc.). Heat load accumulated by cattle over time can also be calculated. The so-called Accumulated Heat Load Units (AHLU) index is based on the number of hours that the HLI remains above a given threshold (nominally 89). The ALHU index addresses the second limitation because it combines the intensity and duration of cattle’s exposure to heat load.

The HLI and AHLU index have recently been incorporated by MLA into a web-based heat load forecast service http://www.katestone.com.au/mla/index.html. The Dairy Australia Grains2Milk project has developed web-based tool which estimates heat load forecast based on region, herd composition, production level and weather forecast (http://www.coolcows.com.au/index.htm) to assist Australian dairy farmers and their advisers to estimate management decisions. One of the goals of our recent work has been the development of a tool to incorporate the HLI and AHLU index for dairy herds under different conditions. Such a tool would be a considerable advance on this current web-based tool enabling producers to predict heat events and implement appropriate management and nutritional interventions. To this end we have developed the Dairy Risk Assessment Program (DRAP).

The development of the DRAP software package has required the collection, sorting, entry and re-coding of many thousands of individual cow observation data points and weather data from numerous climate databases. The accumulation of these data have led to the development and refinement of mathematical algorithms using current scientific literature to produce a user friendly software package designed to assist users in predicting heat loads in dairy cow herds. This software package is designed to be used by the dairy industry to better manage cows during times of elevated environmental temperatures by equipping producers, managers, and dairy industry personnel with Heat Load Index (HLI) values calculated based upon site information, stock characteristics, management practices, and mitigation variables specific to their dairy production unit. Furthermore, the DRAP software package can also be used by the dairy operator to predict adjusted HLI values based upon changes to their variable inputs, for example, the HLI value will be
adjusted in a favourable direction if extra water troughs are installed, greater areas of shade are provided, water within troughs is kept cool, or cow coat colour is more white than black. The desirable increase in the DHLI value as a result of altering facets of the dairy production unit will lead to a lesser incidence of animals deemed to experience extreme stress and high stress during times of elevated environmental temperatures. The achievement of lowering the incidence of heat stress in a dairy herd is beneficial to overall production efficiency. Although this is the first time the software package has been presented in its functional form, we are confident that the background calculations using the variable algorithm inputs entered by the user will accurately predict the average dairy heat load index (DHLI) probability of a dairy cow.

The algorithm that is used to calculate the basal dairy heat load index (DHLI) is:

$$\text{DHLI} = 9.82 + (0.49 \times \text{RH}) + (1.15 \times \text{BGT}) - (0.3 \times \text{WS}) + \exp(-\text{WS} + 2.6)$$

Where BGT is black globe temperature ($= 3.8159 \times \exp(0.0713 \times \text{air temperature})$), RH is the relative humidity and WS is wind speed. The base heat load for the model cow equals 64 and heat load starts to accumulate once the DHLI exceeds 64. The model cow parameters used in this algorithm assumes can be found in Table 1.

### Table 1: Model cow characteristics for the Dairy Risk Assessment Program (DRAP)

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<table>
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<tr>
<td>1</td>
<td>Not adapted to heat</td>
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<tr>
<td>2</td>
<td>Healthy</td>
</tr>
<tr>
<td>3</td>
<td>50% black coat colour</td>
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<tr>
<td>4</td>
<td>Producing 20-25 litres milk/day</td>
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<tr>
<td>5</td>
<td>60 – 12 days in milk</td>
</tr>
<tr>
<td>6</td>
<td>Has access to only limited shade of ~ 0 to 2 m²/cow</td>
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<tr>
<td>7</td>
<td>The cows nutrition regime consists of 80% grazing</td>
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<tr>
<td>8</td>
<td>Has a body condition score (BCS) of 3</td>
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Using the parameters stated above, entered into the model, the threshold value equals 64. At a threshold of >64 body heat of the cow increases hence heat stress of the dairy cow is predicted to become evident. The threshold of the cow can be altered by entering values of farm components for the specific dairying system under the three categories of stock characteristics (genotype, coat colour, health status and days on feed) management practices (provision of shade, temperature of water in the water troughs and the level of manure management) and mitigation (the use of additional water troughs, use of a ration that has been specifically designed to reduce metabolic heat load and the strategic cleaning of areas where wet manure accumulate) measures.

The DRAP model is continually being refined but an example of some of the effects of changes form the model cow on the threshold value are shown in Table 2.

### Table 2: An example of some of the impacts of modification to the model cow characteristics for the Dairy Risk Assessment Program (DRAP)

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<table>
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<tbody>
<tr>
<td>1</td>
<td>Cows adapted to heat + 4</td>
</tr>
<tr>
<td>2</td>
<td>Shade 4 to 5 m²/cow + 2</td>
</tr>
<tr>
<td>3</td>
<td>Greater than 80% white + 1 (requires further refinement)</td>
</tr>
<tr>
<td>4</td>
<td>Cooling infrastructure at the dairy + 2</td>
</tr>
<tr>
<td>5</td>
<td>Sick or lame cows adjustment - 5</td>
</tr>
<tr>
<td>6</td>
<td>Total mixed ration (TMR) - 1 (requires further refinement)</td>
</tr>
<tr>
<td>7</td>
<td>Milk production &gt;30 L/d - 3</td>
</tr>
<tr>
<td>8</td>
<td>Body Condition Score (BCS) &gt;4 + 1 (requires further refinement)</td>
</tr>
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The DHLI and AHL have been run real time over summer of 2011/2012 using BOM data from BOM weather stations in dairy regions and verified against production performance. The DRAP model is currently being reformatted to fit into the Cool Cows (http://www.coolcows.com.au/index.htm) format and it is envisaged that this web-based tool will provide dairy farmers with a tool to accurately predict when heat events are likely to occur. If an event is imminent then the dairy farmer can then implement strategies to ameliorate heat stress and much of our other research has focussed on some nutritional that may be used.

**PHYSIOLOGICAL IMPACT OF HEAT STRESS IN DAIRY COWS**

Lactating dairy cattle are particularly susceptible to heat stress due to the high metabolic load of milk synthesis and visceral metabolism associated with high feed intakes needed to sustain lactation. Some physiological responses to heat stress, such as increased respiration rate, are clinically obvious and have been well documented in lactating animals. For instance, in heat-stressed cattle approximately 15 % of internal (core) heat load is lost via increased respiration rate (McDowell et al. 1976) which can increase from 20 - 40 to >150 breaths per minute (Silanikove 2000). Respiration rates are easily observed and therefore commonly measured to qualify the severity of heat
stress as being either low (20 – 60 breaths per minute), medium (60 – 80 breaths per minute), high (80 – 120 breaths per minute) or severe heat stress (>150 breaths per minute) (Silanikove 2000).

In order to further quantify some of the physiological impacts of heat stress on performance in dairy cows DiGiacomo (2011) conducted a study with high-yielding dairy cows. Briefly, the study involved lactating Holstein dairy cows (~100-120 days in milk (DIM)) balanced by parity, milk yield (MY) (~35-40 kg/day), gestational status and body condition score (~2.75) were housed in environmental chambers at the University of Arizona. All cows were subjected to two treatments; a thermoneutral (18°C, 20 % humidity (THI 64) and a 12 hour light and 12 hour dark cycle) period which lasted for 7 days (week 1) followed by a heat stress period which lasted for 14 days (weeks 2 and 3), meaning that each animal acted as its own control. The heat stress period mimicked a typical Arizona summer day with a cyclical daily temperature (~29-40 °C (maximum THI 82 from 0700 to 2300 hours, 20 % humidity, remaining at THI 73 from 0000 to 0700 hours with a 12 hour light and 12 hour dark cycle). All cows were offered a total mixed ration (TMR) ad libitum.

Milk yield was decreased from 32 to 27 and 23 kg during the first and second weeks of heat stress, respectively (P<0.001) (Figure 1). Similarly, dry matter intake (DMI) was decreased from 25.5 kg/day to 20.2 and 18.8 kg/day during the first and second weeks of heat stress, respectively (P<0.001). Milk fat and protein % and yields were also decreased after 2 weeks of heat stress (see DiGiacomo, 2011). As anticipated both rectal temperature (Figure 2a) and respiration rate (Figure 2b) were increased (P<0.001) during heat stress as were skin temperatures on the rump and shoulder (data not shown). Despite the decrease in feed intake during heat stress, plasma non-esterified fatty acid (NEFA) concentrations were not altered by heat stress (P=0.28) whereas plasma glucose was decreased (4.0 vs 3.8 mmol/L, P=0.02) and urea nitrogen was increased (3.7 vs 4.7 mmol/L, P<0.001) (DiGiacomo, 2011). Heat shock protein (HSP)70/90 and heat shock factor (HSF) 1 mRNA were all able to be detected in the white blood cells of the lactating cattle, under both thermoneutral and heat stress conditions. The expression of HSP90, and to a lesser extent HSP70, were altered by day (P=0.06 and P=0.04 respectively) such that both HSP70 and HSP90 mRNA expression were increased during heat stress, with the increase in HSP90 expression occurring later than that seen for HSP70. In a subsequent study where lactating dairy cows with a similar basal milk production were subject to a similar thermal load (THI of 64 vs 72.5) there were similar impacts on milk production and physiological measures of heat stress (Hall et al. 2012). Thus, it appears that heat stressed dairy cows decrease feed intake and milk yield but based on plasma NEFA do not increase the mobilisation of lipids to meet the deficit in energy balance as is the case in lactating ruminants during thermoneutral conditions (Bauman et al. 1988; Dunshea et al. 1989,1990; Sechen et al. 1990).
Others have also found that in lactating cattle, heat stress reduced feed intake and increased basal and glucose stimulated insulin concentrations, while adipose tissue reserves were not mobilised (Rhoads et al. 2009; Schwartz et al. 2009; Wheelock et al. 2010). It remains unknown why insulin levels are increased in heated ruminants, but is thought to be part of the general processes allowing animals to acclimate to heat (Achmadi et al. 1993). Also, plasma prolactin concentrations are increased in heat stressed mammals, with evidence suggesting that prolactin modulates sweat gland function (Alamer 2011), and is involved in maintaining electrolyte and water balance in the heat stressed mammalian gut, kidney and mammary gland (Collier et al. 1982; Faichney and Barry 1986). Prolactin also influences carbohydrate activity by directly influencing pancreatic functions to increase insulin secretion (Bole-Feytsot et al. 1998), while also reducing the number of insulin receptors in adipose tissue (McNamara 1991). Thus, a heat induced increase in circulating prolactin levels may be partially responsible for the associated insulin resistance. We recently found that sheep exposed to a mild level of heat (-36°C for 6-7 hours daily) had increased plasma prolactin levels at 1500 hours compared to sheep maintained in thermoneutral conditions (19-24°C) even though rectal temperatures were not increased (DiGiacomo 2011). This is intriguing and perhaps indicates that exposure to heat influences metabolism even though physiological signs of clinical heat stress (increased rectal temperatures and respiration rates) are not seen. Regardless, it appears that the lactating dairy cow which is already more insulin resistant that its dry counterpart becomes even more insulin resistant during heat stress.

It is somewhat surprising that heat stressed cattle do not mobilise adipose tissue reserves, as is the case in chronically underfed animals (Dunshea et al. 1988) or in lactating ruminants housed under thermoneutral conditions (Bauman et al. 1988; Dunshea et al. 1990; Sechen et al. 1990). The reasons for this remain unknown since adipose tissue from heat stressed animals is equally as responsive to lipolytic signals as adipose tissue from underfed animals housed under thermoneutral conditions (Rhoads et al. 2009). In non-lactating growing cattle (O’Brien et al. 2010) and in sheep (Achmadi et al. 1993) plasma glucose levels are lower in heat stressed animals, but not those housed in thermoneutral conditions but experiencing a decline in intake. Decreased glucose levels and the lack of adipose tissue mobilisation seen in heat stress ruminants may be a direct response to increased circulating insulin levels, although this remains to be elucidated (Rhoads et al. 2009). It is possible then that improvement in insulin sensitivity may offer a means of reducing the impact of heat stress on lactating dairy cows.

### NUTRITIONAL STRATEGIES TO AMELIORATE HEAT STRESS

Mammals, including ruminants, become insulin resistant during pregnancy and lactation as a normal means of diverting nutrients away from body tissues and towards priority tissues such as the fetus or lactating mammary gland. Animals that are heavily fattened such as late finished cattle and sheep also become insulin resistant (Dunshea et al. 2008). However, insulin resistance is associated with an impaired ability to regulate temperature and so it is likely that animals in these conditions will be less able to cope with heat stress events (Dunshea et al. 2008). The fundamental thermoregulatory strategy of any mammal, including dairy cattle, is to maintain a body core temperature higher than ambient to allow heat to dissipate via conduction, convection, radiation, and evaporation (Collier et al. 2006). When ambient temperature conditions approach body temperature, the only viable route of heat loss is evaporation; if ambient conditions exceed body temperature, heat flow will reverse and the animal becomes a heat sink. In order to assist with evaporation from the skin, during heat exposure there is an increase in blood flow to, and sweating from, the skin of cattle and other ruminants (Choshniak et al. 1982) in order to dissipate heat. It is possible that insulin resistance might contribute to an increased heat load in lactating dairy cows, pregnant cows and sheep and fattening livestock. Genetic selection for improved insulin sensitivity or dietary agents that improve insulin sensitivity may help alleviate heat stress. Dietary agents may include the antidiabetic compounds such as chromium and thiazolidinediones as well as the osmolyte betaine (Dunshea et al. 2008). There have been fewer studies in ruminants than in pigs and poultry, but there is some evidence that dietary betaine can reduce heat stress and improve feed intake and growth performance in beef cattle (Cronje et al. 2005; Loxton et al. 2007) and sheep (DiGiacomo 2011). Also, there is now evidence that insulin resistance causes oxidative damage and that supranutritional supplementation with anti-oxidants may mitigate against heat stress, at least in sheep (Chauhan et al. 2012). Finally, by slowing down the fermentation of starch in the rumen it may be possible to decrease the heat increment of feeding and allow ruminant to better handle heat stress.
INSULIN RESISTANCE, HEAT TOLERANCE AND DIETARY CHROMIUM

In addition to the effects that insulin resistance has on tissue carbohydrate metabolism, there is now increasing evidence that diabetic individuals suffer from thermal intolerance, exhibiting an inability to control body temperature (Ohtsuka et al. 1995). In part, this is because skin blood flow and skin thickness are reduced in diabetic individuals (Forst et al. 2006), thereby reducing the ability to thermoregulate. In this context, chronic treatment with the insulin sensitiser, rosiglitazone increases skin blood flow and improves the ability to thermoregulate in diabetic humans. It is possible that other dietary agents that might enhance insulin sensitivity may improve the ability of ruminant animals, including dairy cattle, to handle heat stress. One such compound may be the insulin-mimic, chromium.

Chromium (Cr) is an essential trace element and plays a key role in carbohydrate, fat and protein metabolism through potentiating the action of insulin (Mertz 1993). It is generally accepted that Cr exerts its effect on glucose metabolism as a component of the glucose tolerance factor. (Amoikon et al. 1995) reported that CrPic increased insulin sensitivity as assessed by increased glucose clearance rate and decreased glucose half-life during a glucose tolerance test and insulin challenge test. Also, CrPic is able to increase the rate of insulin internalization and glucose uptake into skeletal muscle cells (Evans and Bowman 1992). Positive physiological and production responses to dietary chromium (Cr) supplementation have been observed in sheep exposed to external stressors, such as transportation stress (Al-Mufarrej et al. 2008; Kraidees et al. 2009) and heat stress Smantha et al. 2008; Sahin et al. 2002b; Sahin et al. 2002a; Sahin et al. 2005). Dietary CrPicolinate (CrPic) has been shown able to increase feed intake in quail (Sahin et al. 2002a; Sahin, 2010) and increase milk yield and feed intake in Holstein cows under during periods of high ambient temperature (Al-Saiady et al. 2004). Also, dietary nano-CrPic can improve feed intake in finisher pigs during mid-summer (Hung et al. 2011). The positive feed intake response under high ambient temperature indicated that dietary Cr may be able to ameliorate the negative physiological responses of animal under heat stress. Therefore, we conducted a study under controlled heat stress conditions to determine if dietary CrPic could improve insulin sensitivity and the ability to handle heat stress in sheep, our model ruminant for heat stress research (Hung 2012).

In order to quantify some of the physiological impacts of heat stress and dietary chromium on performance, insulin sensitivity and physiology in sheep Hung (2012) conducted a study in controlled environmental rooms. Briefly, the study involved Merino sheep that were subject to one of three diets (0, 200 and 400 ppm added nano-CrPic) and 2 temperature regimes. The two temperature regimes were thermoneutral (22°C and 80% relative humidity constant over the day) and heat stress (40.4°C and 54% relative humidity from 0900 h until 1700 h then declining to thermoneutral) for 3 weeks. Insulin sensitivity was assessed using the intravenous glucose tolerance test (IVGTT) during the third week of treatment.

Rectal temperature increased in response to heat stress (39.29 vs 39.92°C for thermo-neutral and heat stress condition, respectively, P<0.001, sed=0.029) (Figure 3a). Rectal temperatures were greatest at 17:00 (39.21, 39.76, and 39.85°C at 09:00, 13:00 and 17:00 respectively, P<0.001, sed=0.036). There was in interaction between temperature and time such that sheep exposed to thermo-neutral and heat stress conditions had the highest rectal temperature at 17:00 and the lowest at 09:00, and these temperatures were higher in heat stressed sheep at 13:00 and 17:00 (39.18, 39.28, and 39.28°C vs 39.15, 40.32, and 40.48°C at 09:00, 13:00 and 17:00 for thermo-neutral and heat stress stress condition, respectively, P<0.001, sed= 0.05). In addition, there was an interaction between pooled dietary nrCrPic and temperature (39.25 vs 39.31°C, and 39.98 vs 39.89°C, in control and pooled nrCrPic diet for thermo-neutral and heat stress condition, respectively, P=0.031, sed=0.043). Similar effects were seen for skin temperature (data not shown).

Heat treatment increased respiration rate (78.1 vs 167.9 breaths per min for thermo-neutral and heat stress condition, respectively, P<0.001, sed=2.82) (Figure 3b). Respiration rates were highest at 17:00 and lowest at 09:00 (77.4, 142.4 and 149.2 breaths per min, at 09:00, 13:00 and 17:00, respectively, P<0.001, sed=3.45). There was no main effect of pooled dietary nrCrPic in respiration rate (P=0.361). However, there is an interaction in between temperature and pooled nrCrPic (70.9 vs 81.7 breaths per min, and 171.5 vs 166.1 breaths per min, in control and pooled nrCrPic diet for thermo-neutral and heat stress condition, respectively, P=0.008, sed=4.22). The & rectal temperature was significantly increased by heat treatment (0.072 vs 1.117°C for thermo-neutral and heat stress condition, respectively, P<0.001, sed=0.046) and decreased by dietary nrCrPic (0.554 vs 0.675°C for control and pooled nrCrPic diet, respectively, P=0.02, sed=0.049).
Figure 3: Effect of heat load on a/ rectal temperature and b/ respiration rate in sheep during thermoneutral conditions (open symbols) or heat stress (closed symbols). Dietary treatments were either 0 ( ), 400 (Δ) or 800 (○) ppb nano-Crpic. See text for details of thermal treatments. The standard error of the difference for the interaction between thermal treatment x diet x time is displayed. See text for significance of main effects and interactions. Data are from Hung (2012).

Heat treatment significantly reduced weight gain of sheep (128 vs -37 g/day for thermo-neutral and heat stress conditions, respectively, \( P<0.001 \), sed=35.9) while dietary nCrpic increased weight gain (2 vs 67 g/day for control and pooled nCrpic diet, respectively, \( P=0.049 \), sed=38.1). Water intake was significantly increased by heat treatment (3.51 vs 4.41 L/day for thermo-neutral and heat stress condition, respectively, \( P=0.045 \), sed=0.433). Feed intake was reduced by heat treatment (1343 vs 1163 g/day for thermo-neutral and heat stress condition, respectively, \( P=0.003 \), sed=51.4) and increased by dietary nCrpic supplementation (1171 vs 1294 g/day control and pooled nCrpic diet, \( P=0.045 \), sed=53.6). Furthermore, heat treatment significantly decreased fed conversion efficiency (FCE) (0.086 vs 0.037 for thermo-neutral and heat stress condition, respectively, \( P<0.001 \), sed=0.031), whereas there was no effect of pooled nCrpic in FCE (\( P=0.15 \)).

Basal glucose concentration tended to be lower in sheep fed with nCrPic (4.83 vs 4.32 mmol/L for control and pooled nCrPic diet, respectively, \( P=0.062 \), sed=0.248), but higher in heat stress treatment animals (4.21 vs 4.80 mmol/L for thermo-neutral and heat stress condition, respectively, \( P=0.022 \), sed=0.234). The peak glucose concentration of glucose after IVGTT was decreased (\( P=0.001 \)) by dietary nCrPic as was the area under the plasma glucose versus time curve. There were mean effects of temperature (\( P=0.004 \)), pooled nCrPic (\( P=0.002 \)) and time (\( P<0.001 \)) in insulin response to glucose challenge. There was temperature × time (\( P=0.002 \)) and pooled nCrPic ×time (\( P<0.001 \)) interaction in insulin concentration response to glucose infusion. Temperature reduced basal insulin concentration (14.1 vs 12.0 mU/L for thermo-neutral and heat stress condition, respectively, \( P=0.026 \)) although basal insulin concentrations were unaffected by dietary nCrPic (\( P=0.369 \)). However, sheep fed with nCrPic diet had lower plasma insulin responses to the IVGTT (\( P=0.004 \)). Heat stressed animals also had lower insulin responses to IVGTT (\( P=0.015 \)). Taken together these data indicate that dietary nCrPic can improve the ability of sheep to handle heat stress and that at least some of these effects may be via improved insulin sensitivity. These observations need to be extended in lacating dairy cows before recommendations can be made to supplement lactating dairy cows with dietary Crpic when a heat event is imminent. Importantly, (Al-Saiedy et al. 2004) have already shown that dietary Cr increases feed intake and milk production over non-supplemented controls in lactating Holstein dairy cows during periods of high ambient temperature.

**DIETARY BETAINE**

Betaine is a naturally occurring amino acid derivative (tri-methyl glycine) found in many plant and invertebrate species. Physiologically, betaine has an important osmoregulatory action and can serve as a methyl group donor via S-adenosyl-methionine. When incorporated into pig diets, betaine has been reported to improve growth performance by reducing the maintenance energy requirement of the animal (Schrama et al. 2003; Suster et al. 2004). This occurs through reducing the need for sodium/potassium pumping to maintain cellular osmolarity. In addition, dietary betaine has been reported to increase protein deposition and carcass leanness in pigs (Suster et al. 2004; Dunshea et al. 2009) and improve water holding capacity and reduce drip loss in meat (Dunshea et al. 2005). Also, dietary betaine can improve the integrity of gut mucosal cells and reduce the severity of some enteric infections in poultry (Matthews and Southern, 2000; Klasing et al. 2002). (Cronje et al. 2005) has suggested that that heat stress and it’s manifestations is...
a disease of the gut and that dietary betaine may assist by improving gut integrity. There have been fewer studies in ruminants than in pigs and poultry, but there is some evidence that dietary betaine can reduce heat stress and improve feed intake and growth performance in beef cattle (Cronje et al., 2005; Loxton et al., 2007). Importantly, albeit with small numbers (Loxton et al., 2007) found that dietary betaine supplementation reduced the incidence of heat toughening (an indication of heats stress or inability to dissipate heat) from 5/6 carcasses to 1/7 carcasses ($\chi^2=6.8$, $P=0.009$).

Interestingly, there is some evidence from in vitro studies of a complex interplay between extracellular osmolality, betaine and intracellular induction of HSP. Both hypotonicity (Zhang et al., 2003) and hypertonicity (Sheikh-Hamad et al., 1994) induced HSP70 expression in a range of rat tissues and a kidney cell line, respectively. In the latter study, induction of HSP induced by hypertonicity was attenuated by the presence of betaine in the medium, presumably by subsequent accumulation of betaine within the cell normalizing the tonicity between the medium and cytosol. In this same study, betaine inhibited the induction of HSP70 in response to elevated temperature, possibly by stabilizing proteins within the cell. On the hand, betaine increasing expression of heat shock protein during heat stress in primary bovine mammary epithelial cells (BMEC) obtained from pregnant Holstein dairy cows (Xiao et al., 2012). In this latter study, the morphology of control BMECs indicated distinct cell degradation after 8 h of heat exposure, which was absent in 25 mM betaine-treated BMECs. We have conducted a series of studies in sheep, beef cattle and lactating dairy cows to investigate the effects of dietary betaine during heat stress.

In order to quantify some of the physiological impacts of heat stress and dietary betaine on performance, insulin sensitivity and physiology in sheep, (DiGiacomo et al., 2012) conducted a study in controlled environmental rooms. Briefly, the study involved Merino sheep that were subject to one of three diets (0, 2 and 4 g betaine/day) and 2 temperature regimes. The two temperature regimes were thermoneutral (21°C and 57% relative humidity constant over the day) and heat stress (36 °C and 57% relative humidity from 0900 h until 1700 h then declining to thermoneutral) for 3 weeks.

There was a significant main effect of betaine on rectal temperatures such that sheep fed 4 g betaine/day had higher rectal temperatures than those fed 0 and 2 g betaine/day, and those fed 2 g betaine/day had lower rectal temperatures than those fed 0 g betaine/day (Figure 4a) (39.7, 39.6 and 39.8 °C for 0, 2 and 4 g betaine/day respectively, $P<0.001$). There was an interaction between time and treatment such that rectal temperatures from all treatments were highest at 1700 hours, while the sheep supplemented with 4 g betaine/day had higher rectal temperatures than sheep receiving 0 and 2 g betaine/day treatments at all times (39.4, 39.8 and 39.8 °C, vs. 39.3, 39.8 and 39.9 °C vs. 39.5, 39.9 and 40.1 °C for 0, 2 and 4 g betaine/day at 0900, 1300 and 1700 hours respectively, $P<0.001$). There was an interaction between day, temperature and time to alter rectal temperature ($P=0.02$), following the same pattern for these individual factors whereby rectal temperatures were greater in heat stressed sheep, highest at 1700 hours and higher at the end compared to the beginning of the experiment. Rectal temperature increased during week 3 (39.7, 39.7 and 39.8 °C for weeks 1, 2 and 3 respectively, $P=0.02$), although there was an interaction ($P=0.003$) between dietary betaine and week such that the sheep consuming 4 g betaine/day had the highest rectal temperature during week 3, whereas those fed 2 g betaine/day had their lowest rectal temperature in week 3.

Figure 4: Effect of heat load on a/ rectal temperature and b/ respiration rate in sheep during thermoneutral conditions (open symbols) or heat stress (closed symbols). Dietary treatments were either 0 ( ), 2 ( ), or 4 ( ) g betaine per day. See text for details of thermal treatments. The standard error of the difference for the interaction between thermal treatment x diet x time is displayed. See text for significance of main effects and interactions. Data are from DiGiacomo (2011).
Heat treatment increased respiration rate (87 to 134 breaths min\(^{-1}\) for thermoneutral and heat, respectively, \(P<0.001\)) (Figure 4b). Respiration rates were highest at 1700 and lowest at 0900 hours (88, 121 and 124 breaths min\(^{-1}\) for 0900, 1300 and 1700 hours respectively, sed 1.1, \(P<0.001\)). Sheep supplemented with dietary betaine given at a 2 g betaine/day had a decreased respiration rate, and 4 g betaine/day an increased respiration rate (113, 102 and 116 breaths min\(^{-1}\) for control, 2 and 4 g betaine/day respectively, \(P <0.001\)). The maximum respiration rate reached by an individual animal throughout the experiment was 240 breaths min\(^{-1}\) and was achieved on days 17 and 21. There were 1-2 instances of open mouth panting throughout the experiment, although this was not a common occurrence. Respiration rate increased (\(P<0.001\)) over the duration of the study (110 to 117 breaths min\(^{-1}\), for days 1 and 21 respectively). There was no interaction between dietary betaine and heat treatment on respiration rate. There was an interaction between day and heat treatment for respiration rate such that sheep exposed to thermoneutral conditions had consistently lower respiration rates than heat stressed sheep, and while there were daily fluctuations both heat treatments resulted in increased respiration rates on day 21 compared to day 1 of the experiment (85 vs. 93 and 133 vs. 142 breaths min\(^{-1}\) for thermoneutral and heat stress days 1 and 21 respectively). There was also an interaction between day, heat treatment and time (\(P<0.001\)) such that respiration rate were greater in heat stressed sheep, highest at 1700 hours and higher at the end compared to the beginning of the experiment.

The data presented in this experiment demonstrated the novel finding that there are dose responses to dietary betaine supplementation in sheep. At the appropriate concentration, dietary betaine may assist sheep to counter heat stress as dietary betaine supplemented at 2 g betaine/day decreased rectal temperature, respiration rate and heart rate. However, at the higher 4 g betaine/day concentration rectal temperature, respiration rate and heart rate were increased. The high dose of dietary betaine can increase the metabolic heat load, perhaps by increasing hepatic and renal workloads. It is possible that there are different dose response curves for the various functions of betaine that may contribute to the variations in response to betaine. This at lower, betaine may reduce heat production and protect against heat stress whereas at higher doses betaine may stimulate hepatic fatty acid oxidation and increase heat load. Certainly, even higher doses of betaine decrease plasma NEFA indicating either a decrease in lipid mobilisation or an increase in lipid oxidation (DiGiacomo 2011).

In a subsequent study we investigated the effects of betaine during heat stress in lactating dairy cows we conducted a study in environmental chambers at the University of Arizona similar to that outlined previously. Briefly, a total of twenty four (24) healthy Holstein cows sourced from a commercial dairy, free of mastitis, of 90 to 150 days in milk production, and producing 40-45 kg milk per day were assigned to one of 3 dietary treatments. Cows were housed in one of two environmental rooms of the Agricultural Research Complex at the University of Arizona for 31 days. Each room held a maximum of six cows, with the study design using two replicates of 12 cows per replicate. Furthermore, each replicate was assigned a four period experimental design (a 7 day adaptation period, 7 days of thermoneutral conditions, 14 days of heat stress and a 3 day recovery period). Cows were supplemented with either 0, 35 or 75 g betaine per day (Hall et al. 2012).

Dietary betaine increased milk yield and protein % during the thermoneutral period (\(P<0.01\)) but there were no differences between treatments in total milk production or % protein during heat stress. Feed and water intake decreased (\(P<0.01\)) during heat stress with betaine treated. The cows on the control diets had higher pm respiration rates under heat stress (\(P<0.04\)) than those fed betaine, but lower body temperature under heat stress compared to betaine treatments (\(P<0.05\)). Vaginal temperatures were higher in betaine treated cows and were highest in those fed 35g betaine per day. Thus, betaine increased milk and protein production in thermoneutral conditions and was associated with reduced feed and water intake and slightly increased body temperatures during HS at least at the doses tested.

This study showed some positive benefits of betaine in dairy cows under control conditions but not during heat stress. It is possible that the dose of betaine was such that the effects on liver glucose and fatty acid metabolism resulted in increased heat production which counteracted the effect of betaine on acting as an osmolyte and reducing sodium-potassium pumping. The effects on milk yield under thermoneutral conditions were encouraging enough to warrant further work at lower doses to see whether betaine is protective against heat stress in dairy cows. The results from this study need to be more fully explored.

**OTHER DIETARY STRATEGIES**

Heat stress, along with many other stressors such as insulin resistance, can cause oxidative stress and damage. Therefore, there is interest in the use of antioxidants to reduce susceptibility to heat stress. Recently, we have shown that dietary supplementation of sheep with supranutritional levels of inorganic selenium and Vitamin E can improve the ability of sheep to handle heat stress (Chauhan et al. 2012). These results need ot be confirmed in lactating dairy cows.
One means of decreasing the susceptibility of a ruminant animal to heat stress is to reduce the heat of fermentation and the simplest way to do this is to reduce feed intake during under hot conditions (Russell, 2007). Another possible way to decrease the heat of fermentation is to reduce the amount of ruminal fermentation of starch through increasing the amount of starch that escapes ruminal fermentation (Russell, 2007). A problem for Australian dairy farmers is that in most years the most reliable and cheapest grain available is wheat which has a very rapid rate of rument fermentation, especially when compared to maize (Dunshea et al. 2012). A recent study conducted at Ellinbank using infra-red thermography has shown that dairy cows fed wheat-based diets have higher average flank temperatures as well as greater differences between left and right flank temperatures than dairy cows fed maize-based diets (Ian Bland, unpublished observations). Therefore, feeding maize- rather than wheat-based diets may improve the ability of dairy cows to handle heat stress. Alternatively, treating wheat with starch binding agents that reduce the rate of rumen fermentation of wheat may also provide a means of reducing the heat increment of fermentation (Dunshea et al. 2012).

CONCLUSION

We have developed the DRAP to provide a tool for dairy producers to be able to evaluate the likelihood of an imminent heat stress even occurring so that the farmer can then make management decisions to mitigate against heat stress. These decisions may involve management interventions such as providing shade or additional water troughs or implementation of nutritional strategies. Some of these nutritional strategies include dietary CrPic, betaine and antioxidant supplementation or altering the rate of starch fermentation. Dietary CrPic increased feed intake and daily gain during heat stress in sheep while reducing rectal temperature and respiration rate. At least some of the mode of action was through reversing the effect of heat on the antioxidant potential of the sheep. This project will provide farmers the tools to better predict heat stress events using the DRAP and now have some dietary interventions (chromium, betaine and antioxidants) that they can use to mitigate heat stress.

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Supplementation of hand-reared calves with nucleotides from birth to 3 weeks of age and effects on health and immunity

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ABSTRACT

Calf morbidity and mortality is a significant economic problem in the Australian dairy industry. The ability to improve calf health and immunity and reduce subsequent rates of death and disease is therefore vitally important. Dietary supplementation with nucleotides has been shown to be effective in improving health and immunity of young calves, but the results have been variable. This study investigated their effectiveness for improving health and immune responses of calves up to 3 weeks of age. There was no effect of nucleotides on growth, the incidence or severity of diarrhoea, serum IgG concentration, or cellular immunity, but calves supplemented with nucleotides suffered from higher rectal temperatures. Whilst further investigation is warranted, nucleotide supplementation does not affect neonatal calf growth, serum IgG concentration, or cellular immunity, but does influence clinical disease symptoms.

Keywords: Nucleotides; morbidity; diarrhoea; calf immunity

INTRODUCTION

Calf mortality in Australia is between 2 and 10% (Moran, 2002), with morbidity rates higher. High morbidity and mortality places significant economic burden on producers in terms of loss of replacement heifers, treatment of sick calves (Kehoe et al. 2008) and the impact on first lactation productivity (Svensson and Hultgren, 2008). Therefore, improving health and immunity of young calves is vitally important.

Nucleotides are semi-essential nutrients and are required in large amounts by the immune system (Uauy et al. 1990). Two recent studies have investigated dietary supplementation of calves with a mixture of adenine, cytosine and uridine (Kehoe et al. 2008) and the impact on first lactation productivity (Svensson and Hultgren, 2008). Therefore, improving health and immunity of young calves is vitally important.

MATERIALS AND METHODS

Forty purebred Friesian bull calves were obtained at 2-5 days of age from the Department of Primary Industries (DPI) Victoria Ellinbank Centre between July and September 2009. Calves were reared with a maximum of 3 calves per 2.5 x 3.0m pen in a naturally ventilated Ecoshelter® (Redpath Ecoshelters®, Bendigo East, Victoria, Australia) on the La Trobe University Agricultural Reserve (Bundoora, Victoria). Calves were randomly assigned to two treatment groups; control (CON, n = 20) or nucleotides (NUCL, n = 20) and treatments commenced at 5 days of age.

Calves were individually fed Veanavite Full Cream Extra (Rivalea Australia, Corowa, N.S.W.) calf milk replacer (CMR) twice daily at approximately 0800 and 1600 hours, with CON calves fed CMR only and NUCL calves fed CMR plus 1g/feed (2g/day) of mixed nucleotides (Ascogen™, Chemoforma, Augst, Switzerland). Water and oaten hay were available ad libitum and calf meal (Southern Livestock Nutrition, Murgeheboluc, Victoria, Australia) was made available when the oldest calf in the pen was 5 days of age.

Calves were scored daily for rectal temperature, eye and nasal discharge, coughing and faecal consistency, as well as feeding and general behaviours. The percentage of study days on which calves presented with each score was then calculated. Calves were weighed at the commencement of the study and at 10, 14 and 19 – 20 days of age. Blood samples were taken by jugular venipuncture at 5, 14 and 19 – 20 days of age.

Whole blood smears were made for analysis of differential leukocyte counts under oil immersion
with Giemsa-staining and total numbers of leukocytes were determined from whole blood samples within 48 hours. Serum samples were collected from blood clotted for 24 hours at 4°C and centrifuged at 3000 x g for 15 minutes. Serum IgG concentration was measured by capture-ELISA using a Bovine IgG ELISA Quantitation Kit (Bethyl Laboratories Inc., Montgomery, TX, USA).

Statistical differences between groups were analysed using IBM SPSS Statistics 19.0 (‘GradPack’, IBM Corporation, Somers, NY, USA). Data was tested first for normality and analysed using the Independent Samples T-Test when data was normally distributed and the Mann-Whitney U Test when data was not normal. Data was significant when \( p < 0.05 \).

**RESULTS**

Calf liveweight did not differ throughout the study period between CON and NUCL calves and within the first 2 weeks of life, weight gain did not differ between the two groups. Over the 3 week study period, however, NUCL calves had slightly higher weight gain (7.5 ± 0.8 % initial LW), in comparison to CON calves (6.8 ± 0.7 % initial LW), although this was not significantly greater (Table 1).

**Table 1**: Liveweight (kg, LW) and weight gain (% of initial LW) of Friesian bull calves hand-reared from 5 days to 3 weeks of age fed commercial CMR without additives (CON, \( n = 20 \)) or CMR supplemented with mixed nucleotides at 2g/day (NUCL, \( n = 20 \)) (means ± SEM)

<table>
<thead>
<tr>
<th>Liveweight (kg)</th>
<th>Weight gain (% initial LW)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>5 days</td>
</tr>
<tr>
<td>CON</td>
<td>44.3 ± 1.0</td>
</tr>
<tr>
<td>NUCL</td>
<td>43.4 ± 1.1</td>
</tr>
</tbody>
</table>

Faecal consistency was not significantly affected by treatment throughout the study period (Figure 1), although during the first 2 weeks of life, NUCL calves tended to present more often with loose faeces (15.5 ± 3.2%) in comparison to CON calves (10.0 ± 2.7%). There was no significant effect of treatment on the incidence of thin or watery faeces during the first 2-3 weeks of life, although NUCL calves tended to present with thin and watery faeces less often than CON calves (Figure 1).

**Figure 1**: The incidence of total abnormal and loose, thin or watery faecal consistency (% study days, means ± SEM) within the first 2 and 3 weeks of life of Friesian bull calves hand-reared with commercial CMR without additives (CON, \( n = 20 \)), or CMR supplemented with mixed nucleotides at 2g/day (NUCL, \( n = 20 \)).

There were no significant treatment differences in the incidence of eye, or nasal discharge, coughing, feeding, or general behaviours throughout the 3 week study period. By contrast, NUCL calves presented with rectal temperatures of 40.0°C and above on a greater percentage of study days than CON calves (5.9 ± 1.9% vs. 1.0 ± 0.5%, \( P < 0.05 \)). There were no significant differences between groups for the incidence of moderately high (39.5 – 39.9°C) rectal temperatures.
Serum IgG concentration did not differ significantly between CON and NUCL calves throughout the study period, although NUCL calves had slightly lower concentrations initially (8.95 ± 2.08 mg/ml vs. 10.82 ± 1.38 mg/ml) (Figure 2). Although CON calves (-2.77 ± 1.34 mg/ml) had a greater numerical change in serum IgG concentration throughout the 3 week study period in comparison to NUCL calves (-0.88 ± 0.96 mg/ml), the difference was not significant (Figure 2).

There were no significant differences between CON and NUCL calves in numbers of total leukocytes or the percentages of differential leukocyte subsets throughout the study period (Table 2). However, at 14 days of age, CON calves tended to have lower numbers of total leukocytes (73.7 ± 6.5 x10^5/ml whole blood) in comparison to NUCL calves (80.9 ± 6.3 x10^5/ml whole blood). At the same age, CON calves also had a higher percentage of lymphocytes (62.3 ± 4.1 vs. 56.8 ± 4.6%) and a lower percentage of neutrophils (25.2 ± 4.0 vs. 31.5 ± 4.2%) and N:L ratio (0.5 ± 0.1 vs. 0.8 ± 0.2) than NUCL calves. At approximately 3 weeks of age, these results were reversed.

**Table 2:** Total leukocytes (x 10^5)/ml whole blood and percentage of cells per differential leukocyte subset in whole blood of Friesian bull calves hand-reared from 5 days to 3 weeks of age fed CMR without additives (CON, n = 20) or CMR with 2g/day additional nucleotides (NUCL, n = 20) (means ± SEM)

<table>
<thead>
<tr>
<th>Age (Days)</th>
<th>Total Leukocytes (x10^5)/ml whole blood</th>
<th>Lymphocytes (%)</th>
<th>Monocytes (%)</th>
<th>Neutrophils (%)</th>
<th>Basophils (%)</th>
<th>Eosinophils (%)</th>
<th>N:L Ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>CON 58.0 ± 4.7</td>
<td>57.3 ± 3.4</td>
<td>11.0 ± 2.1</td>
<td>31.3 ± 3.8</td>
<td>0.3 ± 0.1</td>
<td>0.2 ± 0.1</td>
<td>0.7 ± 0.1</td>
</tr>
<tr>
<td></td>
<td>NUCL 59.1 ± 5.3</td>
<td>56.5 ± 3.8</td>
<td>14.1 ± 2.0</td>
<td>29.1 ± 4.0</td>
<td>0.3 ± 0.2</td>
<td>0.2 ± 0.1</td>
<td>0.8 ± 0.3</td>
</tr>
<tr>
<td>14</td>
<td>CON 73.7 ± 6.5</td>
<td>62.3 ± 4.1</td>
<td>11.4 ± 2.1</td>
<td>25.2 ± 4.0</td>
<td>0.7 ± 0.3</td>
<td>0.4 ± 0.2</td>
<td>0.5 ± 0.1</td>
</tr>
<tr>
<td></td>
<td>NUCL 80.9 ± 6.3</td>
<td>56.8 ± 4.6</td>
<td>11.1 ± 1.7</td>
<td>31.5 ± 4.2</td>
<td>0.2 ± 0.1</td>
<td>0.4 ± 0.2</td>
<td>0.8 ± 0.2</td>
</tr>
<tr>
<td>19–20</td>
<td>CON 80.8 ± 5.6</td>
<td>59.7 ± 4.5</td>
<td>11.3 ± 1.4</td>
<td>27.4 ± 4.3</td>
<td>0.5 ± 0.3</td>
<td>1.1 ± 0.3</td>
<td>0.8 ± 0.2</td>
</tr>
<tr>
<td></td>
<td>NUCL 74.1 ± 4.5</td>
<td>60.7 ± 4.0</td>
<td>17.2 ± 2.8</td>
<td>21.2 ± 4.0</td>
<td>0.5 ± 0.2</td>
<td>0.4 ± 0.2</td>
<td>0.5 ± 0.1</td>
</tr>
</tbody>
</table>

**DISCUSSION AND CONCLUSION**

The lack of effect on calf growth was consistent with previous work in this laboratory (Kentler, 2012) and that of (Kehoe et al. 2008). In contrast to previous work (Kehoe et al. 2008, Kentler, 2012) however; there was no effect of nucleotide supplementation on faecal consistency. Previous work suggested that nucleotide supplementation was most effective during the first two weeks of life (Kentler, 2012), but the expected reduction in overall abnormal faecal consistency or diarrhoea severity was not seen here. Additionally, (Kehoe et al. 2008) observed reductions in diarrhoea severity from 2-4 weeks of age, but the effect was not evident beyond 4 weeks of age.

Nucleoside transporters located in the brush border membrane of calf intestine are fully functional at birth, with transport capacity and expression genetically fixed and not altered by rumen maturity (Theisinger et al. 2002). Differences in calf genotype, therefore, are likely to alter uptake of supplemental nucleotides and subsequent effects on immune response. Therefore, whilst nucleotide supplementation may effectively reduce diarrhoea severity in some calves (Kehoe et al. 2008, Kentler, 2012), their usefulness for improving disease symptoms may be limited in others.

Although nucleotide supplementation did not affect diarrhoea incidence, rectal temperatures were increased in NUCL calves in comparison to controls. Nucleotide supplementation has been
associated with increased respiratory disease in infants (Hawkes et al. 2006) and increased duration of subclinical disease in calves (Kehoe et al. 2008). An increase in rectal temperature is indicative of clinical disease. However, increased rectal temperature was not accompanied by increased diarrhoea incidence, or severity, or respiratory illness and the relationship between nucleotide supplementation and rectal temperature is difficult to explain. Identification of specific pathogens responsible for disease symptoms in calves would be beneficial in understanding this relationship.

The lack of effect of nucleotide supplementation on circulating IgG and numbers of leukocytes was consistent with previous studies (Kehoe et al. 2008, Hawkes et al. 2006, Kentler, 2012). However, (Mashiko et al. 2009) observed increases in mucosal immune response and positive effects on T-lymphocyte function as a result of nucleotide supplementation. This suggests that whilst nucleotide supplementation did not affect the immune parameters observed in this study, they may exert their effects on other aspects of the immune response.

Further research is necessary to determine the relationship between calf genotype and nucleotide uptake and utilisation and the exact nature of the effect of nucleotides on the immune response requires further investigation. However, it is clear that nucleotide supplementation does not affect growth, cellular immunity, or serum IgG concentration in young dairy calves, and the effect on clinical disease symptoms such as diarrhoea and rectal temperature is variable.

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Treatment of subclinical endometritis in dairy cows with a non-steroidal anti-inflammatory drug

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ABSTRACT

Subclinical endometritis (SCe) is a uterine pathology characterised by an increased proportion of polymorphonuclear cells (PMN) in the uterus postpartum, and is negatively associated with fertility. Recent reports indicate that poorer reproductive outcomes among cows with SCe are associated with local and possibly systemic inflammation, rather than uterine bacteria. Reducing inflammation may therefore be an option to negate the negative effects on reproduction. Normal uterine involution is however, a prostaglandin-mediated inflammatory event. Therefore, the hypothesis tested was that treatment with a non-steroidal anti-inflammatory drug (NSAID), 21-31 days postpartum, would reduce the severity (i.e. average PMN %) of uterine pathology at 42 days postpartum, without lengthening the postpartum anovulatory interval (PPAI). To test this, dairy cows (n = 213) were paired by calving date and Day 14 pmn %, then randomly assigned to treatment with a NSAID (Carprofen 1.4 mg/kg liveweight, n = 103) between 21-31 days postpartum or left as untreated controls (n = 108). In this study, ≥ 14% PMN in the Day 14 cytological sample was defined as SCe. Whilst there was a trend (P=0.09) for fewer SCe treatment cows to have ovulated by day 28 postpartum, NSAID treatment had no effect (P> 0.1) on PMN % at Day 42 or PPAI. The lack of a NSAID treatment effect was possibly because the level of inflammation was too low to detect a treatment response. Therefore, it is concluded in this study where inflammation was low, that a NSAID treatment applied between 21-31 days postpartum was not beneficial.

Keywords: subclinical endometritis; anti-inflammatory; reproduction; dairy cow.

INTRODUCTION

Subclinical endometritis (SCE) is characterised by an increased proportion of polymorphonuclear cells (PMN) in the uterus after calving (Dubuc et al. 2010). Subclinical endometritis is negatively associated with time to first ovulation, submission and conception rate (Barlund et al. 2008; Burke et al. 2010). A recent report indicates that poorer reproductive outcomes among cows with SCE may be associated with local and potentially systemic inflammation, and not necessarily the presence of bacteria in the uterus (McDougall et al. 2011). Studies conducted by (Green et al. 2009) and (Burke et al. 2010) demonstrated that cows with SCE have elevated concentrations of globulin, aspartate aminotransferase and glutamate dehydrogenase, indicating systemic inflammation. These outcomes led to the hypothesis that treatment with a non-steroidal anti-inflammatory drug (NSAID) will improve reproductive outcomes in cows with a high proportion of PMN in the uterus. In this study, this hypothesis was tested using a NSAID that non-selectively inhibits the action of the cyclooxygenase enzyme and prevents the secretion of prostaglandins, which are pro-inflammatory molecules (Sordillo et al. 2009). The timing of NSAID treatment is an important consideration as prostaglandin-mediated inflammation is a normal part of the uterine involution process (Barlund et al. 2008). To allow uterine involution to proceed unimpeded, treatment was delayed until 21-31 days postpartum. Therefore, the specific hypothesis tested was that treatment with a NSAID, 21-31 days postpartum, would reduce the average PMN % of uterine pathology at 42 days postpartum, without lengthening the postpartum anovulatory interval (PPAI).

MATERIALS AND METHODS

Experimental design

A total of 213 multiparous cows (Holstein-Friesian, n=136; Holstein-Friesian x Jersey, n=77) from Scott Farm (DairyNZ), Hamilton were used in this study between May and October 2011 with an average age of 5.4 ± 2.16 years and a live weight of 445 ± 56.3 kg. Prior approval for animal use was obtained from the Ruakura Animal Ethics Committee, Hamilton, New Zealand (# 12294). The cows grazed a ryegrass-white clover pasture mix with a target post-grazing residual of 1,600 kg DM/ha, and were supplemented with maize silage and grass silage.

To ensure that the control and NSAID treatment groups were balanced for PMN %, a uterine cytology sample was taken at 14 days postpartum. Using
a randomised block design, cows were paired by calving date and Day 14 PMN % before being randomly allocated to either the control or NSAID treatment group.

**Uterine cytology**

Uterine endometrial cytology samples were collected and analysed, as described by (Burke *et al.* 2010), on days 14-17 (Day 14) and days 42-45 (Day 42) postpartum. Cows were defined as having SCE if the uterine cytology sample had ≥14% PMN at Day 14, or >7% at Day 42. Cure of SCE (SCE cure rate) was defined as a cow that had SCE at Day 14 but that had ≤7% PMN at Day 42.

**Anti-inflammatory treatment**

The NSAID used was Carprieve LA (Norbrook NZ Ltd, Auckland, New Zealand: active ingredient Carprofen 50 mg/mL). Carprofen has an estimated plasma half-life of 45-65 hours (NZFSA 2010); therefore, to get an extended period of anti-inflammatory action, the treatment was administered in three doses (1.4 mg/kg liveweight) over a 9-day period between 21-31 days postpartum. The most recent live weight was used to calculate the correct drug dose.

**Postpartum anovulatory interval**

Progesterone was measured in plasma collected weekly from 3 to 54 days postpartum and was analysed using an RIA kit (Progesterone Coat-a Count, Siemens., Los Angeles, CA). The average intra-assay co-efficient of variance was 10.2% and the minimum detectable level was 0.08 ng/mL. Progesterone data were used to determine the PPAI, which was defined as the interval from calving to the first sample day that plasma progesterone concentration was ≥ 1 ng/mL.

**Statistical analysis**

The Day 14 and Day 42 PMN % were analysed using linear models. Angular transformation of PMN % was used for analyses but the raw means are presented to help with interpretation as the conclusions were similar.

For the rest of the statistical analyses, a PMN group was calculated using the Day 14 PMN % results and included in the analyses as a fixed effect: High PMN group (top 25%, n=53, PMN ≥14%), Medium PMN group (middle 50%, n=105, PMN 2-13%), and Low PMN group (bottom 25%, n=53, PMN ≤1%). To illustrate possible associations of PMN group, only the Low (healthy cows) and the High PMN (SCE cows) group data will be presented as the conclusions are similar.

The proportion of cows ovulated by a specified date postpartum was analysed using generalised linear models with binomial error distribution. The PPAI was analysed using a proportional hazards regression, a method of survival analysis. A significant effect for all results was declared at $P <0.05$.

**RESULTS**

**Polymorphonuclear cell percentage**

The distribution of PMN % for Day 14 and Day 42 postpartum for all cows is presented in Figure 1. The average Day 14 PMN % was 9.9%. Average PMN % at Day 42 was not affected by the NSAID treatment, 1.4% and 1.7% for the control and the NSAID group respectively (SED = 0.5). The SCE cure rate for the control and NSAID group was 92.3% and 96.3% respectively.

![Figure 1: Polymorphonuclear cell (PMN) percentage distribution for all cows from Day 14 and Day 42 uterine endometrial cytology samples.](image)

**Postpartum anovulatory interval**

There was a trend ($P=0.09$) for the High PMN group to have a lower proportion of cows ovulated by 28 days postpartum (Table 1), but not at any other measurement times. The NSAID treatment had no effect on the proportion of cows ovulated by a specified date postpartum (Table 1), and no interactions between Day 14 PMN % and treatment were detected. Survival analysis results demonstrate that there was no effect of the NSAID treatment on PPAI, and no association between PMN group and PPAI ($P>0.1$).

**DISCUSSION AND CONCLUSION**

In this study, NSAID treatment had no effect on the average Day 42 PMN % or on PPAI. Results do not support the hypothesis that a NSAID treatment from Day 21 is beneficial for reducing PMN %, but indicate that NSAID does not negatively affect PPAI when administered at this time postpartum.
Table 1: Association between Day 14 polymorphonuclear cell group, and the effect of treatment on, the proportion of cows ovulating (progesterone \(\geq 1\) ng/ml) by the specified days postpartum

<table>
<thead>
<tr>
<th>Days</th>
<th>Group</th>
<th>SED</th>
<th>P-value</th>
<th>Group</th>
<th>SED</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>21</td>
<td>Low PMN</td>
<td>0.13</td>
<td>0.06</td>
<td>Control</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>28</td>
<td>Low PMN</td>
<td>0.36</td>
<td>0.09</td>
<td>NSAID</td>
<td>0.15</td>
<td>0.05</td>
</tr>
<tr>
<td>35</td>
<td>High PMN</td>
<td>0.53</td>
<td>0.10</td>
<td>NSAID</td>
<td>0.32</td>
<td>0.07</td>
</tr>
<tr>
<td>42</td>
<td>High PMN</td>
<td>0.60</td>
<td>0.19</td>
<td>NSAID</td>
<td>0.45</td>
<td>0.07</td>
</tr>
<tr>
<td>45</td>
<td>High PMN</td>
<td>0.65</td>
<td>0.33</td>
<td>NSAID</td>
<td>0.46</td>
<td>0.07</td>
</tr>
</tbody>
</table>

1Days postpartum
2The polymorphonuclear cell (PMN) group from uterine samples collected on Day 14 postpartum; Low PMN = Low PMN group (\(\leq 1\%\) PMN); High PMN = High PMN group (\(\geq 14\%\) PMN)
3NSAID = non-steroidal anti-inflammatory drug

The lack of treatment effect for all variables investigated may have been the consequence of the low average Day 14 PMN %, and the high self-cure rate by Day 42 (>90% in control cows). Based on results from a previous study (Meier and Burke, unpublished data), it was expected that approximately 30% of the cows would have a PMN % greater than 18% at Day 14 postpartum (18% is the PMN cut-off most commonly used for uterine samples taken early postpartum (Kasimanickam et al. 2004; Green et al. 2009)). However only 19% of cows had a PMN % greater than 18% at Day 14 in the current study. Therefore, the failure to detect an effect of NSAID in the current study may have been due to the level of inflammation being too low to detect a treatment response.

Additionally, the NSAID treatment may have been applied too late in the postpartum period to be beneficial. There was a tendency for a negative association between SCE (as assessed by Day 14 PMN % in this study) and the proportion of cows ovulated by 28 days postpartum; therefore the treatment may have had a beneficial effect if applied earlier in the postpartum period. To support this hypothesis, cows treated with aspirin (a NSAID) for the first five days postpartum by Trevisi and Bertoni (2008) had a greater first-service conception rate and required less services per conception than untreated cows.

There was no negative association between Day 14 PMN % and PPAI, which is in contrast to the negative association between PMN % and PPAI reported by (Burke et al. 2010). A possible reason for the lack of association is that the level of inflammation in this study may have been too low to detect a difference between the PMN groups, or too low to affect PPAI.

In conclusion, in this study with a low level of inflammation in the studied cows, a NSAID applied between 21-31 days postpartum was not an effective treatment to reduce uterine inflammation at 42 days postpartum. The lack of treatment effect in the current study may have been due to a lower than expected level of inflammation (as indicated by PMN %), the high self-cure rate or the delayed timing of the NSAID treatment relative to calving date. However, the results demonstrate that a NSAID applied at this time does not negatively affect PPAI.

**ACKNOWLEDGEMENTS**

The authors thank the DairyNZ Scott Farm staff and technicians for their assistance with data collection, Barbara Dow for statistical analysis assistance, and Kelly Buckle for cytology microscopy (IVaBS, Massey University, Palmerston North, New Zealand). This research was funded by New Zealand dairy farmers through DairyNZ Inc (AN808) and the Ministry of Business, Innovation and Employment (UOAX0814).

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Innate immune proteins as biomarkers for mastitis and endometritis

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ABSTRACT

Subclinical infections of the mammary gland and reproductive tract of dairy cattle cause significant production losses through decreased milk yield and lowered fertility. In the absence of overt signs of infection, there are no simple, reliable, diagnostic tools to accurately identify cows with these conditions, some of which may progress to a clinical stage at a later date. A search was undertaken to identify proteins in milk and reproductive tract secretions that could serve as the basis for a biomarker-based diagnostic test. A 2D gel-based proteomic analysis of milk and of uterine secretions revealed a number of proteins whose abundance was altered with mastitis or endometritis. Western blotting and ELISA indicated that the levels of two of these proteins, the cathelicidins and S100A12 were increased 25 ± 3 fold, and 29 ± 6 fold, respectively, in milk from 8 cows with clinical mastitis, compared with milk from uninfected quarters. The levels of these proteins correlated strongly with somatic cell count in the milk (r=0.85 and 0.93 for cathelicidin and S100A12, respectively). Changes in milk lactoferrin were less dramatic (7.9 ± 0.2 fold). In the uterine secretions, cathelicidins and S100A9 were increased (2 and 3-fold, P> 0.001; respectively) in secretions from cows with uterine infections, as assessed by uterine cytology, and were correlated (r = 0.87 and 0.64, respectively) with the percent of neutrophils in uterine cytological samples. Cathelicidins and S100 proteins may have value as a basis for screening cattle for mucosal infections.

Keywords: Mammary; uterine; bovine; infection; inflammation; lactoferrin; cathelicidin; S100;

INTRODUCTION

Mastitis and post-partum endometritis are two of the most significant infectious diseases of cattle. Mastitis is a significant economic cost to dairy industries worldwide (Viguier et al. 2009), while endometritis causes reduced fertility, with consequent loss of genetic gain through culling of empty cows (LeBlanc 2008). Mastitis is normally first detected through clinical signs and confirmed through a positive Rapid Mastitis Test, or through elevated Somatic Cell Count (SCC) in a herd test sample. Delayed detection can lead to a more prolonged course of treatment and reduced milk production. Similarly, sub-clinical endometritis can be difficult to diagnose but results in delayed return to oestrus, reduced conception rates, and failure to conceive if unresolved. There are currently no sensitive and reliable tests suitable for screening herds for “pre-clinical” mammary gland or reproductive tract infections (i.e. infections that are asymptomatic but may progress to more serious disease if host natural defences are inadequate to control them). There is, therefore, a need for improved methods to screen herds for early onset or pre-clinical mastitis (Viguier et al. 2009).

The presence of pathogens on mucosal surfaces results in the induction of a range of responses by the host aimed at controlling the incipient infection. These include the production of molecules that mediate local and systemic responses as well as stimulation of secretion of a range of antimicrobial proteins and peptides (Smolenski et al. 2007; Boehmer et al. 2010; Ibeagha-Awemu et al. 2010; Wheeler et al. 2012). These responses have only been partially characterised (Wheeler et al. 2012). A proteomics-based approach was used to identify proteins secreted into milk or in reproductive tract secretions during an infection, together with a preliminary evaluation of their merit as biomarkers.

MATERIALS AND METHODS

Five Holstein-Friesian dairy cows in mid-lactation were experimentally infected in two of their udder quarters by inoculation with Streptococcus uberis via the teat, using previously described procedures (Smolenski et al. 2011). Approval was obtained from the Ruakura Animal Ethics committee. Milk was collected from all quarters prior to inoculation and from the nine infected quarters at the first milking at which clinical signs of mastitis first appeared, which ranged from 24-48 h after inoculation. A sub-sample from each quarter was analysed for SCC, using a commercial service, and a second sample was collected aseptically for bacteriological analysis to confirm infection status. A sub-sample of each was also stored for protein analysis. The remainder of the samples were processed to create separate pools of whey and milk fat globule membrane proteins, as previously described (Smolenski et al. 2007). Milk samples
were also collected from the infected quarter in eight cases of naturally-occurring mastitis at the time of first diagnosis. These samples were analysed for SCC and the presence of mastitis pathogens, and a subsample analysed for protein variables. Quarters were infected with a range of pathogens, including *S. uberis*, *P. aeruginosa*, *S. aureus*, *S. dysgalactiae*, coagulase-negative *Staphylococcus* and *E. coli*. The uterine status of each of 46 multiparous cows without overt clinical endometritis was assessed approximately 3 wk post-partum by taking samples within the uterus using cytobrushes. The recovered material was spread on microscope slides, fixed and stained with Giemsa stain, and the proportion of polymorphonuclear neutrophils (%pmn) amongst the somatic cells determined by a trained cytologist. The cytobrush was then washed with 1 ml of buffered saline and the cells pelleted. The supernatants were subjected to western blot analysis.

The pools of individual whey and milk fat globule membrane samples from uninfected and infected quarters, and representative uterine samples with <5% and > 30% PMN were subjected to 2D electrophoresis (two gels per sample) and the protein spots visualised by Coomassie staining, as previously described (Smolenski et al. 2007). The 2D gel images were captured using a scanning densitometer (GS-800, Bio-Rad) and the spots quantified using the PDQuest software package (Bio-Rad). Spots that appeared by visual inspection to be altered in abundance were excised, subjected to MALDI-TOF mass spectrometry and the mass spectra used to address the NCBI non-redundant mammalian amino acid sequence database, restricted to bovine using the MASCOT software package.

For western blot analysis, the milk and uterine fluid samples were subjected to SDS polyacrylamide gel electrophoresis, the proteins transferred to nitrocellulose membranes, and selected proteins were detected by incubation with antibodies raised against them, following previously described procedures (Smolenski et al. 2011). The blots were probed with the following antibodies; an anti-bovine lactoferrin IgG (Bethyl Laboratories), IgG directed against the cathelin domain that is common to all bovine cathelicidins, IgG directed against bovine S100A9 and IgG directed against S100A12. All but the lactoferrin antibody were raised in rabbits using synthesised peptides as immunogens, according to standard procedures. A direct ELISA was developed in-house. Briefly, 0.1 ml of sample (10-fold dilution of milk) or protein standard in diluted milk matrix was coated on the surface of the plate, washed and probed with an anti-cathelicidin nanobody expressed in M13 bacteriophage. After washing, the signal was detected using a peroxidase-conjugated anti-M13 secondary antibody (GE Healthcare). An intra-assay CV of 15% with a linear range of 20-120 ng/ml was obtained.

The relative abundance of individual proteins was estimated by capturing chemiluminescence signals from the western blots using a CCD camera-based instrument (Chemi-Doc, Bio-Rad). The intensity of each signal was determined by densitometry using the QuantityOne software package (Bio-Rad) and the result expressed as fold change, relative to the milk sample from the same quarter before inoculation or an uninfected quarter, in the case of naturally occurring mastitis. For the uterine proteins, signal intensities were plotted against %PMN in the cytology samples. Correlation analyses was undertaken using the statistical functions within Microsoft Excel 2010.

**RESULTS**

Visual inspection of the 2D gels of pooled milk fraction samples from experimentally infected quarters or from the same quarters before inoculation resulted in 123 spots that appeared to be consistently altered greater than two-fold in abundance between the uninfected and infected milk samples. Mass spectrometry of these excised spots resulted in the positive identification of 41 distinct proteins. The change in abundance of lactoferrin, cathelicidin and S100 family members were particularly prominent. A similar 2D gel analysis of reproductive tract secretions resulted in ten spots that were apparently altered in abundance between the low and high %PMN samples. Mass spectrometry identified four of these proteins to be lactoferrin, S100A9, peptidoglycan recognition protein 1 (PGLYP1) and cathelicidin family members.

Western blot analysis of the nine individual milk samples from inoculated quarters taken before and after the inoculation with *S. uberis*, confirmed that lactoferrin, cathelicidins, S100A9 and S100A12 were consistently increased in abundance in milk collected during a mastitis infection (Figure 1). Western blotting of the post-partum uterine proteins from the 46 animals revealed large variability in the abundance of lactoferrin, PGLYP1, cathelicidins, and S100A9 between the samples. Representative western blots of 15 samples are presented in Figure 2.

Quantification analysis indicate that cathelicidin and S100A12 responded particularly robustly to infection (25 ± 3 fold, and 29 ± 6 fold, respectively). The abundance of cathelicidin concentrations in milk were highly correlated (r = 0.87) with SCC, for both naturally occurring and experimentally induced mastitis (Figure 3). Similarly, S100A12 levels were highly correlated with SCC (r = 0.88).
Lactoferrin concentration, on the other hand, was increased to a much lesser extent (7.9 ± 0.2 fold) and was poorly correlated with SCC (r = 0.40). In the uterine samples, the cathelicidins and S100A9 were increased (2 and 3-fold, P> 0.001; respectively) in secretions with greater than 30% PMN. The levels of the cathelicidins (Figure 4) and S100A9 correlated with the abundance of neutrophils in the uterine cytological samples (r = 0.87 and 0.64, respectively). Changes in lactoferrin were not as marked and were not correlated with %PMN.

**DISCUSSION AND CONCLUSION**

Results confirm earlier studies, wherein milk lactoferrin and cathelicidin concentrations were increased during mammary infection (Smolenski et al. 2011; Harmon et al. 1975), and extend a previous report that the S100 family of proteins are present in milk during mastitis (Lutzow et al. 2008). Lactoferrin is also known to be expressed in the reproductive tract in response to steroid hormones of the oestrous cycle (Dixon and Gibbons 1979). However, this is the first report quantifying and comparing the responses of these proteins to infections in the mammary gland with those in the reproductive tract.

The responses of the individual proteins to infection are distinct between the mammary gland and uterus. This is most likely because they are secreted from different cell types in response to different signals. Cathelicidins and S100 family members are known to be present in neutrophils (Lippolis and Reinhardt 2005), explaining the high correlation of their abundance with SCC in milk and %PMN in reproductive tract secretions. On the other hand, lactoferrin is produced by a wider range of cell types (Teng 2002) and has a relatively high basal abundance in milk, lesser responsiveness to infection and possible responsiveness to steroid hormones in some tissues. This may explain the lack of a significant correlation with SCC in milk or %PMN in reproductive tract secretions in this study.

The data presented here provide candidate biomarkers that could be used in conjunction with SCC and conductivity (for mastitis), and cytological assessment (for endometritis) to better inform cow management decisions. It is possible that the use of several biomarkers in parallel may provide more specific diagnostic information than is possible with a single biomarker. Such an approach could provide additional information on the stage of infection or type of pathogen involved. Further work could address this possibility. The commonality of responses between infections in the mammary gland and uterus suggests that diagnostic information could be produced for both mastitis and endometritis, using a single technological platform. Further research is warranted to evaluate the potential of the cathelicidins and S100 family members in the diagnosis of mammary and uterine infections.

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Advantages of using lactation length, mating and pregnancy data to improve the genetic evaluation of fertility based on calving interval in dairy cows

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2Dairy Futures Cooperative Research Centre, Bundoora, Vic, 3083, Australia

ABSTRACT

Due to lack of good quality fertility data on large numbers of cows, genetic evaluation for fertility in Australian dairy cattle is based on calving interval (CI) and days from calving to first service (CFS) interval. In this study the advantages of using additional traits such as lactation length (LL) and mating and pregnancy data were assessed. The genetic correlation of fertility traits such as CFS, first service non-return rate and pregnancy rate with CI was strong. LL was also highly correlated with CI suggesting that it can be used instead of CI for cows that do not calve again. The use of the additional fertility traits and LL increased the reliability of sires’ estimated breeding values from 33% (when only CI was used) to 38% (when all traits were used) for sires with 30 or more daughters. Implementing a multi-trait genetic evaluation could help to improve the reliability of sire EBVs for these traits and thus minimise the ongoing genetic deterioration in fertility traits in Australian dairy cattle.

Keywords: fertility traits; correlations; breeding values.

INTRODUCTION

Fertility levels in dairy cattle have been declining (e.g. Liu et al. 2008; Sun et al. 2010; InCalf Project, 2011). Recent estimates show that both protein yield and CI have increased by about 1 kg and 0.5 days per annum respectively, over the past decade in Australian Holstein cattle (Australian Dairy Herd Improvement Scheme: ADHIS). The impact of low fertility on profitability in seasonal calving herd is twice that in year-round calving herds (Haile-Mariam et al. 2010). Selecting for fertility by including it in the total profit index, can help to stop the downward genetic trend and assist in achieving compact seasonal calving and breeding patterns.

Genetic evaluation for fertility in Australia is currently based on calving interval (CI) and days from calving to first service interval (CFS) because data on other fertility traits are not available on a sufficiently large number of cows. CI can be determined for herd recorded cows that have calved at least twice. However, cows with poor fertility are often culled before they calve again, which biases estimated breeding values (EBVs) of bulls. Recent ADHIS data show that when the evaluation is based on CI up to 85% of the non-pregnant cows that do not re-calve are excluded (unpublished data). The exclusion of cows that do not calve again from the genetic evaluation could also contribute to the already low reliability of sire EBVs for fertility.

The objective of this analysis was to identify a set of fertility and other indicator traits that can complement genetic evaluation on CI by helping to minimise the inherent bias in it and thereby increasing the reliability of bulls EBVs. The study assessed the improvement in reliability of fertility evaluation as a result of using lactation length (LL), mating and pregnancy data in a multi-trait genetic fertility evaluation.

MATERIAL AND METHODS

Calving, LL, pregnancy and mating data of cows were extracted from the ADHIS database. Calving records between January 1998 and July 2011 were selected. However, no pregnancy data were recorded before 2000 and most cows that calved after 2009 did not have CI because they did not re-calve or their re-calving data did not reach ADHIS by July 2011. Bulls used in the artificial insemination programs with at least 5 daughters were included in the study. Traits considered for the study were CI, LL, pregnancy rate (PR), CFS and 25-day first service non-return rate (FNRR). CFS measures the ability of cows to show heat early after calving and FNRR measures the ability of cows to conceive when mated. The decision to consider all matings recorded throughout the mating season (rather than those within a specific period) was based on earlier analyses of In-Calf data which showed higher heritability (h2) estimates when all matings were considered (Haile-Mariam et al. 2003). All cows with at least one valid record for one of the traits were included in the analyses with missing data for other traits. CI, LL and CFS longer than 500, 450 and 210 days were set at the maximum of 501, 451 and 211 days, respectively. This was done assuming that the reasons for extremely longer intervals are environmental rather than due to genetics. For the study, three different analyses were
performed. First, genetic parameters were estimated based on a five-trait model fitting herd-year-season of calving, month of calving or mating and age at calving as fixed effects and sire with relationship as a random effect. Secondly using genetic parameters estimated above, EBVs were calculated based on 1st crop daughters (i.e. daughters of progeny test bulls) using: Model 1: CI only; Model 2: CI and CFS; Model 3: CI and LL; Model 4: CI, LL and CFS; Model 5: CI LL, CFS and PR; Model 6: CI LL, CFS, PR and FNRR. Reliability of bulls’ EBVs from the prediction error variance were calculated for bulls with ≥ 30 daughters with CI records to assess the increase in reliability due to the inclusion of additional fertility and predictor traits. Thirdly, to compare the predictive ability of the different models, EBVs were calculated using the 5-trait model (Model 6) based on data of all daughters except 1st crop (i.e. 2nd crop and later). Then, correlations were calculated between EBVs for CI from this 5-trait model (2nd crop and later) and those from models 1 to 6 for CI (1st crop daughters). For EBV calculations, an animal model including all relationships was fitted in addition to the fixed effects used in the model to estimate genetic parameters. All data were analysed using ASReml (Gilmour et al. 2009).

**RESULTS**

Summary statistics are presented in Table 1; showing that of the cows with previous calving dates a large number of cows did not have PR and mating data. Of importance, is that the proportion of cows with PR data has more than doubled between 2003 and 2009. Over the years the means for the interval traits such CI, LL and CFS have increased steadily showing a deterioration in fertility. These increases also partly reflect the increase in proportion, over recent years, of herds that practice extended lactation. The h² estimates of the traits varied from as low as 0.02 for first service non-return rate to 0.04 for PR, CI and LL (Table 2). Genetic correlations of CI with LL, CFS, PR and FNRR were strong; particularly, the genetic and environmental correlations between CI and LL which were both high. This suggests that LL can be used as predictor of CI for cows that do not calve again. Residual correlations between CI and other traits except LL were lower than genetic correlations.

**Table 1:** Means and standard deviations (SD) plus proportion of cows with valid records (Prop) used for analyses of fertility traits over the study period 1998 to 2009

<table>
<thead>
<tr>
<th>Traits</th>
<th>1998</th>
<th>2003</th>
<th>2009</th>
</tr>
</thead>
<tbody>
<tr>
<td>CI, days</td>
<td>386</td>
<td>50</td>
<td>71</td>
</tr>
<tr>
<td>LL, days</td>
<td>333</td>
<td>46</td>
<td>56</td>
</tr>
<tr>
<td>CFS, days</td>
<td>76</td>
<td>27</td>
<td>12</td>
</tr>
<tr>
<td>PR (%)</td>
<td>-</td>
<td>-</td>
<td>0</td>
</tr>
<tr>
<td>FNRR %</td>
<td>57</td>
<td>50</td>
<td>8</td>
</tr>
</tbody>
</table>

CI=calving interval; LL=lactation length; CFS=calving to first service; PR=pregnancy rate; FNRR=first service non-return rate.

**Table 2:** Genetic parameters for the multi-trait fertility model (genetic correlations above diagonal, heritabilities in bold on the diagonal and residual correlations below diagonal)

<table>
<thead>
<tr>
<th>Traits</th>
<th>CI</th>
<th>LL</th>
<th>CFS</th>
<th>PR</th>
<th>FNRR</th>
</tr>
</thead>
<tbody>
<tr>
<td>CI, days</td>
<td>0.04</td>
<td>0.94</td>
<td>0.68</td>
<td>-0.89</td>
<td>-0.66</td>
</tr>
<tr>
<td>LL, days</td>
<td>0.84</td>
<td>0.03</td>
<td>0.64</td>
<td>-0.79</td>
<td>-0.62</td>
</tr>
<tr>
<td>CFS, days</td>
<td>0.50</td>
<td>0.35</td>
<td>0.02</td>
<td>-0.74</td>
<td>-0.33</td>
</tr>
<tr>
<td>PR (%)</td>
<td>-0.49</td>
<td>-0.34</td>
<td>-0.01</td>
<td>0.04</td>
<td>0.70</td>
</tr>
<tr>
<td>FNRR %</td>
<td>-0.39</td>
<td>-0.32</td>
<td>0.04</td>
<td>0.13</td>
<td>0.02</td>
</tr>
<tr>
<td>Phen. Var.</td>
<td>2451.2</td>
<td>2174.5</td>
<td>450.7</td>
<td>948.5</td>
<td>2227.3</td>
</tr>
</tbody>
</table>

CI=calving interval; LL=lactation length; CFS=calving to first service; PR=pregnancy rate; FNRR=first service non-return rate.
For young bulls with ≥ 30 first crop daughters, the EBV reliability for CI increased from an average of 33% when only CI data was used to 38% when CI was analysed with the other fertility and predictor traits (Table 3). When bulls with ≥ 60 progeny were considered the increase in reliability of EBVs also showed the same trend with the addition of more traits (results not presented). In both situations this improvement in reliability is mainly due to including LL because about 11% of the cows in the dataset had only LL. The advantage of including the partially recorded fertility traits such as PR and CFS was to improve the timeliness of the EBVs for fertility. Another advantage of the use of a multi-trait model was that the standard deviation of sire EBVs for CI increased by up to 13% showing that the scope for selection can be increased by multi-trait analyses of CI. When the rank correlation between EBVs of bulls for CI from 1st and 2nd crop daughters was used as a measure of predictive ability of models, the correlations increased in accordance with the number of traits included in the model (Table 3). Again, LL was largely responsible for this increase.

**DISCUSSION AND CONCLUSION**

The h² of the all the traits included in the multi-trait model is low and in agreement with the literature (Haile-Mariam et al. 2003; Liu et al. 2008). Higher h² values for traits such as CI, CFS, FNRR, etc. were reported by (Sun et al. 2010). The main reasons for including these traits in the multi-trait model are that they can be used instead of CI (e.g. LL) for cows that do not calve again and are measures that can be recorded before CI (PR, CFS and FNRR) and can thus improve the timing of genetic evaluations for fertility. Also traits such as PR, CFS and FNRR could be available on cows that do not calve again. The improvement in the reliability of EBVs for CI of bulls as a result of multi-trait models is largely because those cows that did not have CI data will generally have some other fertility or LL data. Thus the EBVs produced will be more reliable and less biased compared to EBVs from using CI only. These results compare favourably to those of (Sun et al. 2010) where a multi-trait analyses involving 4 fertility traits increased reliability only marginally when all traits are recorded on all cows.

The increase in reliability of sire EBVs in Table 3 are comparable to those observed by (Sun et al. 2010) where they analysed fertility traits with milk yield traits. In the current study milk yield was not used as predictor of fertility because the genetic correlations between milk yield and some fertility traits can be influenced by management decisions. For example, the correlation of milk yield with traits such as CI and CFS are stronger (0.41) than those with PR and FNRR (-0.18); traits less affected by management (Haile-Mariam et al. 2012). This perhaps suggests that factors other than poor fertility such as high milk yield and the desire of farmers to delay mating to maximise milk output may also lead to longer CI. Using the correlation between CI and milk yield to predict fertility could have the unintended effect of partially discounting the value of animals with high genetic potential for milk. Any advantage that will be gained from using milk yield can be captured by including LL in the multi-trait models as the genetic correlation between LL and milk yield is reasonably high (Haile-Mariam et al. 2012).

**Table 3:** Reliability of sire EBVs for CI based on 1st crop daughters from different models (1 to 6) and correlation between EBVs for CI from 1st crop daughters estimated using different models (1 to 6) and from 2nd crop daughters using model 6

<table>
<thead>
<tr>
<th>Traits in the model</th>
<th>Reliability</th>
<th>Correlations</th>
</tr>
</thead>
<tbody>
<tr>
<td>CI only</td>
<td>0.33</td>
<td>0.72</td>
</tr>
<tr>
<td>CI, CFS</td>
<td>0.34</td>
<td>0.72</td>
</tr>
<tr>
<td>CI, LL</td>
<td>0.37</td>
<td>0.74</td>
</tr>
<tr>
<td>CI, CFS, LL</td>
<td>0.38</td>
<td>0.74</td>
</tr>
<tr>
<td>CI, CFS, LL, PR</td>
<td>0.38</td>
<td>0.75</td>
</tr>
<tr>
<td>All 5 traits</td>
<td>0.38</td>
<td>0.75</td>
</tr>
</tbody>
</table>

¹CI=calving interval; LL=lactation length; CFS=calving to first service; PR=pregnancy rate; FNRR=first service non-return rate.

²For 2337 sires ≥ 30 daughters.

³Based on EBV of 190 sires with ≥ 30 first crop and ≥ 60 second crop and later daughters.

In countries where a seasonal calving system is practiced and where cows are normally inseminated over a relatively short time period, the usefulness of traits such as non-return rate is believed to be limited (Harris et al. 2005). However, in the current analyses it was observed that FNRR could be a useful addition for predicting fertility. The genetic correlation between CI and FNRR was -0.66 (Table 2), similar to the correlation between CI and 6-week In-calf rate (Haile-Mariam et al. 2003). In that study, we also found that FNRR has a genetic correlation of 0.86 with 6-week In-calf rate, which is similar to the genetic correlation between FNRR and PR in the current study. The h² of FNRR in both the current and previous analyses (Haile-Mariam et al. 2003) are similar to those reported in the literature (Liu et al. 2008; Sun et al. 2010).

In conclusion, if cows that are culled due to poor
fertility, their information on LL and other fertility traits can be used to predict a fertility EBV of their sires that is less biased and more reliable than when using CI only. The use of pregnancy and mating data means that more reliable EBVs on fertility will be available to the dairy industry as a tool to reduce genetic deterioration in fertility. Further increases in reliability of EBVs and more opportunity for improving the fertility of the national herds is possible if the quality and quantity of the fertility data that reaches the ADHIS improves. More mating and pregnancy data can also be used as a tool to improve fertility management at the farm level.

ACKNOWLEDGEMENTS

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Reproductive performance of dairy cows in a pasture based Automatic Milking System research farm: a retrospective analysis

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ABSTRACT

A retrospective study of 365 cows with 798 lactations was conducted to identify the production and health traits associated with reproductive outcome variables in an Automatic Milking System (AMS) research farm. Generalised linear mixed model analyses were performed to determine the factors associated with the outcome variables (100-day pregnancy rate and conception within two inseminations). In 36% of lactations, cows were pregnant by 100 days in milk (DIM) and in 75% of lactations, cows had conceived within two inseminations. Cows that were first inseminated after d 79 of lactation were less likely (odds ratio: 0.18, \(P < 0.001\)) to be pregnant by 100 DIM compared with cows first inseminated before d 79 of lactation. Moreover, cows that showed first oestrus after d 57 of lactation had a reduced likelihood (odds ratio: 0.57) of being pregnant by 100 DIM compared with cows showing first oestrus before d 57 of lactation. Cows that were producing milk with a fat to protein ratio in the range of 1.21 to 1.30 had the highest odds (odds ratio 2.0) of conceiving compared to cows that were producing milk with a fat to protein ratio less than (or equals to) 1.09. Cows in the bottom two quartile of milk production (100-day cumulative milk yield of 1950 kg or less) were less likely (\(P < 0.05\)) to conceive within two inseminations compared with cows producing more than 2521 kg. Cows were more likely to be pregnant by 100 DIM if they were detected in oestrus and inseminated sooner, and were not within the bottom two quartiles for milk production.

Keywords: reproduction; automatic milking system; pregnancy rate; conception.

INTRODUCTION

Automatic milking systems (AMS) are becoming increasingly popular due to the growing costs of labour, reduced labour availability and increased desire for improved lifestyle in many dairy countries (Lind et al. 2000). Whilst there have been some studies (Kruip et al. 2000; Kruip et al. 2002; Weiss et al. 2004) conducted to determine the reproductive performance and to identify predictor variables affecting reproduction in AMS in intensive housing systems, the findings have been variable and cannot necessarily be extrapolated to pasture-based systems. Therefore, we analysed a 5-year dataset from an AMS research farm to quantify the reproductive performance as described by the outcome variables; 100-day pregnancy rate and conception rate within two inseminations. In addition we aimed to identify predictor variables affecting these two outcome variables.

MATERIALS AND METHODOLOGY

The dataset from the AMS research farm (Elizabeth Macarthur Agricultural Institute, Camden, Australia) was comprised of 798 lactations from 365 cows for the period 1 April 2006 to 30 April 2011. The predictor variables investigated were parity, breed, age at calving, season of calving and insemination, year of AMS commissioning, milking frequency, milk yield and early lactation milk composition (1st 100 days in milk; DIM), periparturient and lactational disorders, calving to first oestrus and calving to first insemination interval. The reproductive outcome variables analyzed in this study were: (1) 100-day pregnancy rate and (2) conception rate within two artificial inseminations; both measured as binary variables.

Both continuous and categorical variables were initially assessed using descriptive measures. Calving to first oestrus and calving to first insemination interval were categorized into two groups based on median values; the other predictor variables were categorized into quartiles for the purpose of analysis. The associations between the predictor and outcome variables were analysed by generalized linear mixed model (PROC GLIMMIX; SAS Inst. Inc., Cary, NC) with cow considered as a random effect. Parity, calving season, age at calving and 100-day milk yield were included in each final model to avoid confounding effects of these factors.

RESULTS

Descriptive statistics of outcome variables

Among 798 lactations studied, 787 lactations were considered for final analysis. The 100-day pregnancy rate was 36% \((n = 279)\) and conception rate at first and second service (combined) was 75% \((n = 517)\).

Predictor variables affecting the 100-day pregnancy rate

Cows that were first inseminated after d 79 of lactation were about 6 times less likely (odds ratio: 0.18, \(P < 0.001\)) to be pregnant by 100 DIM compared with cows first inseminated before d 79 of lactation. Moreover, when first oestrus was detected more than...
57 days post calving, the likelihood of being pregnant at 100 DIM was reduced compared with when first
oestrus was detected prior to 57 DIM (odds ratio = 0.57, \( P = 0.014 \)). When 100 DIM average fat to
protein ratio was greater than 1.30, cows had lower
(odds ratio = 0.73) 100-day pregnancy rate compared
with cows producing milk containing average fat
protein ratio at a range of 1.21 to 1.30 (Table 1).

**Table 1:** Generalized linear mixed model results for the
outcome variable, 100-day pregnancy rate based on 798
lactations of 787 cows recorded at the research farm

<table>
<thead>
<tr>
<th>Step</th>
<th>Predictor variables</th>
<th>Class</th>
<th>( n )</th>
<th>OR</th>
<th>95% CI</th>
<th>( P )-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Calving to first insemination (d)</td>
<td>( \leq 79 )</td>
<td>233</td>
<td>1.00*</td>
<td>-</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td></td>
<td></td>
<td>&gt;79</td>
<td>218</td>
<td>0.18</td>
<td>0.1-0.3</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Year</td>
<td>Year 1</td>
<td>63</td>
<td>1.00*</td>
<td>-</td>
<td>0.014</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Year 2</td>
<td>90</td>
<td>0.83</td>
<td>0.4-1.9</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Year 3</td>
<td>98</td>
<td>0.79</td>
<td>0.4-1.8</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Year 4</td>
<td>122</td>
<td>0.34</td>
<td>0.2-0.8</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Year 5</td>
<td>78</td>
<td>1.40</td>
<td>0.5-3.9</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Calving to first oestrus (d)</td>
<td>( \leq 57 ) days</td>
<td>221</td>
<td>1.00*</td>
<td>-</td>
<td>0.027</td>
</tr>
<tr>
<td></td>
<td></td>
<td>&gt;57 days</td>
<td>230</td>
<td>0.57</td>
<td>0.3-0.9</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>Fat to protein ratio (average for 1st 100 DIM)</td>
<td>( \leq 1.09 )</td>
<td>117</td>
<td>1.00*</td>
<td>-</td>
<td>0.033</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1.10 to 1.20</td>
<td>111</td>
<td>1.33</td>
<td>0.7-2.6</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>1.21 to 1.30</td>
<td>114</td>
<td>2.00</td>
<td>1.0-3.9</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>&gt;1.30</td>
<td>109</td>
<td>0.73</td>
<td>0.4-1.5</td>
<td></td>
</tr>
</tbody>
</table>

1Step refers to the step at which each variable entered the statistical model.
Results are presented as the odds ratios (OR), Wald confidence interval (CI) and probability values.

*Reference category.

**Predictor variables affecting the probability of conception within two inseminations**

Cows that gave birth to twins were less likely (odds ratio: 0.51, \( P < 0.05 \)) to conceive within the first two
inseminations compared with cows having a singleton
birth (at the given lactation). In addition, cows reported
to have a 100-day cumulative milk yield greater than 2521 kg were more likely (\( P < 0.05 \)) to conceive within
two inseminations compared with cows at lower 100-
day cumulative milk yields (Table 2).

**Table 2:** Generalized linear mixed model analysis results for the outcome variable, probability of conception
within two inseminations

<table>
<thead>
<tr>
<th>Step</th>
<th>Predictor variables</th>
<th>Class</th>
<th>( n )</th>
<th>OR</th>
<th>95% CI</th>
<th>( P )-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Twin birth</td>
<td>Yes</td>
<td>22</td>
<td>0.51</td>
<td>0.43-0.65</td>
<td>0.003</td>
</tr>
<tr>
<td></td>
<td></td>
<td>No</td>
<td>616</td>
<td>1.00*</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>100-day milk yield (kg)</td>
<td>( \leq 1950 )</td>
<td>156</td>
<td>1.00*</td>
<td>-</td>
<td>0.048</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1951 to 2521</td>
<td>162</td>
<td>1.00</td>
<td>0.90-1.12</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>2522 to 3044</td>
<td>163</td>
<td>1.33</td>
<td>1.20-1.50</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>&gt;3044</td>
<td>157</td>
<td>1.16</td>
<td>1.01-1.28</td>
<td></td>
</tr>
</tbody>
</table>

1Step refers to the step at which variable entered in the statistical model.
Results are presented as the odds ratios (OR), Wald confidence interval (CI) and probability values.

*Reference category.
Overall average 100-day milking frequency was 1.9 ± 0.45 times/cow/day. This variable was tested as a predictor variables in the model, but milking frequency was not significantly associated with either of the outcome variables in the dataset presented here.

**DISCUSSION AND CONCLUSION**

Calving to first oestrus interval and calving to first insemination interval were associated with reduced probability of pregnancy by 100 DIM. These findings are similar to those reported in studies by (Washburn et al. 2002) and (Muhammad et al. 2011). High incidence of abnormal resumption of postpartum ovarian cycles, reduced oestrus detection efficiency and decreased oestrus expression are all common causes for extended calving to insemination intervals (Muhammad et al. 2011). Cows in the 2nd highest quartile of milk production were more likely to conceive within two inseminations compared with cows in the lower milk production quartiles. This finding is consistent with the findings of (López-Gatius et al. 2006), but inconsistent with (Windig et al. 2005). The factors that caused the lower producing cows to fall into those quartiles were most likely also associated directly with a reduction in reproductive performance. Such factors would likely include poor health and/or a reduced intake or higher negative energy balance. Whilst high production levels in early lactation are often reported to be associated with delayed and/or reduced conception (Windig et al. 2005), this was not apparent in the dataset presented here and is most likely a reflection of the absolute production levels.

Some researchers (Kruip et al. 2002; Weiss et al. 2004) found no association of increased milking frequency in AMS with a delay in resumption of ovarian cyclicity or increased days to conception. However, others have reported a negative association between milking frequency and reproductive performance. The low incidence of extreme high milking frequencies in our study may explain the absence of this relationship; only 1% of cows averaged 3 or more milkings/day during the first 100 DIM.

Fat to protein ratio was significantly associated with the probability of being pregnant by 100 DIM and cows with a ratio in the range from 1.21 to 1.30 had the highest 100-day pregnancy rate. (Geishauser et al. 1997) reported the range of fat protein ratio from 1.35 to 1.5 as the recommended threshold values beyond which individual cows were regarded as being at higher risk for energy deficiency or metabolic or other diseases.

Whilst the incidence of twin births was relatively low (22 cows, 3.6% births), they were negatively associated with conception rate after two inseminations, and 36.4% of cows that had twins also suffered retained fetal membranes.

One of the challenges of working with historical data is that the decision making that sits behind the management is often not captured, which creates some difficulties with interpretation of results. It is likely that the dataset presented here was also impacted by factors which included (but would not be limited to) shifting from split to year-round calving and increasing herd size and therefore reduced voluntary culling. Whilst the 100-day pregnancy rate (36%) is considerably lower than the industry benchmark of 58% (Incalf, 2007), the interpretation of the results needs to take into account managerial decisions and farm specific factors rather than emphasizing this as a general outcome pertaining to AMS. It will be necessary to perform detailed analyses of other outcome variables (e.g. calving to conception interval and number of AI/conception) directly or indirectly related to the primary measures of the reproductive performance. Moreover, the associated known or unknown predictor variables are required to be resumed or identified.

**ACKNOWLEDGEMENTS**

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The effect of space allowance during transport on welfare of bobby calves

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ABSTRACT

Transport of bobby calves is a contentious animal welfare issue for the dairy industry in Victoria. The objective of this study was to examine the effects of floor space allowance on calf welfare during transport. The treatments consisted of floor space allowances of 0.2, 0.3 or 0.5 m²/calf. Each pen contained 4 animals and a total of 432 male dairy calves (Friesian and Friesian-cross) at an average weight of 38kg. Calves were observed by video during transport and for 12 hours after transport. Behavioural measurements included lying during transport and 12 hours after transport. Blood samples were analysed for creatine kinase (CK). While space allowance did not affect the average time spent lying, there was a difference in the variation in time spent lying ($P<0.001$), as expressed by the standard deviation (sd). There was also a reduction in the number of posture changes in truck pens with the lowest space allowance ($P<0.001$). CK was also increased ($P<0.001$) in calves transported at 0.2m²/calf, compared with both 0.3 and 0.5m²/calf. The results of this study indicate that from an animal welfare perspective, floor space allowance during transport of average sized calves (average 38kg) should be at least 0.3m² per calf.

Keywords: bobby calves; transport; animal welfare.

INTRODUCTION

Transport of bobby calves is a contentious animal welfare issue for the dairy industry in Victoria. Factors that affect the welfare of young calves during transport include calf age, transport duration and conditions (Knowles et al. 1997; Todd et al. 2000; Eicher, 2001; Cave et al. 2005). Overcrowding of bobby calves during transportation can result in injury and death, and calves which are recumbent during transportation in crowded pens have difficulty standing and can be trampled. Young calves show a preference for lying during transport (up to 70% of the trip duration, Eicher and Morrow-Tesch, 2000). The new Australian Animal Welfare Standards and Guidelines for the Land Transport of livestock stipulate that space allowance during transport should be sufficient for calves to lie on their sternum during transport, however no specific space allowance is specified. Young calves are vulnerable to the stresses of transport (Grigor et al. 2001; Cave et al. 2005) and the conditions during transport need further research to develop appropriate welfare standards for the transport of bobby calves. The objective of this study was to examine the effects of floor space allowance on calf welfare during transport as well as effects of calf age and flooring type on calf welfare, although this paper reports on the effect of space allowance only.

MATERIALS AND METHODS

Calves were collected directly from commercial farms and transported for 12 hours in a custom-made cattle truck. The truck was fitted with 9 pens, with movable divisions to change stocking densities. The experimental design was a 3 x 3 x 3 factorial plan. Stocking density and age were allocated according to a matrix design, with flooring substrate linked to a stocking density at each trip. The treatments consisted of floor space allowances of 0.2, 0.3 or 0.5 m²/calf in a Latin square arrangement for each trip. Additional treatments were balanced over the different space allowances and consisted of age (3, 5 and 10 day old) and flooring in the truck (solid steel, steel mesh and straw) but are not reported here. Calves were observed by video during transport and for 12 hours after transport. Each pen contained 4 animals and a total of 432 male dairy calves (Friesian and Friesian-cross) at an average weight of 38kg were transported during 12 trips. After transport animals were unloaded and housed in pens in the same groups of 4, with a pen size of 3 x 3.8 m (2.1 m²/calf), where they were observed for another 12 hours during recovery. Blood samples were taken 1 hour after feeding in the morning, after which the animals were loaded onto the truck. Further blood samples were taken immediately after transport and 12 hours after transport. Behavioural measurements included lying and posture changes between lying and standing during transport, and lying during 12 hours after transport. Blood samples were analysed for creatine kinase (CK), as a measurement of muscle damage due to bruising or muscle fatigue.

RESULTS

Statistically significant effects of space allowance on animal welfare indicators were found (Table 1). While space allowance did not affect the
average time spent lying, there was a difference in the
variation in time spent lying ($P<0.001$), as expressed
by the standard deviation (sd). There was also a
reduction in the number of posture changes in truck
pens with the lowest space allowance. ($P<0.001$).

CK was increased ($P<0.001$) in calves transported
at 0.2 m$^2$/calf, compared with both 0.3 and 0.5 m$^2/$
calf, with more than double the concentration of
CK recorded in animals transported at 0.2 m$^2$/calf
compared with the other stocking densities. Calves
transported at 0.3 compared with 0.5 m$^2$/calf also
showed some elevation of CK.

**Table 1:** Effect of space allowance on behaviour and
physiology before, during and after transport and
after 12 hours of recovery (back-transformed means
in parentheses)

<table>
<thead>
<tr>
<th>Measurement</th>
<th>0.2 m$^2$/calf</th>
<th>0.3 m$^2$/calf</th>
<th>0.5 m$^2$/calf</th>
<th>sed</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time spend lying (%) during transport</td>
<td>52</td>
<td>45</td>
<td>52</td>
<td>3.2</td>
<td>0.069</td>
</tr>
<tr>
<td>Lying (%) sd</td>
<td>20</td>
<td>13</td>
<td>12</td>
<td>2.1</td>
<td>$&lt;0.001$</td>
</tr>
<tr>
<td>Square root of posture changes</td>
<td>3.2 (10)</td>
<td>4.0 (16)</td>
<td>4.1 (17)</td>
<td>0.16</td>
<td>$&lt;0.001$</td>
</tr>
<tr>
<td>Log$_{10}$(CK) Before loading</td>
<td>2.10 (120)</td>
<td>2.02 (100)</td>
<td>2.14 (140)</td>
<td>0.044</td>
<td>$&lt;0.05$</td>
</tr>
<tr>
<td>After 12h transport</td>
<td>2.69 (490)</td>
<td>2.30 (200)</td>
<td>2.17 (150)</td>
<td>0.052</td>
<td>$&lt;0.001$</td>
</tr>
<tr>
<td>After 12h recovery</td>
<td>2.42 (260)</td>
<td>2.16 (130)</td>
<td>2.06 (110)</td>
<td>0.050</td>
<td>$&lt;0.001$</td>
</tr>
</tbody>
</table>

**DISCUSSION AND CONCLUSION**

The increase in variation in lying time and
decrease in posture changes of calves provided with
0.2 m$^2$/calf of space indicate that they may find it
difficult to rise once they are lying down, or find the
space to lie down when standing up. The elevated
level of CK observed in calves transported with
0.2 m$^2$/calf (and to a lesser extend in calves with
0.3 m$^2$/calf) indicates that these calves are either
either more fatigued (Warriss *et al*. 1995) and/or suffer
increased bruising (Tarrant, 1990). (Todd *et al*.
2000) found similar results, with the level of creatine
phosphokinase (CPK) significantly elevated in calves
transported for 12 hours at 0.2 compared to 0.4 m$^2/$
calf. The new Animal Welfare Standards for Land
Transport of livestock stipulate that space allowance
during transport should be sufficient for calves to lie
don their sternum during transport. It appears
that calves transported at 0.2 m$^2$ are somewhat
restricted in changing posture between lying and
standing, resulting in an increase in either bruising
or muscle fatigue. The results of this study indicate
that from an animal welfare perspective, floor space
allowance during transport of average sized calves
(average 38 kg) should be at least 0.3 m$^2$ per calf.

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Effects of shade type and shade amount on the behaviour and physiology of dairy cattle

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ABSTRACT

Access to shade in warm weather is beneficial for welfare and production. We examined design features of shade that are likely to be important for efficient cooling: the degree of protection from solar radiation and the amount of shade provided. Increasing levels of protection from solar radiation resulted in increasing use of shade and lowering of minimum body temperature; shade use was more than twice as high when shade cloth blocking 50 or 99% from solar radiation was provided compared with 25% protection (SEM: 0.22). Cows preferred greater protection from solar radiation (72% of cows chose the 50 or 99% shade option over the 25% option, SE: 3.5 and 3.9, respectively). Increasing the amount of shade available resulted in greater use (24 vs. 50% of observations for 2.4 m² shade/cow and 9.6 m² shade/cow, respectively, SE D: 1.7) and lower respiration rates. Simultaneous use of the shade was greater when 9.6 m² shade/cow was provided (15 vs. 0% of observations for 2.4 m² shade/cow and 9.6 m² shade/cow, respectively). The degree of protection from solar radiation is an important design feature of effective shade for dairy cattle and provision of shade for all cows to use simultaneously is beneficial for cooling.

Keywords: behaviour; body temperature; heat load; respiration rate; shade; solar radiation.

INTRODUCTION

Exposure to summer weather affects the behaviour, physiology and production of cattle. Cows will readily use shade in warm weather and the provision of shade can alleviate negative effects of increased heat load (Roman-Ponce et al. 1977), however, little is known regarding design features of effective shade. This paper summarizes three published studies (Tucker et al. 2008, Schütz et al. 2009, 2010) examining design features of shade that are likely to be important for efficient cooling: the degree of protection from solar radiation and the amount of shade provided.

MATERIALS AND METHODS

In experiment 1, the behavioural and physiological responses of groups of cattle with access to shade cloth blocking 25, 50, or 99% solar radiation (n=3 groups/treatment, 3 animals/group) were studied. In experiment 2, groups of cows were exposed to three treatment combinations to study the preference for shade type: pair-wise simultaneous presentation of shade cloth that blocked: 50 and 99%, 25 and 50%, and 25 and 99% of solar radiation in a cross-over design (n=9 groups/comparison, 3 animals/group). In experiment 3, the behavioural and physiological responses of cattle that had access to 2.4 m² or 9.6 m² shade/cow (shade cloth blocking 99% of solar radiation, n=4 groups/treatment, 10 animals/group) were studied. A detailed description of the experiments are presented in (Tucker et al. 2008) and (Schütz et al. 2009, 2010).

RESULTS

Shade use increased with higher levels of protection from solar radiation (25%: 1.3h, 50%: 3.0h, 99%: 3.3h/15.5 h, SEM: 0.22, P<0.001) and increased with solar radiation levels (P<0.001, Figure 1). Cows with more protection from solar radiation had lower minimum body temperature (25%: 37.9°C, 50%: 37.9°C, 99%: 37.7°C, SEM: 0.05). Seventy-two percent of the cows preferred shade that blocked 50 (SE: 3.5) or 99% (SE: 3.9) solar radiation (P<0.001) over the 25% option.

Shade use was greater when 9.6 m² shade/cow was provided compared to 2.4 m² (50 vs. 24% of observations, SED: 1.7, P<0.001) and increased with heat load (Figure 2). There were fewer aggressive interactions (a forceful physical contact) in the shade (10.7 vs. 3.2 physical contacts/m²/5.8 hrs for 2.4 m² and 9.6 m² shade/cow, respectively, SED: 3.16). Cows with access to 9.6 m² shade/cow used the shade simultaneously whereas the cows with 2.4 m² shade/cow were never observed using the shade at the same time. For example, simultaneous use was observed in 15 vs. 0% of observations on the day of the experiment with highest heat load index (HIL = 95) for the cows in the 9.6 and 2.4 m² shade/cow treatment, respectively. Cows with access to 9.6 m²/ cow had lower respiration rates (57, 51 breaths/min for 2.4 m² and 9.6 m² shade/cow, respectively, SED: 2.1, P = 0.007) compared with cows in the 2.4 m² shade/cow treatment.
DISCUSSION AND CONCLUSION

The results suggest that dairy cattle are able to distinguish between shade that block different amounts of solar radiation, and prefer more protective shade. Shade use increased in warm weather, which is in accordance with other studies (Kendall et al. 2006) and indicates that the importance of shade increases in warm weather. The amount of shade also influences its effectiveness. When sufficient shade amount was provided for all cows to use simultaneously, there were fewer aggressive interactions and cooling effects were more marked. In conclusion, shade should be provided for all cows to use simultaneously and block at least 50% solar radiation.

ACKNOWLEDGEMENTS

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Genetics of feed efficiency and feeding behaviour traits in Holstein heifers

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ABSTRACT

Data from a 2-year feeding trial of growing Holstein heifers (n=842) were used to examine the heritability of feeding behaviour traits and their relationships with Residual Feed Intake (RFI), which is a measure of feed efficiency. Five feeding behaviour traits were analysed: number of meals (nm), feeding duration (FD), dry matter intake (DMI), eating rate (ER) and meal size (MS). All 5 traits were moderately heritable. Two of the traits were genetically correlated with RFI (DMI and FD; 0.45 and 0.27 respectively), and two traits had modest phenotypic correlations with RFI (DMI and ER; 0.52 and 0.23 respectively). The results suggest that feeding behaviour may differ between efficient and inefficient animals and may be useful for selecting animals with better feed efficiency. However, the limitation is that measurement of DMI is still required.

Key words: feeding behaviour, residual feed intake, dairy

INTRODUCTION

Feed efficiency is an important trait that has a major influence on production costs in the dairy industry. Although Residual Feed Intake (RFI), which is the difference between actual and predicted dry matter intake, is gaining popularity as a measure of feed efficiency. However, measuring RFI is expensive and time consuming. Thus, it is of interest to evaluate alternative traits, such as feeding behaviour, to determine if these may indirectly predict feed efficiency.

In human and rodent studies, there is evidence relating meal frequency, meal size and eating speed to different metabolic rates and obesity (e.g. Heinrichs 2001; Scisco et al. 2011). Recent studies also suggest there may be modest phenotypic/genetic correlations in beef cattle between RFI and meal frequency (Kelly et al. 2010), and feeding duration (Durunna et al. 2011). However, these estimates are very imprecise. Currently, there are no published estimates of these correlations for dairy cattle.

The main objectives of this study were to estimate genetic and phenotypic parameters for RFI and feeding behaviour traits in growing dairy heifers. It is hypothesised that the results will be useful in determining which of these traits influence feed efficiency in young dairy heifers, and whether feeding behaviour could be used to select for more efficient dairy cattle.

MATERIALS AND METHODS

The experiment was run in three batches over a two year period, with a total of 842 Holstein-Friesian heifers aged around 6 months. In each batch, around 300 heifers were measured for individual ad libitum feed intake across a 56 day test period. Details of experimental design and management are given in (Williams et al. 2011).

Feed intake data was recorded for each meal event using automated feeders. Five feeding behaviour traits were calculated from these data (Table 1).

Genetic parameters were estimated using linear mixed models in the ASreml package (Gilmour et al. 2006). The model was:

\[ y_{ijk} = \mu + farm_i + batch_j + pen_k + b_1 age + b_2 lwt + animal + e_{ijk} \]

Here, animal estimates the additive genetic variation modeled as \( A\sigma^2_g \). Two alternative A matrices were used: one from pedigree relationships, and the other a genomic relationship matrix (GRM) calculated using the heifers’ genotype data. All heifers were genotyped with the Illumina High Density Bovine SNP chip, which comprises 777,963 SNP markers (San Diego, CA). A full description of the genotype data, the quality control process and construction of the genomic relationship matrix can be found in (Pryce et al. 2012).

Univariate and bivariate models were run for each trait to check the significance of fixed effects and to obtain starting values for the (co)variance components. A multivariate model was then used that included all six traits, fitting only the significant fixed effects \((P<0.01)\) for each trait. (Co)variances estimated from the multivariate model were used to estimate heritability and genetic/phenotypic correlations.

RESULTS

The abbreviation for the traits and their means across batches (± S.D.) are shown in Table 1.
Table 1: Summary for feeding behaviour traits

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Definition</th>
<th>Across all 3 batches</th>
</tr>
</thead>
<tbody>
<tr>
<td>NM</td>
<td>Number of meal events, num/day</td>
<td>13.5±1.3</td>
</tr>
<tr>
<td>FD</td>
<td>Feeding duration, hr/day</td>
<td>2.4±0.3</td>
</tr>
<tr>
<td>DMI</td>
<td>Dry matter intake, kg/day</td>
<td>8.2±0.6</td>
</tr>
<tr>
<td>ER</td>
<td>Eating rate, kg/hr</td>
<td>3.9±0.8</td>
</tr>
<tr>
<td>MS</td>
<td>Meal size, kg/meal</td>
<td>0.7±0.1</td>
</tr>
</tbody>
</table>

Genetic parameters estimated for the traits are shown in Table 2. As mentioned before, two genetic matrices were used in the model (pedigree and GRM). However, convergence problems were encountered with the pedigree matrix. Thus, only the results estimated using the multivariate GRM model are presented. As shown in Table 2, all feeding behaviour traits were found to be moderately heritable. Two traits (DMI and FD) had moderate genetic correlations with RFI (0.45 and 0.27 respectively), and two traits (DMI and ER) had moderate phenotypic correlations with RFI (0.52 and 0.23 respectively).

Table 2: Heritability estimates (on the diagonal), genetic and phenotypic correlations (above and below the diagonal respectively) for Residual feed intake (RFI), number of meals (NM), feeding duration (FD), dry matter intake (DMI), eating rate (ER) and meal size (MS)

<table>
<thead>
<tr>
<th></th>
<th>RFI</th>
<th>NM</th>
<th>FD</th>
<th>DMI</th>
<th>ER</th>
<th>MS</th>
</tr>
</thead>
<tbody>
<tr>
<td>RFI</td>
<td>0.40 (0.09)</td>
<td>-0.07 (0.17)</td>
<td>0.27 (0.15)</td>
<td>0.45 (0.13)</td>
<td>0.06 (0.16)</td>
<td>-0.06 (0.16)</td>
</tr>
<tr>
<td>NM</td>
<td>0.05 (0.04)</td>
<td>0.45 (0.08)</td>
<td>0.03 (0.14)</td>
<td>0.03 (0.16)</td>
<td>-0.01 (0.15)</td>
<td>-0.80 (0.06)</td>
</tr>
<tr>
<td>FD</td>
<td>0.11 (0.04)</td>
<td>-0.04 (0.04)</td>
<td>0.50 (0.09)</td>
<td>0.48 (0.12)</td>
<td>-0.81 (0.04)</td>
<td>-0.23 (0.14)</td>
</tr>
<tr>
<td>DMI</td>
<td>0.52 (0.03)</td>
<td>0.09 (0.04)</td>
<td>0.32 (0.04)</td>
<td>0.46 (0.09)</td>
<td>0.11 (0.14)</td>
<td>0.18 (0.15)</td>
</tr>
<tr>
<td>ER</td>
<td>0.23 (0.04)</td>
<td>0.10 (0.04)</td>
<td>-0.80 (0.01)</td>
<td>0.23 (0.04)</td>
<td>0.46 (0.09)</td>
<td>0.13 (0.14)</td>
</tr>
<tr>
<td>MS</td>
<td>0.06 (0.04)</td>
<td>-0.76 (0.02)</td>
<td>0.10 (0.04)</td>
<td>0.13 (0.04)</td>
<td>-0.04 (0.04)</td>
<td>0.48 (0.09)</td>
</tr>
</tbody>
</table>

**DISCUSSION**

In our study, the moderate heritability estimates of all feeding behaviour traits are in agreement with the findings published for beef cattle (Robinson and Oddy 2004; Durunna et al. 2011). Further, the moderate genetic correlations of RFI with DMI and FD are in agreement with other studies (e.g. Robinson and Oddy 2004; Nkrumah et al. 2007). The genetic correlations between RFI and the other three traits (NM, ER and MS) were not significantly different from zero. In comparison to genetic correlations published for these traits elsewhere (e.g. 0.34±0.30 between RFI and NM in Nkrumah *et al.* 2007 and 0.18±0.31 between RFI and ER in Durunna *et al.* 2011), the precision of our estimates is comparatively good. This may be due to a larger population size and the use of a GRM to estimate the genetic (co)variance components.

The moderate to strong positive phenotypic correlation between RFI and DMI reported here is in agreement with other studies (e.g. Robinson and Oddy 2004; Kelly *et al.* 2010). This confirms that cattle with higher DMI have poorer feed efficiency (i.e. higher RFI), and implies that animals with high intake use energy less efficiently for growth compared to those with lower intakes. It would be useful to understand if high DMI governed by a relatively larger MS can cause biological inefficiencies in animals (i.e. hinder rumen fermentation). However, the phenotypic correlation between RFI and MS (0.06) implies that meal size shows no effects on RFI. Moreover, RFI and ER had a moderate phenotypic correlation in our study, whilst it was not significantly different to zero in (Durunna *et al.* 2011). The biological differences of gender/stage of growth may be a possible explanation, with growing heifers in our study, and finished steers in theirs.
CONCLUSION

Some feeding behaviour traits have moderate to strong genetic and phenotypic correlations with RFI (DMI, ER and FD). DMI is used in the calculation of RFI and thus is not a feeding behaviour trait, while FD is an indirect measure of DMI. Heifers that eat for a longer period are obviously expected to eat more. Therefore, we conclude that although feeding behaviour may help to achieve our goal of indirectly selecting more efficient cattle, the limitation is that a measure of intake is still required. Furthermore, genomic selection tools for the trait of interest, i.e. RFI may be better than indirect selection criteria. In addition, eating rate (ER) was phenotypically correlated to RFI and DMI. This is of interest, because it implies that cattle that eat slowly can improve feed efficiency, although it is not effective to use ER as a selection criterion to genetically improve RFI.

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FEEDBASE & NUTRITION
Abstract

A high proportion of the Australian and New Zealand dairy industry is based on a relatively simple, low input and low cost pasture feedbase. These factors enable this type of production system to remain internationally competitive. However, a key limitation of pasture-based dairy systems is periodic imbalances between herd intake requirements and pasture dry matter (DM) production, caused by strong seasonality and high inter-annual variation in feed supply. This disparity can be moderated to a certain degree through the strategic management of the herd through altering calving dates and stocking rates, and the feedbase by conserving excess forage and irrigating to smooth seasonal forage availability. Australasian dairy systems are experiencing emerging market and environmental challenges which includes increased competition for land and water resources, decreasing terms of trade, a changing and variable climate, an increasing environmental focus that requires improved nutrient and water use efficiency and lower greenhouse gas emissions. The integration of complementary forages has long been viewed as a means to manipulate the home grown feed supply, to improve the nutritive value and DM intake of the diet, and to increase the efficiency of inputs utilised. Only recently has integrating complementary forages at the whole farm system level received the significant attention and investment required to examine their potential benefit. Recent whole-of-farm research undertaken in both Australia and New Zealand has highlighted the importance of understanding the challenges of the current feedbase and the level of complementarity between forage types required to improve profit, manage risk and/or alleviate/mitigate against adverse outcomes. This paper reviews the most recent systems-level research into complementary forages, discusses approaches to modelling their integration at the whole farm level and highlights the potential of complementary forages to address the major challenges currently facing pasture based dairy systems.

Keywords: complementary forages, pastures, dairy farming systems, modelling.

Introduction

The Australian dairy industry production has a current value of AU$3.9 billion and is the country’s third largest rural industry behind beef and wheat, producing 9.1 billion litres of milk and exporting $2.75 billion of product in 2010/11 (Dairy Australia 2011a). The New Zealand dairy industry produced 17.3 billion litres of milk valued at NZ$10 billion in 2010/2011(DairyNZ 2011), making it the country’s largest export earner. The major competitive advantage of both the Australian and New Zealand dairy industries, relative to other countries in the developed world, is the efficient production of milk from a relatively cheap feed source; the home grown feedbase (Dillon et al. 2005).

Pasture grasses are the dominant forage source throughout each of the dairy regions of Australia and New Zealand (Doyle et al. 2000; Holmes 2007). Home grown forage consumption is a key determinant in dairy business success (Mitchell 1998; van Bysterveldt 2005). However, as farms move closer to achieving a ceiling level of production from their current feedbase and natural resource base, the question that is often proposed is, “Where is the next major gain in the feedbase?”. Intensifying the farm system to achieve a higher level of pasture consumption from a business that is currently using over 70% of its pasture production potential often comes with substantial additional costs and risk. Additional increases in home grown forage consumption do not always achieve the predicted improvements in profit. In some regions it is often considered more effective to purchase more land than intensify the current enterprises, especially if the land is not suited to further increases in stocking rate. Unfortunately, the opportunity to purchase additional land in many regions is limited because of encroaching urbanisation and increasing land prices. Consequently, dairy businesses are seeking new and complementary pasture species, conserved forages and novel concentrates/by-products to supplement their pasture based systems (Clark et al. 2007).
The use of forage species to complement the feedbase with respect to quantity, nutritive value or seasonality of feed produced (from here on referred to as complementary forages) is not a novel idea. Complementary forages have been adopted successfully across dairy farming systems in Australia and New Zealand for many years. Forage sources that potentially complement the perennial ryegrass (*Lolium perenne* L.) feedbase include annual forage species, legumes (both pastures and crops), forbs, and other perennial grasses. These complementary forages have received greater research, development and extension focus in recent years to increase forage DM production potential (both grazed and conserved), manipulate nutritive value, achieve greater productivity gains, increase farm profitability, lower business risk and to compensate declining terms of trade.

This paper briefly reviews the strengths and weaknesses of the current dairy feedbase system throughout Australia and New Zealand and examines the current adoption of complementary forages. The paper also examines the external pressure of decreasing land and water availability and reviews the most recent systems-level research into complementary forages. The key factors influencing the success of integrating complementary forages are discussed. The paper also details modelling complementary forages and explores how challenges such as a changing and variable climate and a carbon constrained economy may influence the feedbase and the role that complementary forage may play in alleviating these challenges.

**MANAGING THE FEEDBASE**

Due to varying climates, availability and cost of land, water and feed, milk payment schedules, personal preferences and knowledge base, a wide spectrum of dairy production systems has evolved in both Australia and New Zealand (Table 1). In Australia, dairy farms are categorised into five varying farming systems (Dairy Australia 2011b). According to national farm survey results (Dairy Australia, 2010), 30% of Australian dairy farms are classified as farming system 1 (grazed pasture and other forages with < 1.0 tonne grain/concentrates fed in bail), 50% in system 2 (grazed pasture and other forages with > 1.0 tonne grain/concentrates fed in bail), 11% in system 3 (pasture grazed for most or all of year with a partial mixed ration on feed pad with or without grain/concentrates fed in bail), 5% in systems 4 (pasture grazed for less than nine months per year with partial mixed ration on feed pad with or without grain/concentrates fed in bail) and 2% in system 5 (zero grazing, cows housed and fed total mixed ration). In New Zealand, in the past 15 years, systems have changed such that they now range from 100% pasture systems through to systems where 50% or more of feed is imported from outside the pasture area (Macdonald et al. 2010). There are also five classes of dairy systems in New Zealand, based on the proportion of total feed consumed comprised by imported feed, and whether imported feed is used for dry cows, lactating cows or both (Kolver and Hedley 2006). Imported feed is defined as any feed used for dairy cows that is not grown on the milking platform area (area directly utilised by lactating dairy cows). This includes silage conserved on support land (areas of land not directly utilised by lactating dairy cows) or crops grown on support land fed to dairy cows either while milking, or during the non-lactating period. It also includes feed purchased from outside the farm business. In 2010/11, 13% of New Zealand dairy farm were classified as system 1 (no imported feed), 30% in system 2 (between 4 and 14% feed imported which is used for dry cows only), 35% in system 3 (10 to 20% of feed imported which is used for dry cows and to extend lactation), and 22% in systems 4 and 5 (> 20% feed imported, with some imported feed used all year round for lactating cows in system 5) (Clark et al. 2012).
Table 1: The regional milk supply, climatic zone, main feed source and farming system for each of the major dairy regions of Australia and New Zealand

<table>
<thead>
<tr>
<th>Australian Region</th>
<th>% of milk supply</th>
<th>Australian Climatic Zone</th>
<th>Main Feed Source and Farming System (FS)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gippsland regions of Victoria</td>
<td>24%</td>
<td>Temperate: no dry season warm summer</td>
<td>Non-irrigated perennial ryegrass/white clover pasture, (39% FS 1, 53%, FS 2, 8% FS 3)</td>
</tr>
<tr>
<td>South West Victoria</td>
<td>23%</td>
<td>Temperate: distinctly dry (and warm) summer</td>
<td>Non-irrigated perennial ryegrass/white clover pasture, (41% FS 1, 47%, FS 2, 8% FS 3, 2% FS 4, 2% FS 5)</td>
</tr>
<tr>
<td>Northern irrigation and North East regions of Victoria, Riverina and upper Murray region of New South Wales</td>
<td>20%</td>
<td>Grassland: warm persistently dry</td>
<td>Irrigated perennial ryegrass (19% FS 1, 48% FS 2, 15% FS 3, 15% FS 4, 2% FS 5)</td>
</tr>
<tr>
<td>Tasmania</td>
<td>8%</td>
<td>Temperate: no dry season, mild summer</td>
<td>Irrigated and Non-irrigated perennial ryegrass/white clover pasture (66% FS 1, 26% FS 2, 6% FS 3)</td>
</tr>
<tr>
<td>Eastern New South Wales</td>
<td>8%</td>
<td>Temperate: no dry season, hot summer</td>
<td>Irrigated and non-irrigated temperate and subtropical annual and perennial grasses (15% FS 1, 51% FS 2, 15% FS 3, 15% FS 4, 4% FS 5)</td>
</tr>
<tr>
<td>Northern New South Wales to Far North Queensland</td>
<td>7%</td>
<td>Temperate: moderately dry winter warm summer</td>
<td>Irrigated and Non-irrigated perennial ryegrass/white clover pasture, annual grasses and legumes (20% FS 1, 58% FS 2, 12 FS 3%, 3% FS 4, 7% FS 5)</td>
</tr>
<tr>
<td>South Australia</td>
<td>6%</td>
<td>Temperate: high rainfall: cold winter</td>
<td>Non irrigated annual grasses, irrigated perennial grasses, subtropical pastures (19% FS 1, 60% FS 2, 8% FS 3, 10 FS 4%)</td>
</tr>
<tr>
<td>South West Western Australia</td>
<td>4%</td>
<td>Temperate: high rainfall: dry and hot summer</td>
<td>Non-irrigated perennial ryegrass/white clover pasture; maize silage; some maize grain (5% FS 1; 27% FS 2; 38% FS 3; 24% FS 4 and 7% FS 5)</td>
</tr>
<tr>
<td>New Zealand Region</td>
<td>% of milk supply</td>
<td>New Zealand Climatic Zone</td>
<td>Main Feed Source and Farming System (FS)</td>
</tr>
<tr>
<td>Waikato/Bay of Plenty/Central Plateau</td>
<td>33%</td>
<td>Temperate, high rainfall: often dry summer</td>
<td>Non-irrigated perennial ryegrass/white clover pasture; maize silage; some maize grain (5% FS 1; 27% FS 2; 38% FS 3; 24% FS 4 and 7% FS 5)</td>
</tr>
<tr>
<td>Lower North Island including Taranaki</td>
<td>19%</td>
<td>Temperate, high rainfall: occasional dry summer</td>
<td>Non-irrigated perennial ryegrass/white clover pasture; maize silage (9% FS 1; 26% FS 2; 37% FS 3; 18% FS 4, and 10% FS 5)</td>
</tr>
<tr>
<td>North and South Canterbury</td>
<td>17%</td>
<td>Cool-temperate high rainfall: cold winter, irrigated in summer</td>
<td>Irrigated perennial ryegrass/white clover pasture; kale (grazed) for winter feed on support land; increasing use of cereal grain (1% FS 1; 5% FS 2; 45% FS 3; 38% FS 4, and 10% FS 5)</td>
</tr>
<tr>
<td>Otago/Southland</td>
<td>17%</td>
<td>Cool-temperate high rainfall: cold winter, rarely dry summer</td>
<td>Non-irrigated perennial ryegrass/white clover pasture; kale (grazed) and swedes (grazed) for winter feed on milking platform or support land (7% FS 1; 26% FS 2; 40% FS 3; 24% FS 4, and 3% FS 5)</td>
</tr>
<tr>
<td>Northland/Auckland</td>
<td>7%</td>
<td>Temperate, high rainfall: frequently dry (and warm) summer</td>
<td>Non-irrigated perennial ryegrass/white clover pasture, often with significant presence of kikuyu (volunteer); maize silage (10% FS 1; 35% FS 2; 32% FS 3; 16% FS 4, and 6% FS 5)</td>
</tr>
<tr>
<td>West Coast/Tasman/Marlborough</td>
<td>4%</td>
<td>Temperate, high rainfall: rarely dry summer</td>
<td>Non-irrigated perennial ryegrass/white clover pasture (15% FS 1; 40% FS 2; 35% FS 3; 9% FS 4, and 1% FS 5)</td>
</tr>
</tbody>
</table>

Australia milk production by region for 2010/11, sourced from Dairy Australia (2012)
Major feed source for Australian zones and Farming system adapted from (Barlow 2008) and Dairy Australia (2011b). Feed source for NZ farm system types for 2010/11 from DairyBase (DairyNZ, Diane Sutton, pers. comm.).
The major competitive advantage of grazed pasture based dairy systems is the ability to produce milk at a low cost (Dillon et al. 2005). Pasture based dairy systems, in particular those utilising perennial ryegrass, also possess a range of other positive attributes including a relatively high forage nutritive value, ease of pasture establishment, responsiveness to nitrogen (N) fertiliser, perenniality in conducive environments and a vast body of knowledge relating to its management (Holmes et al. 2002). However, in most of the temperate regions, under rain-fed conditions, there is a bimodal distribution of pasture growth with the majority of this growth occurring in spring and a secondary peak occurring in autumn (Rawnsley et al. 2007b). This results in substantial feed gaps and periods of oversupply throughout the year (Figure 1). In the northern dairy regions of subtropical Australia, the combination of warm-season and cool-season pastures, with conserved forages, grains and by-products, is used to support milk production throughout the year (Callow et al. 2005). Producers have to manage the feedbase to provide feed of adequate quantity and nutritive value as feeds are often higher in fibre content and lower in digestibility (viz. C₄ summer grasses) compared with C₃ grasses (Farina et al. 2011b; Garcia et al. 2008).

The constraints associated with the seasonality of forage supply and nutritive value has long been recognised. Jacobs and McKenzie (2003) recommended prioritising feedbase research into exploring the integration of other forage species with varying seasonal growth patterns to even out forage supply and to develop cropping combinations that achieve high DM yields and are of high nutritive value. This has led to a strong focus on the integration of complementary forage across dairy systems in both Australia and New Zealand.

Dairy producers have long recognised the limitations associated with seasonality of pasture supply and large year-to-year variations in annual pasture production. They have adapted strategic management responses such as calving date, stocking rate, use of irrigation, and forage conservation to lessen these influences and improve the balance between feed demand and supply. One of the most common uses of complementary forages is to smooth out the supply of forage throughout the year and to reduce the reliance on conserved feed and concentrates to fill feed gaps (Pritchard et al. 1991). Examples of this include the use of alternative pasture grasses that extend the growing season into summer, e.g. tall fescue (Festuca arundinacea Schreb.) in South West Victoria (Chapman et al. 2008b) and in the Waikato region of New Zealand (Clark et al. 2010) or growing summer forage crops (namely forage brassicas) in southern Australia and New Zealand to provide late summer/early autumn forage (Clark et al. 1996; Jacobs et al. 2001). In this situation, forages are often grown as part of the pasture renovation cycle so that the cost of the renovation is offset against the extra forage grown by the crop (Notman 1994). Use of winter cereals in the South Island of New Zealand (de Ruiter et al. 2002) and in southern Australia (Jacobs et al. 2009) has the potential to provide additional highly digestible forage in early to mid-winter, a period when growth rates of perennial grasses are low. The use of single-graze winter cereals, such as forage oats (Avena sativa L.) and Doubletake triticale (x Triticosecale), on the South Island of New Zealand, yield up to 5.5 t DM/ha by mid-July after a March sowing (de Ruiter et al. 2002). Likewise, multiple grazing of Doubletake triticale through winter provides a flexible forage source with the potential for a further 13.5 t DM/ha harvested for silage in late spring (de Ruiter et al. 2002).

Complementary forages can be used to manipulate seasonal feed supply on the milking platform and milking support areas. The use of...
brassica crops such as kale (Brassica oleracea var. acephala) or swedes (Brassica napus var. napobrassica), and fodder beet (Beta vulgaris L.) for winter feed on dairy support land in the South Island of New Zealand is an example of this strategy. This allows higher stocking rates to be sustained on the milking platform than would otherwise be possible due to low winter pasture growth rates (Judson et al. 2010) and also allows farm pasture cover to increase to target levels for the start of calving in early spring. Common practice is to plant these crops on support areas in mid-spring (generally mid-October to early November), and feed them in winter at allowances of 10-14 kg DM per cow per day (plus forage supplement, such as silage or straw) for 50-70 days before cows return to the milking platform for calving. Crop yields of 12 to 18 t DM/ha for kale and swedes, or 20 t DM/ha for fodder beet are commonly achieved in Canterbury and Southland (Judson and Edwards 2008; Judson et al. 2010). While there are some health concerns with forage brassica-or fodder beet-based diets (e.g. nitrate poisoning, acidosis) these can be effectively managed by adapting cows onto crops through a transition period and use of fibre supplements (Judson et al. 2010). This complementary forage strategy, largely developed by dairy farmers, has helped facilitate a doubling of cow numbers in the Canterbury and Southland region over the past 10 years (Anonymous 2002; DairyNZ 2011).

Complementary forages have been used to improve and balance the nutritive value of the diet being offered to dairy cows. Maize (Zea mays L.) silage has been successfully integrated into dairy systems both in Australia and New Zealand (Pritchard et al. 1989). Maize is high in starch and fibre, and low in protein and complements a diet that is low in fibre and high in protein such as those observed in winter and early spring pasture. The use of forage brassicas over summer and early autumn in southern Australia enables the addition of a high energy, low fibre feed during a period where available pasture and conserved hay or silage are all high in fibre (Farina et al. 2011a).

Complementary forage options have also been adopted to gain more from a limited resource base. Forage crops can be up to 250% more water use efficient than shallow rooted pasture species such as perennial ryegrass and the DM yield potential of forage crops often exceeds that of a pasture over the same period. In Victoria, the water use efficiency for total water received (irrigation plus rainfall) of turnips (Brassica rapa L.) was 48 kg DM/mm (Jacobs and Ward 2003) and millet (Echinochloa utilis cv. Ohwi and Yabuno) was 28.1 kg DM/mm compared with 22.2 kg/DM mm for perennial ryegrass (Jacobs et al. 2004). Similarly in subtropical South East Queensland, the water use efficiency for maize for total water received was 46 kg DM/mm, which was two to three times higher than for annual ryegrass (Callow and Kenman 2004). In New South Wales under non-limiting N and water conditions, irrigation and total water use efficiency of maize ranged from 61 to 70 and from 36 to 42 kg DM/mm, in paddock and plot scale experiments, respectively (Garcia et al. 2008; Islam and Garcia 2012b). Irrigation use efficiency of forage rape (Brassica napus L. cv Goliath) ranged from 47 kg DM/mm (Garcia et al. 2008) to 80 kg DM/mm (Islam and Garcia 2012a). Total water use efficiency of forage rape was 29 kg DM/mm (Garcia et al. 2008). Clearly, integrating forage crops in a farming system can be viewed as a way to maximise water use efficiency (t DM produced per ML of irrigation water applied) and land yield potential (t DM produced/ha of available land). However, the decision to grow a forage crop should not be based on such metrics alone but on how the crop complements the whole farm system including both farm profit and risk. This requires a detailed understanding and analysis of the whole system.

INTEGRATING COMPLEMENTARY FORAGES AT THE WHOLE OF SYSTEM LEVEL

Garcia and Fulkerson (2005) highlighted the need to develop dairy systems with greater productivity to alleviate the increased competition for agricultural land and water in New South Wales, and also the long-term declining terms of trade. This led to detailed component and farm system experimentation examining the potential of complementary forage rotations (CFR) under irrigation. In a 3 year field study (Garcia et al. 2008) produced 42 t DM/ha.yr from a CFR comprising of an annual sequence of maize, forage rape and a legume (Persian clover, Trifolium repesinatum L. or maple pea, Pisum sativum L). This was compared to the pasture (control) treatment [kikuyu grass (Pennisetum clandestinum) over-sown with short-rotation ryegrass (Lolium multiflorum L)] which yielded 17 t DM/ha.yr. A complementary forage (CF) system whole-farm study was also established in which the CFR and pasture on the farmlet area was proportioned at a ratio of 35:65. In the CF system over 26 t DM/ha.yr were utilised and yielded 2,159 kg milksolids (MS)/ha from home grown feed (Farina et al. 2011a). The 2-year physical dataset generated in this study was used as a basis of a comprehensive modelling study that included the combination of
biophysical models (APSIM, DairyMod and Farmax Dairy Pro), budgeting software (NSW DPI Milk Biz Whole-Farm Budgeting Program version 3.2.1) and risk analysis software (@Risk version 4.0.5, Palisade Corporation, Newfield, NY). The study compared the economic impact and potential risks (associated with climatic and feed price variability) of the CF system and a pasture plus concentrate system. On average the CF system achieved over 30% more operating profit/ha than the pasture plus concentrate system (S.R Farina unpublished data). Also, the CF system was less sensitive to both climatic (due to higher and more uniform responses to irrigation water used in summer for high-yielding forage crops) and feed price (due to lower dependence on bought-in feed) variability than the pasture plus concentrate system. The study demonstrated the economic sustainability of intensification options based on increasing home-grown feed through better use of complementary forages.

(Chapman et al. 2006) also identified the need for continued productivity gains on-farm to counter declining terms of trade. In southern Australia it was clear that top producers are already achieving close to the ceiling of pasture production potential from the traditional perennial ryegrass base. Whilst the CFR and CF system work proposed by Garcia and Fulkerson (2005) addressed the limitations of land and water availability (Farina et al. 2011a; Garcia et al. 2008), further work in southern Australia addressed the strong seasonality associated with perennial ryegrass in a non-irrigated environment, the high inter-annual variation in pasture production and the limited pasture persistence (Chapman et al. 2006; Chapman et al. 2008a). (Chapman et al. 2008a) proposed for the non-irrigated dairy regions of southern Australia that home grown forage consumption could be increased by 30%, by integrating other pasture species and forage crops into the perennial ryegrass pasture base. It was hypothesised that a 30% improvement in home forage consumption would lead to a 30% improvement in return on assets. Initial modelling by (Chapman et al. 2008b) identified that the 30% improvement in production could be obtained through the inclusion of a double crop (winter forage cereal and summer brassica) and a more active summer pasture (tall fescue) system (also termed complementary forage (CF) system) compared to a perennial ryegrass only system (RM). They also concluded that the herbage accumulation in the CF system was more consistent across years than RM system. It was suggested that such a system would provide farmers with a more predictable operating profit from year to year (Chapman et al. 2008c). When tested within a four-year farmlet experiment, the increase in DM production was confirmed with on average 31% more home grown forage being consumed per hectare in the CF system compared to the RM system (Cullen et al. 2012a). However, this only translated into a 3% higher return on assets, much less than expected because of the strong performance and profitability of the perennial ryegrass base farm; generally low DM yields of summer brassica crops related to drier-than average climatic conditions; lower than expected consumption rates and nutritive value of whole crop silage made from winter-grown cereals; and failure of tall fescue-based pastures to improve the seasonal distribution of pasture supply (Cullen et al. 2012a). Compared to RM system, the profitability of the CF system fluctuated more in the face of year-to-variability in growing season conditions and milk price, and therefore carried higher business risk. Subsequently, these farmlets were modified and continued for a further two years. Key modifications included a higher stocking rate in the RM system and for the CF system, a focus on high rates of perennial ryegrass renovation using grazeable forage options and thus reducing the reliance that the CF system previously had on high amounts of conserved forage from winter cereals. Results from the second year of this revised experimental design (first year was considered a transition year) showed that 16% more home grown forage was consumed from the new CF system and this resulted in a 10% increase in return on assets (Cullen et al. 2012a).

While the initial CF system was capable of growing more feed and enabling greater consumption of home grown feed per hectare, the additional costs associated with forage conservation, feeding out and DM losses through this process, coupled with greater exposure to poor seasons (short springs and dry summers) meant that this did not translate to significantly greater profit. Furthermore, the perennial ryegrass system performed above expectation and highlighted that there is further opportunity for many producers to exploit this potential. When the CF system was re-designed and focused on producing more feed for direct grazing, associated costs were reduced and the system became more profitable and offers potential for the future.

Compared to southern Australia and New Zealand, the feedbase systems utilised within the subtropical dairy regions of northern Australia are more varied. A relatively common and simple feeding system in northern Australia is grazed tropical grasses during summer, grazed temperate pasture during winter, conserved feed fed out in autumn and grain based concentrate fed during milking throughout the year, with cows batch-calved during autumn and...
spring. More complex partial mixed ration systems calve all year and use detailed ration formulation and feed-out systems, with varying amounts of crops and pastures for grazing and conservation, usually with some irrigation (Chataway et al. 2010a). In 2000, milk producers in northern Australia were required to make rapid adjustments to their production systems to enable them to compete in a newly deregulated market. Studies were initiated to evaluate the effect of intensifying dairy production on profitability in the context of the whole farm system. Five different production systems considered to have relevance to northern Australia were modelled. Four of these systems maintained a grazed forage base and had the potential to increase milk output three-fold by increasing milking cow numbers and level of purchased supplementary feed without having to expand the land area. The fifth feedlot system involved feeding a total mixed ration comprised of grain, maize silage, barley silage, and lucerne hay (Callow et al. 2005). A field evaluation of the modelled milk production systems was conducted over four years with five farmlets established in a subtropical environment of southeast Queensland (Chataway et al. 2010b). For the grazed systems, mean annual milk yield per ha ranged from 866 kg MS (1.9 cows/ha) for a system based on rain-fed tropical pastures to 1,619 kg MS (3.0 cows/ha) where cows were fed temperate and tropical irrigated forages. For the feedlot herd, annual milk yield of 2,924 kg MS/ha (4.3 cows/ha) was achieved through the use of high levels of concentrates (approximately 3 t DM/cow). Decreased DM production caused by adverse environmental conditions with below average rainfall and restrictions on irrigation was offset by purchasing conserved fodder ranging from 0.3 to 1.5 t DM/animal. While these farmlets showed that it was relatively simple to achieve high milk production from intensifying farming systems (Chataway et al. 2010b), it was difficult to define the appropriate phasing and sizing for each dairy system to match labour and budgetary constraints. Unpredictable environmental conditions, poor seasonal growth and uncertainty in milk price increase the risk of business failure particularly during periods of rapid intensification (Walker et al. 2007).

In the Waikato region of New Zealand, a ‘Super Productivity’ system was operated for three years, with the aim of lifting total annual production to 1,750 kg MS/ha, compared to the 1,500 kg MS/ha (including off-farm area used for growing maize silage), deemed to represent the upper level of production achieved in the New Zealand dairy industry up to 2006/07 (Glassey 2009). The forage plan for the system sought to provide all the feed needed for this production from within the farm milking platform area. The forage plan was based on replacing old pasture with new perennial ryegrass and white clover (Trifolium repens L.) cultivars; and growing forage crops (mainly maize, followed by annual ryegrass) on 25% of farm area, which were expected to yield a minimum of 29 t DM/ha per year (Glassey 2009). Compared to a benchmark all grass farm system, the Super Productivity farm aimed for an additional 3.8 t DM/ha consumed to support higher per cow production and an additional 0.5 cow/ha. Over the three years of the study, estimated DM and feed energy production were within 1% of target, but production per cow fell 11% below target due to fewer than expected days in milk resulting from failure to shift the seasonal pattern of feed production sufficiently to extend lactation into late autumn. An additional 2.8 t DM/ha was grown on the Super Productivity farmlet compared to the benchmark farmlet, of which 2.0 t DM/ha came from increased pasture herbage accumulation (partly explained by an additional 33 kg N fertiliser per ha per year), and 0.8 t DM/ha from the crops grown. While the Super Productivity system resulted in an additional 340 kg MS/ha, costs of production were higher ($3.08/kg MS versus $2.65/kg MS in benchmark), operating expenses were $1297/ha greater, and mean return on assets was 7.3% versus 6.0% per annum in the benchmark system. Glassey (2009) concluded that the Super Productivity farmlet “required both consistently higher payouts and improved feed production for it to be reliably superior in profitability to the benchmark farm.”

In examining the performance of perennial ryegrass compared to alternative systems in South West Victoria, (Chapman et al. 2008c) found that in good years (defined as having early autumn and long spring growth) integrating complementary forages into the feedbase could not exceed the profitability of the perennial ryegrass only feedbase. However, in average or poor years (e.g. shorter growing seasons), integrating complementary forages could match and exceed the profitability of a perennial ryegrass only feedbase. In the cool temperate growing regions of Tasmania where perennial ryegrass has been shown to achieve production in excess of 20 t DM/ha under irrigation (Rawnsley et al. 2007b) and also under rain-fed conditions in the high rainfall (>1000 mm/yr) regions (Cotaching and Burkitt 2011), replacing a productive perennial base with an annual forage crop is rarely economically viable. In this environment annual forage crops are more effective when integrated as either part of a renovation cycle or used to improve the utilisation of support land (Pembleton and Rawnsley 2011; Rawnsley et al. 2007a).
While most of the studies described above have concentrated on manipulating feed supply (quantity), feed nutritive value and DM intake can also limit milk production especially in summer and autumn in the absence of irrigation. (Woodward et al. 2008) extended the idea of complementarity by designing a system based largely on legumes to deliver forage of higher nutritive value (mimicking a forage ‘total mixed ration’, FMR), and comparing production and profit with a system based on conventional perennial ryegrass-white clover pasture. Each system was represented by a farmlet located in the Waikato region, New Zealand. The FMR system, which included lotus (Lotus corniculatus L.), lucerne (Medicago sativa L.), white clover and red clover (Trifolium pratense L.), resulted in lower total DM production than the ryegrass/white clover control (mean over two years of 15.5 and 18.7 t DM/ha per year, respectively) but higher milk production (+7.7% per cow and per hectare), most of which was captured in the late summer-autumn period due to higher nutritional value of the diet. Averaged across the two years of the trial, the FMR system increased economic farm surplus by 11%. However, (Woodward et al. 2008) noted that the finding of higher profitability in FMR should be treated cautiously, since the experiment was conducted for only two years, and the true persistence of some of the species used (and, hence, costs of pasture maintenance) was not fully tested. On the plus side for the FMR system, the legume-dominant forage base (including lotus, a tannin-containing species) could offer environmental benefits such as reduced methane emissions (Woodward et al. 2004) and a higher proportion of excreted N being partitioned to faeces compared to urine which should reduce the risk of N leaching from urine patches (Haynes and Williams 1993, Fraser et al. 1994). However, these benefits have been difficult to capture in pasture legume mixtures, where the legumes have had poor agronomic performance and associated low abundance and persistence (Edwards et al. 2008).

The collection of complementary forage work undertaken across both Australia and New Zealand highlights the importance of understanding the challenges of the current feedbase and level of complementarity that is needed to improve profit and/or alleviate/mitigate against adverse outcomes. The work undertaken in South West Victoria by (Chapman et al. 2008a) suggests that a greater financial return may be possible from perennial ryegrass-based systems than previously recognized and there was little evidence to support the idea of moving substantially away from the perennial ryegrass base in pursuit of greater profits. However, (Cullen et al. 2012a) highlighted that if the focus of the complementary forages is to provide additional grazeable feed and this is integrated into the system as part of a proactive renovation program then there may be opportunity for such options to improve profitability of dairy systems.

We consider that a key feature driving the positive relationship between farm profitability and home grown forage use across Australia and New Zealand is the perenniality and grazeable nature of the current feedbase. Alternative grazed perennial forage species within the family Poaceae (grasses) and from families other than Poaceae should be further explored to address limitations of the current feed base. Edwards and Bryant (2011) highlighted that, in New Zealand, the identification of the appropriate perennial ryegrass ecotypes or combination of ecotypes for a dairy farm is an important decision to improve pasture production, persistence and nutritive value. Current cultivars have a range of flowering times of approximately six weeks and there is a strong relationship between early spring growth and early flowering (Kemp and Culvenor 1994). Edwards and Bryant (2011) suggested sowing paddocks of ryegrasses with different flowering dates on farm will help improve early spring and late spring growth and assist in maintaining pasture nutritive value and DM intakes throughout spring and into summer. While the breeding of perennial ryegrass has focused on improved annual herbage production and it is suggested that this has achieved genetic gains of approximately 0.5% per annum (Woodfield 1999), seasonal distribution of the feed supply and better matching this supply with feed demand during key periods is also considered desirable (Easton et al. 2002).

(Nie et al. 2004) compared deeper rooted perennial grasses (tall fescue, phalaris (Phalaris aquatica L.) and cocksfoot (Dactylis glomerata L.)) with perennial ryegrass for four years in South West Victoria and observed less inter-annual variability in total herbage accumulation and growth rates for these alternative perennial pastures. Similarly, (Christie et al. 2005) found that when dairy cows grazed pasture swards dominated by either prairie grass (Bromus willdenowii Kunth.) or cocksfoot that there was no difference in milk production compared to perennial ryegrass dominant swards. The ability to combine differing species and or cultivars across the milking platform with varying distributions of feed supply and/or nutritive characteristics, whilst maintaining the grazeable nature and perenniality of the feedbase might have been somewhat overlooked in the pursuit of more substantial gains in total annual forage production.
MODELLING COMPLEMENTARY FORAGES

(Lee et al. 2012) highlighted that substantial value could be gained by using growth rate data in a modelling approach, followed by on-farm validation experiments to quantify and extend the potential benefits of combining species on farm. The majority of modelling associated with complementary forages has been undertaken at a biophysical level where observed DM yields have been compared to simulated DM yields. For ryegrass pastures the biophysical model DairyMod (Johnson et al. 2008) has been shown to satisfactorily simulate pasture DM yields across dairy regions of Australia and New Zealand (Cullen et al. 2008) and also under varying management inputs like irrigation (Rawnsley et al. 2009). For complementary forages there is a paucity of modelling information relating to their production and a clear gap exists in the current range of models available to the dairy industry to investigate and predict the interactions between forage crops and other system components. The Agricultural Production Systems Simulator (APSIM; (Keating et al. 2003)), is a biophysical model that was developed to explore interactions between soil, climate, crops and management practices within the Australian broad acre cropping industries and is now used worldwide across a range of agricultural systems. Recent evaluations of the accuracy of APSIM in simulating DM yield, phenology and nutritive characteristics of forage crops grown in the dairy regions of South East Australia (K.G Pemberton unpublished data) concluded that APSIM can be used with confidence to explore the influence of crop management and environment on forage crop DM yield and phenology (Figure 2). However, the ability to simulate herbage nutritive characteristics was somewhat limited and should be the focus of future research and model development.

Figure 2: An example of the ability of APSIM to predict DM yield and phenology of annual forage crops (shown as scatter plots of observed values vs. modelled values) grown in the South East Australian dairy regions. Error bars represent the range in observations where more than one observation made up a data point. Source K.G Pemberton (unpublished data).
Developing and validating models for simulating the growth of complementary forages provides a cost effective approach to the evaluation of inter-annual performance and influence of agronomic management on production (e.g. Pembleton et al. 2011), while also being a means to evaluate the performance of a broad range of crops under future climate scenarios. However, as stated by Jacobs and Woodward (2010) when scaling up from both modelling and component studies there needs to be consideration given for reductions in realised DM yields due to a range of factors that include increases in spatial variation and the ability to impose consistent and timely management as the scale of operation increases. In addition, it is important to evaluate model capacity to capture the complementarity that can exist at the soil and plant level when simulating complementary forage rotations. (Garcia et al. 2007) provided a list of soil-plant complementarity interactions. While forage rotations can be productive in terms of total biomass production, they can also create unforeseen problems, for example, greater soil disturbance than a permanent pasture, a potential decreases in organic matter content and a more difficult environment in which to control weeds (Houlbrooke et al. 2009; Stevenson et al. 1997). Potential positive outcomes can include greater N capture (Kristensen and Thorup-Kristensen 2004), improved nutrient utilisation (Merrill et al. 2002) and increased development and distribution of biopores and microbial communities (Ball et al. 2005). It is therefore critical that our current evaluation of biophysical models not only considers the ability to simulate DM yields but also the interacting components.

THE FUTURE FOR COMPLEMENTARY FORAGES

Although the majority of work on complementary forages has focused on increasing the total biomass grown and the conversion of additional home grown forage into milk, other external and/or future pressures should be considered in deciding whether to integrate complementary forages into the feedbase. An emerging challenge for the Australian dairy industry is to develop productive and profitable systems that are adapted to a warmer and possibly drier climate, rely less on irrigation and minimise greenhouse gas (GHG) emissions per unit of production. Indeed (Cullen et al. 2012b) and (Cullen et al. 2009) showed that the annual DM production of perennial ryegrass in temperate regions such as southern Victoria is likely to decline with more than 2°C warming, in particular if this is associated with lower rainfall and shorter growing seasons. In contrast, in cooler temperate regions like North West Tasmania, warming with associated increases in atmospheric carbon dioxide (CO₂) concentration is expected to increase perennial ryegrass production (Cullen et al. 2012b; Holz et al. 2010). There is an emerging body of evidence to suggest that alternative forage species will play an important role in complementing perennial ryegrass as the main forage source for dairy production in future warmer and drier climates. Perennial species with deeper roots, increased summer activity or tolerance for high temperatures and higher WUE are considered to be desirable traits (Cullen et al. 2009; White and Snow 2012).

Biophysical modelling with APSIM was undertaken to compare the production potential of double cropping forage options to that of rain-fed perennial ryegrass under future climate scenarios (K.G Pembleton unpublished data). Historical climate data from North West Tasmanian and South West Victoria along with two warmer and drier future climate scenarios were used. The warmer and drier climate scenarios were created by scaling the historical weather data by a 1°C or 2°C increase in mean air temperature, with a corresponding 10% (+1/-10’ scenario) or 20% (+2/-20’ scenario) decline in rainfall, with atmospheric CO₂ concentrations of 435 ppm and 535 ppm, respectively. The +1/-10 and +2/-20 climate scenario represent possible climates in 2030 and 2050, respectively (IPCC 2000; CSIRO and BoM 2007). This modelling suggests that in the cool temperate climate of North West Tasmania there appears no benefit in shifting away from a perennial ryegrass base to a double cropping system although in the relatively warmer and drier climate of South West Victoria the potential DM yield benefits of moving to a complementary forage system appear likely to increase under a future climate scenario (Figure 3 upper panels). While there was only between a 0 and 2.5% increase in the risk of crop failure between the baseline and future climate scenarios for the forage systems shown in Figure 3, some other forage systems investigated (data not shown) which involved later sowings of the spring/summer crops had up to a 25% increase in the risk of crop failures. One of the major limitations to the success of double and triple cropping systems is the limited time window to establish successive crops (Garcia and Fulkerson 2005).

The biophysical modelling data presented in Figure 3 (upper panels) were then used within the dairy farm system model Dairy Predict (Walker and Simpson 2006) to explore the inclusion of the annual forage system on 20% (selected as intermediate level between 10 and 30%) of the milking area within a perennial ryegrass based system for a North West Tasmanian and a South West Victorian dairy farm.
(B.R. Cullen unpublished data). The inclusion of an annual forage cropping system into the perennial pasture base reduced the gross margin of the North West Tasmanian dairy farm under both the current and future climatic scenarios (Figure 3 lower panels). In contrast, the gross margin of the South West Victorian dairy farm remained steady when an annual forage system was included under the baseline scenario, and increased with the inclusion of the annual forage cropping system under both future climate scenarios. This highlights that while in some environments under current climatic conditions, complementing temperate pastures with annual forage crops may only be marginally economically viable, their inclusion in the future may assist to mitigate some of the negative consequences of climate change on farm profitability.

![Figure 3: Box-plots (5th, 10th, 25th, 50th, 75th, 90th, and 95th percentile, with dotted mean line) of the annual forage yield of perennial ryegrass pastures and forage cropping systems (upper panels) and the gross margin of pasture based dairy farms incorporating annual forage crops onto 20% of the milking area under current (baseline), 2030 (+1°C -10% Rain) and 2050 (+2°C -20% Rain) climate scenarios (lower panels). Source K.G Pembleton (unpublished data) and B.R Cullen (unpublished data).](image)

The farm systems described in Figure 3 were assessed for their GHG emission profiles using the industry recognised greenhouse accounting tool DGAS (Christie et al. 2011). This analysis showed there was little difference in the GHG emission intensity of milk production (kg CO₂e/kg MS) between the feedbase options and the climate scenarios, indicating limited potential to manipulate the forage base to mitigate the emissions associated with milk production (B.R Cullen unpublished data). However, it is important to note that the emission estimates are based on current GHG inventory methods only, and that future research quantifying GHG emissions associated with differing complementary forage systems may potentially lead to changes in the inventory calculations. For example, (Woodward et al. 2004) found lower methane emissions per unit of MS when animals were fed diets based on Lotus corniculatus compared to those fed perennial ryegrass. While perennial pasture species lend themselves to low-input systems of production, the increased pasture DM yield required to support modern dairy production has reduced their nutrient use efficiency (particularly N use efficiency). (Garcia et al. 2008) identified that a complementary forage rotation based on maize, forage rape and Persian clover (Trifolium resupinatum L.) had over a 100% improvement in N use efficiency compared to that of an intensively managed pasture based on kikuyu (Pennisetum clandestinum Höchst.) annually oversown with annual ryegrass. These findings highlight the potential that the integration of complementary forages may have for improving N use efficiency and lowering the GHG emissions per unit of milk production, although significantly more research is needed to quantify this.

The intensification of the pasture base through higher stocking rates has resulted in some producers coming close to reaching their ceiling of pasture consumption per ha and only modest increases in stocking rate are foreseen. In conjunction, some dairy regions are also forecasting significant industry growth. For example in Tasmania, the dairy industry is entering a major expansion phase with significant investment and increases in the milk processing capacity leading to a projected increase in demand for milk of up to 40% over the next 5 years (DairyTas 2012). Similarly, projected industry growth of 60 to 65% is anticipated in the South Island of New Zealand over the next 20 years (DairynZ 2010). Although some industry growth can be expected through the intensification of existing dairy businesses, these potential large increases in milk demand are likely to result in non-dairy marginal areas (e.g. run off blocks) and other farm enterprises (e.g. cropping, beef and sheep) being converted into milk producing land.

Although this potential industry growth in these regions is viewed as being extremely positive,
there are a number of potential difficulties when moving dairying into marginal non-traditional environments. The integration of complementary forages could play a significant role in alleviating such challenges as lower soil fertility/poorer soils, reduced availability of irrigation water and a more marginal environment with respect to climatic extremes and pasture production.

**CONCLUSION**

Studies integrating complementary forages at the whole-of-farm system, particularly in the temperate environment of southern Australia and New Zealand, which are most favourable to perennial ryegrass pasture production, have found little evidence for major improvements in farm profits when moving away from this pasture based system. This is most likely due to the overarching benefits of the grazeable and perennial nature of the pasture base in comparison to the cutting and conservation required to maximise the utilisation of many annual forage crops. This highlights that for regions that are most conducive to maintaining a perennial and grazeable feedbase, opportunities exist to integrate grazeable perennial forage species to address some of the limitations of the ryegrass base. The findings of other studies reported in this paper have highlighted that complementary forages do have the capacity to alleviate some of the limitations of the pasture base and their adoption has the potential to advance the dairy industry particularly in dairy regions with constrained land and water availability. Efforts to understand their integration at the whole-of-farm system have been invaluable and further understanding is required to support their advancement, particularly if limitations of the pasture base have the potential to become more prevalent into the future due to a changing climate, increasing demands for greater environmental stewardship, dairy moving into more marginal environments and increasing competition for land and water resources. Enhancing our understanding and ability to simulate the growth and development of complementary forages and their complementarity at both a biophysical and whole of system level is viewed as important to further advancement of the Australian and New Zealand dairy industries.

**ACKNOWLEDGMENTS**

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Increasing the starch availability of sorghum grain for ruminants through dry heat popping

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ABSTRACT

Sorghum grain is a relatively cheap and abundant grain source for Queensland dairy farms. However, the starch digestibility of sorghum within the rumen is limited by starch structure and the protein/starch matrix within the grain. To increase the rate and extent of ruminal starch digestion, dry popping using dry heat was compared to other common processing methods. Sorghum grain was processed using eight different processing methods: rolled (R), hammer-milled (HM), disc-milled (DM), dry-popped (DP), dry-popped and disc-milled (DPM), dry-popped and hammer-milled (DPMH), semi-popped and disc-milled (SPDM) and steam-rolled (SR). The treatments were fermented in an in-vitro system according to Goering and Van Soest (1970) using rumen fluid from two fistulated steers. Data used for rate estimations were in-vitro starch fermentation residues, fermented for 0, 3, 7, 12, 18, 24, 36 and 48 hr. A first order decay was used in SAS (2008) to estimate the rates of digestion, assuming no lag or indigestible starch present. Digestion rates were derived using the 7h starch digestibilities of Roe (1994) and pair-compared to the rates estimated using the non-linear procedure. The non-linear model resulted in R² values between 0.92 and 0.99 and rates of starch degradation between 4.9 and 11.6 %/h. The DPM and DPMH treatments had the highest rates (P<0.05) and the HM, R and DM treatments were the lowest, with DP, SPDM and SR sorghum being intermediate. Dry popping of sorghum grain in conjunction with disc or hammer-milling increased the in vitro starch digestibility when compared to conventional processing methods.

Keywords: Sorghum grain, popping, processing, starch, digestibility, in vitro

INTRODUCTION

Sorghum grain is a relatively cheap and abundant grain source for Queensland dairy farms. Approximately 40-60% of dairy farmers throughout Queensland use sorghum as their main starch source for milk production (D. Barber, pers. comm.). However, many dairy farmers struggle to achieve higher production levels due to the lower digestibility of sorghum grain. While sorghum grain is high in starch (ranging between 62 and 66%), the outer coating and the protein/starch matrix of the grain prevents all of the starch from being digested by the animal. Steam flaking or rolling is a process used to increase starch availability of grain and improve its degradation in the rumen by heating the starch with steam. However the availability of steam flaking or rolling is limited in parts of Queensland and the lower dry matter content of steam flaked/rolled sorghum (78-86% DM) poses handling and reduced shelf-life issues on-farm for dairy farmers. As an alternative, it may be possible to increase the starch availability and degradability of sorghum by popping the grain using dry heat. The process of popping the grain has the potential to increase ruminal starch availability through gelatinisation of the starch molecule and increased surface area for microbial attachment and degradation. The aim of the experiment was to increase the starch availability of sorghum grain and assess the rumen degradability through a residual starch in vitro fermentation experiment conducted over 48 hours.
the grain did not fully pop and was separated using a 5 mm sieve and used in the semi-popped treatment. The hammer-milled (H and DPH) and disc-milled (DM, DPD and SPD) treatments were ground to 2 and 1.2 mm, respectively, to represent industry best practice for milled grain size using these processing methods. All other treatments were ground to 4 mm (R, DP and SR) to represent mastication.

**Fermentation Method**

Buffer was made up for each run on the day of inoculation according to the method of Goering & Van Soest 1970. In 250 ml plastic bottles (Nalgene 3120-0250), 0.75 grams of each treatment was combined with 40 ml of pre-warmed buffer (39°C). The bottles were randomly allocated in the water bath, warmed to 39°C and purged with CO₂ for 2 hours prior to inoculation with rumen fluid. Inoculum was obtained from two rumen fistulated steers that were fed 3 kg of cracked sorghum/steer·d⁻¹ and ad libitum access to kikuyu/ryegrass pasture. One litre of rumen fluid was taken from each steer and filtered through 4 layers of cheesecloth and glass wool and mixed in equal parts in a pre-warmed 4 litre schott bottle while being saturated with CO₂. Each bottle was inoculated with 10 ml of rumen fluid, mixed with the medium and sample by swirly gently and fermented with a positive pressure of CO₂ for their allocated time period. Treatment bottles were placed on ice when removed for 10 minutes and stored at 4°C to stop fermentation.

**Starch analysis of the fermented samples and statistical analysis**

Distilled water was added to the treatment bottles which were then centrifuged. The supernatant was removed and the remaining sample was analysed for starch concentration. Total starch in the fermented sample residue was analysed using the AOAC method (Megazyme total starch kit, AA/AMG, Megazyme International, Ireland) and an automated spectrophotometer. Samples were corrected for dry matter content and the data used for rate estimations were in-vitro starch fermentation residues, fermented for 0, 3, 7, 12, 18, 24, 36 and 48 hours. A first order decay was used in SAS (2008) to estimate the rate of digestion, assuming no lag or indigestible starch present. The Marquardt option of nonlinear regression in SAS was chosen. Parameters of the digestion model estimated by nonlinear regression were analysed by the general linear models procedure of SAS (2008) and included factors for replicate and sample. Main effects and significant differences between treatment means were detected using the Student-Newman-Keuls procedure (SAS, 2008). Digestion rates were also derived using the 7 hour starch digestibilities of Roe (1994) and pair-compared to the rate estimates obtained with the non-linear procedure (SAS 2008), using Tukey’s pair comparison test. Statistical significance was tested at P<0.05.

**RESULTS**

Starch content of the processed sorghum was the same across all treatments (Table 1). At 7 hours, the digestibility and rate of degradation was the highest for the two dry-popped and milled treatments (DpD, DPH) and lowest for the three standard processing methods (R, HM, DM), with the remaining treatments being intermediate (DP, SPD, SR). DP and SPD sorghum were higher (P<0.05) than SR sorghum (Table 1). The nonlinear model estimated rates of starch degradation between 4.9 and 11.6 %/h (P<0.05). The 7h and nlIn kd values were similar (P=0.65), except for the DM, HM and SR treatments which were underestimated. The non-linear model accounted for a high level of variations with R² values between 0.92 and 0.99. Fermentation for 48 hrs was necessary to reach complete digestion for all treatments.

**Table 1:** In-vitro starch digestibility at 7 hours and degradation rates obtained using the formula by Roe (1994) or the nonlinear (NLIN) procedure in SAS, of eight processing methods of sorghum grain

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Starch %</th>
<th>7h digestibility (%)</th>
<th>kd-7h (%/h)</th>
<th>kd-NLIN (%/h)</th>
<th>R²-NLIN</th>
</tr>
</thead>
<tbody>
<tr>
<td>Disc-milled*</td>
<td>70.2</td>
<td>16.3</td>
<td>2.6</td>
<td>4.9</td>
<td>0.933</td>
</tr>
<tr>
<td>Dry-popped</td>
<td>71.5</td>
<td>48.1</td>
<td>9.4</td>
<td>9.6</td>
<td>0.986</td>
</tr>
<tr>
<td>Dry-popped &amp; disc-milled</td>
<td>70.2</td>
<td>53.2</td>
<td>10.9</td>
<td>11.5</td>
<td>0.991</td>
</tr>
<tr>
<td>Semi-popped &amp; disc-milled</td>
<td>70.8</td>
<td>49.7</td>
<td>9.8</td>
<td>9.0</td>
<td>0.998</td>
</tr>
<tr>
<td>Dry-popped &amp; hammer-milled</td>
<td>70.4</td>
<td>55.2</td>
<td>11.5</td>
<td>11.6</td>
<td>0.997</td>
</tr>
<tr>
<td>Hammer-milled*</td>
<td>70.2</td>
<td>24.0</td>
<td>3.9</td>
<td>5.1</td>
<td>0.936</td>
</tr>
<tr>
<td>Rolled</td>
<td>69.6</td>
<td>28.6</td>
<td>4.8</td>
<td>4.5</td>
<td>0.929</td>
</tr>
<tr>
<td>Steam-rolled*</td>
<td>71.2</td>
<td>39.3</td>
<td>7.1</td>
<td>9.7</td>
<td>0.981</td>
</tr>
</tbody>
</table>

a,b,c,d,e Means within a column differ (P < 0.05); * kd-7h and kd-NLIN differ (P < 0.05)
DISCUSSION

Dry-popping and grinding sorghum increased the in-vitro digestibility of starch relative to steam rolling and the three standard processing methods (rolling, hammer-milling and disc-milling). Huntington (1996) and (Theurer et al. 1999) also reported an increase in ruminal starch digestibility with steam flaking compared to dry rolling sorghum grain. (Theurer et al. 1998) stated that the increased digestibility of starch from steam flaking is through disruption of the protein matrix and disorganisation of the starch granules. Dry popping is likely to have a similar effect through the gelatinisation of the starch and an increase in surface area for microbial attachment from the explosive action of popping with dry heat. Steam-rolled sorghum had a 37% higher digestibility compared to rolled sorghum which was similar to (Theurer et al. 1999) and Huntington (1996) (41% and 31% respectively). Dry popping then hammer-milling increased the starch digestibility by 93% compared to rolled sorghum at 7 hours. Similar rates to the standard processing methods were seen by (Wester et al. 1992) with sorghum grain varieties processed through a 1 mm screen. Dry popping and grinding sorghum grain increased starch digestibility relative to dry popping, steam rolling and grinding only, which suggests that the combination of gelatinisation and increasing surface area through heating and grinding respectively, will improve the starch availability of sorghum grain in the rumen.

CONCLUSION

Dry popping of sorghum grain has a greater potential than steam rolling to increase ruminal starch digestibility and degradability at 7 hours in the rumen when the grain is disc or hammer-milled after being popped.

ACKNOWLEDGEMENTS

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New Developments in our knowledge of 25 OH Vitamin D requirements for dairy and beef cattle

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ABSTRACT

This review aims to summarise the benefits of dietary 25 OH Vitamin D supplementation for improving both calcium metabolism at parturition and increasing the efficiency of phosphorus absorption. Hypocalcaemia at parturition in dairy cows is a major economic cost to the dairy industry and has significant animal welfare implications. Hypocalcaemia may result in an increased rate of associated metabolic diseases and a significant reduction in milk yield in the subsequent lactation. Phosphorus feed supplements and fertilisers continue to increase in price as the world supply of phosphorus approaches peak production. It has been established that in the bovine, phosphorus supplements for both growing heifers and dairy cows are only absorbed at a rate of between 50 to 70%, which has economic and environmental consequences. Vitamin D and its metabolites are responsible for the active control of both calcium and phosphorus absorption and utilisation in mammals. However, due to the complexity of Vitamin D metabolism, supplementation with commercial Vitamin D3 to achieve improvements in macro mineral balance has been shown to be largely ineffective and may have adverse health implications. On the other hand, supplementation with 25 OH Vitamin D3 to achieve supraphysiological concentrations in plasma is safe and moreover in mice this Vitamin D metabolite has been shown to replace the functions of the very active form of Vitamin D (1,25 (OH)2 Vitamin D3). A series of studies undertaken at the University of New England, Armidale has identified that dietary supplementation with 25 OH Vitamin D3 in cattle increased plasma concentration of 25 OH Vitamin D3 to levels (375 ng/ml) 3 to 4 times the concentrations achievable from exposure to sunlight. The high concentrations of 25 OH Vitamin D3 significantly increased the retention of phosphorus (3 g/d) and calcium (4 g/d) in steers which was reflected in improved mineral digestibility. In a separate study steers supplemented with a combination of both 25 OH Vitamin D3 and anionic salts displayed greater urinary calcium excretion than steers fed anionic salts alone. In dairy cows, immediately prior to parturition, an increase in both urinary calcium excretion and a concomitant increase in dietary calcium absorption permit a greater resistance to hypocalcaemia. In dairy and beef cattle grazing pastures marginal in phosphorus content, an increase in phosphorus digestibility as a consequence of Vitamin D supplementation activity is highly desirable.

INTRODUCTION

Under normal conditions B group vitamins are synthesised from bacterial synthesis in the rumen. However, precursors for Vitamin A and E are often found in green herbage, and if access is not available they can be readily supplemented. Vitamin D on the other hand is not usually found in natural feedstuffs and is obtained by exposure of skin to solar ultra violet radiation. In skin epithelial cells a cholesterol derivative (7Dehydrocholersterol) is converted to previtamin D3, which normally is immediately converted to Vitamin D3. In the liver, Vitamin D3 undergoes hydroxylation to 25 OH Vitamin D (25-vitD) and finally, in kidney tissue, 25-vitD undergoes further hydroxylation to produce the very active form of the vitamin 1,25(OH)2 Vitamin D (1,25-vitD) (DeLuca, 2004).

The vitamin D status of animals is quantified by the concentration of 25-vitD in plasma (DeLuca, 2004). In the temperate geographical regions of the world the plasma concentrations of 25-vitD are highest in summer and lowest in late winter reflecting the seasonal changes in solar ultra violet B radiation. (Hymoller et al. 2009) in Denmark (latitude 56 north) observed that plasma 25-vitD in dairy cows ranged from 20 ng/ml in summer to less than 5 ng/ml in winter. In Armidale, NSW (latitude 31 South) steers in summer exhibited levels of 45 ng/ml (McGrath et al. 2012a). However, it has been known for sometime that the maximum observed plasma concentrations of 25-vitD of 80-100 ng/ml in both humans and animals under intense natural sunlight is principally due to a rapid photo destruction of the pre-vitamin D3 to non-active products before it can be converted to Vitamin D3 (Webb et al. 1989).

Although the natural synthesis of cholecalciferol in skin cannot achieve high levels of plasma 25-vitD above the stated range of 80-100 ng/ml, large oral doses of 25-vitD do not appear to be degraded by rumen bacterial activity (Hymoller and Jensen, 2010) and result in marked elevations in plasma 25-vitD concentrations (McGrath et al. 2012a). It now
appears that 25-vitD appears to possess very similar biological activities to that of the 1,25-vitD when in super physiological concentrations in plasma (Rowling et al. 2007). The actions of 1,25-vitD in the absence of parathyroid hormone are extremely beneficial for prevention of hypocalcaemia in parturient dairy cows (Bar et al. 1985) and increasing the rate of absorption of phosphorus in both beef and dairy cattle (Rizzoli et al. 1977). However, unlike 25-vitD, 1,25-vitD has a short half-life and very small amounts are toxic.

This article aims to review recent studies of 25-vitD in bovine. The aim of the review is to summarise these studies and demonstrate how 25-vitD can be used to beneficially manipulate calcium and phosphorus metabolism in cattle. The article will present implications of the research and areas that require further investigation.

METHOD

This review summarises studies that were undertaken within a post-doctoral thesis (McGrath, 2012). The individual experiments have been published within various formats, namely Animal Production Science, Animal and various conferences proceedings. This review utilises information garnered from these studies, as well as several studies by other authors.

A detailed account of the materials and methods can be found within each published article. However, in summary, studies were undertaken utilising fistulated steers as models. 25-vitD was added to the diets, through the fistula or by slow release intra-rumen bolus. Urinary calcium excretion was measured by total collection or by spot samples adjusted for creatinine concentration.

DISCUSSION

25-vitD and macro mineral digestion

Vitamin D is responsible for active absorption of both calcium and phosphorus absorption from the dietary tract (Deluca, 2004). Phosphorus is seldom a major limiting nutrient for cattle production in temperate regions due to the extensive use of fertilisers and the use of high phosphorus containing feedstuffs. In these regions a reduction of phosphorus usage is now important in order to reduce feed costs and adverse environmental impacts. In the north of Australia, however, the importance of providing phosphorus as a limiting nutrient for cattle production has been recognised for decades (Ternouth, 1990).

| Table 1: Mean mineral balance for calcium and phosphorus in animals offered a low quality forage diet with and without supplements of 25-vitD (McGrath et al. 2012a) |
|-----------------|--------|--------|
|                  | 25-vitD | Control|
| Calcium (g/d)    |        |        |
| Feed            | 66.4   | 65.7   |
| Faeces          | 55.8   | 60.7   |
| Urine           | 2.5*   | 0.9    |
| Retained        | 8.1*   | 4.1    |
| Phosphorus (g/d)|        |        |
| Feed            | 26.4   | 26.1   |
| Faeces          | 17.2*  | 20.4   |
| Urine           | 1.1    | 0.9    |
| Retained        | 8.0*   | 4.9    |

*Means within rows differ (P < 0.05)

In ruminants, active phosphorus digestibility is unable to be increased as 1,25-vitD production is regulated by plasma calcium concentration (Abdel-Hafeez et al. 1982). However on low phosphorus diets increases in absorption have been achieved by the use of 1,25-vitD (Rizzoli et al. 1977). Early work by (Hollis et al. 1977) reported increased plasma concentrations of calcium and phosphorus in heifers when plasma 25-vitD concentrations exceeded 200 ng/ml following injections of massive doses. In a study involving a cationic rich forage diet by (McGrath et al. 2012a), animals supplemented with 3.25 mg of 25-vitD per day exhibited plasma concentrations of over 300 ng/ml compared with levels in control animals of 45 ng/ml and in this situation significant improvements in both phosphorus and calcium retention, dietary absorption and an increase in plasma concentration of both minerals was recorded.

Synergy between dietary supplementation of 25-vitD and the use of anionic salts

Dietary manipulation in the 3-4 week period prior to calving aimed at reducing potassium intakes concurrent with the use of magnesium and anionic salts is now common place in the dairy industry as a means of reducing metabolic disorders (particularly hypocalcaemia) and improving feed intake and milk yield (DeGroot et al. 2010). It has been argued that the creation of a compensated metabolic acidosis increases the sensitivity of tissues to parathyroid hormone resulting in increased bone calcium resorption, increased intestinal absorption of calcium, increased urinary excretion of calcium and importantly an increased production of 1,25-vitD in the kidney (Horst et al. 2005).
The extent of the interaction between the dietary cation/anion difference (DCaD) of a diet and supplementation with 25-vitD was investigated in a study in which total daily urine calcium excretion was accurately determined (McGrath et al. 2011). The results of this study clearly illustrate that elevated blood plasma concentrations of 25-vitD were incapable of generating significant increases in urine calcium output in the absence of a compensated metabolic acidosis resulting from the use of a diet containing a DCaD of -120 mEq/kg (Figure 1).

Similar synergistic associations between additional anionic salts in pre-calving diets and supplements of 25-vitD on daily urine calcium output have also been reported (Wilkens et al. 2012; McGrath et al. 2012b). Furthermore, calcium losses in urine of the order of 6-7 g/day due to the feeding of anionic salt supplements has been demonstrated previously in dairy cows (Van Mosel et al. 1994) and it has been argued that prolonged periods of calcium excretion without an increase in calcium availability from the diet could be detrimental to the cow at calving. (Lean et al. 2006) suggested that cows fed precalving diets that are severely anionic for long periods show greater propensity for hypocalcaemia due to protracted bone calcium resorption. However, (McGrath et al. 2012a) demonstrated that 25-vitD increased dietary calcium absorption. Furthermore, an analysis of the concentration of the bone degradation marker (serum crosslaps (CTx)) undertaken in the PhD thesis of McGrath (2012) demonstrated that the use of the vitamin did not increase the amount of bone calcium resorption during conditions of compensated metabolic acidosis (Figure 2).

Parathyroid hormone (PTH) activity enhances the conversion of 25-vitD to 1,25-vitD in order to stimulate bone calcium removal and increase renal absorption of calcium by the kidney tubules (Horst et al. 2003). It would seem therefore that the combination of dietary supplements of 25-vitD together with anionic salts would have a synergistic effect for preventing extreme hypocalcaemia in dairy cattle. This was confirmed by (Wilkens et al. 2012) who demonstrated that cows who were supplemented with a combination of anionic salts and 25-vitD maintained a higher plasma calcium concentration at parturition.

Figure 1: Urinary calcium excretion is increased by a combination of anionic salts in the feed and intra-rumen administration of 25-vitD. DCaD −120 ($\sigma$). DCaD 150 ($\sigma$). Linear regression: $y = 0.065x + 1.34$ (R$^2 = 0.62$) (McGrath et al. 2011).

Figure 2: Plasma crosslaps concentration (CTx ±SE) in steers offered either a cationic or anionic forage diet, with or without intra-ruminal supplementation of 25-vitD and monensin. Collection 1 was 2-3 days after the initial treatment with 25-vitD and collection 2 was approximately 10 days later (McGrath, 2012).

The complementary nature of compensated metabolic acidosis and 25-vitD appears to successfully negate severe hypocalcaemia by several actions. Firstly, in the weeks prior to calving daily supplements of 25-vitD will increase calcium absorption at a time when calcium would be removed from bone in order to buffer the effects of the anionic salts (McGrath et al. 2012a). Thus leaving available skeletal calcium intact and able to meet more severe demands. Secondly, providing 25-vitD ensures adequate production of 1,25-vitD when PTH levels are elevated at calving, and the metabolic acidosis achieved by the anionic salts will also ensure that the tissues are very sensitive to the action of this hormone (Horst et al. 2003). Thirdly, the extra calcium being absorbed from the diet is contributing to an increase in urinary calcium turnover due to the state of compensated metabolic acidosis. This calcium is instantly conserved when PTH is secreted, allowing a large reserve of calcium to be immediately available during the greatest period of calcium stress (Schonewille et al. 1999).

**IMPLICATIONS AND FUTURE RESEARCH**

Elevated concentrations of plasma 25-vitD (>200 ng/ml) increase the absorption of both calcium and phosphorus from the digestive tract in bovine. This aspect of vitamin D activity can be utilised to benefit several aspects of both the dairy and beef industries. In extensive grazing conditions utilisation of 25-vitD may enable cattle to utilise sub-optimal
supplies of dietary phosphorus. While in intensive conditions supplementation with 25-vitD may permit diets lower in phosphorus or calcium to be fed, this may include total mixed rations or supplemental feeds.

It has been demonstrated that the addition of 25-vitD and anionic salts to the transition diet of dairy cows helps maintain plasma calcium concentration at parturition. However, utilisation of 25-vitD during lactation may also be of benefit. An increase in utilisation of dietary calcium and phosphorus, as well as replacing skeletal minerals during the early stages of lactation may have both physiological and environmental benefits.

In view of the relatively small quantities of active 25-vitD required to elevate plasma levels of the vitamin above threshold values, it is difficult to accurately provide such amounts under free access paddock supplementation systems. Moreover, in the north of Australia the pronounced wet season physically prohibits supplementation at exactly the correct time of year when phosphorus becomes the first limiting nutrient (ie; when there is protein and energy in available herbage). In this situation a slow release rumen bolus device consistently releasing the critical daily dose of 25-vitD would circumvent the problems of supplementation. Such a device would also have great application in dairy heifer grazing systems in order to increase and maintain good frame score and bone density. The use of a slow release bolus would be a powerful experimental tool to evaluate this concept in large numbers of cows in split herd design experiments where the feeding management would not need to be compromised by expensive differential supplement delivery systems.

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The efficiency with which metabolisable energy is used for live weight gain differs between feed types

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ABSTRACT

In four experiments, 187 non-lactating cows were grouped into one of five treatments (Control, pasture, pasture silage, maize silage, maize grain, palm kernel expeller). All treatment groups were fed inside and offered fresh autumn pasture to estimated maintenance requirements (0.55 MJ metabolisable energy (ME)/kg liveweight^{0.75}/d) and approximately 20 MJ ME/d for pregnancy and activity (Control treatment). Cows, other than Control cows, were additionally offered their treatment feed at one of two levels (2.5 and 5 kg DM/d), and were compared with the unsupplemented Control to determine the efficiency of use of energy for liveweight gain (kg). The kg of Past and Msil was 0.34 and 0.47, respectively, in line with published literature. The kg of Psil (0.50) was greater than expected, but consistent with the kg for spring pasture, indicating that the ensiling process did not decrease the efficiency with which the feed is used for liveweight gain. Palm kernel expeller had the greatest kg (0.61), probably due to its greater fat content. The kg for Mgr was surprisingly low (0.38). In conclusion, Past was less efficient for liveweight gain than PKE and also tended to be less efficient than Psil and Msil. PKE was more efficient than Mgr and tended to be better than Msil, and Psil tended to be more efficient than Mgr. These results confirm differences between feeds in the efficiency of use of ME for liveweight gain and provide important information to ensure cows reach the desired BCS targets.

Keywords: efficiency of liveweight gain; supplement; energy; dairy cattle; non-lactating.

INTRODUCTION

The correct body condition score (BCS) at calving (BCS 5 for mature cows and 5.5 for first and second calvers; 10-point-scale) is important to enable dairy cows to achieve milk production, reproduction and health targets (Roche et al. 2009). An exact knowledge of the efficiency with which feeds are used for live weight (Lwt) gain is essential to develop an action plan for farmers relating to dry period length and feed availability.

Although net energy requirements for tissue gain are available (ARC 1980; CSIRO 2007; NRC 2001), information on the efficiency with which metabolisable energy (ME) from different feeds is used to gain Lwt under grazing conditions is lacking. For example, fresh autumn pasture has been assigned an efficiency for Lwt gain (k_g) of 0.33, but this figure is based on Lwt gain in sheep (Waghorn and Barry 1987). More importantly, (MacRae et al. 1985) reported efficiencies that were approximately 30% greater than this in poor quality autumn pasture (k_g = 0.43). As autumn pasture remains the primary dry cow feed for Lwt gain in seasonal calving grazing systems, actual feed requirements for Lwt gain are important. Although k_g figures are available for pasture silage, the origin of these are unclear, and there is no relevant information on the k_g for palm kernel expeller in dairy cows, which is a common feed ingredient for BCS and Lwt gain in late lactation and during the dry period in New Zealand and Australian grazing systems.

The objective of this experiment was to determine the amount of ME required for Lwt gain from pasture and commonly used supplementary feeds in non-lactating pregnant dairy cows, which will facilitate the estimation of k_g for these feeds under temperate grazing conditions.

MATERIALS AND METHODS

Cows

Four experiments were conducted in autumn (April to June) 2009 and 2011 with 187 non-lactating, multiparous Holstein-Friesian and Holstein-Friesian x Jersey cross dairy cows. Cows were offered their feed allowance in the Calan gate facilities at Lye Farm (DairyNZ, Hamilton, NZ) for 38 ± 2 days. Average cow Lwt and day of gestation were 525 ± 54 kg and 206 ± 18 days, respectively.

Feeding regime

Cows were blocked on age, day of gestation and Lwt, and randomly allocated to one of eleven treatment groups. Cows in the control group were fed an estimated maintenance level of freshly cut pasture (0.55 MJ ME/kg^{0.75}; Holmes et al. 2002), plus an additional allowance for activity and pregnancy (~20 MJ ME/d; Holmes et al. 2002). Cows in the
remaining treatment groups were offered the Control diet of freshly cut pasture and either 2.5 (Low) or 5.0 kg DM (High) of fresh pasture (Past), pasture silage (Psil), maize silage (Msil), maize grain (Mgr), or palm kernel expeller (PKE). Supplements were offered first at approximately 0800, followed by the Control diet. Animals were kept indoors for approximately seven hours, after which they were released onto a bare paddock until the next morning.

**Feed and dry matter intake**

Daily individual feed offered and refused was recorded, and a representative sample of all feeds offered was collected and dried to determine their dry matter (DM) content. A second sample was dried at 60°C, ground through a 2.0 mm sieve (Christy Lab Mill, Suffolk, UK), bulked weekly, and analysed for nutrient composition by wet chemistry (DairyOne, Ithaca, NY). For pasture and pasture silage, metabolisable energy (ME) was estimated from in vitro DM digestibility (DMD*0.172-1.707: CSIRO, 2007). Feed quality values are reported in Table 1.

**Table 1:** Means (± standard deviations) for main feed components (% dry matter unless otherwise stated) measures of five evaluated feeds

<table>
<thead>
<tr>
<th>Sample Type</th>
<th>Maize grain</th>
<th>Maize silage</th>
<th>Autumn Pasture</th>
<th>Spring pasture silage</th>
<th>Palm kernel expeller</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dry matter (% fresh)</td>
<td>85.3 (7.08)</td>
<td>39.5 (5.51)</td>
<td>15.0 (3.63)</td>
<td>28.5 (3.86)</td>
<td>92.9 (7.94)</td>
</tr>
<tr>
<td>MJ ME/kg DM*</td>
<td>14.1 (0.11)</td>
<td>10.3 (0.42)</td>
<td>12.4 (0.64)</td>
<td>11.6 (0.56)</td>
<td>11.0 (0.66)</td>
</tr>
<tr>
<td>Crude fat</td>
<td>3.7 (0.39)</td>
<td>3.1 (0.52)</td>
<td>4.1 (0.92)</td>
<td>4.1 (2.33)</td>
<td>9.6 (0.79)</td>
</tr>
<tr>
<td>Starch</td>
<td>71.7 (2.03)</td>
<td>38.0 (2.86)</td>
<td>1.1 (1.07)</td>
<td>1.0 (0.72)</td>
<td>0.4 (0.27)</td>
</tr>
<tr>
<td>24hr in-vitro true digestibility</td>
<td>95.6 (1.08)</td>
<td>73.6 (2.82)</td>
<td>82.1 (3.81)</td>
<td>76.9 (3.91)</td>
<td>52.4 (3.01)</td>
</tr>
</tbody>
</table>

* MJ ME for pasture and pasture silage are estimated from DairyOne IVTD: IVTD*0.172-1.707; MJ ME for maize grain, palm kernel expeller and maize silage are converted from Meal to MJ by factor 4.186.

**Lwt/BCS change**

In all experimental periods, individual BCS was recorded once weekly (Macdonald and Roche 2011; 10-point scale). Individual Lwt was recorded once weekly in 2009 and three times per week in 2011.

**Statistical analyses and calculations**

Changes in Lwt and BCS over the experimental periods were analysed using mixed models fitted with REM in GenStat (VSN-International 2011), including period, treatment and interactions of period and treatment as fixed effects and cow as a random effect. Contrasts of treatments were included in the analyses to test differences between control and feed supplement, between feed types, between feed supplement amounts, and to test for an interaction between supplement and supplement amount. Regression analysis was used to predict Lwt gain from supplement DM intake and ME intake for each supplement, and the amount of supplement required for one kilogram of gain was calculated from these results. The k was estimated from the energy required for 1 kg Lwt gain (MJ ME), assuming 25 MJ NE/kg Lwt (Holmes et al. 2002).

**RESULTS**

Dry matter intake, ME intake, BCS and Lwt gain results are presented in Table 2. On average, Control cows consumed 7.5 kg DM/cow/d, with total DMI for the other treatments ranging from 9.3-9.8 and 10.4-11.9 kg DM for the Low and High allocations, respectively. Daily average ME intake was 95 MJ ME for Control cows and ranged from 114-127 and 125-157 MJ ME for the supplemented groups in the Low and High allocations, respectively.

Compared with Control cows, Lwt gain/d was greater (P<0.001) in cows fed supplements, and greater (P<0.001) for High compared with Low feed allocations, irrespective of feed type. However, feed type also affected Lwt gain (P<0.001), with cows on the Past treatment gaining less Lwt than cows on the other treatments (Table 2). A similar effect of feed type also tended (P=0.07) to be evident for BCS change.
Table 2: Average daily dry matter intake (DMI) and metabolisable energy (ME) intake (MEI), daily liveweight (Lwt) and body condition score (BCS) gains, and estimated efficiency of use of metabolisable energy for Lwt gain (k̄). Control cows were fed an estimated maintenance level of fresh pasture (0.55 MJ ME/kg0.75) and an additional allowance for activity and pregnancy (~20 MJ ME). Cows in the remaining treatments were fed the Control diet and one of two feeding levels (Low = 2.5 and High = 5.0 kg DM).

<table>
<thead>
<tr>
<th>Treatments</th>
<th>Control maize grain</th>
<th>Maize silage</th>
<th>Pasture</th>
<th>Pasture silage</th>
<th>Palm kernel expeller</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Low</td>
<td>High</td>
<td>Low</td>
<td>High</td>
<td>Low</td>
</tr>
<tr>
<td>Base pasture</td>
<td>7.5</td>
<td>7.3</td>
<td>7.0</td>
<td>7.1</td>
<td>9.4</td>
</tr>
<tr>
<td>DMI (kg DM/d)</td>
<td>NA</td>
<td>2.5</td>
<td>4.8</td>
<td>2.8</td>
<td>4.9</td>
</tr>
<tr>
<td>Supplement intake (kg DM/d)</td>
<td>NA</td>
<td>0.22</td>
<td>0.84</td>
<td>0.97</td>
<td>1.09</td>
</tr>
<tr>
<td>Total DMI/d (kg)</td>
<td>7.5</td>
<td>9.8</td>
<td>11.9</td>
<td>10.0</td>
<td>11.7</td>
</tr>
<tr>
<td>MEI/d</td>
<td>94.6</td>
<td>127.1</td>
<td>156.8</td>
<td>119.1</td>
<td>136.2</td>
</tr>
<tr>
<td>Lwt change/d</td>
<td>0.22</td>
<td>0.84</td>
<td>1.27</td>
<td>0.97</td>
<td>1.09</td>
</tr>
<tr>
<td>BCS change/d</td>
<td>0.01</td>
<td>0.02</td>
<td>0.03</td>
<td>0.02</td>
<td>0.02</td>
</tr>
<tr>
<td>MJ MEI/kg Lwt gain</td>
<td>66.1</td>
<td>52.9</td>
<td>73.5</td>
<td>50.4</td>
<td>40.8</td>
</tr>
<tr>
<td>k̄g</td>
<td>0.38</td>
<td>0.47</td>
<td>0.34</td>
<td>0.50</td>
<td>0.61</td>
</tr>
</tbody>
</table>

a) the difference between control vs. remaining treatments; b) differences between supplement treatments; c) differences between feeding level (irrespective of supplement type); d) interaction between supplement and feeding level.
The average ME intake required above maintenance, activity and pregnancy for Lwt gain is presented in Table 2. On average, 66, 53, 74, 50, and 41 MJ ME was required per kg of Lwt gain in cows fed Mgr, Msil, Past, Psil and PKE, respectively. This is equivalent to a $k_g$ of 0.38, 0.47, 0.34, 0.50, and 0.61, respectively. Pasture ME was used with lower efficiency ($P<0.01$) for Lwt gain than PKE, and also tended to be less efficient than Psil ($P=0.07$). PKE was used more efficiently than Mgr ($P<0.05$).

**DISCUSSION AND CONCLUSION**

Results confirm differences in the $k_g$ of feeds commonly used for BCS and Lwt gain during the dry period. The average energy required per kg of Lwt gain was greatest for Past, which was approximately 30% less efficient ($k_g=0.34$) than Psil and Msil (Table 2), but consistent with values reported by (Holmes et al. 2002; $k_g=0.33$) and CSIRO (2007; $k_g=0.34$) for autumn pasture. The $k_g$ of Msil (0.47) was similar to that outlined in NRC (2001; $k_g=0.42$).

Pasture silage had a $k_g$ of 0.50, consistent with the currently published value of 0.47 for spring pasture (Holmes et al. 2002), and in line with the reported values of CSIRO (2007) where spring pasture had a greater $k_g$ than autumn pasture. These results indicate that the process of ensiling in this study did not interfere with the quality of the forage. Interestingly, the $k_g$ of Mgr was 20% lower ($k_g=0.38$) than the values published in NRC (2001; $k_g=0.47$). The reason for the low $k_g$ for Mgr is not clear, but it may be due to differences in the partitioning of ME as it relates to varying end-products of digestion associated with feed type. The high starch content of Mgr (Table 1) may result in a greater production of propionate, rather than acetate, in the rumen (Rook 1964). Propionate is a major contributor to gluconeogenesis in the ruminant, and glucose serves as the main energy source for the conceptus (Battaglia 1978; Molina et al. 1991), with rapidly increasing demands during the second half of pregnancy (Bruckmaier and van Dorland, 2010). Thus, it is possible that a significant proportion of the energy in Mgr was used for conceptus metabolism instead of Lwt gain.

Cows fed PKE required the least energy for Lwt gain (40.8 MJ ME/kg Lwt), resulting in a $k_g$ of 0.61. This may be the result of higher fat concentrations in the PKE supplement (9.6% DM; Table 1). Because glucose serves as the main energy source for foetal growth (Battaglia 1978; Molina et al. 1991), the dam partitions glucose to the gravid uterus, preferentially utilising NEFA for energy and body reserves of the dam; thus, the greater availability of NEFA from the PKE diet would be expected to provide more energy for the dam rather than the conceptus. The ME utilised by the conceptus was not measured in the present experiment; therefore, further research investigating the effect of starch-based feeds and PKE in mid-gestation on foetal growth, is required to validate or refute these hypotheses.

The results of this study confirm differences between feeds in the efficiency of use of ME for Lwt gain and provide important information for on-farm feed budgeting to ensure cows reach the desired BCS targets. Further research should focus on reasons for the high $k_g$ of PKE, as well as the lower $k_g$ of high starch feeds offered in mid- to late gestation.

**ACKNOWLEDGEMENTS**

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Impact of integrating forage crops on commercial pasture based dairy farms

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Faculty of Veterinary Science, The University of Sydney, Camden, NSW 2570, Australia

ABSTRACT

The pasture-based dairy industry in Australia has been investigating ways to increase the quantity of forage produced above that of grazed pasture alone. In recent years a new technology of a complementary forage rotation was reported to be able to grow 40tDM.ha in one year. It involved a triple crop rotation that would be grown on 35% of the farm area. This has been termed a complementary forage system. This concept has been tested at a research farm level but not in a commercial farming situation. The aim of this study was evaluate the potential impact of implementing a CFS using a modeling approach on 8 case study farms across two different dairying regions. The results showed that 7 of the 8 farms could benefit from utilizing a CFS through an increase in total forage yields across the farm resulting in a higher operating surplus. Due to the impact on total forage yield, the largest benefits of implementing a CFS can be seen by farms that have relatively lower pasture utilization. Further research should be directed at fully understanding the cost and risks of implementing a CFS as all the present modeling has been conducted in a steady state. Irrigation water use efficiency of the CFS on commercial farms warrants further investigating.

Keywords: Pasture, forage crops, pasture-based dairy

INTRODUCTION

The pasture-based dairy industry in Australia has been looking for ways to increase the quantity of forage produced above that of grazed pasture. An option for farmers to increase the quantity of forage produced on farm is to integrate crops and pastures in sequence. The use of complementary forage crops to provide additional home-grown feed in a pasture based dairy system has been investigated by (Garcia et al. 2008). Garcia and Fulkerson (2005) developed a concept of a system of forage crops that could be grown in sequence and potentially increase the production of home-grown forage above the yield of pasture alone. This system was termed a complementary forage rotation and involved growing maize as a bulk silage crop, forage rape for an autumn grazing and a field pea crop for silage.

To investigate this concept further (Garcia et al. 2008) conducted a paddock scale experiment under full irrigation resulting in a yield of over 40tDM. ha.yr for the 3 years of the experiment. (Garcia et al. 2007) conducted a modeling exercise of these results and concluded that the optimal area for the CFR in a commercial dairy would be 35% of the land area with the other 65% left as pasture for grazing.

This CFR concept was then further explored by (Farina et al. 2011) by conducting a farmlet study integrating the CFR with pasture and this was termed a complementary forage system (CFS). It was found that it was possible to achieve over 25tDM.ha.yr yield across the whole farm (33.1tDM.ha.yr from CFR, 22.4tDM.ha.yr from pasture) and over 27,000 litres. ha.yr of milk. (Farina et al. 2011) concluded that a triple crop complementary forage system had the potential to allow an increase in production from the same land area without the need for additional bought-in feed.

The economic impact of this fully irrigated CFS on a commercial farm has been investigated by (Alford et al. 2009) by utilising a whole-farm economic model of a representative farm constructed from various information sources including the physical data from the trial conducted by (Farina et al. 2011), ABARE, and the NSW DPI. It was concluded from this work that even at the lower realized production levels that (Farina et al. 2011) reported compared to (Garcia et al. 2008) the CFS compares profitably with other strategies to increase production such as increasing pasture utilization and concentrate feeding level.

A limitation of (Alford et al. 2009) and (Farina et al. 2011) economic analyses is that they used a representative farm rather than a real case study farm. Malcolm (2004) suggested that the use of real case study farms enhance the use of model farms when evaluating new technologies and outlined the limitations of using representative farms.

With this background information it was decided that the next logical step would be to investigate the impact of a CFS on a commercial farm. In this study we hypothesized that the use of a CFS on real commercial case study dairy farms will provide a profitable way to increase milk production from the land resource already available to the farmer independent of their current production levels.
MATERIALS AND METHODS

The Case Study Farms

Eight commercial dairy farms from two regions, four from northern Victoria and four from the Hunter Valley region of NSW form the basis of this study. Production data was collected from each of the case study farms on a fortnightly basis during the years 2009-2011 and each farm has at least 12 months information recorded. The collection of the information has allowed the case studies to be developed in more depth than using historical annual point-in-time records, which provides a robustness needed to validate the modeling work. The case study farms are described in Table 1.

Table 1: Description of the case study farms used as the basis for modeling the potentiality of the CFS

<table>
<thead>
<tr>
<th></th>
<th>Northern Victoria</th>
<th>Hunter Valley</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Farm 1</td>
<td>Farm 2</td>
</tr>
<tr>
<td>Area (ha)</td>
<td>110</td>
<td>353</td>
</tr>
<tr>
<td>Peak Herd Size</td>
<td>250</td>
<td>675</td>
</tr>
<tr>
<td>Concentrate Fed (tDM/lactation)</td>
<td>1.0</td>
<td>1.9</td>
</tr>
<tr>
<td>Milk Solids (kg/ha)</td>
<td>874</td>
<td>955</td>
</tr>
<tr>
<td>Home grown feed (% of total diet)</td>
<td>76%</td>
<td>63%</td>
</tr>
<tr>
<td>Grazed pasture utilisation (tDM/ha)</td>
<td>5.7</td>
<td>5.2</td>
</tr>
<tr>
<td>Total forage utilization (tDM/ha)</td>
<td>7.7</td>
<td>7.05</td>
</tr>
<tr>
<td>Operating Surplus ($/ha)</td>
<td>$1646</td>
<td>$1456</td>
</tr>
<tr>
<td>Feed Costs ($/ha)</td>
<td>$1518</td>
<td>$1919</td>
</tr>
</tbody>
</table>

Modeling Logic

A modeling approach was used to simulate the physical production characteristics and economics of the eight case study farms. The general modeling logic was to use UDDER (Larcombe, 1989) to model the physical production characteristics of each of the case study farms and then use the outputs from UDDER as inputs into MilkBiz (NSW, DPI) to analyse the financial impact of each scenario. This modeling methodology has previously been validated by (Chapman, et al. 2008) with the difference being that they used “RedSky” for the financial analysis of the outputs from UDDER.

Forage Yields

The timing of management decisions and yields of the complementary forage rotation adopted in this study was drawn from the previous work of (Garcia et al. 2008) and (Islam et al. 2012). The cost of the various forages was taken from the economic study of the CFS by (Alford et al. 2009). The CFR yields and cost for each region are outlined in Table 2.

Table 2: Yield and cost of the forage crops used in the triple crop complementary forage rotation (CFR), adapted from APSIM (CSIRO) and (Islam et al. 2012)

<table>
<thead>
<tr>
<th></th>
<th>Northern Victoria</th>
<th>Hunter Valley</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Maize</td>
<td>Forage Rape</td>
</tr>
<tr>
<td>Yield (tDM/ha)</td>
<td>16.2</td>
<td>10.5</td>
</tr>
<tr>
<td>Cost $./ha</td>
<td>$2900</td>
<td>$815</td>
</tr>
<tr>
<td>Wastage</td>
<td>15%</td>
<td>30%</td>
</tr>
<tr>
<td>Cost $./tDM</td>
<td>$211</td>
<td>$111</td>
</tr>
<tr>
<td>Quality (MJME/kgDM)</td>
<td>9.5</td>
<td>11.4</td>
</tr>
</tbody>
</table>
Management Decisions

The forage cropping management timing was adapted from (Islam et al. 2012). The maize was planted in October and harvested in February on 35% of the farm area. After the maize was harvested the 35% of the farm area was divided into two portions with forage rape and field peas grown on half (17.5% of the farm area) and the other half being return to pasture assuming the same growth rates as the base farm model. Forage rape was available for grazing from 20th April until 26th July but limited to 5kg per head per day. Field peas were planted following the forage rape.

The following restrictions were also placed on making management decision in UDDeR.

- An increase in milking cow number was allowed on each farm in proportion to the increase in forage yields from the CFS based on quality (MJME/kgDM);
- all bought-in forage was replaced with the extra forage grown in the CFS;
- no change was made to the level of concentrate feeding per cow to avoid the concentrate feeding affecting the milk response;
- total lactating cow intake was limited to intake in the base farm scenario so as to limited the influence of diet on per cow production;

Model Validation

The fitness of the model to the actual farm data was determined by using the Root of the Mean Square Prediction Error (RMSPE) method on four production elements of total farm milk solids, total farm fat, total farm protein, and total farm litres. Once the RMSPE was below 20% it was determined that the model was calibrated sufficiently.

RESULTS

Physical production

Peak herd size was increased on every farm as a result of being able to grow a larger quantity energy through the increase in forage production on each farm (Table 1.). Farms with relatively low stocking rates were able to increase the number of milking cows at the peak number by up to 73%.

Seven of the case study farms showed an increase in milk solids production with the largest relatively increases for those farms coming from a relatively low base.

Table 3: Physical production indicators for a simulated complementary forage system (CFS) using UDDeR (Larcombe, 1989) and MilkBiz (NSWDPI) on eight case study dairy farms in two dairying regions

<table>
<thead>
<tr>
<th>Farm</th>
<th>Farm 2</th>
<th>Farm 3</th>
<th>Farm 4</th>
<th>Farm 5</th>
<th>Farm 6</th>
<th>Farm 7</th>
<th>Farm 8</th>
</tr>
</thead>
<tbody>
<tr>
<td>Peak Herd Size</td>
<td>368</td>
<td>1080</td>
<td>722</td>
<td>361</td>
<td>189</td>
<td>283</td>
<td>597</td>
</tr>
<tr>
<td>% change from base</td>
<td>47%</td>
<td>60%</td>
<td>4%</td>
<td>52%</td>
<td>35%</td>
<td>73%</td>
<td>32%</td>
</tr>
<tr>
<td>Milk Solids (kg,ha)</td>
<td>1242</td>
<td>1497</td>
<td>1920</td>
<td>1133</td>
<td>1763</td>
<td>1651</td>
<td>2770</td>
</tr>
<tr>
<td>% change from base</td>
<td>42%</td>
<td>57%</td>
<td>&lt;1%</td>
<td>70%</td>
<td>28%</td>
<td>60%</td>
<td>27%</td>
</tr>
<tr>
<td>Home grown feed (% of total diet)</td>
<td>76%</td>
<td>63%</td>
<td>65%</td>
<td>75%</td>
<td>73%</td>
<td>65%</td>
<td>53%</td>
</tr>
<tr>
<td>% change from base</td>
<td>n/c</td>
<td>n/c</td>
<td>18%</td>
<td>3%</td>
<td>4%</td>
<td>3%</td>
<td>13%</td>
</tr>
<tr>
<td>Total forage utilization (tDM, ha)</td>
<td>10.9</td>
<td>11.7</td>
<td>13.2</td>
<td>9.57</td>
<td>16.1</td>
<td>12.2</td>
<td>17.5</td>
</tr>
<tr>
<td>% change from base</td>
<td>41%</td>
<td>66%</td>
<td>&lt;1%</td>
<td>52%</td>
<td>37%</td>
<td>76%</td>
<td>52%</td>
</tr>
</tbody>
</table>
Economic Performance

The key economic performance indicators from the MilkBiz output show the potential change in operating surplus with the incorporation of forage crops on each of the case study farms. Increases in operating surplus were affected by the increasing in feed costs of the CFS compared to the base feed profile. Six of the farms modelled showed a substantial increase in operating surplus of between 16% and 40%. One farm showed only a minor increase in operating surplus of 1.5% and one farm actually had decrease in operating surplus of -19% compared the base year.

Table 4: Key economic indicators of a simulated complementary forage system (CFS) on eight case study farms using the MilkBiz (NSWDPI) financial analysis model

<table>
<thead>
<tr>
<th>Northern Victoria</th>
<th>Hunter Valley</th>
</tr>
</thead>
<tbody>
<tr>
<td>Farm 1</td>
<td>Farm 2</td>
</tr>
<tr>
<td>Operating Surplus ($/ha)</td>
<td>$2008</td>
</tr>
<tr>
<td>% change from base</td>
<td>22%</td>
</tr>
<tr>
<td>Feed Costs</td>
<td>$2619</td>
</tr>
<tr>
<td>% change from base</td>
<td>72%</td>
</tr>
</tbody>
</table>

The operating surplus reported as an output of MilkBiz is defined as \((\text{operating surplus}) = (\text{total dairy receipts}) - (\text{total overhead cost} + \text{total variable costs})\).

DISCUSSION AND CONCLUSION

The main objective of this study was to examine the effect of implementing a CFS on eight case study dairy farms across two dairy regions with the hypothesis being that incorporating a forage crop rotation will increase profitability. The results from the eight farms show that on six of the farms there is a clear economic advantage in incorporating a CFS to increase the total forage yields, milking cow number and resultant increase in milk production. One of the farms showed only a small (1.5% on base year) increase in operating surplus. This can be attributed to the increase in costs, especially feed costs, associated with the CFS.

One farm showed a 19% decrease in operating surplus after incorporating the CFS. An explanation for this result is that the farm was not able to substantially increase the forage yields compared to the base year. The forage crops that were used in the base year scenario were cheaper per unit of dry matter fed and so feed costs increased in the CFS scenario. While it would not be recommended for a farm to decrease profitability it needs to be recognized that this farm had an operating surplus of $2361/ha under the CFS scenario which was 17% higher than the next most profitable farm in the region. This result is supported by (Chapman, et al. 2012) who found that incorporating a double crop forage rotation into a grazed pasture based dairy decreased operating surplus by 33% to $1746/ha. Further investigation needs to be completed as to the conditions that would be required for a farm such as this to need to use a CPS incorporating such things as irrigation water use efficiency and changes in alternate feed prices. It also needs to be noted that the quality of maize used in the model is less than recorded when monitoring the case study farms. The energy of the maize silage in the CFS model was 9.5MJME/kgDM where as the maize silage tested on farm consistently gave results of 10.1 to 10.5 MJME/kg DM.

When all of the eight farms are compared the largest impact of utilizing a CFS on profitability is a result of increasing total forage yield. This is despite the realistic yield variations between regions used in the modeling, which in reality is considered conservative. These results show that the CFS technology can be applied across a range of farms and production systems with positive results. Total forage yields increased for three of the four farms located in Northern Victoria by 41%, 66% and 52% respectively for farms 1, 2 and 4. In the Hunter Valley the total forage yield increases were 37%, 76%, 52% and 42% for farms 5, 6, 7 and 8 respectively. The only farm to show a decrease in total forage yield was farm 3 located in northern Victoria. This farm already has a reasonably high total forage yield and the CFS replaced some of the relatively cheap pasture and crop silage with more expensive maize silage.

It appears from the results shown in Table 4 that farms with lower total forage harvest at a base year can actually benefit more from incorporating a CFS than those farms who are already harvesting relatively larger amounts of forages. It is quite possible that in reality a farmer who is able to only harvest moderate quantities of pasture could see a large increase in total forage harvest with the incorporation of forage crops. These forage crops would require different management skills compared to managing pasture grazing but in many respects this management is more simple and easy to get correct.
This paper shows that incorporating a CFS into a pasture-based dairy system can be profitable but it is not without risk. It is recommended that risk be looked at in further research especially considering the results of this study using conservative yields and costs that have been validated with actual farmers' yields. It would be beneficial to have an analysis of the risks that farmers need to consider when growing each of these crops including a seasonal analysis of where forage crops can fit into the feed base depending on the market and environmental conditions.

A limitation of this study is that it is examining the case studies in a steady state. This means that any additional cost or investment to implement a CFS have not been accounted for. It would be beneficial to examine the cost of implementing this technology on these farms and determine the appropriate payback period. It would also be beneficial to look at the impact on the water use efficiency of each of the feedbase systems and sensitivity of forage yields and costs for each of these farms.

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REFERENCES


Behaviour of dairy cattle during the periparturient period and its relationship to illness after calving

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SHORT SUMMARY

Changes in animal behaviour can be used for the early identification of sick animals. The period around parturition is a time when dairy cattle are at greatest risk of disease; monitoring behaviour during this time may help improve herd health and management.

ABSTRACT

The periparturient period, typically defined as the period immediately before and after calving, is a challenging time for dairy cows that must cope with physiological, metabolic and endocrine changes as well as a variety of environmental and management related stressors. These challenges likely contribute to the high incidence of disease observed during the weeks following parturition. Changes in behaviour during the period around parturition can be used to identify animals that are ill or at risk of disease. The aim of this review is to summarize current knowledge on the behavioural changes during the periparturient period and how these relate to illness in dairy cattle. We provide an overview of the concept of sickness behaviour, describe changes in feeding behaviour, social behaviour, and resting behaviour around parturition and how these behaviours differ between animals that become ill after parturition and those that remain healthy. This review focuses primarily on dairy cattle raised within indoor group-housed systems as the majority of our work has been focused in this area; however, literature related to pasture-based dairy production system and other farm animal species is also discussed. Reduced feeding time and intake, increased standing time, restlessness, and a reluctance or inability to successfully compete for access to resources are some examples of the behavioural changes that have been associated with illness after calving. Using behaviour to identify sick animals and those at increased risk of becoming ill will facilitate prompt treatment and provide opportunities to identify management strategies that prevent disease thus improving overall herd health and animal welfare.

Keywords: farm animals, sickness behaviour, parturition, health, welfare

INTRODUCTION

In mammalian species the transition from pregnancy to motherhood is a time of great change (Pawluski and Galea 2008; Pawluski et al. 2011) as the mother undergoes physiological, metabolic, and physical adjustments to accommodate pregnancy, parturition and the onset of lactation (Grattan et al. 2001). Environmental and management related changes are also commonly imposed on farmed animals during this period, and these changes may be additional stressors during the already difficult transition from pregnancy to lactation. For example, dairy cows often face a number of dietary changes and social regroupings, and primiparous cattle encounter novel conditions such as the milking parlour.

One of the primary challenges for dairy cattle during the periparturient period is the increase in nutrient requirements to support the onset of lactation at a time when feed intake, and thus nutrient supply, lags far behind (Drackley 1999). Although it is not clear exactly what combination of factors regulate intake around calving, these factors are likely associated with physiological state (e.g. discomfort associated with end of pregnancy, health status), environment (e.g. pen changes; disruption in social environment) and management (e.g. changes in diet formulation). Because the amount of energy obtained from dietary sources is insufficient to meet requirements, most cattle will experience a period of negative energy balance after calving, with this energy deficit being most pronounced during the first few weeks following calving (Grummer et al. 2004). Insulin resistance and increased non-esterified fatty acid (NEFA) mobilization are some of the homeorhetic adaptations that occur in dairy cattle during the periparturient period in order to increase the availability of energetic substrates; however, these physiological adaptations also place cattle at increased risk for health disorders after calving (Bell 1995; Drackley 1999).
For dairy cattle raised in intensive indoor production systems, disease and mortality rates are high during the weeks following parturition; nearly 75% of all disease occurs within the first month of calving (see reviews by Grummer 1995; Goff and Horst 1997; Ingvarsen et al. 2003; Ingvarsen 2006) often with as many as 30 to 50% of all postpartum cows being affected in some way (Le Blanc 2010). Incidence of disorders including mastitis, metritis, dystocia, ketosis, and retained placenta have been reported to be lower in dairy production systems that offer access to pasture (e.g. Bendixen et al. 1986; Washburn et al. 2002; White et al. 2002; Bruun et al. 2002); however, in extensive pasture-based systems parturition may be induced with glucocorticoids in some cattle (a practice that is currently under veterinarian supervision) in order to maintain a short seasonal calving interval. These animals may be at increased risk for challenges associated with immunosuppression and an increased incidence of retained placenta after calving (MacDiarmid and Cooper, 1982; Murray et al. 1982). High rates of disease around parturition is not unique to dairy cattle as farrowing has also been reported to be an important risk factor for sow mortality (Chagnon et al. 1999; Anil et al. 2008); with approximately 40% of all sow deaths occurring within the first few days of farrowing (Chagnon et al. 1999). Farm animals that become ill during this period are more likely to die at a younger age (e.g., Anil et al. 2008) and are less productive (e.g., Mulligan and Doherty 2008) throughout their life cycle.

Considerable research has focused on physiology, metabolism and nutrition of the periparturient animal, but despite advances in our understanding of these areas, disease and mortality rates around parturition remain high. Survey findings, representing approximately 83% of dairy cows in the U.S., have discovered that most disorders affecting periparturient dairy cows have increased in prevalence over the last 10 years (1997–2007, USDA 2008). We believe that an understanding of dairy cattle behaviour during the period around calving may provide additional insight into the high incidence of disease during this time.

Recent research has begun to focus on the value of behaviour as a disease indicator in animals (reviewed by Weary et al. 2009). For example, early work in this area found that healthy feedlot steers spent 30% more time at the feed bunk then morbid (bovine respiratory disease) steers (Sowell et al. 1998). When an electronic feed monitoring system was used, morbidity in feedlot steers could be identified 4 days earlier than conventional methods that typically involve visual observation of clinical symptoms (Quimby et al. 2001). Due to the high incidence of disease around parturition, researchers have become increasingly interested in understanding relationships of feeding, resting and social behaviour around parturition with subsequent health and performance.

The aim of this review is to summarize current knowledge regarding the behavioural changes that occur during the periparturient period including the relationship that these behaviours have to illness in dairy cattle. We begin with an overview of the concept of sickness behaviour and the theory behind its relationship to disease. Next we describe key behavioural changes that occur around parturition and how alterations in these behaviours may relate to illness. Given our own expertise we will place particular emphasis on the role of feeding and social behaviour. We also review the literature on behavioural responses to common farm management practices around parturition drawing on examples that describe the effects of space restriction, housing conditions and social groupings. This review focuses primarily on dairy cattle raised within intensive (indoor), group-housed systems with total mixed ration (TMR) feeding as the majority of our work has been completed in this area; however, literature related to extensive pasture-based dairy production systems will also be discussed. To supplement our discussion further, we provide other examples from the human, swine and rodent literature, where applicable. Lastly, we have attempted to identify gaps in the literature in the hope that this will stimulate further research in this area.

**SICKNESS BEHAVIOUR**

Behaviour changes when animals are ill. These changes, commonly termed “sickness behaviours” can include decreases in exploratory activity, reproductive activity, food and water intake, grooming and other social behaviours (Hart 1988). Originally it was believed that these behavioural changes resulted from the debilitating effects of illness but more recently researchers have suggested that these behavioural changes may be a coordinated approach to facilitate recovery and that sick animals are motivated to perform these behaviours (Hart 1988; Dantzer and Kelley 2007). Sickness behaviours help the animal to conserve and redirect energy to important physiological functions such as the immune system and these behaviours can also facilitate the febrile response that is important for combating infection. Components of the immune system have also been found to drive these behaviours directly. Specifically, pro-inflammatory cytokines such as interleukin-1 (IL-1) released by activated immune
cells communicate with the hypothalamus to control behaviour through the release of hormones (Dantzer and Kelley 2007). Cytokine induced hypophysia, for example, reduces intake of important micronutrients (e.g. zinc or iron) needed to support pathogen growth and thus in this manner decreased intake could facilitate recovery (Aubert 1999).

Stock people and veterinarians have long used sickness behaviours as clinical indicators of disease; however, it is important to note that the expression of these behaviours can be context-dependent and influenced by other motivational states (Millman 2007). For example, pigs infected with porcine reproductive and respiratory syndrome (PRRS) virus conserve heat by spending more time lying in contact with other pigs compared to non-infected pigs (Escobar et al. 2007). The expression of this behaviour is also influenced by ambient temperature. (Sutherland et al. 2007) found that when pigs were infected with PRRS but housed in an environment with an ambient temperature of 32 °C they spent less time lying in contact with another pig compared to infected pigs housed at a temperature of 24 °C. These results highlight the importance of ensuring behaviours of sick animals are appropriately interpreted as they may be influenced by a number of factors other than the disease.

Physiological stress is also related to immunity and therefore is likely also associated with sickness behaviours. Corticosteroids are well known for their anti-inflammatory properties. Studies have shown that when cattle or swine are exposed to high concentrations of cortisol there is a decrease in the ability of lymphocytes to proliferate, cytokine production (e.g. IL-2) drops, and neutrophil function is impaired (Westley and Kelly 1984; Blecha and Baker 1986; Salak et al. 1993). Other work, however, has shown that activation of the hypothalamic–pituitary–adrenal (HPA) axis does not negatively alter immunity (e.g. cytotoxicity of natural killer cells was not affected when exogenous cortisol was administered to pigs; Salak-Johnson et al. 1996). These differences may be attributed to the nature of the stressor. During acute stress, such as an injury that challenges the integrity of the body, stress hormones are more likely to be associated with priming the immune system in a manner that prepares it for invading pathogens and subsequent infection (Carroll and Forsberg 2007). However, when the stressor is chronic the effects of stress hormones on the immune system shift and become less preparatory and more suppressive (Sapolsky et al. 2000).

The immunosuppressive effects associated with chronic or persistent stress contribute to differences in disease susceptibility for stressed and non-stressed animals. Peter and Bosu (1987) reported that cows developing retained placenta after calving had higher serum cortisol concentrations 6 d prior to parturition in comparison with cows that remained healthy. (Hopster et al. 1998) found that cattle with the greatest physiological stress response to a novel environment also had the greatest immunosuppression when exposed to an endotoxin-induced mastitis challenge. Surprisingly, despite the potential for numerous environmental and social stressors during the periparturient period in dairy cattle and the high incidence of disease after calving, little research has explored the effects of stressors on subsequent behaviour and immunity.

**BEHAVIOUR AROUND PARTURITION AND ITS RELATIONSHIP TO DISEASE**

The onset of maternal care is the most obvious behavioural change during the periparturient period and has been the subject of much research (rats: Rosenblatt et al. 1988; pigs: Algers and Uvnäs-Moberg 2007; cattle: von Keyserlingk and Weary 2007; sheep: Dwyer 2008). Studies conducted primarily with rats and sheep have shown that there is a cascade of neuroendocrine changes that occur in late pregnancy and during parturition that stimulate the onset of maternal behaviour. Hormones including estradiol, progesterone, prolactin, and oxytocin have been demonstrated to be important in regulating these behaviours (Bridges 1984; Rosenblatt et al. 1988).

Maternal behaviour can be considered to encompass all those behaviours expressed by the gestating or lactating mother that facilitate offspring survival including, changes in feeding, resting, and social behaviour. However, maternal behaviour is also commonly used to describe the suite of behaviours expressed by the mother in late gestation (e.g. nest building) and those behaviours directed towards the offspring throughout lactation until the young are weaned (Dwyer 2008).

Illness during the period around parturition may interfere with normal maternal behaviour and affect the survival and development of offspring (e.g. providing maternal milk or thermoregulation; Bahr et al. 1998). These consequences are especially important in systems such as extensive beef operations or swine production, where the mother provides care for her young as opposed to dairy production systems where the calf is generally removed from its mother soon after birth. Below we describe in more detail behavioural changes that occur around parturition (see also Table 1) and how these vary with illness.
Table 1: Summary of the key behavioural adaptations observed in dairy cattle during the periparturient period

<table>
<thead>
<tr>
<th>Behavioural Adaptation</th>
<th>Stage Relative to Parturition</th>
<th>Description of Behaviour</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Isolation-seeking</td>
<td>d 0</td>
<td>Pasture Beef Cows: increased distance from nearest neighbor</td>
<td>Lidfors et al. 1994</td>
</tr>
<tr>
<td>Rumination</td>
<td>-9 h to +3 h</td>
<td>Rummation activity declines (nadir at +3 h)</td>
<td>Houwing et al. 1990</td>
</tr>
<tr>
<td></td>
<td>d -1 and d 0</td>
<td>Standing bouts increase by 80%</td>
<td>Huzzey et al. 2005</td>
</tr>
<tr>
<td>Increased Restlessness</td>
<td>d -1 to d +1</td>
<td>Longer standing times than pre- or post-partum</td>
<td>Huzzey et al. 2005</td>
</tr>
<tr>
<td></td>
<td>-3 h to +3 hrs</td>
<td>% of time standing nearly doubles during 3 h after calving relative to 3 h before</td>
<td>Houwing et al. 1990</td>
</tr>
<tr>
<td></td>
<td>Periparturient</td>
<td>Healthy cows: Prepartum DMI stable until d-1 where it drops significantly; intake then recovers postpartum following a slight drop on d -1 from day of calving intake level</td>
<td>Huzzey et al. 2007</td>
</tr>
<tr>
<td>Food Intake</td>
<td>Prepartum</td>
<td>40% depression in DMI beginning d -2 to d 0</td>
<td>Vazquez-Añon et al. 1994</td>
</tr>
<tr>
<td></td>
<td>Prepartum</td>
<td>36% decline (cows) and 26% decline (heifers) in DMI beginning d -21 to d 0</td>
<td>Vandehaar et al. 1999</td>
</tr>
<tr>
<td></td>
<td>Postpartum</td>
<td>DMI increases 1.5 to 2.5 kg/week over first 21 d of lactation</td>
<td>Bertics et al. 1992; Kertz et al. 1991</td>
</tr>
<tr>
<td>Feeding Activity (Cow)</td>
<td>Periparturient</td>
<td>Longer feeding times pre-partum than postpartum (healthy cows)</td>
<td>Huzzey et al. 2005; Huzzey et al. 2007</td>
</tr>
<tr>
<td></td>
<td>Periparturient</td>
<td>More meals postpartum than pre-partum</td>
<td>Huzzey et al. 2005</td>
</tr>
<tr>
<td>Allogrooming</td>
<td>d 0</td>
<td>Time spent licking calf is greatest during hours following delivery</td>
<td>Edwards and Broom 1982; Metz and Metz 1986; Edwards 1983</td>
</tr>
<tr>
<td>Nursing (Calf)</td>
<td>Postpartum</td>
<td>Nature (e.g. beef cow-calf operations): calf suckles 25 min/d (6-8 meals) during first month</td>
<td>Vitale et al. 1986</td>
</tr>
<tr>
<td>Standing Time</td>
<td>Periparturient</td>
<td>Similar pre- and post-partum; longest daily standing times around calving</td>
<td>Huzzey et al. 2005</td>
</tr>
</tbody>
</table>

1 d 0 = day of calving; negative days (hours) refer to the prepartum period; positive days (hours) refer to the postpartum period
Feeding behaviour

Nutrient requirements increase during the final weeks of pregnancy to support the final stages of foetal growth and prepare the mammary gland for lactation. Following parturition nutrient requirements remain high to support the demands of lactation and therefore changes in feeding behaviour around parturition are important to the overall health of the animal. In rats, food intake increases by up to 50% during pregnancy and up to 300% during lactation compared to non-pregnant rats (reviewed by Augustine et al. 2008). However, in many mammalian species food intake declines in the days before parturition. For instance, intake generally show declines in sows 3 to 4 d before parturition (Hurnik 1985). In dairy cattle, a decline in dry matter intake is typically observed 2 to 3 weeks before parturition followed by a gradual increase in dry matter intake during the weeks following calving (Grummer et al. 2004); time spent feeding follows a similar pattern as dry matter intake before and after calving in dairy cattle (Huzzey et al. 2005).

The decline in intake before parturition is associated with endocrine changes that also occur during this time (Ingvartsen and Andersen 2000). In most mammalian species estradiol levels gradually increase at the end of pregnancy and peak just before parturition (reviewed by Rosenblatt et al. 1988); increased levels of this hormone have been associated with depressed food intake (Czaja and Goy 1975; Blaustein and Wade 1976; Gong et al. 1989) and altered feeding behaviour, including decreases in meal size and meal frequency (Blaustein and Wade 1976; Geary and Asarian 1999; Eckel 2004).

Nutritional status before calving may also be an important regulator of intake during the periparturient period, with feed intake affected by hormones such as leptin and insulin (Broberger 2005). Cattle that are over-fed (150% of National Research Council (NRC) recommendations for NE) late in pregnancy have higher concentrations of NEFA in circulation due to decreased tissue responsiveness to insulin, higher BHBA concentrations, and lower DMI after calving relative to cattle that are not over-fed (80 to 100% of NRC recommendations for NE) during late pregnancy (Dann et al. 2006). Similar to dairy cattle, there is a decline in the ability of insulin to suppress NEFA mobilization during late gestation in humans (Cantalano et al. 2002). In pigs, an increased back fat depth at farrowing is associated with greater serum leptin concentration (Estienne et al. 2000), greater insulin resistance and lower feed intake (Weldon et al. 1994a; Weldon et al. 1994b).

Aside from hormonal signals associated with depressed intake, other physiological factors can also influence food intake and feeding behaviour. For example, the size of the foetus may affect intake of cows and small ruminants in late gestation; the growing foetus is thought to reduce space available in the abdomen for the rumen causing animals to eat less (Stanley et al. 1993; Laporte-Broux et al. 2011). Individual animal factors can also influence feed intake during this period. For instance, multiparous sows are generally less prone to reductions in food intake than primiparous sows perhaps due to the previous experience of the multiparous sows with the stressors during the farrowing period (Lawrence et al. 1994).

Several studies have shown that both feeding behaviour and feed intake change in response to illness during the periparturient period and that these changes occur well before clinical signs of disease are evident. (Urton et al. 2005) showed that Holstein dairy cows diagnosed with acute metritis (uterine infection) after calving spent less time at the feed bunk beginning 12 days before calving; for every 10-min decrease in feeding time, cows were twice as likely to be diagnosed with metritis after calving. In a follow-up study, (Huzzey et al. 2007) found that metritic cows also had lower DMI as far back as 2 weeks before calving and 3 weeks before clinical signs of disease (Figure 1A). (Goldhawk et al. 2009) reported that cows that were diagnosed with subclinical ketosis within 1 week after calving spent less time at the feed bunk, visited the feeder less often, and consumed less feed during the week before calving and the 2 week period after calving (Figure 1B).
Figure 1: Differences in dry matter intake (kg) between cows that remain healthy throughout the first 21 days of lactation and those with severe metritis (A), subclinical ketosis (B) and subclinical hypocalcemia (C). Data is adapted from Huzzey et al. 2007 (A), Goldhawk et al. 2009 (B), and Jawor et al. 2012 (C).

Postpartum illness is not always associated with lower feed intake before calving. Cows that were diagnosed with subclinical hypocalcemia within 24-h after calving (serum calcium concentration ≥ 1.8 mmol/L, without clinical milk fever) had greater dry matter intake during the 2 week period leading up to calving; after calving dry matter intake tended to be higher only during week +2 relative to calving (Figure 1C; Jawor et al. 2012). In that study cows with subclinical hypocalcemia were producing nearly 6 kg/d more milk during the first 4 weeks of lactation; however, increased prepartum intake cannot be explained by an increase in nutrient requirements to support higher milk yield after calving as these cows were not yet lactating. Higher levels of feed intake pre-partum may interfere with the regulation of feed intake post-partum, as well as calcium metabolism, but more work is required to elucidate the mechanism of action. Cows with subclinical hypocalcemia made fewer visits to the water trough during the first 2 weeks after calving and tended to make fewer visits to the feed bins during weeks 1 and 3, suggesting that they used these resources more efficiently around calving.

Feeding behaviour around calving also differs for cattle that develop claw horn lesions later in lactation compared with those that maintain good hoof health (Proudfoot et al. 2010). Claw horn lesions, including sole haemorrhages and sole ulcers, are a major cause of lameness in cattle. These lesions become clinically visible approximately 8 to 12 weeks after calving but develop during the period around calving (Chapinal et al. 2009). Cows with lesions during mid-lactation consumed feed at a faster rate during the 2-week period before calving and consumed approximately 5 kg more DMI during the 24 h after calving, relative to cows without lesions that were fed the same diet (Proudfoot et al. 2010). A high rate of intake is associated with feed sorting for small particles which, when combined with a higher feed intake, may increase risk for ruminal acidosis (DeVries et al. 2007; Fairfield et al. 2007). Unfortunately, this study could not confirm that increased intake contributed to acidosis-related changes in the hoof. Future work is encouraged to identify the possible mechanisms by which the development of lesions may be affected by feeding behaviour around calving.

The research described does not allow us to determine if changes in health are the result of changes in feeding behaviour, or vice versa. Differences in feeding behaviour might be due to undiagnosed disease, with the behavioural changes exacerbating the original condition, or increasing the risk of the animal succumbing to other ailments (Weary et al. 2009). Given the frequent regroupings that result in a dynamic group composition (von Keyserlingk et al. 2008) during the periparturient period, other factors such as the social environment and management may also influence aspects of feeding activity and consequently also be related to subsequent health.

Social behaviour

Dairy cattle are social animals and readily establish social relationships that can influence other aspects of behaviour including feeding and resting activity (Val-Laillet et al. 2008). Social behaviour may include any activity that involves two or more individuals, such as aggression associated with competition for resources and allogrooming associated with the formation of social bonds. These types of behaviours, which generally offer longer-term benefit, are predicted to decline more rapidly than behaviours such as feed intake, as animals divert resources with long-term value to those of immediate importance such as thermoregulation or
feed intake (Weary et al. 2009). Declines in social activities such as allogrooming (grooming a conspecific) are recognized as sickness behaviours in laboratory animals (Hart 1988; Dantzer and Kelley 2007). While some social behaviours around calving have been well described including those related to the cow-calf bond, other social behaviours, often related to management changes at calving, including interacting with unfamiliar individuals and competing for resources, have received less attention. Even less research has explored the relationship between social behaviour and disease in dairy cattle around the calving period.

Maternal aggression is important for the defence of offspring (Bosch and Neumann 2012). Studies conducted primarily with laboratory animals demonstrate changes in this behaviour during the periparturient period (Caughey et al. 2011). For instance, aggressive behaviour in laboratory rats (defined as an increased frequency of attacks or threats toward an intruder rat in the home cage) increase gradually during the last days before parturition (day 16 through day 19; gestation period in rats: 19–22 days) with maximal aggressive responses a few hours before parturition (Rosenblatt et al. 1994; Caughey et al. 2011). These behaviours are likely modulated in part by hormonal fluctuations such as oxytocin and vasopressin, among other neurotransmitter systems (reviewed by Bosch and Neumann 2012). Although aggression drops immediately following parturition, it increases again during early lactation and then reduces again at weaning (Caughey et al. 2011). Aggression has been also described in farm animals in the hours before labour in sows (defined as single or multiple lunge towards pen-mates; Arey et al. 1992) and ewes (defined as an increase frequency of attacks towards another neonatal lamb; Dwyer 2008). To date no work has examined changes in aggressive behaviour in dairy cattle around parturition with subsequent disease risk but we suggest that this may be a promising area of inquiry.

Allogrooming is another behaviour that is important around parturition. Cows spend much of the first few hours after birth licking the calf; this behaviour is important for stimulating calf activity, including circulation, urination and defecation (Metz and Metz 1986). Licking can occupy nearly 30 to 50% of a dam’s time during the first hour after birth (Edwards and Broom 1982). It has also been suggested that licking of the newborn calf is essential in establishing the maternal-infant bond. Young are at increased risk of being abandoned when the mother is prevented from licking them (Klopf er et al. 1964; Hudson and Mullord 1977). Failure to lick is more common in first lactation animals than multiparous animals (Edwards 1983). To date there has been no work examining the relationship between disease around calving and the expression of allogrooming behaviour.

In extensive production systems, establishing a strong bond between the dam and her calf is important as she provides protection and nourishment to the young neonate (von Keyserlingk and Weary 2007). However, most dairy cattle production systems separate cow and calf within 24 h following parturition, with the intention of reducing time available for the establishment of strong social bonds. The time to separation may be shorter for cattle raised indoors compared to those raised on pasture since calving pens in barns typically in a location that can be frequently monitored by farm staff. Several studies have shown that the behavioural responses of cows to separation from their calf (i.e. increased vocalization, time with head outside pen, and standing time) are greater the longer that the pair is allowed to remain together following calving (e.g. after 4 h or 2 weeks; Weary and Chua, 2000; Flower and Weary, 2001). Increased stress associated with delayed cow-calf separation may influence the health and incidence of disease in cows following calving; however, this relationship has yet to be investigated and we encourage further work in this area as it may be particularly relevant to beef operations and pastoral dairy operations.

In nature cows will typically suckle their calf approximately 25 min per day during the first month and divide this time into approximately 6–8 sucking events (Vitale et al. 1986); this process is very different than the twice or three times daily milking routine used on most commercial dairy operations following cow-calf separation (von Keyserlingk et al. in press). (Dahl et al. 2004) reported that somatic cell counts were lower in cows milked 6 times per day in the first 21 days compared to cows only milked three times per day. These authors suggested increased milking frequency early in lactation influences the mammary gland capacity to resist mastitis. The question therefore arises as to whether failure to express maternal behaviours such as nursing can influence the health status of the cows. More work is needed to clearly establish the links between suckling/milking frequency and udder health and whether the prevention of certain aspects of the maternal behaviour may also have detrimental effects on health.

Competition is another important aspect of social behaviour in dairy cattle and during the period around calving cows may face a number of management related changes that can influence this behaviour. These changes may include movements
to new pens or pastures to accommodate production stage (e.g. non-lactating pregnant vs. lactating) and changes in stocking density, situations that can alter the social dynamics of cattle reared in groups; these management practices will be discussed in detail later in this review. Competitive behaviour can be expressed in physical (e.g. butting, pushing) or non-physical ways (e.g. eye contact, threatening to butt, etc.). Aggressive competitive behaviour is described as the physical action of an animal to make another animal (usually lower ranked) withdraw from a resource (Fraser and Broom 2007). This behaviour can cause fear, lead to injury or affect other aspects of behaviour such as feeding or resting times. For example, (Proudfoot et al. 2009a) found that when cows reared in a free-stall barn were overcrowded during the period around calving, there was an increase in competitive displacements from the feeding area and cows tended to have lower intake during the prepartum period relative to cows fed in a non-competitive environment.

In many farm animal species social competition is regulated by dominance relationships between individuals (Drews 1993). For example, dominance at the feed bunk may be defined as having priority of access to the feed bunk (e.g. feeding first) or being more successful at displacing others from the feed bunk, particularly in situations where feeding space is limited. Previous work has shown that level of success in competitive interactions during the period around calving may be related to postpartum disease risk. (Huzzey et al. 2007) reported that cows that developed metritis after calving displaced others from the feed bunk less often before calving, relative to cows that remained healthy. These sick cows also spent less time feeding and consumed less feed during the periods of the day when feed bunk occupancy was highest; this period corresponded to the hours following fresh feed delivery, a time when cows are highly motivated to eat and when feed palatability and quality are highest (DeVries and von Keyserlingk 2005). Peak feeding time, however, is when the feed bunk is most crowded and therefore when competition for feed is greatest, suggesting that cows that go on to become sick after calving lack the motivation to compete for access to feed before calving and may benefit from more feeding space during this time. Similarity, (Goldhaw et al. 2009) reported that cows that developed subclinical ketosis within 1 week of calving were less likely to be socially engaged at the feed bunk up to two weeks before calving. Research conducted with goats has also shown that when feeding space is restricted near the end of gestation, doe’s are at increased risk for developing pregnancy toxaemia (Mavrogiani and Brozos 2008) likely due to the increased frequency of aggressive competitive interactions which limit the ability of some animals to gain access to feed (Conway et al. 1996). The results of these studies suggest that prepartum social interactions may play an important role in disease susceptibility. However, similar to the relationships between feeding behaviour and disease, the question remains as to whether the changes in health are the result of changes in social behaviour, or vice versa. We encourage further work in this area to understand the mechanisms by which social behaviour and health may be related.

**Standing and lying behaviour**

During the period immediately around parturition animals become increasingly restless, likely due to the discomfort associated with the delivery process. (Huzzey et al. 2005) reported that among dairy cattle, daily standing time during the days around calving (d-1 to d+1) were on average 2 h longer than during the 10 days prior to calving and 1 h longer than during the 10 days after calving. This study also found that the frequency of standing bouts (transitions between lying and standing) increased by 80% during the days around calving further suggesting that cattle were more restless, likely due to calving discomfort. Similarly, farrowing sows increase the number of times they change positions from lying to standing as parturition approaches, with this behaviour peaking between 12 to 6 hours prior to birth of first piglet (Vestergaard and Hansen 1984). Cattle that have difficulty in delivering the calf (dystocia) transition from lying to standing positions more frequently than cows without dystocia beginning 24 h before calving (Proudfoot et al. 2009b).

Lameness has not traditionally been considered a disease associated with parturition, likely because hoof pathologies are generally not noticed until mid-lactation for cattle raised indoors; hoof lesions, however, take months to become visible and it is likely the period around calving where the lesions first begin to develop (Cook and Nordlund 2009). Decreased free-stall use and increased standing time on hard surfaces such as concrete are associated with increased risk of developing hoof lesions and lameness (Webster 2002; Tarlton et al. 2002). For cattle raised on pasture, lameness may develop from cattle being herded daily to and from the milking parlour on poorly maintained trails or races, long periods standing, and being shifted to concrete yards while waiting to be milked (Chesterton et al. 1989). Consequently, changes in standing and lying behaviour during the period around calving may be an important factor influencing subsequent lameness risk in cattle. Recent work has begun to show how the physiological and behavioural changes during the calving period among cattle raised indoors increase
the risk of lameness later in lactation (Knott et al. 2007; Proudfoot et al. 2010). Cows diagnosed with lesions in mid lactation stood on average 2 h/d more during the 2 week period before calving compared to cows that were not lame and spent 4 h/d more time standing during the 24 h period following calving (Proudfoot et al. 2010). These differences were driven by an increase in the time spent ‘perching’ with the front 2 feet in the lying stall, suggesting that longer standing times and standing with 2 feet in a stall during the period around calving can serve as early indicators of lameness later in lactation.

Longer standing times around parturition have also been associated with subclinical hypocalcemia in dairy cattle. Cows diagnosed with subclinical hypocalcemia within 24 h of calving, spent nearly 3 h longer standing during the 24-h period preceding parturition compared to cows with normal plasma calcium concentrations (Jawor et al. 2012). These authors hypothesized that calcium-deficient animals could have experienced additional discomfort and therefore longer standing times during the calving process if labour was prolonged due to weak uterine contractions; calcium is essential for proper myometrial smooth muscle cell contractility (López-Bernal 2003). More research, however, is encouraged to understand the mechanisms by which metabolic disorders around calving relate to standing and lying behaviour.

**THE EFFECTS OF CATTLE MANAGEMENT ON BEHAVIOUR**

Management during periparturient period affects various aspects of behaviour and therefore may also be related to disease risk. Below we discuss the behavioural responses to common farm management practices around parturition drawing on examples that describe the effects of space restriction, housing conditions and social re-groupings. A summary of these effects is also provided in Table 2 along with recommendations for management changes that may improve behaviour and thus health in dairy cattle kept in indoor housing.

**Table 2.** The effects of common management practices on dairy cattle behaviour and suggested changes in management to improve behaviour and health during the periparturient period.

<table>
<thead>
<tr>
<th>Management Practice</th>
<th>Behavioural Consequence</th>
<th>Recommendations</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Restricted Feed Bunk Space</td>
<td>• Increased competition • Lower feeding time • Longer inactive standing • Increased feeding rate • Variable effects on DMI</td>
<td>• Provide 76 cm of linear bunk space per animal (or 1 headlock / cow) • Headlocks reduce competition • Post-rail barriers may decrease inactive standing • Increase frequency of fresh feed delivery to increase feeding time</td>
<td>Behaviour: Olofsson 1999; Huzzey et al. 2006; Proudfoot et al. 2009a Recommendations: DeVries et al. 2005; Huzzey et al. 2006; NFACC 2009</td>
</tr>
<tr>
<td>Restricted Lying Space</td>
<td>• Increased competition • Lower lying time • Increased lameness risk • Sacrifice feeding time to rest</td>
<td>• Provide 1 lying stall / cow in free-stall pen • Provide 15 m² / cow in individual maternity pens</td>
<td>Behaviour: Fregonesi et al. 2007a; Metz 1985 Recommendations: NFACC 2009</td>
</tr>
<tr>
<td>Regrouping / Pen Changes</td>
<td>• Lower dry matter intake on day of regrouping • Increased feeding rate • Decreased rumination • Increased displacements from feeder • Allogrooming reduced</td>
<td>• Avoid moving single animals • Limit number of pen moves • Avoid overcrowding in regrouped pen</td>
<td>Behaviour: von Keyserlingk et al. 2008; Schirmann et al. 2011 Recommendations: Grant and Albright 2001; Cook and Nordlund 2004; NFACC 2009</td>
</tr>
<tr>
<td>Inappropriate Lying Stall Design or Management</td>
<td>• Longer standing times • Increased lameness risk • Increased Perching</td>
<td>• Widen stalls or move neck rail further back from curb to decrease 2-foot standing • Clean stalls regularly and re-bed to increase lying time • Use deep-bedded stalls to decrease lameness risk</td>
<td>Behaviour: Tucker and Weary, 2004; Fregonesi et al. 2007b; Tucker et al. 2005 Recommendations: Tucker et al. 2004; Fregonesi et al. 2009; Drissler et al. 2005 Chapinal et al, in press</td>
</tr>
</tbody>
</table>
Studies exploring the effect of space availability on dairy cows raised indoors have found that overstocking the feed bunk (Proudfoot et al. 2009a) and lying stalls (Fregonesi et al. 2007) to the extent that animals cannot eat or lie down simultaneously, increases aggressive competitive displacements. Animals that are less successful at this competition must be active at less favoured times, avoid activity when certain dominant animals are active, or tolerate less preferred places (Galindo and Broom 2000). Research has shown that socially subordinate animals (those that are the least successful at displacing others from the overstocked resource) have the greatest improvements in activity (e.g. feeding times) when they are provided more space (DeVries et al. 2004).

Increased competition due to overstocking can also affect other aspects of behaviour. For example, multiparous cows that were overstocked at the feed bunk (2 cows to 1 feeding station) during the week before calving had lower feed intakes relative to cows that were not crowded (Proudfoot et al. 2009a). Similarly, research with pigs has shown that reducing pen size or increasing group size can decrease daily feed intake and appetite in these animals (Walker 1991; Gonyou and Stricklin 1998). Overstocking during the time around calving was also associated with an increase in feeding rate among multiparous cows, with those cattle that were the least successful in competitive interactions at the feed bunk having the highest rates of intake (Proudfoot et al. 2009a). Overstocking also results in longer periods of inactive standing, as cows wait by the feeder to gain access to feed (Olofsson 1999; Huzzey et al. 2006; Proudfoot et al. 2009a). Certain feed bunk designs may help reduce displacement frequency during periods of overstocking for cattle reared indoors (DeVries and von Keyserlingk 2006; Huzzey et al. 2006). Providing physical separation between the necks of cattle, as with a head-lock feed barrier, or between the bodies of cattle, as with specially designed feeding stalls (DeVries and von Keyserlingk 2006), has been shown to decrease displacement frequency during periods of overstocking when compared with more open feed barrier designs (e.g. post-rail feed barrier) (reviewed by von Keyserlingk and Weary 2010). More research is required to determine if the use of these types of feed barriers during the periparturient period can reduce disease risk.

Extensive pastoral dairy production systems do not experience the same stocking density pressures (cows per unit of area) as in intensive indoor production. Although cattle housed on pasture do engage in aggressive interactions, these occur less frequently compared with cows housed indoors (Phillips and Rind 2001). Low forage availability or variable quality pasture may, however, still lead to competitive feeding environments. In free-roaming grazing cattle, preferences for plant communities were found to be proportional to the relative differences in quality (preference for higher crude protein percentage) and quantity of preferred forage (Senft et al. 1985); if high-quality feeding sites are limited on pasture, cattle may engage in increased competitive interactions in order to obtain access to the best foraging locations. However, to our knowledge no work has looked specifically at whether competitive interactions take place or increase in these situations therefore, this may warrant investigation.

Longer standing times can also occur when there are problems in cow housing or management; for example, cows housed in pens with little or wet bedding, or restrictive neck rails spend more time standing than those with dry stalls and neckrails that are located further back in the stall (Tucker and Weary 2004; Fregonesi et al. 2007b; Fregonesi et al. 2009). Perching with 2 front feet in the stall during the period around calving has also been linked to restrictive stall design (Tucker et al. 2005; Fregonesi et al. 2009). Research has shown that cows spend less time perching when the stalls are designed in such a manner as to allow cows to stand fully inside the stall (e.g., by widening the stall or moving the neck rail further from the rear curb; Tucker et al. 2004; Fregonesi et al. 2009). In pasture-based systems, larger herd sizes or grazing cattle on pastures located a long distance from the milk parlour, can lead to longer times spent walking to and from the milking parlour and longer times spent standing on concrete waiting to be milked (Stafford and Gregory 2008); this may be a risk factor for lameness (Chesterton et al. 1989).

Under natural conditions animals often isolate themselves from their herd mates in the hours immediately before parturition (von Keyserlingk and Weary 2007). For example, although cows are naturally gregarious, the onset of maternal behaviour in free ranging cattle begins at the point when a cow isolates themselves from herd mates and chooses a nesting site for the delivery of the calf (Lidfors et al. 1994). On intensively managed dairy farms cattle are generally moved to an individual maternity pen next to the prepartum group or left to calf in large group pens where there is typically little to no space for them to isolate themselves from the rest of the herd. The inability to seek and obtain an isolated space for calving may be stressful to cattle and this increased stress may play a role in subsequent health; this hypothesis however has not been experimentally tested and further research in this area is encouraged.

Confinement production systems, such as tie-stalls for dairy cows and gestation stalls for sows,
limit the ability of animals to engage in any form of exercise, prevent the animal for being able to turn around, and limit her ability to groom. Rats subjected to restraint during gestation show signs of depressive behaviour and elevated cytokines (O’Mahony et al. 2006) and increased anxiety postpartum (Pawluski et al. 2011). Pregnant sows are generally kept in individual crates that restrict movement and this may increase stress around parturition (de Groot et al. 2007). Confinement systems may represent potential stressors capable of negatively affecting behaviour and physiology, and thus may contribute to an increased risk for health or production related complications around parturition. There is some evidence suggesting that lack of exercise (in sows) is a risk factor for coliform mastitis (Ringarp 1960; Hoy 2002); however, the role of space restriction and subsequent disease risk requires further investigation. We suggest that behavioural changes associated with restrictive environments may put animals at greater risk of impaired immune function and disease but more work is required to test these predictions.

In many farm animal production systems it is common practice to mix unfamiliar animals into new groups at various stages of production. On intensively managed dairy farms, for example, the periparturient period may include up to 4 to 5 group changes; cows are typically moved from a far-off (non-lactating group) to a close-up group (within 3 weeks prepartum) to an individual maternity pen for the calving event, and then to the main lactating herd after calving. Similarly, during the spring calving season on extensive pastoral dairy operations cattle are brought together to form mobs (high density groups of grazing cattle) according to stage of production; in these systems cattle will also undergo several group changes which may include moving cattle through a dry (non-lactating) cow mob, springer mob, colostrum mob, and finally into the main grazing herd. Regrouping may have negative consequences for both behaviour and health. Research with dairy cows raised indoors has shown increased aggression in the days following regrouping (von Keyserlingk et al. 2008). (Schirmann et al. 2011) found that cows that were more aggressive at regrouping also reduced their intake, feeding rate, rumination activity and number of lying bouts during the period following mixing with unfamiliar individuals. Regrouping has also been shown to disrupt the behaviour of pigs by increasing aggressive interactions prior to the establishment of a new stable social hierarchy (Couret et al. 2007). Sows that have been moved into a new social group develop more skin lesions (as a result of aggressive behaviour), avoid high ranking or resident animals, have higher cortisol concentrations and lower weight gains, relative to sows that are not regrouped (Arey and Edwards 1998; Hayne 2000 and Gonyou 2003; O’Connell et al. 2004; Jarvis et al. 2006; Couret et al. 2007). Future work in this area should focus on gaining a better understanding of individual responses to regrouping during the period around calving, and how this management practice influences an animal’s susceptibility to disease after parturition. Work is also needed to ascertain the effects of regrouping cattle housed on pasture, particularly in cases where animal densities are high or resources may be limiting.

Around parturition dairy cattle must cope with a host of environmental and management related stressors which may include high stocking densities, new social groups, confinement systems, or novel environments (e.g. movement to maternity pen or milk parlour for the first time). Animals choose different strategies to cope with stressful environments, and some strategies are more successful than others. In a recent review, (Proudfoot et al. 2012) described how behavioural responses of individuals to stressful management practices can be different and are related to each individuals “coping style”. Two distinctive coping styles have been described: 1) proactive coping, which is characterized by territorial control and aggressive behaviour in response to a stressor, and 2) reactive coping, which is characterized by low-aggression and conservation-withdrawal type behaviours in responses to a stressor. For example, in an environment where cattle are overstocked at the feed bunk a proactive coping strategy may be to actively engage in competitive interactions at the feed bunk in order to achieve bunk access during the peak feeding periods (i.e. following fresh feed delivery) whereas a reactive coping strategy would be to wait until later times in the day to feed, when bunk occupancy is lower and there is little need to compete for access to the feed. Both of these strategies result in the cow gaining access to the feed, but the manner in which they do so is different. Interestingly, studies have shown that these two coping styles are characterized by different physiological profiles. Animals exhibiting a reactive coping strategy tend to have greater activation of the hypothalamic-pituitary-adrenal axis with greater concentrations of circulating cortisol (see Koolhaas et al. 1999). Sustained over-activation of hypothalamic-pituitary-adrenal axis with greater concentrations of circulating cortisol has been linked with immunosuppression in dairy cows (Hopster et al. 1998) and pigs (Tuchscherer et al. 2004), suggesting that this coping style may also be an important factor influencing disease risk around parturition. We suggest that future research aimed at exploring the relationship between behaviour and health during the periparturient period, also consider individual coping strategies.
CONCLUSION

The periparturient period is a critical time for dairy cattle that must cope with physiological and environmental adjustments that threaten their health and welfare. Many animals have difficulty making the transition from pregnancy to lactation, as evidenced by the high incidence of disease that occurs during the weeks immediately following parturition. An expanding body of literature shows that behavioural changes around parturition not only identify which animals are sick but also which animals are at increased risk for becoming sick. As such, behavioural monitoring may be useful to inform management adjustments that facilitate disease prevention or to promptly identify animals in need of treatment. Key behavioural changes associated with illness after parturition include reduced feeding time, lower feed intake, long periods of inactive standing, restlessness, and an inability or reluctance to socially compete for important resources such as the feed bunk or lying stalls. Stockpersons can use these changes to identify management strategies that improve health around the transition period.

Future research should combine measures of nutrition, metabolism, physiology and immunology during the periparturient period with these key behavioural changes to identify the most effective management strategies that will reduce the incidence of disease around calving.

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 Gestational Stress Leads to Depressive-Like Behavioural and Immunological Changes in the Rat. *Neuroimmunomodulation*. **13**, 82-88.


Nutritional management of the transition cow in the 21st century – a paradigm shift in thinking

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ABSTRACT

The transition period is defined as the 6 to 8 wk encompassing late pregnancy and early lactation, involving coordinated changes across multiple tissues and an enormous increase in nutrient requirements. Failure to transition successfully results in reduced dry matter intake, milk production, delayed oestrus, failure to conceive, and increased incidence of metabolic and infectious diseases, many of which are inter-related. Modern technologies have enabled the measurement of transcriptional changes in genes involved in multiple biochemical pathways across the transition period, enabling a better understanding of the implications of management and nutritional changes on cow health and productivity. The effect of pre-calving dry matter intake on subsequent cow health and productivity is discussed, with results of recent experiments challenging the long-held recommendations for nutritional management of transition dairy cows. The physiological role of fatty acids, in addition to the role of fat as an energy source is discussed, as is the lack of information on production responses to protein intake and metabolisable protein supply. Immune dysfunction and metabolic disorders are discussed and, finally, knowledge gaps and future research areas are identified.

BACKGROUND

The 6 to 8 week (wk) period of transition between late pregnancy and early lactation poses an enormous metabolic challenge to the high-yielding dairy cow. Failure to adequately meet this challenge through a series of complex homeorhetic adaptations can result in a range of inter-related metabolic diseases, suboptimal production and high rates of culling in early lactation (Curtis et al. 1985; Goff and Horst, 1997b; Godden et al. 2003). The major metabolic hallmarks characterising the transition period in healthy and functionally compromised cows have been described in numerous reviews (e.g. Bell, 1995; Goff and Horst, 1997b; Drackley et al. 2001). Recently, this literature has been extended to describe some of the molecular mechanisms underpinning metabolic adaptations in the peripartal cow (Loor, 2010). Many other reviews have summarised the diverse array of nutritional management strategies proposed to minimise metabolic dysfunction and the risk of disease in the periparturient period (Grummer 1995; Horst et al. 1997; Overton and Waldron, 2004). Despite decades of intensive metabolic research and the trialling of numerous nutritional strategies to maintain dry matter intake (DMI) and control the mobilisation of body stores of fat, calcium, and, to a lesser extent, protein in early lactation, the incidence of metabolic disease and impaired performance remains high in both intensively managed confinement and more extensive pasture-based systems. The purpose of this review is to integrate recent research findings with previous knowledge of transition cow metabolism and nutrition, and to offer some new insights into key elements of successful management of the transition cow.

ADAPTING TO LACTATION ONSET – PHYSIOLOGICAL CHANGES AND MOLECULAR REGULATION

Changes in nutrient requirements

The dramatic increases in nutrient requirements following parturition have been quantified in terms of mammary demands for synthesis of milk lactose, fat and protein versus the lesser pre-partum needs of the conceptus for glucose, fatty acids (FA) and amino acids (Bell, 1995). Changes in calcium and other mineral requirements have been estimated similarly (Goff and Horst, 1997b). Briefly, it was estimated that in a Holstein cow producing 30 kg milk at 4 days post-partum, the mammary requirements for glucose, FA and amino acids are, respectively, 2.7, 4.5 and 2.0 times those of the gravid uterus during late pregnancy, and the estimated mammary requirement for energy is 3.0 times that of the uterus (Bell, 1995). Similarly, Goff and Horst (1997b) estimated that the mammary requirement for calcium to produce 10 kg colostrum on the day (d) of parturition is more than double that for foetal growth in late gestation. Additional nutrient requirements of non-mammary tissues also undergoing peripartal hypertrophy, such as the liver and gut, will add to the challenge.

Since average values for DMI increase by only about 30% between late pregnancy and d 4 of lactation, much of the abruptly increased requirements for specific nutrients and energy must be met by increased hepatic gluconeogenesis and...
the mobilisation of body stores of fat, protein and calcium. Indeed, (Reynolds et al. 2003) and (White et al. 2012) confirmed a major increase in hepatic gluconeogenesis in cows between 1 wk pre-partum and 1 wk post-partum.

The massive mobilisation of body fat is achieved by a combination of increased lipolysis and decreased rates of lipogenesis and FA re-esterification in adipose tissue, leading to the net release of non-esterified FA (NEFA) and glycerol into the bloodstream (Bell, 1995; Drackley et al. 2001; Roche et al. 2009). The homeorhetic changes required to achieve this tissue mobilisation appear to be primarily under genetic control (McNamara and Hillers, 1989), with little nutritional influence during the first 5 wk of lactation (Roche et al. 2006; McCarthy et al. 2007; Roche et al. 2009). Plasma NEFA are efficiently used for mammary triacylglycerol (TAG) synthesis and can be oxidised in most non-mammary tissues. In addition, glycerol is a readily assimilated precursor for hepatic gluconeogenesis.

Mechanisms of a more moderate mobilisation of amino acids from, so-called, labile tissue protein reserves are less well understood. However, evidence points to suppression of protein synthesis and possibly, increased proteolysis in skeletal muscle (Bell et al. 2000). In the immediate post-partum period, there also appears to be some diversion of amino acids from splanchnic tissue synthesis and secretion of export proteins that may support much of the suddenly increased hepatic requirement for glucogenic substrate for at least a few days after calving (Bell et al. 2000).

Adaptations to increase the blood supply of calcium very soon after calving include increased resorption of bone stores, increased intestinal active transport and decreased urinary excretion of calcium (Horst et al. 2005).

Homeorhetic and homeostatic regulation of physiological changes associated with the transition from pregnancy to lactation

The concept of homeorhesis implies the agency of endocrine or neuroendocrine factors capable of responding to physiological and environmental changes and of simultaneously influencing disparate metabolic functions in multiple tissues. Such a role has been convincingly demonstrated for growth hormone (GH) in lactating dairy cows, based on detailed observations of metabolic, physiological and molecular responses to treatment of cows with exogenous GH and to changes in endogenous GH secretion induced by altered physiological and metabolic states (Bauman, 2000; Etherton and Bauman, 1998). These include most of the previously described metabolic adaptations that underpin increased fat mobilisation and hepatic gluconeogenesis during the transition state (Roche et al. 2009), which, most notably, are associated with a marked and sustained increase in circulating GH concentrations (Block et al. 2001; Roche et al. 2005; Roche, 2007).

The likely positive effects of GH on the mobilisation of body fat stores and increased gluconeogenesis in transition cows are associated with attenuation of its usually potent stimulation of hepatic synthesis of IGF-1 and its binding proteins (Boisclair et al. 2006; Lucy et al. 2009). This effect has been attributed to a 50% decrease in hepatic GH receptor abundance at parturition, which gradually increases during the first 14 (Radcliff et al. 2003) to 50 days (Lucy et al. 2009; Grała et al. 2011) post-partum and appears to be directly influenced by prevailing insulin concentrations, which, in turn, are determined by energy balance (EBAL) and/or dietary carbohydrate type (Rhoads et al. 2004; Grała et al. 2011). Periparturient suppression of the trophic influences of IGF-1 on skeletal muscle and other tissues is consistent with net release of amino acids and reduced glucose utilisation by peripheral tissues in support of mammary and hepatic metabolic demands.
Decreased EBAL and insulin concentrations during the transition period are also likely to be responsible for marked decreases in adipose synthesis and blood concentrations of the hormone, leptin, soon after calving (Block et al. 2001; Leury et al. 2003). In ruminants, as in rodents, this anorexigenic peptide appears to act principally on the hypothalamus to regulate DMI and peripheral metabolism, indicating that the prolonged depression in leptin concentrations during early lactation may assist the concomitant recovery of DMI and EBAL (Boisclair et al. 2006).

The known physiological actions and peripartal blood profiles of several other hormones, including oestradiol-17β, progesterone, placental lactogen, prolactin and cortisol, are consistent with putative homeorhetic influences on dairy cattle during late pregnancy and early lactation. However, convincing evidence of a causative role in homeorhetic processes has yet to be provided.

**Molecular regulation of homeorhesis**

Most research evidence to date, although derived mainly from rodent work, indicates that changes in expression of messenger RNA (mRNA) exert a major influence on physiological function. Many of the homeorhetic changes discussed previously correspond with changes in transcript abundance (i.e. abundance of mRNA) for key genes, indicating that molecular changes underpin the physiological perturbations associated with the transition from pregnancy to lactation (Loor, 2010). With advancing technology enabling more targeted molecular assays in multiple tissues, knowledge of the mechanisms underpinning peripartal homeorhetic changes and, arguably more importantly, the effect of environmental factors on peripartal metabolism continues to increase. Information published up to early 2010 on changes in expression of hepatic genes associated with lipid, carbohydrate and nitrogen metabolism in transition dairy cattle was reviewed recently (Table 1: Loor, 2010). In general, changes in mRNA expression correspond with changes reported in biochemical studies. For instance:

- increased peroxisomal -oxidation (Grum et al. 1996) in liver immediately post-partum is consistent with the increased hepatic expression of acyl-CoA oxidase (Loor et al. 2005), the rate-limiting enzyme in this pathway
- increased blood NEFA and the decreased body fat mass immediately post-partum are consistent with the decrease in expression of several lipogenic enzymes in adipose tissue (Sumner-Thomson et al. 2011; Ji et al. 2012) and corresponds with lower enzymatic rates (McNamara et al. 1995)
- copious synthesis of milk fat, protein, and lactose post-partum is consistent with the marked increase in nutrient utilisation (Bell, 1995), enzyme activity (Mellenberger et al. 1973), and expression of key enzymes in mammary tissue (Bionaz and Loor, 2008; Bionaz and Loor, 2011; Bionaz et al. 2012)
- the peripartal decrease in GH receptor expression in liver coincides with low circulating concentrations of IGF-1 and correspondingly high concentrations of GH (Lucy et al. 2009; Grala et al. 2011)
- the increase in the liver’s ability to use alanine for glucose synthesis after calving (Overton et al. 1998; Reynolds et al. 2003) is consistent with an increase in mRNA expression for the enzymes pyruvate carboxylase (PC) and phosphoenolpyruvate carboxykinase (PEPCK1: Greenfield et al. 2000; Hartwell et al. 2001; van Dorland et al. 2009; White et al. 2012)
**Table 1:** Evaluation of the pattern of change of key metabolic pathways in liver, adipose, and mammary tissue of dairy cattle from late-pregnancy to early post-partum. Adapted and expanded from the summary by Loor (2010), (Sumner-Thomson *et al.* 2011), (Bionaz *et al.* 2012), and (Ji *et al.* 2012).

<table>
<thead>
<tr>
<th>Pathway</th>
<th>Biological process</th>
<th>Time post-partum</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Liver</strong></td>
<td></td>
<td>First week</td>
</tr>
<tr>
<td>Ureagenesis</td>
<td>Arginine biosynthesis</td>
<td>No change to decrease</td>
</tr>
<tr>
<td>Glucose metabolism</td>
<td>Glycolysis and TCA cycle</td>
<td>Modest increase</td>
</tr>
<tr>
<td>Growth hormone signalling</td>
<td>IGF-1 binding/transport</td>
<td>Decrease</td>
</tr>
<tr>
<td>Gluconeogenesis</td>
<td>Glucose synthesis</td>
<td>No change to modest increase</td>
</tr>
<tr>
<td>Lipoprotein metabolism</td>
<td>Synthesis of lipoprotein</td>
<td>Decrease</td>
</tr>
<tr>
<td>Cholesterol metabolism</td>
<td>Synthesis and transport</td>
<td>No change to decrease</td>
</tr>
<tr>
<td>Fatty acid transport</td>
<td>Cellular uptake</td>
<td>Modest increase</td>
</tr>
<tr>
<td>Fatty acid oxidation</td>
<td>Mitochondrial and peroxisomal degradation of long-chain fatty acids</td>
<td>Modest increase</td>
</tr>
<tr>
<td>Fatty acid esterification</td>
<td>Long-chain fatty acid transfer into triacylglycerol</td>
<td>Increase</td>
</tr>
<tr>
<td>Ketogenesis</td>
<td>Synthesis of ketone bodies</td>
<td>Decrease</td>
</tr>
<tr>
<td>Lipid droplet formation</td>
<td>Desaturation and cytosolic lipid storage</td>
<td>Modest increase</td>
</tr>
<tr>
<td><strong>Adipose</strong></td>
<td>Lipogenesis and adipogenesis; transcriptional regulation; glucose uptake</td>
<td>Marked decrease</td>
</tr>
<tr>
<td>Lipolysis</td>
<td>Hormone-stimulated and basal lipolysis</td>
<td>Modest increase</td>
</tr>
<tr>
<td>Insulin signalling</td>
<td>IRS-1 phosphorylation</td>
<td>Decrease</td>
</tr>
<tr>
<td>Insulin signaling pathway</td>
<td>Gene expression</td>
<td>Decrease</td>
</tr>
<tr>
<td>Fatty acid transport and nutrient use</td>
<td>Long-chain fatty acid uptake, transport, and lactate utilisation</td>
<td>Modest decrease</td>
</tr>
<tr>
<td><strong>Mammary</strong></td>
<td>Fatty acid synthesis, triacylglycerol synthesis, cholesterol and sphingolipid synthesis, desaturation</td>
<td>Marked increase</td>
</tr>
<tr>
<td>Lipid metabolism</td>
<td>Lactose synthesis</td>
<td>Marked increase</td>
</tr>
<tr>
<td>Carbohydrate metabolism</td>
<td>Oxidative phosphorylation and Krebs cycle</td>
<td>Increase</td>
</tr>
<tr>
<td>Energy metabolism</td>
<td>His, Val, Leu, and Ile metabolism</td>
<td>Increase</td>
</tr>
</tbody>
</table>

1Data encompass analyses of subcutaneous adipose biopsies harvested at -30 or -14 days from calving and at 7, 14, and 21 days post-partum.
2From (Sumner-Thomson *et al.* 2011) using microarrays.
3From (Ji *et al.* 2012) using *in vitro* phosphorylation assay and quantitative reverse-transcription (RT) polymerase chain reaction (PCR).
4From Bionaz and Loor (2008, 2011) and (Bionaz *et al.* 2012).
The emphasis in dairy cattle physiology research, to date, has focussed on metabolic enzymes. However, as in the case of homeorhesis, tissue responses are coordinated by a complex network of proteins that “share” information arising from cues (e.g. hormones and metabolites) from within the organ or from the external milieu (e.g. the blood). These networks have evolved so that tissues can accurately respond to external signals and either maintain homeostasis or provide priority to certain physiological functions (e.g. milk production); hence, regulation of mRNA transcription plays a pivotal role in coordinating physiological function during the transition period (Figure 1).

The proteins responsible for the regulation and accessing of genetic information (i.e. transcription regulators) have evolved to function together in regulatory modules or multi-protein complexes that possess many different activities. An example of such regulation is the involvement of peroxisome proliferator activated receptors (PPAR) in the coordination of liver and skeletal muscle adaptations to fasting and under-nutrition. In rodents, the PPAR (α, γ, and δ) are activated by saturated and unsaturated long-chain FA (LCFA), essentially as a function of the intracellular concentration; for example, fasting and under-nutrition enhances influx of LCFA to liver and increases the availability of LCFA that bind to and activate PPAR (Figure 1). These nuclear receptors represent one of the best-studied models of metabolic control at the molecular level. The pathways that can be affected by nuclear receptors encompass not only FA oxidation and ketogenesis but also gluconeogenesis and ureagenesis (Mandard et al. 2004). Evidence for the existence of a functional PPARα network in ruminant liver has been obtained in neonatal calves, in which injection of a specific pharmaceutical ligand led to upregulation of several PPARα target genes (Litherland et al. 2010). The net result of an increase in mRNA expression is an increase in abundance of the functional protein, which, given that availability of substrate is not limiting, should lead to an overall increase in flux through the pathway (e.g. FA oxidation, gluconeogenesis, and ureagenesis: Figure 1).

**Figure 1:** Schematic model of nutrient metabolism in liver and the underlying molecular adaptations that allow for synthesis of energy (ATP), ketone bodies, urea, triacylglycerol (TAG), very-low density lipoproteins (VLDL), and glucose. Gene symbols for key enzymes in mitochondrion and peroxisomes are in capitals. Incoming non-esterified fatty acids (NEFA) can serve as activators of peroxisome proliferator activated receptor-alpha (PPARα), thus, helping to coordinate metabolic adaptations to dietary fatty acids or negative energy balance. This scheme underscores the central role of liver in coordinating adaptations occurring not only through diet (i.e. nutrient provision) but also in peripheral tissues during catabolic states (e.g. adipose and muscle during negative energy balance).

**Summary**

The transition from pregnancy to lactation is a significant metabolic challenge, with almost instantaneous, several-fold increases in the requirement of cows for energy, protein and minerals. A successful transition involves the initiation and coordination of changes in multiple organs that facilitate the provision of these nutrients to the cow and, more specifically, to the mammary gland, often at the considerable expense of other tissues; this coordination of metabolic priorities is termed homeorhesis and there is increasing evidence that peripartal changes in the transcript abundance of genes involved in key metabolic pathways underpin this orchestration of changes in seemingly unrelated tissues. An increasing knowledge of metabolic pathway integration and more targeted functional laboratory assays are providing scientists with a greater opportunity to explore the effects of environment on these important metabolic changes. These data will improve the understanding of management and nutrition on the success or failure of a cow’s transition and help provide recommendations to farmers on ways that optimise this important and potentially costly period of the cow’s lactation.
**DRY MATTER INTAKE**

Profile of change in periparturient dry matter intake

Intake regulation is complex. The central nervous system undertakes the homeostatic role of sensing nutrient intake and body reserves, integrating the information, and regulating energy intake and/or energy expenditure (Roche et al. 2008). Information regarding metabolic state can be transmitted to the intake control centres of the brain by a diverse array of signals, such as stimulation of the vagus nerve or metabolic “feedback” factors derived from the pituitary gland, adipose tissue, stomach/abomasum, intestine, pancreas, and muscle (Woods et al. 1998). These signals act directly on the neurons located in the arcuate nucleus of the medio-basal hypothalamus, a key site for integration of hunger (orexigenic) and satiety (anorexigenic) responses in the brain.

In most situations, the “drive to eat” increases with energy requirements (Woods et al. 1998; 2000; Roche et al. 2008). A major exception to this rule appears to be the pre-partum dairy cow, whose DMI is reported to decline during the weeks preceding parturition (Coppock, 1972; Lodge et al. 1975; Bertics et al. 1992) despite increasing energy requirements for foetal growth and lactogenesis (Bell, 1995). However, this decline is not universal. For example, (Coppock et al. 1972) reported no decline in DMI until dietary starch concentration exceeded 25% of the ration DM. This is consistent with the decline in DMI in sheep intravenously infused with oestrogen when offered starch-containing pellets but not when offered hay (Forbes, 1972; Forbes, 2007). The effect of oestrogen on selection against starch-containing feeds appears to be moderated by body condition score (BCS; Weston, 1996), with the decline in DMI greater in higher BCS animals. Consistent with the effect of a dietary forage:concentrate ratio on the peripartum decline in DMI, Roche (2006) reported no decline in DMI in the weeks preceding calving in dairy cows fed a 50:50 mixture of fresh pasture and dry feeds appears to be moderated by body condition score (BCS; Weston, 1996), with the decline in DMI greater in higher BCS animals. Consistent with the effect of a dietary forage:concentrate ratio on the peripartum decline in DMI, Roche (2006) reported no decline in DMI in the weeks preceding calving in dairy cows fed a 50:50 mixture of fresh pasture and pasture hay, irrespective of whether the cows were fed to energy requirements or restricted to 80% of energy requirements.

Recent research from von Keyserlingk’s group at University of British Columbia has added further to the understanding of factors regulating the peripartum decline in DMI. Seminal work associating behavioural and DMI changes before calving with post-calving diseases (Huzzey et al. 2007; Goldhawk et al. 2009) has highlighted that cows which succumb to either ketosis or metritis after calving have a lower DMI pre-calving, but there was no evidence of a change in feeding behaviour or DMI until the onset of parturition in those that remained healthy post-calving. Considering data on disease prevalence, the “average” herd profile of DMI change during the weeks before calving would indicate a decline in DMI; however, the data imply that this is associated with an unidentified, non-evident malaise pre-partum rather than a natural decline associated with impending parturition. Consistent with the putative influence of this “non-evident pre-partum malaise” on post-partum health, (Burke et al. 2010a) reported an increase in subclinical uterine inflammation 28 to 42 days post-calving in cows that had lower concentrations of blood albumin pre-calving than their non-affected counterparts. Thus, (Huzzey et al. 2007) and (Burke et al. 2010a) identified changes to animal behaviour and physiology prior to evident pathology. The low blood albumin was suggested by (Burke et al. 2010a) to reflect liver dysfunction in this situation.

Collectively, these data indicate that the peripartum decline in DMI is a result of interactions between management, nutrition, and pregnancy-related hormonal changes and, although common, is not an immutable parturition-related phenomenon. Starch-based feeds have been reported to contribute to the decline in DMI, which, furthermore, has been associated with poor health post-calving. Additional research is required to determine the dietary and management factors that may be contributing to the liver inflammation/dysfunction that is putatively associated with the failure of cows to transition successfully and whether mitigation strategies will result in improvements to health and productivity during early lactation.

The importance of pre-calving dry matter intake and energy balance

Epidemiological and metabolic research undertaken over recent decades has been interpreted to support the original recommendation to “prime” or “steam up” the cow several weeks before calving (Boutflour, 1928), based on a positive association between pre-calving plasma NEFA and the incidence of metabolic disease (Dyk et al. 1995), and a negative association between liver TAG accumulation and pre-partum energy intake (Bertics et al. 1992). However, closer examination of the latter two reports reveals inconsistencies in the derived conclusions; for example, there was no effect of pre-partum DMI on liver TAG content at 4 wk post-partum, but cows in the high pre-calving DMI group had greater plasma NEFA and almost double plasma -hydroxybutyrate (BHBA) concentrations of the low pre-calving DMI group at 2 wk post-partum (Bertics et al. 1992). These results are consistent with more recent US (Douglas et al. 2006) and NZ (Roche et al. 2005) research reporting a linear
relationship between early post-partum live weight loss and pre-calving DMI. Also, research studies in Europe (Agenas et al. 2003; Holtenius et al. 2003), the US (Dann et al. 2006; Douglas et al. 2006) and NZ (Roche et al. 2005; Roche, 2007) provided no evidence that a pre-calving increase in plasma NEFA negatively affects post-partum metabolism or disease incidence. In fact, cows that were feed-restricted for several weeks before calving had increased capacity for hepatic gluconeogenesis and -oxidation, reduced hepatic TAG accumulation and a reduced risk of milk fever and ketosis (Holtenius et al. 2003; Loor et al. 2006; Roche et al. 2005; Roche, 2007). Thus, contrary to accepted dogma, high energy intakes pre-calving may increase the risk of metabolic diseases in early lactation.

The collective literature points to a deficiency in the epidemiological research model, from which associations are often extended to reflect cause and effect before the underlying physiology is properly considered. It is now apparent, that both post-partum disease and metabolic indicators of negative energy balance before calving had increased capacity for hepatic gluconeogenesis and -oxidation, reduced hepatic TAG accumulation and a reduced risk of milk fever and ketosis (Holtenius et al. 2003; Loor et al. 2006; Roche et al. 2005; Roche, 2007). Thus, contrary to accepted dogma, high energy intakes pre-calving may increase the risk of metabolic diseases in early lactation.

The drain of nutrients by the conceptus and mammary gland places considerable nutrient demand, above maintenance, on the cow during the final weeks pre-calving. Additional factors, however, have resulted in the belief and recommendation that the provision of non-fibre carbohydrates (NFC) as an energy source will improve the transition success of the dairy cow. Assumed benefits are believed to result from three factors:

- the ability of NFC to stimulate ruminal papillae development;
- acclimatisation of the rumen microorganisms to the high NFC ration offered post-calving;
- provision of a more readily available supply of nutrients, such as glucose, for the conceptus to prevent maternal loss of energy reserves.

Papillae development

Because of the results of one study (Dirksen et al. 1985), providing feeds high in NFC pre-calving is often recommended to enhance papillae development. However, such a recommendation is an over-extrapolation of those results, wherein papillae development was improved in cows fed a high grain diet compared with those fed a poor-quality forage (straw). In comparison, (Andersen et al. 1999) compared cows fed a more typical forage-based ration for non-lactating dairy cows (pasture silage) with cows supplemented with ~4 kg DM of barley in the morning. Macroscopic and histological examinations of the rumen epithelia indicated no differences between the two diets. This result is consistent with the predominant influence of ruminal butyrate production on rumen papillae development and maintenance (Sakata and Tamete, 1979) and the fact that supplementation with cereal concentrates has little effect on ruminal butyrate production in cows fed fresh pasture or pasture silage (Dalley et al. 2001).
**Rumen adaptation**

When highly fermentable carbohydrates are introduced into the diet the production of volatile FA (VFA) increases, reducing rumen pH. This change in pH exerts selective pressure on the microbial population and needs to be undertaken gradually, thereby allowing a stable fermentation pattern to continue. Of the reasons cited earlier for a greater level of NFC in the pre-calving diet, this reason is, arguably, the most valid. However, (Hernandez-Urdaneta et al. 1976) disputed the need to feed concentrates pre-calving for ruminal adaptation as cows in their study could be changed from prep-artum diets of nearly all forage to high concentrate diets (60% concentrates) post-partum without any adverse effects on feed intake, rumen fermentation or milk production. In contrast, (Weimer et al. 2010) noted that although rumen pH and VFA patterns returned to normal within 24 hours (h) in cows subjected to an exchange of ruminal contents, changes to the microbial population took up to 61 days. This is consistent with the low rumen pH following concentrate feeding 28 days post-partum reported by (Andersen et al. 1999) in cows that were supplemented with barley pre-calving. Considering there was no difference in ruminal epithelium histology, this difference could be a result of different populations of ruminal microorganisms and associated differences in the efficiency of degradation of NFC. This may mean that gradual adaptation to the post-calving diet is worthwhile, particularly if it is substantially different in NFC content to the pre-calving ration.

Further research on the length of time required for ruminal transition between feeds offered to grazing dairy cows is needed to minimise digestive disturbances and maximise transition success.

**Gluconeogenic precursors to spare maternal reserves**

As the primary sources of energy used for conceptus metabolism are glucose, lactate, and amino acids (see review by Bell, 1995), the provision of gluconeogenic precursors could be expected to reduce the catabolism of labile protein stores and reduce the need for mobilisation of FA from adipose tissue for -oxidation in peripheral tissues. In support of this, a number of studies (see review by Overton and Waldron, 2004) reported increased DMI, reduced NEFA and BHBA, and increased post-partum milk production in cows supplemented with NFC sources pre-calving. However, as reported by Overton and Waldron (2004), the majority of these studies were confounded by energy intake as well as carbohydrate source. (Smith et al. 2008) in TMR-fed cows and (Roche et al. 2010) in pasture-fed cows evaluated isoenergetic diets that differed in their carbohydrate composition: (Smith et al. 2008) compared 34 and 40% NFC and (Roche et al. 2010) compared 13 and 32% NFC in the pre-partum ration. Post-calving milk yield, composition and secreted NE, and BCS change were not affected by pre-calving carbohydrate type in either TMR or pasture-fed cows, refuting the hypothesised benefits of pre-calving dietary NFC inclusion. (Roche et al. 2010) did highlight treatment differences in metabolic parameters, however, with lower blood albumin concentrations pre-calving and during the colostrum period in cows on the high NFC diet. Blood albumin, a negative acute phase protein, is an indicator of liver health, declining in situations of liver dysfunction. These data imply a potentially negative effect of NFC on peripartum metabolism in pasture-based systems that requires further investigation.

In apparent support of a lack of a benefit from changing pre-calving dietary carbohydrate composition, results from a recent study indicated that providing a cow with NFC instead of structural carbohydrate, under otherwise isoenergetic conditions, will not “spare” maternal tissue stores (Mandok et al. 2012). Results, in fact, indicate a less efficient conversion of energy to live weight gain from high starch feeds compared with high NDF feeds in late gestation dairy cows. It was hypothesised that the high NFC feeds would result in increased ruminal lactate and propionate production, increased hepatic expression of PEPCK1 and, therefore, gluconeogenesis, with the resultant glucose (and potentially lactate) being utilised by the conceptus for energy, while the acetate production from structural carbohydrate would increase de novo lipogenesis. Mechanisms aside, the data do not support a use of NFC in preference to structural carbohydrates as a means of sparing maternal tissues in late gestation.

**The importance of dietary fat**

Over the past fifteen years, there has been substantial interest in the effect of lipid supplementation during the periparturient period for improving liver metabolism and health (Grum et al. 1996; Selberg et al. 2004, 2005; Douglas et al. 2004; Petit et al. 2007; Andersen et al. 2008; Ballou et al. 2009; Hayirli et al. 2011). The degree of lipid supplementation has been mostly within the range of traditional recommendations (e.g. 3-4% of supplemental lipid to not exceed ~6% of DM as total lipid).

The primary aim in the studies undertaken during the 1990s was to provide additional energy in the form of fat to help thin cows replenish adipose stores during the dry period (Grum et al. 1996); however, evidence from rodent studies at that time also sparked interest in the potential of LCFA to manipulate liver lipid metabolism around parturition
and prevent TAG accumulation (i.e. enhance LCFA oxidation: Drackley 1999). More recent research has explored the effects of saturated, trans, and poly-unsaturated (PU) FA-rich sources on hepatic metabolism (Selberg et al. 2004, 2005; Andersen et al. 2008) and reproduction (Santos et al. 2008).

The roles of specific FA in liver metabolism have been investigated in vitro, with the effects of palmitic acid (16:0) alone or in combination with stearic acid (18:0), oleic, linoleic (18:2n-6), linolenic (18:3n-3), eicosapentaenoic (20:5n-3; EPA), or docosahexaenoic (22:6n-3; DHA) acid on liver metabolism examined using monolayer cultures of calf hepatocytes (Mashek and Grummer 2003). They reported increased BHBA concentrations and oxidation of 14C-palmitic acid to ketone bodies during incubations of 1 mM 16:0 + 1 mM 18:0. Linolenic acid resulted in the highest rates of gluconeogenesis from [14C]-propionic acid and greatest amounts of intracellular glycogen, along with reduced TAG production. An interesting finding was that 22:6n-3 alone or with 20:5n-3 increased cellular TAG content and incorporation of 14C-palmitic acid into cellular TAG. In addition, 22:6n-3 alone decreased metabolism of 14C-propionic acid to glucose in the medium or to cellular glycogen. Although thought provoking, a criticism of this study could be the use of supra-physiological concentrations of each FA (peak total NEFA concentration is rarely greater than 1.5 mM; Drackley, 1999). In addition, isolated hepatocytes incubated for 48 h are sufficiently far removed from the regulatory responsiveness and functioning in cow’s liver tissue (e.g., diminished basal gluconeogenic activity; Donkin and Armantano, 1993) to make them inappropriate for addressing the biological effects of purified FA. Given the limitations in obtaining and maintaining bovine hepatocytes in culture, use of liver tissue collected via biopsy for in vitro studies is a feasible alternative that has not been thoroughly explored.

Intravenous infusions of TAG emulsions from oils with different FA profiles have also been used to study the potential effects of specific FA on liver lipid and carbohydrate (e.g. gluconeogenesis) metabolism (Mashek et al. 2005). Comparisons of tallow (contained 43% 18:1 and 26% 16:0), linseed (contained 51% 18:3n-3, 21% 18:1, and 6% 16:0), and fish oil (contained 32% EPA + DHA, 15% 18:1, and 20% 16:0) emulsions infused over four days into fasted, non-lactating, non-pregnant cows imply that different lipid sources can influence development of fatty liver. Among these oils, linseed resulted in a tendency (P = 0.10) for lower liver TAG compared with tallow and fish oil. Plasma NEFA were also lower with linseed oil, compared with tallow, indicating the supplemental 18:3n-3 might have had an effect on adipose metabolism (Mashek et al. 2005). Considering the primary FA in pasture is also 18:3n-3, these results have implications for grazing systems and the effects of dietary FA require further investigation.

In summary, there is compelling evidence that, in addition to providing energy to the transition cow, specific FA could alter lipid and carbohydrate metabolism in the bovine liver to different extents. A greater knowledge of these effects could be used to positively influence liver metabolism peripartum, thereby reducing liver TAG accumulation and enhancing gluconeogenesis and other important aspects of liver function.

Can the liver be primed to the onset of parturition by feeding fat?

The concept of “priming” liver metabolism ahead of calving so that the level of desired LCFA (e.g. PUFA vs. saturated) is enriched in liver and adipose tissue (Douglas et al. 2006; Andersen et al. 2008; Ballou et al. 2009) merits consideration. However, to test such a hypothesis thoroughly, there is need to design dose-response studies including both saturated and unsaturated LCFA sources and FA combinations representative of the late-pre-partum and early post-partum period. With such an approach, the degree of LCFA enrichment of the liver phospholipid pool or adipose stores could be assessed and how this affects metabolic pathways and, in particular, the molecular targets that regulate liver function. At the core of these studies is the hypothesis that the intracellular concentration of a desired LCFA can be enriched and FA oxidation increased at the expense of esterification. The potential effect of LCFA supplementation could likely go beyond liver and adipose tissue metabolism per se, because work with rodents (Li et al. 2005; Mishra et al. 2004) has provided evidence that the very-long chain PUFA (e.g. EPA, DHA) can reduce production of pro-inflammatory cytokines through effects on gene expression. Inflammation, for example, has been reported to result in fatty liver in rats (Dickerson and Karwoski, 2002) and there is increasing evidence of similar events occurring in the liver of periparturient cows (Loor et al. 2005; 2006; Bradford and Farney, 2010).

Are there potential practical approaches to target nuclear receptors in cow tissues?

In non-ruminants, the direct metabolic effects of LCFA appear linked to their ability to bind and activate nuclear receptors (e.g. PPAR, hepatocyte nuclear factor-4-alpha: HNF4A), with subsequent increases or decreases in expression of sets of genes involved not only in metabolism, but in various cellular functions (e.g. cell proliferation, signal
transduction, apoptosis: Desvergne et al. 2006). Among PPAR, PPARα is highly-expressed in liver of both rodents and dairy cattle, and its activation in rodents increases the expression of all the key enzymes involved in cholesterol synthesis and FA oxidation; PPARα can also directly enhance the synthesis of some apolipoproteins (e.g. apo-AI and apo-AII: Puigserver, 2005; Barish et al. 2006) and gluconeogenic genes. Unlike classical endocrine receptors that bind to high-affinity glandular hormones, PPAR bind to lower-affinity ligands generated from dietary fat or intracellular metabolism and turn on feed-forward metabolic cascades to regulate lipid homeostasis via the transcription of genes involved in lipid metabolism, storage, and transport (Barish et al. 2006; Desvergne et al. 2006). Studies reviewed here and elsewhere (Loor, 2010) indicate that PPAR have biological relevance in ruminants and might represent novel biological targets to optimise liver and adipose adaptations to the onset of parturition. Bovine PPAR also respond to pharmaceutical agonists and LCFA (Thering et al. 2009; Bionaz et al. 2012). Several recent studies have evaluated different types of lipid and their capacity to reduce liver lipid deposition, but results have been inconsistent. For example, (Kulick et al. 2006) used a dry-cow model in which water, tallow, or linseed oil was infused into the abomasum. Contrary to the results of (Mashek et al. 2005), tallow (high in 16:0 and c9-18:1) was more beneficial than linseed oil in reducing liver TAG accumulation during feed restriction. In another recent study (Andersen et al. 2008), saturated fat (16:0 mainly) pre-partum was more efficacious than flaxseeds (high in 18:3n-3) in preventing TAG accumulation at 2 wk post-calving. This appeared to be coupled with numerically greater palmitate oxidation to CO₂ and ketone bodies. Although it is challenging to compare across studies, results appear to be consistent with in vitro results indicating that longer-term incubation with 16:0 (Mashek and Grummer, 2003) enhanced ketogenesis to a greater extent than PUFA. The nRC (2001) indicated a metabolisable protein requirement for their example Holstein cow and heifer during late pregnancy of approximately 900 g/d. However, this estimation did not include an increment for synthesis of mammary tissue, which (Bell et al. 2000) approximated at about 120 g/d, resulting in an overall predicted requirement of between 1,000 and 1,100 g/d. This is unlikely to be an issue in grazing systems where at least 50% of the dry cow diet is provided by high protein forages. However, where fresh forage is not a major component of the pre-partum ration, as in a typical dry cow TMR during the late pre-partum period, this predicted requirement cannot be met without supplemental protein sources and, in particular, ruminally undegradable sources. Consistent with this assessment, modestly positive responses have been reported by increasing level of protein feeding during the pre-partum period (reviewed by Bell et al. 2000). However, there are also indications that excessive supply of crude protein may be detrimental to performance (Putnam et al. 1999; Hartwell et al. 2001); this may be attributed to the apparently impaired capacity of the liver to detoxify ammonia to urea as TAG accumulation increases during the immediate peripartum period (Strang et al. 1998; Zhu et al. 2000).

For dairy cows during the immediate post-calving period, protein requirements and predictions of supply are complicated by both the increased demand for glucoenic amino acids (Reynolds et al. 2003) and the contributions of catabolised body proteins to the overall amino acid pool. (Garcia-Bojalil et al. 1998a, 1998b) fed high protein diets (~21% CP) containing either low (11.1%) or high (15.7%) concentrations of rumen-degradable protein (RDP). They reported decreased milk yields and delays in both follicular development and luteal function in cows fed the ration containing 15.7% RDP. These results have implications for grazing systems, where cows receive RDP well in excess of requirements in early lactation. However, reducing dietary crude protein in the transition period in grazing dairy cows through provision of low protein...
supplements in isoenergetic diets (Roche et al. 2010) did not affect milk production, although it did reduce the duration of post-partum anoestrus (Burke et al. 2010b). The effects of protein in early lactation on milk production, BCS loss, and cow metabolism are important areas for consideration in future research. To the authors’ knowledge, research focused on varying dietary protein supply using metabolisable protein-based approaches for formulating diets has not been conducted.

Summary

Knowledge of the effects of nutrition on the successful transition of a cow through calving has greatly increased in the last decade. Epidemiological evidence of a positive association between pre-calving energy intake and post-calving health and productivity has been superseded by metabolic and molecular evidence of a potential negative relationship between these variables in well-managed dairy systems. In addition, recent research indicates a lack of importance of carbohydrate type pre-calving on post-calving health and productivity, although indications of reduced liver function when grazing cows are provided with high NFC supplements pre-calving requires further investigation. Protein nutrition of the transition cow has been largely ignored, with current recommendations still based on calculated requirements rather than response experiments. In addition, because of the large amount of protein in the diets of grazing animals, a deficiency of protein has not been considered likely; however, possible negative effects of surplus RDP in an animal with reduced hepatic function requires further investigation. Finally, recognition of the functional role of individual FA in addition to fat as an energy source has led to very interesting findings on the effect of FA on liver function. However, in vivo research is lacking; the positive (and negative) effects of individual FA in vitro as well as the increased use of high fat by-products in the dairying systems of Australia and New Zealand indicate a need for future research effort in this area.

PERIPARTURIENT HEALTH PROBLEMS

The transition period, although short, is when the majority of metabolic and infectious diseases occur during the dairy production cycle. The majority of cases of milk fever, ketosis, fatty liver, mastitis and uterine infections occur during this period, with much of the effort during the transition period aimed at prevention of these diseases.

There is a well-reported reduction in aspects of immune function through the calving period, with reduced numbers and effectiveness of immune cells in blood (Nonnecke et al. 2003). Although this is often described as peripartum immune suppression, there is also a heightened peripartum inflammatory response in many tissues (Bradford and Farney, 2010), with increased concentrations of positive acute phase proteins indicating a heightened immune system; for this reason, the peripartum period should not be regarded as a period of immune suppression, but instead as one of immune dysfunction.

Metabolic diseases are complex disorders that occur when the cow’s ability to adjust to a major physiological change (e.g. calving) is compromised. They have been a persistent problem for farmers for centuries, with milk fever first documented in 1793 in Germany (Schultz, 1971) and ketosis reported in the USA as early as 1849 (Udall, 1943). Most metabolic disorders stem from nutritional inadequacy or failure to prime metabolic processes for the change from pregnancy demands to lactational demands. Although this is true for the classical metabolic disorders, there is increasing evidence of a link between nutritional and management factors that contribute to immune dysfunction and non-classical metabolic disorders (e.g. milk fever that occurs before the drain on calcium following the first milking).

These diseases are costly; conservative estimates from New Zealand indicate that the failure of cows to transition successfully through calving costs their dairy industry in excess of $1 billion/year in lost productivity and premature wastage of cows (Roche 2012). A focus of any transition cow management programme should be to ensure that peripartum disease (i.e. both clinical and subclinical) is minimised, thereby maximising the likelihood of an early return to oestrus and a successful pregnancy outcome, increasing DMI and milk production, while minimising the early lactation NEBAL.

Peripartum immune dysfunction

The immune system is impaired during the transition period due to physical, hormonal, and metabolic stresses associated with gestation, parturition, and the onset of lactation (Kehrli et al. 1989; Cai et al. 1994; Mallard et al. 1997). Numerous studies have reported decreases in immune cell concentrations in blood (Park et al. 1992), reduced gene expression for immune components (Madsen et al. 2002), and impaired chemotactic and phagocytic capabilities around parturition when compared with mid-to-late lactation (Mehrzad et al. 2001; Shuster et al. 1996). The state of NEBAL is often characterised by impaired neutrophil function (e.g., Kehrli et al. 1989; Burvenich et al. 2007), including trafficking, phagocytosis, and killing capacity (Burvenich et al. 2007). Lymphocyte numbers decrease around parturition as a function of reduced proliferation (e.g., Kehrli et al. 1989).
There is some in vitro evidence indicating that a marked elevation in blood NEFA and BHBA concentration is one of the causative factors of immune suppression. For instance, NEFA at concentrations typical of the early post-partum period (i.e., 0.5-2 mM) led to greater oxidative burst activity, substantial necrosis, and a decrease in the viability of neutrophils (Scalia et al. 2006). Ketone body concentrations similar to those evident around parturition also impaired the phagocytic and bactericidal capacity of neutrophils, effectively reducing udder defence mechanisms against mastitis pathogens (Suriyasathaporn et al. 2000). Although this effect of NEBAL is well accepted, seminal research using mastectomised cows compared with intact cows indicate that the event of parturition and associated metabolic changes contribute to the immune dysfunction (Nonnecke et al. 2003), but that the lactation-induced NEBAL post-calving sustains the suppression of immune cell function. In addition, the post-partum NEBAL, although a result of failing to coordinate energy intake with energy output at that time-point, may have its origins at an earlier time (Huzzey et al. 2007; Goldhawk et al. 2009), as previously discussed, and may not be corrected through dietary changes post-calving (Roche et al. 2005).

Data from non-ruminant studies indicate that both saturated and polyunsaturated LCFA can alter immune functions through activation of diverse intracellular signalling cascades (e.g. activation of Toll-like receptors and PPAR, inhibition of NF-κB: Sordillo et al. 2009; Contreras and Sordillo, 2011). A recent study provided evidence that saturated FA (16:0 and 18:0) and EPA were more potent than other unsaturated LCFA in upregulating the expression of PPARα and several inflammation-related genes (Bionaz et al. 2012), indicating that enhanced availability of certain LCFA might alter immune cell pathways. From a practical standpoint, however, there are insufficient in vivo data on optimal levels of LCFA to potentially enhance immune cell function of dairy cows during the peripartum period.

**Immune dysfunction exacerbates susceptibility to pathogenic infections during the transition period**

In addition to the sharp decrease in the number of circulating polymorphonuclear (PMN) neutrophils (Park et al. 1992; Detilleux et al. 1995), the decrease in mammary T lymphocytes (Park et al. 1992) from late-pregnancy through calving impairs the cow’s ability to fight pathogens during the early post-partum period. The PMN constitute the primary defence of the innate immune system against invading microorganisms; thus, impairment of PMN function during the transition period exacerbates susceptibility to mastitis and metritis. Consistent with this premise, an increase in the incidence of these diseases has been reported in cows with impaired PMN function before and after parturition (Cai et al. 1994). Respiratory burst activity of PMN is one of the mechanisms used by these cells to fight invading pathogens and data indicate that the severity of clinical mastitis is greater in cows with a low respiratory burst activity (Heyneman et al. 1990).

From a mechanistic standpoint, the marked change in blood steroid concentrations (e.g., cortisol, progesterone, and oestradiol) around parturition contributes to impaired PMN function because it decreases the expression of genes and membrane proteins associated with apoptosis (e.g., FADD, Mcl-1, and TRAF6), protein translation (ribosomal protein S15), normal respiratory metabolism (cytochrome b), and the adhesion receptor L-selectin (Barton et al. 2005; Madsen et al. 2002; Weber et al. 2001). Thus, hormonal changes around parturition affect PMN function at a molecular level. However, the periparturient hormonal changes are short-lived and are unlikely to explain all of the alterations in PMN function throughout the transition period.

The decrease in circulating blood glucose with the onset of lactation is another likely factor associated with the impaired immune function after calving. (Newsholme et al. 1986) reported high activities of hexokinase and glucose-6-phosphate dehydrogenase and low activities of phosphorylase in activated murine macrophages, indicating that glucose is a more important fuel than glycogen and that the pentose phosphate pathway is of high importance within the cell. Most important, glucose is the primary, if not only, fuel source used by macrophages for phagocytosis (Newsholme et al. 1986). It follows then that enhancing glucose availability to immune cells might be a practical means of lessening the severity of immune dysfunction around calving. That idea is partly supported by a recent study that reported that over-feeding a moderate-energy diet during the dry period resulted in greater blood glucose pre- and post-partum and also an increase in PMN phagocytosis after calving (Graugnard et al. 2012). Although such a response might signal a benefit of energy over-feeding from an immune function standpoint, this benefit has to be weighed against the greater likelihood for overfed cows to have elevated concentrations of blood NEFA and liver lipid after calving (see previous section).

**Practical approaches to alleviate immune dysfunction**

There is strong evidence that supplementation of the diet with antioxidants (e.g. vitamin E/α-tocopherol, selenium, vitamin A/β-carotene/retinol, and vitamin C)
is a practical way of enhancing immune cell function and decreasing inflammation (Sordillo et al. 2009). It was also reported recently that supplementation with rumen-protected omega-3 PUFA plus vitamin E from -21 through +21 d relative to parturition resulted in lower postpartum blood concentrations of NEFA, BHBA, bilirubin, and greater α-tocopherol, indicating an overall improvement in liver function and attenuated inflammatory response post-partum (Trevisi et al. 2011). Although ingested PUFA are substantially hydrogenated in the rumen, there is evidence that dietary supplementation with omega-3-rich oils during the peripartal period can enhance the concentration of EPA and DHA in liver phospholipids and adipose tissue TAG (Ballou et al. 2009); these can, in turn, serve as a storage source of these FA and potentially alter molecular pathways regulated by PPAR (Schmitt et al. 2011). Fresh forages, like perennial ryegrass, may, therefore, be beneficial in the peripartum period, being high in both omega-3-rich oils and vitamin E, and having a fast rumen passage rate, ensuring minimal biohydrogenation of the desirable fat. These advantages must be weighed up against the high dietary RDP and dietary potassium, both of which may have negative consequences for dairy cow health.

**Metabolic diseases**

Although the prevalence of metabolic diseases tends to be low in lower yielding pasture-based herds (McDougall, 2001), many farmers face annual problems that are both costly and frustrating. Clinical cases are only part of the problem, with many more cows reportedly suffering subclinical problems when clinical cases are evident. For example, New Zealand research indicates that for every ‘downer’ cow, at least two more cows are clinically hypocalcaemic and 16 have subclinical hypocalcaemia (Roche 2012).

The majority of metabolic diseases occur during the transition period and, although genetic factors influence the risk of these diseases through effects on traits, such as susceptibility to milk fever (Lean et al. 2006; Roche and Berry, 2006) and the rate of BCS loss (Roche et al. 2006; McCarthy et al. 2007), farm management in the weeks around calving has a major effect on the risk of disease.

The two most common metabolic diseases in pasture-based systems are milk fever and ketosis, although it is likely that “fatty liver syndrome” and left displaced abomasum become more common with greater supplement use and higher milk production per cow. All of these diseases have secondary effects, with the occurrence of one disease increasing the risk of another (Figure 2). In addition, they predispose cows to infectious diseases (Curtis et al. 1985), particularly of the udder and uterus, and reduce milk production and fertility. The principal causes of, and strategies to avoid, these metabolic diseases will be reviewed here.

**Milk fever**

Milk fever is best described by its technical name – *parturient hypocalcaemia* –, which means lowered blood calcium around the time of calving. Approximately 90% of milk fever occurs in the 24 h after calving (Roche and Berry, 2006). On average, only 2% of cows are diagnosed with milk fever in pasture-based systems (i.e. “downer cows”: McDougall, 2001). However, laboratory analyses indicate that double this number have less than the clinical threshold of calcium circulating in blood (<1.4 mm) and 33% of cows are subclinically affected (i.e. <2.0 mm; low DMI, reduced milk production: Roche 2012).

Clinical milk fever is reported to reduce lactation yield by 14%, while cows suffering subclinical hypocalcaemia produce 7% less milk (Block 1984). There is also evidence that milk fever increases the risk of ketosis and uterine infections (Curtis et al. 1985) and that 5% of downer cows do not recover (Schultz 1971). The average cost of milk fever is estimated to be $8,000/100 cow herd (Roche 2012).

Although a cow has substantial stores of calcium in her skeleton (~6 kg) and consumes a considerable amount of calcium in food (i.e. a cow eating 10 kg of pasture and pasture silage has 40-80 g calcium in her gastrointestinal tract), blood calcium is under very strict hormonal control; a cow only absorbs from food and resorbs from bones what she requires. This can create an issue at the onset of lactation, when a cow’s requirement for calcium in blood can increase by more than 400% in a day (Goff and Horst, 1997b).
This requires a rapid increase in the absorption of calcium from the intestines and in the resorption of calcium from bone. Anything that interferes with these processes will increase the risk of milk fever.

Many factors affect the cow’s ability to maintain blood calcium during this period.
1. Genetics: Jersey cows are 2.5 to 5 times more likely to experience milk fever than Holstein-Friesian cows (Lean et al. 2006; Roche and Berry, 2006). This effect of breed is well published, with Channel Island breeds having less ability to absorb calcium and secreting more calcium in milk. Within breed, Holstein-Friesian cows of North American genetic origin have lower blood calcium and magnesium concentrations than Holstein-Friesian cows of New Zealand origin (Roche et al. 2001), even when secreting a similar milk energy output, indicating a greater risk of milk fever.

2. Body condition score: Cows that are excessively fat (greater than BCS 6.0) or excessively thin (less than BCS 3.0) at calving are at an increased risk of milk fever (Roche and Berry, 2006).

3. Weather: Milk fever is more likely to occur during wet days and nights, probably because of lower DMI and increased stress. In addition, frosty nights increase the risk of milk fever (Roche and Berry, 2006).

4. Diet: Many dietary factors can contribute to the risk of milk fever:
   - Magnesium intake is, arguably, the single greatest dietary factor determining the risk of milk fever (Lean et al. 2006; Roche and Berry, 2006). Magnesium is essential for the efficient absorption and resorption of calcium; therefore, cows that have low blood magnesium around calving are more likely to get milk fever. In an analysis of 30 years of data from DairyNZ No. 2 Dairy, milk fever prevalence dropped from more than 10% to less than 5% following the introduction of pre-calving magnesium supplementation in the late 1970s/early 1980s (Roche and Berry, 2006). In addition, (Roche et al. 2002) reported that supplementation with magnesium sulphate and magnesium chloride were more effective than magnesium oxide in maintaining periparturient eucaecaemia, despite a lack of effect of differences in dietary potassium and dietary cation-anion difference (DCAD). However, use of these supplements is not practical on all farms.
   - Cows absorb only as much calcium as they require and it takes several days for a cow to alter the proportion of calcium she absorbs from her diet (Braithwaite and Riazuddin, 1971). When the cow calves and her requirements for calcium increase rapidly, she cannot increase the proportion of dietary calcium absorbed sufficiently or quickly enough and milk fever occurs.

Because of this relationship between dietary calcium and calcium absorption, traditional recommendations have been to feed a low calcium diet pre-calving. In theory, this will stimulate the cow to absorb a higher proportion of calcium from her diet, such that, when she calves and is fed a high calcium diet, she will absorb enough calcium to prevent milk fever. This strategy has been demonstrated to be effective on farm (Wiggers et al. 1975). However, it is very difficult to reduce dietary calcium low enough during the dry period to stimulate calcium absorption post-calving sufficiently to prevent milk fever.

Oetzel (1991) and (Lean et al. 2006) noted that very low and very high levels of dietary calcium pre-partum prevented milk fever, with the greatest risk of milk fever occurring between 0.5 and 2.0% DM calcium. These reports have led some to suggest that milk fever can be prevented by supplementing cows with calcium pre-calving. However, the data presented indicate that dietary calcium would need to be greater than 2.0% DM to be effective in milk fever prevention: on average, a dry cow eating 9-12 kg DM of a pasture and pasture silage mix would have to consume a further 300-400 g ground limestone each day for dietary calcium to be sufficiently high to reduce the risk of milk fever. In pasture-based systems, this would rarely be practical.

In contrast to dry cows, the provision of supplementary calcium to colostrum cows, along with magnesium supplementation, will aid in the prevention of milk fever (Roche et al. 2002).

- Dietary potassium also contributes to the prevalence of milk fever, but, at least in pasture-based systems, it does not appear to be as important as many claim. Research undertaken primarily in the USA suggests that potassium is the primary nutritional factor contributing to milk fever through its effect on DCAD (Goff and Horst, 1997a). Because of this, high potassium forages
should be minimised in the weeks before calving (NRC, 2001). If this contraindication were appropriate for pasture-fed cows, 100% of cows would get milk fever due to the high potassium content of temperate pastures. In contrast, incidence of milk fever in pasture-based herds is low (McDougall et al. 2001) and New Zealand data indicated no difference in blood calcium around calving when cows were fed pastures varying from 3.3 to 4.2% DM potassium, the natural range evident in productive temperate pastures (Roche et al. 2002). This does not mean that potassium is unimportant. Potassium interferes with the absorption of magnesium in the rumen and, as magnesium is important for calcium absorption, thereby increases the risk of milk fever. However, it is secondary in importance to magnesium supplementation.

- Feeds that are high in phosphorus increase the risk of milk fever by interfering with the renal activation of vitamin D (Kichura et al. 1982; Reinhardt et al. 1988). Therefore, feeds that are high in phosphorus (e.g. palm kernel extract, distillers grains) should be used with caution in the weeks prior to calving, particularly in herds prone to milk fever.

- The DCAD is calculated from the amount of potassium, sodium, chlorine and sulphur in the diet. The proportion of these minerals in the diet influences the acidity/alkalinity of blood (blood pH; Stewart, 1983) and blood pH affects calcium absorption from the intestine and bone calcium homeostasis (Roche et al. 2007; Van Mosel et al. 1994). Blood pH drops when DCAD is less than 0 meq/kg DM and calcium absorption from the small intestine increases (Roche et al. 2003; Roche et al. 2007). Such a low DCAD is generally not achievable when pasture is a significant part of the ration. Lowering the DCAD through removal of potassium from the ration where practically possible, however, facilitates the use of practical levels of anionic salts and will improve magnesium absorption, thereby reducing the risk of milk fever in some circumstances.

- New Zealand data (Roche, 2007; Roche et al. 2005) indicate that the more feed cows are offered in the 2 wk before calving, the lower the concentration of calcium in blood at calving. The reason for this is unclear; it may be because well-fed cows are receiving more calcium in their diet, reducing the proportion of calcium absorbed, or because they are consuming more potassium pre-calving. Alternatively it may be because well fed cows have lower DM intakes after calving (Roche et al. 2005) and, therefore, reduce their intake of calcium at the time when it is most needed.

**Ketosis**

Ketone bodies (acetone, acetoacetate, BHBA) are intermediates in the breakdown of NEFA that can accumulate in blood when large amounts of body fat are mobilised and there is insufficient carbohydrate to facilitate -oxidation. The clinical state of this disease is referred to as ketosis. Ketosis has long been recognised as an important disorder of energy metabolism during early lactation (Schultz, 1968) and estimates of clinical ketosis incidence over time have consistently ranged from 4 to 16% of cows (Schultz, 1968; Baird, 1982; Merck, 2011). Although there are no published estimates of incidence of clinical ketosis in grazing dairy cows, using blood BHBA concentrations as a reference point, Roche (2012) reported that, on average, 8% of cows in research studies had >2.0 mM BHBA in blood in the weeks post-calving; this is the reported reference concentration indicative of clinical ketosis in North American systems (Duffield et al. 1998).

However, two important evolutions have occurred over the past 15 years in how ketosis is assessed and its implications considered.

- the major focus has shifted from clinical ketosis to the implications of subclinical ketosis in dairy cows
- the importance of timing of ketosis during early lactation has been evaluated

In a dataset involving 1,010 cows from 25 farms (mostly tiestall and component-fed) in Ontario, (Duffield et al. 1998) reported that about 30% of control cows sampled during wk 1 and 2 of lactation had subclinical ketosis, as defined by circulating BHBA>1.2 mM, and (Duffield et al. 1999) concluded that these cows had a greater risk of subsequent left displaced abomasum (odds ratio = 2.60) and metritis (odds ratio = 3.35).

Consistent with the findings of (Duffield et al. 1998; 1999), (Ospina et al. 2010a) determined that cows fed a total mixed ration (TMR) in the North-East United States with serum BHBA>1.0 mM from d 5 to 15 of lactation had a greater risk for the development of left displaced abomasum, clinical ketosis, and either of these disorders or metritis (risk ratios ranging from 4.4 to 6.9). In the same dataset,
cows with serum BHBA greater than 1.0 mM had 393 kg less projected milk for the lactation and 13% lower risk of pregnancy during the 70 d following the voluntary waiting period (Ospina et al. 2010b). In addition, (McArt et al. 2011) determined that 43% of cows (within farm prevalence ranged from 26 to 56%) in four large freestall, TMR-fed herds had at least one circulating BHBA concentration between 1.2 and 2.9 mM when sampled 6 times between 3 and 16 days in milk, indicating that the prevalence of subclinical ketosis is high and also highly variable across farms.

In comparison, Roche (2012) reported that only 12% of cows in a multi-year research database derived from pasture-based diets had blood BHBA concentrations >1.2 mM and that this prevalence was recorded 4 wk post-calving, with <2% of cows presenting with this BHBA concentration during wk 1 and 2 post-calving (Figure 3). The reason for the difference in prevalence between TMR-based and pasture-based systems is not clear, but may reflect differences in milk production and the consequent level of metabolic stress the cow is subjected to during the transition period. Nevertheless, it is consistent with the low overall incidence of metabolic disorders reported for pasture-based systems (McDougall 2001).

![Figure 3: Concentration of -hydroxybutyrate (BHBA) through time in blood of pasture-based transition dairy cows. Data are derived from a research database (Roche 2007; Roche et al. 2005; 2010) and reported by Roche (2012).](image)

The second evolution in the consideration of ketosis relates to timing of incidence during early lactation. Traditionally, ketosis has been thought to have primary onset between 10 days and 8 wk post-calving (Schultz 1968; Baird 1982). In contrast, (McArt et al. 2012) reported that peak prevalence of subclinical ketosis occurred at 5 days in milk when 29% of cows sampled across four large dairy herds had elevated circulating BHBA concentrations. Furthermore, associations of subclinical ketosis with disease outcomes or removal from the herd were much stronger if the onset of subclinical ketosis occurred from 3 to 7 days in milk compared with 8 days in milk or later. However, these data from TMR-fed herds are not consistent with that of Roche (2012) for pasture-based systems, where peak BHBA concentrations occurred at 28 days post-partum (Figure 3). Similarly, Ingvartsen (2006) reported a peak in plasma BHBA concentrations between 4 and 6 wk post-calving, but with increases from wk 1. He also noted, however, that post-calving peak BHBA was affected by pre-calving energy intake, with cows on low energy diets pre-calving having lower plasma BHBA post-calving, consistent with New Zealand observations that over-feeding in the pre-calving period increases the risk of high blood BHBA post-calving (Roche 2007). (Roche et al. 2005) also reported a negative relationship between level of feeding pre-calving and EBAL post-calving, such that a high feeding level pre-calving associated with greater NEBAL post-calving. Consistent with these findings, molecular changes in liver indicate decreased functionality (i.e. -oxidation, gluconeogenesis, ureagenesis) post-calving in cows overfed pre-calving (Loor et al. 2006).

The relevance of reference ranges for BHBA derived in systems where cows are fed high NFC diets needs to be considered for the Australian and New Zealand dairy industries. For example, (Roche et al. 2010) reported that cows fed pasture and pasture silage (NFC=18%) had more than double the circulating concentrations of BHBA than similar cows fed an equivalent amount of metabolisable energy as pasture, pasture silage and 35% DM of the diet as a maize and barley-based concentrate (NFC=40%), despite no treatment differences in the trajectory of BCS change or circulating NEFA concentrations; also, blood albumin concentrations was lower in the high NFC treatment, potentially indicating liver dysfunction. These data indicate a lack of relevance of reference ranges for BHBA derived from systems feeding high NFC diets for pasture-based systems, where plasma BHBA might be a function of ruminal butyrate production and a lack of NFC to provide precursors for hepatic -oxidation of NEFA rather than an indicator of a metabolic disorder per se. Defining relevant reference ranges for BHBA for pasture-based systems should be a research priority.

Fatty liver

Fatty liver disease or hepatic lipidosis is a metabolic disorder that can frequently occur during the transition period. Fatty liver is associated with reduced health status, lower productivity, and impaired reproductive performance (Bobe et al. 2004). “Fat cow syndrome”, commonly related to fatty liver disease (Morrow, 1976), is a major
problem in cows that are over-conditioned at parturition and results in dramatic decreases in DMI, a greater incidence of downer cows, and negative health effects that may be irreversible. Feeding of diets with greater starch content to increase energy density during the dry period can lead to fat cow syndrome, thus indirectly increasing the risk of fatty liver disease and other associated diseases post-partum. Fatty liver can also occur in cows that are not over-conditioned, with reports of up to 50% of dairy cows affected during early lactation (Jorritsma et al. 2001). However, there are very little data on the incidence of fatty liver in pasture-based dairy cows.

As outlined in previous sections, the rapid increase in milk yield, concomitant with physiological changes during the early post-partum period (Bell, 1995), is often characterised by reduced DMI resulting in NEBAL and increased blood NEFA. The NEFA are taken up by the liver at approximately 26% of whole-body NEFA flux (Drackley et al. 2001) and can be:

1. oxidised to obtain energy by mitochondria, peroxisomes or microsomes (Drackley, 1999);
2. partly oxidised to ketone bodies; and
3. re-esterified to TAG. The TAG are stored in the cytosol of hepatocytes or assembled with apolipoprotein-B100 (ApoB100), cholesterol, and phospholipids to synthesise very low density lipoproteins (VLDL) (Shelness et al. 1999).

Excessive TAG accumulation in liver occurs when the hepatic uptake of NEFA exceeds their oxidation and secretion by the liver and it occurs primarily at some point during the first 4 wk post-partum (Bobé et al. 2004). From a biochemical standpoint, the bovine liver can esterify NEFA at a rate in vitro similar to that in simple-stomached species, such as rat, pig and chicken, but the rates of TAG export in VLDL from ruminant liver is markedly lower than those of other species (Pullen et al. 1990). That feature is partly responsible for the consistent increase in liver TAG during the first few weeks post-partum that has been reported in studies over the last 10 years when cows are overfed moderate-energy diets during the dry period (e.g. Dann et al. 2006; Janovick and Drackley, 2010; Ji et al. 2012). While BCS pre-partum provides a practical evaluation of the degree of body fatness, recent evidence indicates that overfeeding energy can lead to a marked increase in visceral adipose tissue mass without appreciable differences in BCS or body weight (Nikkhah et al. 2008) underscoring the importance of nutritional management.

“Starter drenches” in early lactation

Propylene glycol is a glucogenic precursor that has been used for many years as an oral drench in the treatment of ketosis. Available studies consistently demonstrate decreased concentrations of NEFA in plasma, usually accompanied by decreased concentrations of BHBA in plasma in response to propylene glycol administered as an oral drench (Grummer et al. 1994; Christensen et al. 1997; Pickett et al. 2003; Chagas et al. 2007). However, incorporation of propylene glycol into the TMR did not affect concentrations of NEFA and BHBA in plasma (Christensen et al. 1997). Stokes and Goff (2001) reported that administration of an oral drench of propylene glycol for two days beginning at parturition decreased concentrations of NEFA in plasma and increased milk yield during early lactation. Similarly, (Chagas et al. 2007) reported lower blood NEFA concentrations during the first 5
wk post-partum in grazing cows supplemented with propylene glycol for 16 wk post-calving, but reported no effect on milk production. Subsequent experiments in which propylene glycol was administered as a drench beginning at parturition for either two days (Visser et al. 2003) or three days (Lenkaitis et al. 2003) or as part of a combination drench administered for three days beginning at parturition (Visser et al. 2002) reported no productive response to propylene glycol drench. (Chagas et al. 2007) did report reproductive benefits from propylene glycol, however, with an increase in the pulsatile release of luteinising hormone and an earlier return to oestrus in supplemented cows. Overall, research supports that bolus administration of propylene glycol will result in modest and inconsistent effects on metabolic variables; however, the lack of consistent production responses across experiments contraindicate that routine administration of propylene glycol.

Propionate supplements consisting of propionate complexed to Ca or trace minerals potentially could be used to supply substrate for hepatic gluconeogenesis. Published responses to peripartal supplementation with propionate supplements have been mixed. (Mandebvu et al. 2003) reported that feeding approximately 110 g/d of a propionate supplement on a commercial dairy farm did not affect milk yield, but transiently decreased plasma NEFA concentrations and urine ketone score. Stokes and Goff (2001) reported that drenching cows with 0.68 kg of Ca propionate twice during the early postpartal period did not affect early lactation milk yield, or concentrations of NEFA and BHBA in plasma. Part of the reason for the lack of measured responses to propionate supplements could be the amount of propionate provided relative to the amount produced in the rumen. Because Stokes and Goff (2001) did not detect metabolic responses (decreased NEFA and/or BHBA concentrations in plasma) in response to oral administration of a sizable (0.68 kg) bolus of Ca propionate, possibly because of differences in either ruminal metabolism or absorption kinetics of propylene glycol and the propionate supplements. Overall, existing research does not support use of propionate supplements either through the TMR or via bolus.

Monensin is a common rumen modifier provided either through feed premix or in controlled-release capsule (CRC) form. Administration of monensin by CRC during the transition period and early lactation decreased the incidence of subclinical ketosis (>1.2mM) in dairy cows by 50% (Duffield et al. 1999). Over-conditioned cows (BCS > 4.0 at 21 d before expected calving; 5 point scale) supplemented with the monensin CRC produced significantly more milk than unsupplemented controls during early lactation (Duffield et al. 1999). In a subsequent experiment, cows administered the monensin CRC had decreased circulating concentrations of NEFA during the wk immediately preceding calving, but concentrations were not affected during the first wk post-calving (Duffield et al. 2003). In contrast, cows fed 300 mg/d of monensin from 28 d prior to calving until calving did not have altered concentrations of NEFA or glucose during the pre-partum period, but had lower circulating NEFA concentrations during the first wk post-calving and tended to have increased DMI during early lactation (Vallimont et al. 2001). More recently, (Mullins et al. 2012) reported that monensin supplementation by daily top-dress on TMR (400 mg/d) from 21 d before expected calving date until 21 d after calving decreased both mean and peak concentrations of BHBA and liver TAG accumulation.

(Duffield et al. 2008a, 2008b, 2008c) conducted a meta-analysis of effects of dietary supplementation or ruminal administration of monensin on health, production, and reproduction of dairy cows. Across 59 studies, they determined that monensin supplementation reduced circulating BHBA and NEFA concentrations (Duffield et al. 2008a). Across 77 studies, they determined that monensin supplementation decreased DMI slightly but increased both milk yield and milk production efficiency (Duffield et al. 2008b). Finally, across 16 studies monensin supplementation decreased risk for both ketosis and left displaced abomasum; administration by CRC resulted in greater reductions in retained placenta and metritis relative to administration in the diet (Duffield et al. 2008c). In comparison, (Waghorn et al. 2007) reviewed the research undertaken in pasture-based systems in Australia and New Zealand and, again, reported variable results. Australian studies (Lowe et al. 1991) reported a 30 g/cow/d increase in milk protein but these results were not achieved in subsequent trials on 18 dairy farms in Australia (Lean et al. 1994; Beckett et al. 1998), wherein monensin increased milk yield but did not increase milk protein yield. (Waghorn et al. 2007) quoted unpublished experiments in New Zealand and Australia that reported an average increase of 40 g fat and protein/cow/d across the dataset, but only an increase of 23 g in those studies undertaken in New Zealand.

The reason for the inconsistency in milk production responses to monensin is not clear, but it may reflect a negative effect on DMI (Duffield et al. 2008b), or an interaction with diet quality. (Waugh et al. 2005) reported an increased effect of monensin as dietary metabolisable energy declined. These data,
and published evidence of greater responses when diet digestibility declines (McGuffey et al. 2001; Duffield et al. 2008b), suggest that milk production responses to monensin may be highest when pasture quality is low, while the lowest response is likely when pasture quality is highest. Further research is required to determine cow responses under different dietary conditions.

**Summary**

The transition period, although short, is when the majority of metabolic and infectious diseases occur, meaning that significant gains in animal health and productivity could be achieved through understanding the reasons for failure to transition successfully. Immunological and metabolic dysfunction appear to be primary reasons for the high disease incidence and, although some of this appears to be an inevitable function of the parturition event, there is considerable evidence that management and nutritional practices pre- and post-calving contribute. Understanding the molecular and metabolic changes associated with level of feeding and feed ingredients on important biochemical processes will help to validate the advice being provided to farmers and should, therefore, improve cow longevity, reproductive and productive efficiency, and animal welfare.

**CONCLUSIONS AND CONSIDERATIONS FOR FURTHER RESEARCH**

Nutrition and management of the transition cow was highlighted by Boutflour (1928) as a way of improving milk production. During the last 20 years, in particular, knowledge in biochemical and molecular processes associated with a successful transition has dramatically increased. This increased knowledge has resulted in a paradigm shift in thinking about the most appropriate way in which to manage the transition cow. The cow’s greater requirement for energy as she transitions from pregnant to lactating (Bell, 1995) highlighted the need to consider energy and protein nutrition. Subsequent work demonstrated that energy intake and feed composition have important effects on the molecular regulation of biochemical pathways (Loor et al. 2006; Ji et al. 2012), particularly in liver and adipose tissue, the tissues subjected to greatest scrutiny to date, but also conceivably in muscle, mammary and reproductive tissues. The importance of pre-calving nutrition in post-partum health has been highlighted in studies of animal behaviour (Huzzey et al. 2007; Holdhaw et al. 2009), epidemiology of periparturient diseases (Dyk et al. 1995) and force-feeding (Bertics et al. 1992). However, the paradigm shift in thinking is that the relationship between pre-calving energy intake and relevant circulating metabolites, and post-partum health and productivity is, for the most part, not causative (i.e. responses very likely reflect the same metabolic perturbation, but one is not necessarily the cause of the other). Consistent with this hypothesis, attempts to increase energy intake pre-calving have not produced positive animal production or reproduction responses; in fact, metabolic and molecular indices indicate potential benefits to a controlled restriction during the weeks immediately preceding calving. Further research is needed in this area, as there are likely interactions among feed composition, cow BCS, and post-partum nutrition factors (e.g. level of feeding, feed composition).

Because of the focus on pre-partum energy intake, there has been limited research on the effects of dietary protein level, protein type, essential amino acids (e.g. methionine), or individual FA on the success of the cow’s transition through calving. Considering the potential negative implications of excess RDP and the effects of FA on important biochemical processes, research is required in this area. As with all ruminant nutrition studies, due attention must be paid to what is leaving the rumen in addition to what the cow is consuming.

Most importantly, future studies investigating the requirements of the transition cow must involve multiple research disciplines (i.e. from applied nutrition and management to basic physiology). Improved laboratory assays will facilitate a greater understanding of how nutrition and management influence immunological and physiological functions during this important period. These technologies are not intended to replace detailed physiological studies. However, physiological studies that involve arteriovenous flux across important organs or in vitro assays are difficult, time-consuming and expensive, cannot be undertaken across large numbers of animals, and are, sometimes, of questionable in vivo relevance. In comparison, tissue biopsies are relatively easy to undertake and modern technologies (e.g. high throughput molecular and immunological assays) coupled with bioinformatics platforms facilitate the assessment of many biochemical pathways through time in multiple animals. Despite the increasing availability of these technologies, every endeavour must be made to associate transcription and protein changes with tissue metabolic output and whole-animal production level data, to ensure appropriate interpretation of results and robust advice to industry.

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Chicory and plantain management strategies to increase herbage dry matter yield, nutritive value and plant survival

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ABSTRACT

The forage herbs chicory and plantain are becoming increasingly popular in summer-dry regions of both New Zealand and Australia due to their ability to produce a large amount of feed of high nutritive value between spring and autumn. Limited information is available, however, on the effect of grazing management on modern herb cultivars. This experiment aimed to determine the effect of increasing defoliation interval (as measured by pre-defoliation height of the sward) on total DM production, nutritive value and plant survival over two years. From December 2010 to May 2011 (Year One), the total DM yield of chicory was greatest \( (P<0.001) \) when swards were defoliated at 350 or 550 mm (10.8 t DM/ha). Total DM yields of plantain were greater \( (P<0.001) \) than chicory, and increased \( (P<0.001) \) with pre-defoliation height (16.1 t DM/ha). Swards contained predominantly herb leaf (92-95%), and while the metabolisable energy (ME) content of chicory was similar across pre-defoliation heights, during summer the ME content of plantain was reduced \( (P<0.001) \) in swards defoliated at 350 or 450 mm. During Year Two (June 2011 to May 2012), increasing the pre-defoliation height increased \( (P<0.001) \) total annual DM yields of chicory and plantain, increased \( (P<0.001) \) reproductive stem/seedhead development, reduced \( (P<0.05) \) the yield of weed species, and reduced \( (P<0.001) \) herbage ME content in summer for chicory and throughout the year for plantain. Before reproductive development begins, there is greater flexibility with the pre-defoliation height of chicory compared with plantain, with no apparent ill-effect of increasing the pre-defoliation height on chicory. During reproductive development of chicory and plantain, however, swards should be defoliated at 250 mm to minimise production of stem/seedhead and weed species, while maintaining high leaf DM yield and high nutritive value.

Keywords: herb; pre-defoliation height; defoliation interval; rotation length.

INTRODUCTION

Dairy farms in New Zealand and southern Australia rely predominantly on grazed perennial ryegrass \( (Lolium perenne \text{ L.}) \) based pastures for feed. Pasture growth is often limited by soil moisture deficits in the absence of irrigation, leading to feed deficits during summer/autumn. As a result, interest is increasing in alternative forages that have deeper rooting systems and are more drought- and/or heat-tolerant than perennial ryegrass. Two such species include the forage herbs, chicory \( (Cichorium intybus \text{ L.}) \) and plantain \( (Plantago lanceolata \text{ L.}) \). Under rotational grazing with dairy cows, dryland chicory swards generally have an effective life of 1-2 years, with production between 9 and 11 t DM/ha from spring to autumn (Rollo et al. 1998; Glassey et al. 2012). Chicory herbage is highly digestible, and has greater mineral content (e.g. P, S, Mg, Na, Cu, Zn, B) than perennial ryegrass (Li and Kemp 2005; Harrington et al. 2006). Compared with chicory, plantain tends to have a longer growing season, greater annual DM production and greater persistence, but lower nutritive value (Powell et al. 2007; Glassey et al. 2012).

While research on best grazing management practices for chicory has been undertaken (Li and Kemp 2005), there is little information on plantain, and few studies have compared the relative advantages of modern herb cultivars used for dairying. The aim of this experiment was to determine the effect of increasing defoliation interval (as measured by pre-defoliation height of the sward) on chicory and plantain DM production, nutritive value and plant survival, with the hypothesis that increasing the pre-defoliation height would increase herbage production; however, there may be an associated decline in nutritive value, particularly during reproductive development.

MATERIALS AND METHODS

The experiment was conducted in Hamilton, New Zealand \((37°47’S, 75°19’E; 40 \text{ m a.s.l.})\) between September 2010 and May 2012. In mid-October, plots \((1.5 \times 7 \text{ m})\) were sown with chicory (cv. ‘Choice’; 6.7 kg/ha) or plantain (cv. ‘Tonic’; 10 kg/ha) Superstrike® treated seed following a double herbicide spray and full cultivation. Due to low October/November rainfall \((69 \text{ mm}; 37\% \text{ of the 40-year average})\), spray-irrigation was set up and applied as required to keep soil moisture content above...
the permanent wilting point. In total 331 mm of irrigation water was applied during the experiment, bringing the total water applied (irrigation + rainfall) from October 2010 to September 2011 to 1294 mm (12% above the 40-year average annual rainfall).

The experiment was laid out in a split-plot design, with five replicates of eight treatments (four pre-defoliation heights x two residual heights). Defoliation occurred when leaves had grown to heights of 150, 250, 350, or 550 mm for chicory and 150, 250, 350, or 450 mm for plantain, while the residual heights for both species were 30-50 or 60-80 mm. The time taken for swards to reach these heights is reported in Table 1. During winter/early spring, chicory was not defoliated to improve persistence (Li and Kemp 2005), nor was the plantain 450 mm treatment as it did not reach this height.

At every harvest, one 5 x 0.8 m strip was cut from each plot using a forage harvester (Jenquip, Feilding, NZ) set to the desired residual height. Samples of cut herbage were taken and used to determine DM content, botanical composition, and herbage nutritive characteristics (crude protein, soluble sugars and starch, acid and neutral detergent fibre, ash, dry organic matter digestibility (DOMD)) using wet chemistry. Metabolisable energy (ME) content was calculated as DOMD x 0.16 (AFRC 1993). Every three months, four 0.12 m² quadrats were randomly placed in each plot and sown herb plant numbers were counted.

Data were analysed using REML in GenStat (version 14.1; VSN International) as a species x pre-defoliation height x residual height factorial design. There was little effect of residual height; therefore this paper focuses on pre-defoliation height only.

RESULTS

From December 2010 to May 2011 (Year One), the total DM yield of chicory was greatest (P<0.001) when swards were defoliated at 350 or 550 mm (Table 2). Total DM yields of plantain were greater (P<0.001) than chicory, and increased (P<0.001) with increasing pre-defoliation height. In Year Two (June 2011 to May 2012), total DM yields for chicory and plantain were greatest (P<0.01) when swards were defoliated at 550 mm and 450 mm, respectively.

In Year One, herbage harvested from chicory swards consisted of chicory leaf (92%), weed species (e.g. C4 grasses, Solanum nigrum and Modiola caroliniana; 8%) and dead material (1%), while herbage harvested from plantain swards contained plantain leaf (95%), weed species (3%) and plantain seedhead (2%). In Year Two, increasing the pre-defoliation height increased the yield of reproductive stem or seedhead (P<0.001) and decreased the yield of weed species (P<0.05; Figure 1). The DM yield of chicory leaf was similar across all pre-defoliation heights, while the DM yield of plantain leaf tended to be greater for swards defoliated at 450 mm compared with 150 or 250 mm (P = 0.08).

Seasonal metabolisable energy (ME) data is presented in Table 3. In Year One, the ME content of plantain was lower (P<0.01) during summer in swards defoliated at 350 or 450 mm compared with 150 mm. Throughout Year Two, the ME content of plantain decreased (P<0.001) as the pre-defoliation height increased. During summer, chicory ME content was greater (P<0.001) in swards defoliated at 250 mm compared with 150, 350 or 550 mm, while in autumn ME content was lower (P<0.001) in swards defoliated at 150 mm compared with 250, 350 or 550 mm.

Although the plant density of both species declined over time, plantain maintained a greater (P<0.001) plant density than chicory. In December 2011, there was an effect of pre-defoliation height in both species (P<0.05; Figure 2), with plant density reduced in chicory defoliated at 150 or 550 mm and plantain defoliated at 150 mm.

DISCUSSION AND CONCLUSION

As hypothesised, increasing the pre-defoliation height of herb swards increased total DM production, with maximum DM yields of chicory and plantain recorded at pre-defoliation heights of 350-550 and 450 mm, respectively. This positive effect of greater time intervals between defoliation is consistent with previous studies on chicory (Clark et al. 1990; Li et al. 1997; Belesky et al. 1999) and plantain (Labreveux et al. 2004) that tested defoliation intervals of up to eight weeks.

A more important goal than increasing total DM yield, however, may be to maximise herb leaf DM yield, while minimising production of reproductive stem or seedhead with lower nutritive value (Li and Kemp 2005) and weed species. In the second year of this experiment when reproductive development had begun, this criterion identified 250 mm as the optimum pre-defoliation height for both species. (Clark et al. 1990) determined that maximum ‘Grasslands Puna’ chicory leaf DM yield occurred when swards were defoliated every five weeks from October to December. This is a slightly longer defoliation interval than identified here, possibly due to cultivar differences or the shorter experimental length only taking into account part of the reproductive development period.

Increased pre-defoliation heights were generally associated with a decline in herbage nutritive value, with the exception of chicory in Year
One (spring-sown chicory generally doesn’t produce stem during first summer/autumn). The decline in nutritive value was anticipated considering that DM yield of lower quality stem/seedhead increased with increasing pre-defoliation height. Interestingly, the nutritive value of herbage from plantain defoliated at 350-450 mm was also lower during summer of Year One, despite minimal (≤4%) seedhead presence. This indicates that the nutritive value of plantain leaves may decline over time, likely contributing to the lower nutritive value in plantain defoliated at greater heights during the second year.

The ‘optimum’ pre-defoliation height for chicory and plantain requires a balance between leaf DM yield and herbage nutritive value. Before reproductive development begins, there is greater flexibility with the defoliation management of chicory compared with plantain, with no apparent ill-effect of increasing the pre-defoliation height of chicory on any measured variable. During reproductive development however, chicory and plantain swards should be defoliated at 250 mm to minimise production of stem/seedhead and weed species, while maintaining high leaf DM yield and high nutritive value. Modelling and milk production response studies are required to determine the impact of pre-defoliation height on a whole farm system.

ACKNOWLEDGEMENTS

The authors acknowledge the technical assistance of the Lye Farm technicians and the statistical expertise of Barbara Dow. This experiment was funded by New Zealand dairy farmers through DairyNZ.

REFERENCES


**Table 1:** Time taken (weeks) for chicory and plantain to reach 150, 250, 350 or 450/550 mm

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<td>Mid- to late autumn</td>
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<tr>
<td>Winter to mid-spring</td>
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<td>Mid- to late spring</td>
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**Table 2:** Yields (t DM/ha) from chicory and plantain swards defoliated at 150, 250, 350 or 450/550 mm over two years

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<thead>
<tr>
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<th>SED (within herb)</th>
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<td>550</td>
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<td>12.7</td>
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SED, standard error of the difference; S, species; D, pre-defoliation height; S x D, species by pre-defoliation height interactions; NS, not significant.

**Table 3:** Metabolisable energy content of herbage from chicory and plantain swards defoliated at 150, 250, 350 or 450/550 mm over two years

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SED, standard error of the difference; S, species; D, pre-defoliation height; S x D, species by pre-defoliation height interactions; NS, not significant.
Figure 1: Yield of herb leaf (black), herb stem/seedhead (diagonal lines) and weed species (white) during Year Two from (a) chicory and (b) plantain swards defoliated at 150, 250, 350, or 450/550 mm.

Figure 2: Plant density of the sown herb species in (a) chicory and (b) plantain swards defoliated at 150 (dotted lines), 250 (dashed lines), 350 (dash-dot lines), or 450/550 mm (solid lines) over two years. Error bars indicate the standard error of the difference between defoliation height data.
Impact of lax and intense grazing on chicory utilisation and survival

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ABSTRACT

A chicory (Cichorium intybus L.) crop was established on a commercial dairy farm in Waikato, New Zealand, to investigate the impact of lax vs. intense (target 10 vs. 5 cm post-grazing height) rotational grazing on chicory performance over two summers (2010-2011 and 2011-2012). The crop was grazed by mid-lactation Friesian-Jersey cross dairy cows. During the first summer, there were significant differences between post-grazing height for the first three grazing periods but not the fourth (9.8 vs. 6.5 cm for lax and intense grazing, respectively, when averaged over four grazing periods; P<0.05). Total dry matter (DM) production was similar for both treatments in the first summer (averaging 7.6 t DM/ha, P>0.05). Nutritive characteristics and forage DM consumed in both treatments was similar (averaging 11.7 MJ metabolisable energy/kg DM, 73.3% DOMD, 24.5% CP and 6.2 t DM/ha consumed), but chicory shoot density was greater under lax than intense grazing in March 2011 (82 vs. 62 shoots/m², respectively; P<0.001). In the second summer, when chicory became reproductive, no significant difference in post-grazing height was achieved over two grazing rotations (averaging 21.3 and 14.3 cm for lax and intense grazing, respectively). There was no significant difference between treatments in chicory nutritive characteristics (averaging 12.8 MJ ME/kg DM, 80.0% DOMD and 25.0% CP), chicory total DM production (2.0 t DM/ha), forage DM consumed or shoot density (19 shoots/m²). The variability in post-grazing height demonstrates how difficult it is for farm managers to achieve a prescribed post-grazing height in chicory, particularly during reproductive stem development. Grazing interval, rather than post-grazing height, may be a more useful recommendation for optimal chicory production and utilisation.

Keywords: Cichorium intybus; grazing intensity; grazing severity; dry matter production.

INTRODUCTION

Chicory (Cichorium intybus L) generally provides better quality feed than ryegrass-based pastures over summer-autumn, with high metabolisable energy (ME) content, even when chicory typically becomes reproductive in its second summer (Clark et al. 1990b; Waugh et al. 1998). Supplementing a pasture-based diet with chicory can, therefore, increase milk production over summer and autumn (Waugh et al. 1998; Minné et al. 2012). In the North Island of New Zealand, these benefits have led to increased use of chicory on dairy farms, with thousands of hectares sown annually (Moloney and Milne 1993).

Grazing management strongly influences chicory performance, with the ultimate aim of maximising leaf growth and utilisation while minimising stem development. With this aim in mind, (Clark et al. 1990a) recommended defoliation intervals of 1, 2 or 4 weeks to 10 cm height or 4-weekly defoliation intervals to ground level. Cutting to ground level did, however, reduce subsequent regrowth and chicory plant density. (Li et al. 1994) also demonstrated the impact of grazing intensity on stem development, with stem yields increasing by 117% as the post-grazing height rose from 5-10 to 10-15 cm.

Many studies on chicory performance are from cut swards (e.g. Clark et al. 1990a) or have been done under controlled conditions (e.g. Li et al. 1994). While this is essential for developing an understanding of chicory responses to grazing, to develop practical guidelines it is useful to test research recommendations on commercial farms where conditions are more variable. Therefore, a study was undertaken to determine if a proficient farm manager could achieve a prescribed post-grazing height to optimise chicory performance. The aim was to compare the impact of lax vs. intense grazing (10 vs. 5 cm target post-grazing height) on chicory DM production, nutritive value, forage consumed and chicory shoot density. Based on previous research, it was hypothesised that total DM production and shoot density would be greatest under lax grazing; however, nutritive value may be compromised.

MATERIALS AND METHODS

The commercial dairy farm was in the central Waikato region of New Zealand (38°5’25”, 175°20’51”). Pure chicory (cv. ‘Choice’ Superstrike-coated seed was direct-drilled at 3.5 kg seed/ha into a 2.8 ha paddock in September 2010 after glyphosate application to the existing pasture. The paddock was divided into six 0.5 ha plots, with three replicates of the two grazing intensity treatments (lax vs. intense) in a randomised complete block design.
The chicory was grazed four times during the first summer, over six days on each occasion, beginning 10 January 2011, 31 January, 25 February and 23 March 2011. The 490 Friesian-Jersey cross dairy cows grazed one of the six 0.5 ha plots for several hours before afternoon milking for each of the six days. Cows were removed from plots approximately an hour earlier under lax than intense grazing treatments; timing of removal was based on visual assessment by the farm manager. From 23 March until 24 November 2011, all plots were grazed in common on a 30-40 day round to approximately a 10 cm residual. The intensity treatments were again imposed when the crop was grazed over six days, beginning 2 January and 13 February 2012. After the mid-February grazing, herbicide was applied to the crop due to poor crop performance. Throughout the study, grazing decision rules were based on the feed availability, resulting in 21 and 40-day rotations during the first and second summers, respectively.

Pre- and post-grazing, four randomly located 0.2 m² quadrats per plot were cut to ground level and oven-dried for 48 hours at 80°C to estimate DM yield. Chicory shoots were counted in the post-grazing quadrats after cutting. The height of fifty randomly chosen chicory plants was also measured from the highest leaf tip to the ground pre-and post-grazing. Fifty chicory leaves from different plants within a plot were randomly selected before grazing, oven-dried for 48 hours at 60°C and analysed for nutritive value using wet chemistry (Calvert 2012). All data were analysed with GenStat 13.2 (Genstat 2010) using a one-way ANOVA for each of the years.

RESULTS

Pre-grazing, chicory height was similar under lax and intense grazing, except for February 2012 when chicory was taller in the lax treatment (P<0.05; 75 vs. 56 cm; Figure 1). In summer 2011, post-grazing height averaged 9.8 and 6.5 cm under lax and intense grazing, respectively (Figure 1); close to the targets of 10 and 5 cm. Differences between treatments in post-grazing heights were significant in January and February, but not March, 2011. In 2012, post-grazing heights did not differ between treatments (P>0.05, Figure).

**Figure 1:** Pre- and post-grazing height (cm) of chicory under lax and intense grazing on a commercial dairy farm over two summers. Bars indicate standard errors of differences for comparisons between treatments pre- and post-grazing. Asterixes (*) denote significant differences. Pre-grazing lax: (■); pre-grazing intense: (□); post-grazing lax: (■); and post-grazing intense: (□).

In the first year (2011), chicory had greater (P<0.05) pre-grazing mass under lax than intense grazing on two occasions, and a higher post-grazing residual on one occasion (Table 1). However, the amount of DM consumed from January to March 2011 was similar for both treatments (Table 1). Total DM yield from establishment to 20 April 2011 (the grazing after the last treatment grazing) was also similar, averaging 7610 kg DM/ha.

In the second year (2012), chicory had greater pre-grazing mass under lax than intense grazing on one occasion (P<0.05, Table 1). DM produced between the two grazings (i.e. difference between the January residual and February pre-grazing mass, Table 1) was not significantly different, averaging 2020 kg DM/ha. Forage DM consumed during the February grazing (i.e. pre-grazing mass minus post-grazing residual) was also not significantly different, averaging 2140 kg DM/ha (P>0.05, Table 1).

There was no effect of grazing intensity on chicory nutritive characteristics at any time during the experiment (Table 2, P>0.05). Over the two summers, ME content ranged from 11.3 to 12.5 MJ ME/kg DM, dry organic matter digestibility (DOMD) from 70 to 82% and crude protein (CP) content from 18 to 29%.
Table 1: Chicory pre- and post-grazing mass and DM consumed under lax and intense grazing on a commercial dairy farm over two summers

<table>
<thead>
<tr>
<th>Year</th>
<th>Pre-grazing DM (kg DM/ha)</th>
<th>Post-grazing residual DM (kg DM/ha)</th>
<th>DM consumed (kg DM/ha)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Lax</td>
<td>Intense</td>
<td>sed</td>
</tr>
<tr>
<td>2011</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>10-Jan</td>
<td>4510</td>
<td>4380</td>
<td>600</td>
</tr>
<tr>
<td>29-Jan</td>
<td>1840</td>
<td>1670</td>
<td>136</td>
</tr>
<tr>
<td>25-Feb</td>
<td>3170</td>
<td>2130</td>
<td>281 *</td>
</tr>
<tr>
<td>23-Mar</td>
<td>2250</td>
<td>1800</td>
<td>158 *</td>
</tr>
<tr>
<td>20-Apr</td>
<td>1580</td>
<td>1270</td>
<td>141</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DM</td>
<td>consumed</td>
<td>(January-March)</td>
<td></td>
</tr>
<tr>
<td>2012</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2-Jan</td>
<td>2620</td>
<td>2320</td>
<td>512</td>
</tr>
<tr>
<td>13-Feb</td>
<td>4590</td>
<td>2580</td>
<td>569 *</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DM</td>
<td>consumed</td>
<td>(February)</td>
<td></td>
</tr>
</tbody>
</table>

Treatments were grazed in common from April-November 2011, with the first treatment grazing for the second year occurring on 2 January 2012.

Table 2: Average (± standard deviation) nutritive characteristics of chicory leaves from lax and intensely grazed swards on a commercial dairy farm over two summers

<table>
<thead>
<tr>
<th>ME (MJ ME/kg DM)</th>
<th>DOMD (% DM)</th>
<th>CP (% DM)</th>
<th>ADF (% DM)</th>
<th>NDF (% DM)</th>
<th>Ash (% DM)</th>
<th>SS (% DM)</th>
<th>Starch (% DM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Date</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2011</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>10-Jan</td>
<td>12.3 ±0.45</td>
<td>77 ±2.8</td>
<td>18 ±2.5</td>
<td>21 ±1.5</td>
<td>20 ±1.3</td>
<td>16 ±1.7</td>
<td>14 ±5.3</td>
</tr>
<tr>
<td>29-Jan</td>
<td>11.3 ±0.29</td>
<td>70 ±2.0</td>
<td>25 ±1.6</td>
<td>25 ±1.2</td>
<td>25 ±2.0</td>
<td>20 ±2.1</td>
<td>6 ±1.4</td>
</tr>
<tr>
<td>25-Feb</td>
<td>11.4 ±0.54</td>
<td>72 ±3.3</td>
<td>26 ±1.7</td>
<td>27 ±2.5</td>
<td>30 ±1.6</td>
<td>16 ±2.6</td>
<td>8 ±2.0</td>
</tr>
<tr>
<td>23-Mar</td>
<td>11.9 ±0.32</td>
<td>74 ±2.1</td>
<td>29 ±0.9</td>
<td>28 ±1.4</td>
<td>33 ±1.7</td>
<td>16 ±1.7</td>
<td>9 ±2.7</td>
</tr>
<tr>
<td>2012</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2-Jan</td>
<td>13.1 ±0.21</td>
<td>82 ±1.2</td>
<td>26 ±2.3</td>
<td>28 ±2.3</td>
<td>26 ±3.4</td>
<td>12 ±1.4</td>
<td>12 ±2.2</td>
</tr>
<tr>
<td>13-Feb</td>
<td>12.5 ±0.32</td>
<td>78 ±1.6</td>
<td>24 ±1.9</td>
<td>28 ±3.1</td>
<td>29 ±3.1</td>
<td>14 ±1.2</td>
<td>12 ±2.2</td>
</tr>
</tbody>
</table>

ME, metabolisable energy; DOMD, dry organic matter digestibility; CP, crude protein; ADF, acid detergent fibre; NDF, neutral detergent fibre; SS, soluble sugars.

There were more chicory shoots under lax than intense grazing in March 2011 (P<0.001), but at no other times were differences significant (Figure 2).
DISCUSSION AND CONCLUSION

In the first summer when chicory was vegetative, the actual post-grazing heights were similar to those targeted; these were achieved simply by the farm manager making a visual assessment and removing the cattle from the paddock. During reproductive development in the second summer, however, grazing was patchy. Cows stripped leaves from off the reproductive stems of the chicory plants, but avoided the tough reproductive stems as observed by (Clark et al. 1990b). The leaves remained high in nutritive characteristics. It was observed that some of the reproductive stems were trampled while others remained upright. As a result, target post-grazing heights were not achieved, nor was there any significant difference between treatments in post-grazing height. Therefore, achieving target residual heights on dairy farms is likely to be very difficult in reproductive swards of chicory unless mechanical means are employed.

During the first summer, lax grazing did not affect the total DM produced or consumed; however, it did improve shoot density. Results are consistent with previous research in which severe grazing reduced plant density (Clark et al. 1990a). Similarly, an effect of defoliation intensity on total DM production has also been observed in some studies, although it was generally agreed that defoliation frequency or interval was more important (Li and Kemp 2005, and references therein). Lax grazing did not reduce the nutritive value of chicory leaves, which remained high under both grazing regimes and within the range of values reported elsewhere (Li and Kemp 2005; Waugh et al. 1998).

Of note was the large decline in chicory shoot density between March and December 2011, when it was grazed in common through late autumn, winter and spring. Grazing through winter when chicory is dormant can exhaust carbohydrate reserves, resulting in poor performance in subsequent seasons (Li and Kemp 2005), as was likely the case here. Resting chicory from grazing during winter and early spring should, therefore, increase plant survival and subsequent DM production.

Target post-grazing heights for chicory may readily be achieved under controlled conditions on research farms, or on a commercial dairy farm while the chicory is vegetative. The variability in post-grazing height observed in this study, however, demonstrates how difficult target heights are to achieve on commercial dairy farms with reproductive chicory. Further, even if target post-grazing heights are achieved as during the first summer, the DM production and consumption benefits are negligible. Therefore, factors such as grazing interval that have a greater impact on DM production and persistence than residual height (Li and Kemp 2005) should be the main focus of grazing management.

ACKNOWLEDGEMENTS

Thanks to Phil Señey for providing his crop, cattle and time, and Sarah Cross and Jason Hughes for assistance with field measurements. This experiment was funded by New Zealand dairy farmers through DairyNZ Inc.

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Irrigated mixed sward of annual ryegrass (**Lolium multiflorum**) and kikuyu (**Pennisetum clandestinum**) exceeds 20 t DM/ha/yr utilisation for dairy production

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¹ Agri-Science Queensland (Dairy) University of Queensland (Gatton), Lawes Qld 4343

**ABSTRACT**

Well managed perennial ryegrass (**Lolium perenne**) swards can exceed 20 t dry matter (DM)/ha/yr in Queensland, however minimal feed is produced during summer and they require renovation annually. To exploit the subtropical environment fully, an alternative system is to grow a mixed-sward of short-rotation annual ryegrass (**L. multiflorum**) and tropical grass kikuyu (**Pennisetum clandestinum**). An irrigated grazing demonstration was conducted in Queensland from 2007 to 2009. Ryegrass was oversown into a kikuyu and white clover (**Trifolium repens**) sward in 2007 and 2008 and grazed by 50 to 105 milkers at a stocking rate of 11 to 19 cows/ha/d. Grazing interval was 3-4 leaves/tiller for annual ryegrass (cool-season) and 5-6 leaves/stolon for kikuyu (warm-season) and residual pasture height ranged from 5-9 cm. Utilisation, botanical composition, and forage quality were assessed. Cumulative pasture utilisation in year 1 was 20.3 t DM/ha and 24.6 t DM/ha in year 2 and water use efficiency (WUE) 16.4 and 15.3 kg DM/mm respectively. The additional utilisation in year 2 was achieved from conservation of kikuyu for silage. When botanical composition was averaged across each year, kikuyu recorded the highest values with 59.1 and 76.3% in years 1 and 2. The proportion of white clover declined from 22.5 to 7.8% in years 1 and 2, whereas ryegrass remained constant at 17.6% and 14.6%. Forage quality was highest when ryegrass was actively growing and lowest during summer when kikuyu was the dominant species. A mixed temperate and tropical grass sward can produce nutritious feed throughout the year.

**Keywords:** Tropical pasture; dairy; water use efficiency.

**INTRODUCTION**

There is a continual need to intensify productivity on Queensland dairy farms to offset rising farm production costs and the decline in allocation of water for irrigation. It is possible to further intensify subtropical pasture based systems as field plot evaluation of irrigated pastures demonstrated potential for a two-fold improvement in yield (Lowe *et al.* 1999) when compared with the industry average of 7 t DM/ha/yr (Callow *et al.* 2010). Temperate grasses and clovers have contributed significantly to dairy production by maintaining milk production during the autumn to spring period, and by providing a source of highly digestible forage to optimise milk production and its components (Fulkerson *et al.* 1998). However, during summer the high temperatures and humidity inhibits growth and causes ‘rust’ and plant mortality (Callow *et al.* 2003), which leads to substantially reduced yields in the second year. An alternative is to oversow a short-rotation ryegrass into an established perennial tropical grass such as kikuyu. Kikuyu is a productive and persistent tropical grass which can withstand grazing under high stocking rates and provides reasonably nutritious feed during summer and autumn (Reeves *et al.* 1996). This grass combination has the potential to produce large quantities of highly digestible pasture, and the present study was undertaken over 2 years in Queensland to determine the potential DM utilisation from a grazed pasture comprised of an established sward of kikuyu, oversown each autumn with annual ryegrass.

**MATERIALS AND METHODS**

A grazing study was conducted at Murdralpa Research Station (27°46´S, 152°40’E; altitude 40 m) from May 2007 until June 2009. Following the establishment of kikuyu cv. Whittet and white clover cv. Haifa in autumn 2006, annual ryegrass (cv. Aristocrat II) was broadcast at 45 kg/ha to facilitate increased ryegrass density on 4 June 2007 and 21 April 2008. The field site was 2,26 ha (80 m x 283 m) and irrigation water was applied with a high pressure traveller. The site was strip grazed using electrified tape every 3-4 leaves/tiller for annual ryegrass (during the cool-season) and 5-6 leaves/stolon for kikuyu (during the warm-season) by 50-105 milking cows. Residual pasture height following grazing ranged from 5-9 cm during both summer and winter. When not grazing these pastures, the milking herd received a partial mixed ration to achieve an average milk production of 22 L/cow/d. The site was slashed to 10 cm residual on 11 September, 2 and 26 October 2007, 8 September and 24 November 2008 with the aim of stimulating vegetative tiller production. Kikuyu was slashed to 10 cm residual on 20 March 2007 and mulched to a similar height on 18 April 2008 to suppress growth and assist in the establishment of ryegrass seedlings. Urea fertiliser
(N 46.0%) was broadcast at 60-120 kg/ha after defoliation, the lower application rate coincided with a shorter grazing interval during the warm-season. In total 370 and 473 kg N/ha was applied as urea fertiliser in years 1 and 2 respectively. Irrigation scheduling was determined by monitoring the pattern of soil water content (% volumetric) every 2-3 weeks using capacitance sensors. Irrigation water was applied to supplement rainfall when soil water extraction was observed at 40 cm below ground level and the amount of water applied generally restored soil water content to field capacity.

Prior to grazing, the basal cover of kikuyu, annual ryegrass, white clover and weeds were determined using a modified point quadrat method (Hill et al. 2004). A 0.09 m² quadrat was placed within ten exclosure cages, each cage 1 m² in area, distributed evenly across the study site to visually assess the proportion of cover for each species. The number of ryegrass leaves/tiller and kikuyu leaves/stolon were counted from two randomly selected plants within each cage. Pasture utilisation (t DM/ha) was determined by measuring the average height (cm) of the residual pasture using a rising plate meter (RPM) and harvesting with hand shears the pasture contained within the quadrat (0.09 m²) to the residual pasture height (cm). After sampling, each cage was randomly allocated within the freshly grazed site. The harvested herbage was weighed and a subsample taken from each quadrat and dried in a fan forced oven at 60°C for 48 hrs to determine the DM percentage and ground through a 1 mm screen in preparation for analysis for crude protein (CP), sugars, and neutral detergent fibre (NDF) at Dairy One Forage lab (Ithaca, New York State, USA).

RESULTS

Effective rainfall (≥5 mm and ≤50 mm/d) and cumulative FAO56 evapotranspiration in year 1 was 647 and 1165 mm, in year 2 they were 870 and 1584 mm. To meet the additional water requirements in year 2, a total of 739 mm of irrigation water was applied compared with 590 mm in year 1. Water use efficiency was calculated by dividing the total DM yield recorded in each year by the volume of water applied, the values were similar at 16.4 and 15.3 kg DM/mm in years 1 and 2.

![Figure 1: Mean 30 day rolling average of daily utilisation (kg DM/ha/d) of total pasture (---), kikuyu (-----), annual ryegrass (-----) and white clover (-----).](image-url)
Total pasture utilisation in year 1 was 20.3 t DM/ha from a total of 12 grazings, ranging from a minimum of 0.5 t DM/ha for the first grazing of annual ryegrass to a maximum of 2.7 t DM/ha in January. In year 2 total pasture utilisation was 24.6 t DM/ha from 12 grazings and one harvest for silage in April 2008 which yielded 5.0 t DM/ha. The pattern of average daily utilisation (kg DM/ha/d) was similar in years 1 and 2, with the lowest rates coinciding with the cool-season, and the maximum rates occurring during summer (Figure 1). The average daily utilisation rates for years 1 and 2 were 76.1 ± 10.20 and 62.9 ± 10.50 kg DM/ha/d respectively. There were distinct seasonal differences in the botanical composition of the sward, with ryegrass and white clover dominating the sward during winter and early spring, and kikuyu dominating for the remainder of the year. In year 1, kikuyu accounted for 59.1% of total utilisation (12.0 t DM/ha), and ryegrass and white clover for 17.6 and 22.5% of total utilisation respectively. In year 2, ryegrass was planted 6 weeks earlier but the yield remained similar at 3.6 t DM/ha, while the utilisation of white clover was less than half at 1.9 t DM/ha. The utilisation of kikuyu increased to 18.8 t DM/ha, 76.3% of the total DM production.

The nutritive value of the pasture reflected the botanical composition of the sward, with the highest quality recorded when the proportion of the temperate species was greatest. This occurred from May to November 2008 when NDF values were <60% and CP content greater than 20% (Figure 2). Quality was lower from December to April when the proportion of kikuyu exceeded that of the temperate species. CP and sugar contents tended to decline over the period of the study, associated with an increased kikuyu yield and decreased clover yield in year two.

**DISCUSSION AND CONCLUSION**

This study has demonstrated the potential productivity which can be attained from oversowing with a temperate pasture species in autumn into a tropical grass sward. We recorded over 20.0 t DM/ha of actively growing pasture which was more than double industry average (Callow 2010), with CP values exceeding 20% DM and WUE in the order of 16 kg DM/mm. Although pasture growth during ryegrass establishment was relatively low, this could be offset by staggering paddock establishment several months. (Garcia et al. 2008) recorded 17.0 t DM/ha from the same pasture mix grown in the temperate environment of New South Wales. Both studies show that an irrigated tropical grass pasture over sown with ryegrass annually is capable of high and consistent production of quality forage. The pasture combination offers dairy farmers a comparatively low risk and simple feedbase system to intensify productivity.

**ACKNOWLEDGEMENTS**

We thank DAFF and Dairy Australia for their financial support.

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Grass and Forage Science. 63, 284-300.
Grazing preferences of forages by dairy cows in different seasons


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ABSTRACT

Grazing preferences of 10 forage varieties were studied in different seasons in a “cafeteria” system where adjacent forage monocultures were offered to dairy cows at the same time. Four field pea varieties in spring; three legume forages (soybean, lablab and cowpea) in summer; and 3 brassicas (forage rape, leafy turnips and radish) in autumn-winter were evaluated. Cultivar Sturt, with 37% of total grazing time (TGT) was the most preferred (P < 0.001) but field pea variety Kaspa (13% of TGT) the least preferred. In summer soybean was the most preferred (P < 0.001) legume (69% of TGT), while cowpea was the least preferred (13.8%). Forage rape was the most preferred (P < 0.001) brassica species (45%). In each season, the highest preference ranks coincided with the highest forage DM yields. Strong grazing preferences by dairy cows were demonstrated indicating the potential of forage crops to manipulate behaviour of cows.

Keywords: cow preference; forages; grazing; dairy cows; seasons.

INTRODUCTION

Australian dairy farmers rely predominantly on perennial pastures as the primary source of feed. However, for a herd calving year round, the amount of dry matter (DM) produced from pasture alone is insufficient to meet feed requirements throughout the year due to the seasonal fluctuations of pasture growth and availability (Garcia et al. 2008). The intensification of dairy farming, together with the increased nutrient requirements of genetically improved dairy cows and high cost of purchased feed, indicate the need to investigate high yielding forages that could be used to overcome the seasonal pasture deficit within farms (Farina et al. 2010).

Dairy cows have shown strong levels of preference for specific forages when given the choice (Horadagoda et al. 2009). However, there is a lack of information on cows’ preference of forage options for each season of the year. Therefore, the objective of this study was to test the grazing preferences by dairy cows of a range of high yielding forage species and cultivars over different seasons.

MATERIALS AND METHODS

A series of cow preference studies were conducted at May Farm, University of Sydney, Camden, NSW to investigate the relative cow selection preferences and the DM yield of a range of forages during different seasons. In each study up to 4 species or cultivars of forages were offered at the same time through a unique ‘cafeteria’ system that provided opportunity for an unbiased testing of what animals selected (Horadagoda et al. 2009). Forages were randomly cultivated in treatment plots which were located between an outer circle of 46 m and inner circle of 18 m in diameter.

RESULTS

There were significant differences (P< 0.001) in the relative time cows spent grazing individual forage species/cultivars in each of the seasons. Among the field pea cultivars, Sturt was the most preferred (36.9% of grazing time [GT] ± 4.6) and Kaspa the least preferred (12.6% GT± 3.2) (Table 1). Among the three legumes tested in summer, soybean, and cowpea had the highest DM yields (6.8 t DM/ha) and was also the most preferred brassica variety, whilst radish was least preferred.
Table 1: Cow grazing preference time for the forages studied in each season expressed as the percentage of the relative time spent on grazing each species or cultivar with the SEM and the yield (t Dm/ha) of each forage

<table>
<thead>
<tr>
<th>Season</th>
<th>Forage type</th>
<th>Cow preference (% of grazing time ± SEM)</th>
<th>DM Yield on offer (t Dm/ha ± SEM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Spring</td>
<td>Sturt</td>
<td>36.9 ± 4.6</td>
<td>8.4 ± 0.2</td>
</tr>
<tr>
<td></td>
<td>Yarrum</td>
<td>27.9 ± 3.9</td>
<td>3.2 ± 0.2</td>
</tr>
<tr>
<td></td>
<td>Morgan</td>
<td>19.3 ± 2.3</td>
<td>6.9 ± 0.4</td>
</tr>
<tr>
<td></td>
<td>Kaspa</td>
<td>12.6 ± 1.9</td>
<td>4.8 ± 0.3</td>
</tr>
<tr>
<td>Summer</td>
<td>Soybean</td>
<td>68.8 ± 7.9</td>
<td>6.8 ± 0.7</td>
</tr>
<tr>
<td></td>
<td>Lablab</td>
<td>17.3 ± 3.9</td>
<td>5.8 ± 0.6</td>
</tr>
<tr>
<td></td>
<td>Cow peas</td>
<td>13.8 ± 5.4</td>
<td>5.2 ± 0.7</td>
</tr>
<tr>
<td>Winter-Autumn</td>
<td>Forage rape</td>
<td>45.4 ± 5.2</td>
<td>6.5 ± 0.7</td>
</tr>
<tr>
<td></td>
<td>Leafy turnip</td>
<td>31.6 ± 3.2</td>
<td>5.2 ± 0.9</td>
</tr>
<tr>
<td></td>
<td>Grazer radish</td>
<td>14.1 ± 4.2</td>
<td>3.5 ± 0.6</td>
</tr>
</tbody>
</table>

The grazing preferences of forage species followed by the same letters are not significantly different at (P < 0.05).

Preference for field peas was inversely related to tendril density (Figure 2a and b). In addition to the highest grazing preference, yield of Sturt was also the highest (8.4 t DM/ha when compared to 4.8 t DM/ha for Kaspa).

DISCUSSION AND CONCLUSION

Results confirmed that grazing behaviour is influenced by both forage availability and palatability (Horadagoda et al. 2009). Coincidently in all three seasons, the forage varieties studied that had the highest DM yield were also the most preferred varieties by the cows. Results also indicate that forage peas (Sturt) could be used productively for grazing during spring in NSW, as opposed to being sown for making silage only (Garcia et al. 2008). The nature of the crop canopy in field peas (tendril density) influenced preference. In soybean the erect presentation of leaves and stem made it readily accessible for grazing compared to the other legumes where leaves laid flat and close to the ground (lablab) or the foliage was stunted and bushy in nature (cowpeas). This study also demonstrated that soybean can be grown to overcome summer pasture deficits.

For the brassica species, forage rape was also the most erect forage. Its highest preference may also be related to higher water soluble carbohydrate content (114 g/kg DM) in petioles and stems.

All together, these field studies demonstrated that strong grazing preferences by dairy cows are evident when given free choice and indicate the potential of forage crops to manipulate cows' behaviour, particularly for future automated (robotic) milking systems in which cows voluntarily move to and from paddocks in search of feed incentives (Jago et al. 2002).

REFERENCES


ABSTRACT

The dairy industry in northern Victoria relies on irrigation water to grow a large proportion of its feed. Low and variable irrigation allocations over the last 15 years have caused dairy farmers to reassess their feedbase. A modelling study was undertaken with the objective of determining the irrigation water requirements of five forages commonly used by the dairy industry in northern Victoria. The FAO56 evapotranspiration model was used with 70 years of historical weather data. Model parameters were selected to ensure consistency of modelled and previously measured water requirements. Modelled annual irrigation water-use for perennial pasture, lucerne, maize, long-season annual pasture and short-season annual pasture were 8.3, 7.8, 5.5, 4.7 and 2.8 ML/ha, respectively. The large range in data suggested that “probability of exceedance” curves were a better descriptor of the likely irrigation water requirements than a simple average (and range). These data will be useful to dairy farmers who are planning their management responses during periods when irrigation water availability is limited and variable.

Keywords: evapotranspiration; FAO56; probability of exceedance.

INTRODUCTION

The dairy industry in northern Victoria relies on irrigation water to grow a large proportion of its feed inputs. However, irrigation water requirements can vary markedly from year to year. The FAO-56 model (Allen et al. 1998) has been successfully used in northern Victoria to predict the water requirements of a range of irrigated forages using climatic data (Greenwood et al. 2008, 2009); the exception is the first irrigation of annual forages after a dry period. The objective of this study was to determine the probability distribution of annual irrigation water requirements of five irrigated forages at Tatura in northern Victoria using 70 years of climate data.

MATERIALS AND METHODS

The FAO-56 single crop coefficient model was used to model crop irrigation water requirements on a daily basis for five forage types at Tatura. Climatic data from 1935 to 2005 was sourced from the SILO website (SILO 2011).

The forages used were perennial pasture (perennial ryegrass-white clover), lucerne, maize, long-season annual pasture (Persian clover-Italian ryegrass; irrigated from mid-February to mid-November) and short-season annual pasture (subterranean clover-Italian ryegrass; irrigated from mid-March to mid-October).

Crop coefficients were selected to ensure consistency between the modelled and previously measured (Greenwood et al. 2008 and 2009) annual irrigation water-use. A crop coefficient value of 1.0 was used for all forages except maize. Crop coefficient values for maize were: 0.3 from pre-irrigation to 20 days after sowing, a linear increase over the next 40 days to 1.2, and 1.2 for the remainder of the production period (Greenwood et al. 2008).

Irrigation scheduling was on the basis of cumulative (ET_o-R) (reference evapotranspiration less rainfall) since the last irrigation or runoff event. Values of ET_o-R at which irrigations were scheduled were: perennial and annual pastures >45 mm, lucerne >75 mm, and maize >60 mm. No forages were irrigated between 15 May (or 15 April for lucerne) and 15 August. The maize was sown on 22 November and received its last prior to 22 March.

The modelling rules assumed all irrigation runoff water was captured and reused, no collection and storage of run-off from rainfall, and deep drainage of 1 mm per day whenever estimated soil water deficits indicated surface ponding.

A more complete description of the modelling process and rules are given by (Lawson et al. 2012).

RESULTS

Modelled annual irrigation water-use of the five forage and their ranges over a 70 year period are shown in Table 1. The data were plotted using “probability of exceedance” curves as shown in Figure 1. These curves show the proportion of years (Y-axis) for which irrigation water-use will exceed a certain level (X-axis). For example, annual irrigation water-use for perennial pastures at Tatura will exceed approximately 4.8, 5.9, 7.5 and 9.5 L/ha for 99, 90, 50 and 10% of years, respectively. Consequently, the annual irrigation water-use was between 5.9 and 9.5 ML/ha for 80% of years.
**Table 1:** Average climatic data (1935-2005) and modelled irrigation water-use for Tatura

<table>
<thead>
<tr>
<th></th>
<th>Rainfall</th>
<th>ETo</th>
<th>Perennial pasture</th>
<th>Lucerne</th>
<th>Maize</th>
<th>Long-season annual</th>
<th>Short-season annual</th>
</tr>
</thead>
<tbody>
<tr>
<td>mm/year</td>
<td></td>
<td></td>
<td>ML/ha/year</td>
<td>ML/ha/year</td>
<td>ML/ha/year</td>
<td>ML/ha/year</td>
<td>ML/ha/year</td>
</tr>
<tr>
<td>Average</td>
<td>483</td>
<td>1179</td>
<td>8.3</td>
<td>7.8</td>
<td>5.5</td>
<td>4.7</td>
<td>2.8</td>
</tr>
<tr>
<td>Range</td>
<td>203-927</td>
<td>1067-1340</td>
<td>4.8-10.6</td>
<td>3.4-11.4</td>
<td>3.5-7.0</td>
<td>1.9-6.8</td>
<td>0.6-4.9</td>
</tr>
</tbody>
</table>

**Figure 1:** Modelled irrigation water-use of perennial pasture (PP), lucerne, maize, long-season annual pasture (LSAP) and short-season annual pasture (SSAP) at Tatura for 1935-2005.

**DISCUSSION AND CONCLUSION**

Modelled annual irrigation water-use was closely related to the length of the growing season and was highest for perennial pasture and lucerne, intermediate for maize and long-season annual pasture, and lowest for short-season annual pasture. The large range in annual irrigation water-use suggested that for planning purposes, the probability of exceedance values were a better descriptor of the amount of irrigation water that is required than a simple average (and range). These data will be useful to dairy farmers who are planning their responses to limited availability of irrigation water.

**ACKNOWLEDGEMENTS**

Funding for this project was provided by the Victorian Department of Primary Industries, Dairy Australia and Murray Dairy.

**REFERENCES**


Milk response and feed conversion efficiency of grazed and conserved ryegrass and oats pastures fed at three different levels of grain intake in a subtropical environment

A.R. ANSTIS, D.G. BARBER, M.N. CALLOW, E.J. LITZOW

Agri-Science Queensland, DAFFQ, University of Queensland (Gatton Campus), LAWES Qld 4343

ABSTRACT.

Management of forages to achieve optimum milk production and feed conversion efficiency (FCE) is critical to the profitability of Australian dairy farms. A 20-day feeding experiment was conducted at Mutdapilly Research Station with 72 Holstein Friesian dairy cows in mid lactation. Annual ryegrass (Lolium multiflorum) and forage oats (Avena sativa) were managed using two defoliation methods (grazed and conserved) to achieve forage with high and medium nutritive characteristics (ME, CP and NDF content) respectively, and assessed for FCE (L milk/kg DM), milk yield and composition at three amounts of grain intake (0, 3 and 6 kg grain as-fed/cow.day). Results show that milk yield and protein concentration were increased with increasing grain intake. There was no significant effect on FCE. It was concluded that increasing grain intake when feeding forages that have a medium to high nutritive quality will not increase FCE if forage intake remains high and total DM intake is increased with milk yield.

Key Words: Feed conversion efficiency; grain; ryegrass; oats; pasture; conserved forage.

INTRODUCTION

When transitioning from grazed pasture to conserved forages, there is uncertainty around how to maintain milk yield and profitability when differences in the nutritive value of forage species and stage of maturity at defoliation arise. This uncertainty is often counteracted by adjusting the amount of grain fed. The milk response to grain feeding is variable (Robaina et al. 1998) and does not always result in an increase in FCE, which may be due to substitution (Bargo et al. 2002). The objective of this study was to define the milk production response and FCE of dairy cows offered two temperate forages grown in a subtropical environment, fed as grazed pasture or conserved silage on a feedpad to achieve forage with high and medium nutritive quality (ME, CP and NDF content) respectively, when fed in combination with three amounts of grain intake.

MATERIALS AND METHODS

A 20-day split-split plot feeding experiment consisting of a 10-day adaptation period and a 10-day treatment period was conducted at Mutdapilly Research Station in 2008. Seventy-two Holstein Friesian cows (184 ± 15 days in milk) were randomly assigned to each treatment. Two temperate forage species (annual ryegrass and forage oats) were evaluated under two defoliation methods, either grazed at the recommended grazing time (3 leaf stage for ryegrass and 4 weeks for oats) or delaying defoliation, cutting and conserving as roundbale silage (6 leaf stage for ryegrass and 8 weeks for oats) and fed on the feedpad. The four forage treatments (ryegrass pasture grazed, ryegrass silage fed on the feedpad, forage oats grazed and forage oats silage fed on the feedpad) were replicated twice. The eight plots were divided further into three sub-plots (each with 3 cows) and randomly allocated 0, 3 and 6 kg as-fed/cow.day of a barley/maize grain (50% barley:50% maize) mix offered in the dairy. Pre- and post-grazing measurements and silage intake were recorded daily. Cows were milked twice daily with milk composition samples taken every second day. FCE (L milk/kg DM) was calculated as the solids corrected milk yield (L/cow.day) divided by the feed consumed (kg DM/cow.day).

RESULTS

Forage intake was higher for annual ryegrass compared to forage oats (P<0.01), but was not altered by amount of grain intake or defoliation method (P>0.05). Increasing concentrate intake increased estimated ME intake/day, milk yield and protein concentration. Annual ryegrass increased milk yield and milk protein concentration compared to forage oats (Table 1). There were no significant changes in FCE (P>0.05). A significant forage x defoliation interaction was seen for DM and ME intake and milk fat concentration (P<0.05; data not presented).
Table 1: Effects of forage type, method of defoliation and grain intake on dry matter intake, metabolisable energy intake (MEI), milk yield, milk composition and feed conversion efficiency (FCe)

<table>
<thead>
<tr>
<th>Variable</th>
<th>Forage</th>
<th>Defoliation</th>
<th>Grain intake (kg as-fed/cow.day)</th>
<th>Main effects¹</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Oats</td>
<td>Rye</td>
<td>Grazed</td>
<td>Silage</td>
</tr>
<tr>
<td>DM Intake (kg/day)</td>
<td>18.2a</td>
<td>20.0a</td>
<td>19.7</td>
<td>18.5</td>
</tr>
<tr>
<td></td>
<td>17.4a</td>
<td>18.7a</td>
<td>21.2b</td>
<td>**</td>
</tr>
<tr>
<td>MEI (MJ/day)</td>
<td>199ª</td>
<td>223b</td>
<td>225ª</td>
<td>196ª</td>
</tr>
<tr>
<td></td>
<td>186ª</td>
<td>206ª</td>
<td>240ª</td>
<td>**</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>***</td>
</tr>
<tr>
<td>Milk yield (L/day)</td>
<td>19.8ª</td>
<td>22.4ª</td>
<td>21.4</td>
<td>20.7</td>
</tr>
<tr>
<td></td>
<td>19.5ª</td>
<td>21.3b</td>
<td>22.4c</td>
<td>*</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>***</td>
</tr>
<tr>
<td>Fat (%) m/v</td>
<td>4.01</td>
<td>4.11</td>
<td>4.12ª</td>
<td>3.99b</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>4.14</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>4.00</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>4.04</td>
</tr>
<tr>
<td>Protein (%) m/v</td>
<td>3.08ª</td>
<td>3.32b</td>
<td>3.18</td>
<td>3.22</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>3.12ª</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>3.23b</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>3.25ª</td>
</tr>
<tr>
<td>FCE (L milk/kg DM)</td>
<td>1.26</td>
<td>1.26</td>
<td>1.31</td>
<td>1.21</td>
</tr>
<tr>
<td></td>
<td>1.21</td>
<td></td>
<td></td>
<td>1.36</td>
</tr>
<tr>
<td></td>
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<td></td>
<td>1.28</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1.15</td>
</tr>
</tbody>
</table>

¹ Significance levels: *P = <0.05, **P = <0.01, ***P = <0.001

DISCUSSION AND CONCLUSION

Forage type and grain intake affected the milk response which was consistent with results found by Davison and Elliot (1993). Though ME intake was improved with grazed ryegrass and increasing amount of grain intake, no subsequent improvement was observed in FCE presumably because the amount of substitution was low and the intake of good quality forage was high. However in a review by Beever and Doyle (2007), FCE increased with level of intake and production. It was concluded that increasing grain intake when feeding forages that have a medium to high nutritive quality will not increase FCE when forage intake remains high and total DM intake is increased with milk yield.

ACKNOWLEDGEMENTS

We thank the Queensland dairy industry and Dairy Australia for financial support.

REFERENCES


Increasing home grown forage consumption and profit in non-irrigated dairy systems

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2 Dairy NZ
3 Terneus Agricultural Consulting Pty Ltd, Upwey, Vic 3158.
4 Department of Primary Industries Victoria
5 RedSky Agriculture

ABSTRACT

A farmlet experiment was conducted in south-west Victoria to test the hypothesis that systems based on perennial ryegrass (Lolium perenne L.) with complementary forages can result in 30% higher home-grown forage (HGF) consumption and a 30% increase in profitability compared to a system based on well-managed perennial ryegrass pasture only. A well managed ryegrass farmlet (‘RM’) stocked at 2.25 cows/ha was compared to a complementary forage farmlet (‘CF’), stocked at 2.6 cows/ha and incorporating tall fescue (Festuca arundinaceae schreb.), annual ryegrasses (Lolium multiflorum Lam.) and double cropping (winter cereals and summer brassica forages), over four lactations (2005/06-2008/09). On average, CF had 31% higher HGF consumption than RM but only 2% higher return on assets (ROA). In May 2009 the farmlets were reconfigured with the stocking rate on RM increased to 2.6 cows/ha, and the complementary forages plan revised to focus on high rates of ryegrass pasture renovation with crops (for grazing) used in the renovation program and stocked at 3.1 cows/ha (‘RM Plus’). In 2010/11, RM Plus system harvested 16% more HGF with a 10% increase in ROA compared to RM. The high levels of production and profitability on RM over six years demonstrated untapped potential in perennial ryegrass systems. CF increased HGF consumption by 30%, however the extra profit was not sufficient to warrant major change in the forage base. A forage plan focussing on forages that are directly grazed and integrated into an aggressive pasture renovation program offers promise for increasing profit.

Keywords: dairy, pasture, profitability, complementary forages, perennial ryegrass; tall fescue

INTRODUCTION

The profitability of pasture-based dairy production systems in southern Australia is closely related to the amount of pasture consumed by cows per hectare (eg. Armstrong et al. 2010). The growth of perennial ryegrass is strongly seasonal (winter-spring), which limits gains in pasture consumption. Complementary HGF options have potential for lifting total forage production per hectare, but their impact on profit is not known. A farmlet experiment was conducted in southwest Victoria to test the hypothesis that systems based on perennial ryegrass with complementary forages (‘CF’) can result in 30% higher HGF consumption and a 30% increase in profitability compared to a system based on well-managed perennial ryegrass pasture only (‘RM’).

MATERIALS AND METHODS

A farmlet experiment was conducted on a commercial farm near Terang (38° 14’ S; 142° 55’ E) in southwest Victoria. The region has a temperate climate with the long-term average annual rainfall of 783 mm. The RM farmlet was stocked at 2.25 cows/ha, while the CF farmlet was stocked at 2.9 cows/ha. The experiment ran for four years (2005/06-2008/09). CF combined perennial ryegrass (44% area) with tall fescue (25% area), oversowing of perennial ryegrass with annual and short term ryegrass (16% area) and double cropping (winter cereals for silage and summer brassicas for grazing on 15% area). In May 2009, the stocking rate on RM increased to 2.6 cows/ha to further test the capacity of perennial ryegrass to support profitable feeding systems. A revised forage plan for the alternate farmlet was implemented at the same time, focussing on high rates of perennial ryegrass pasture renovation with forage crops (for grazing) used in the renovation program. This system, renamed ‘RM Plus’, ran for a further two years (2009/10–2010/11). Each farmlet system was stocked with 36 cows; land area was adjusted to achieve the required stocking rate. In the experiment pasture management policies for renovation, fertiliser application and grazing were implemented to optimise growth and consumption. The cost of production and ROA of the farmlets was calculated using the measured farm inputs and production, including actual costs, together with costs for items that could not be determined in a farmlet situation (eg. animal health and shed expenses) and asset values representative of the top 10% of the industry (source: redskyagri.com). Milk prices were $4.45, 4.35, 6.40, 4.75, 4.50 and 5.35/kg MS in the six successive years.
RESULTS

For the first phase of the farmlets, HGF consumption on CF was 31% higher than RM over the first four years of the experiment (means of 9.7 and 7.4 t DM/ha for CF and RM respectively, Table 1). However, average annual ROA for CF was only 2% higher than for RM (12.2 and 12.0% for CF and RM respectively). Comparisons between the RM and RM Plus systems were restricted in 2009/10 by the transition to the new systems. In 2010/11 (phase 2), RM Plus harvested 16% more HGF with a 10% increase in ROA compared to RM, albeit under favourable seasonal conditions (Table 2). Across these two years the difference in cost of production between the RM Plus and RM ($+0.19/kg MS) was less than between CF and RM in the first four years ($+0.30/kg MS).

Table 1: Key production and economic results from RM and CF farmlets (2005-06-2008/09)

<table>
<thead>
<tr>
<th></th>
<th>RM</th>
<th></th>
<th></th>
<th></th>
<th>CF</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>05/06</td>
<td>06/07</td>
<td>07/08</td>
<td>08/09</td>
<td>05/06</td>
<td>06/07</td>
<td>07/08</td>
<td>08/09</td>
</tr>
<tr>
<td>Total HGF consumed (t DM/ha)</td>
<td>7.29</td>
<td>6.48</td>
<td>8.31</td>
<td>7.49</td>
<td>10.82</td>
<td>8.15</td>
<td>10.30</td>
<td>9.39</td>
</tr>
<tr>
<td>HGF % of diet</td>
<td>46.8</td>
<td>56.7</td>
<td>72.8</td>
<td>66.0</td>
<td>53.0</td>
<td>49.2</td>
<td>65.3</td>
<td>57.4</td>
</tr>
<tr>
<td>Milk production (kg MS/ha)</td>
<td>1170</td>
<td>1278</td>
<td>1350</td>
<td>1187</td>
<td>1526</td>
<td>1753</td>
<td>1780</td>
<td>1510</td>
</tr>
<tr>
<td>Cost of production ($/kg MS)</td>
<td>3.08</td>
<td>3.29</td>
<td>3.13</td>
<td>3.01</td>
<td>3.15</td>
<td>3.75</td>
<td>3.45</td>
<td>3.32</td>
</tr>
<tr>
<td>ROA (%)</td>
<td>10.3</td>
<td>7.9</td>
<td>20.5</td>
<td>10.1</td>
<td>11.8</td>
<td>5.9</td>
<td>22.5</td>
<td>10.5</td>
</tr>
</tbody>
</table>

Table 2: Key production and economic results from RM and RM Plus farmlets (2009/10-2010/11)

<table>
<thead>
<tr>
<th></th>
<th>RM</th>
<th></th>
<th></th>
<th></th>
<th>RM Plus</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>09/10</td>
<td>10/11</td>
<td></td>
<td></td>
<td>09/10</td>
<td>10/11</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total HGF consumed (t DM/ha)</td>
<td>8.68</td>
<td>9.68</td>
<td>9.34</td>
<td>11.29</td>
<td>1396</td>
<td>1546</td>
<td>1691</td>
<td>1893</td>
</tr>
<tr>
<td>HGF % of diet</td>
<td>59.0</td>
<td>66.6</td>
<td>54.7</td>
<td>59.7</td>
<td>2.84</td>
<td>2.60</td>
<td>3.11</td>
<td>2.71</td>
</tr>
<tr>
<td>Milk production (kg MS/ha)</td>
<td>1396</td>
<td>1546</td>
<td>1691</td>
<td>1893</td>
<td>9.3</td>
<td>17.6</td>
<td>8.9</td>
<td>19.4</td>
</tr>
</tbody>
</table>

DISCUSSION AND CONCLUSION

The high levels of production and profitability obtained in the RM farmlet over six years demonstrated the untapped potential of perennial ryegrass based systems. CF increased home grown forage consumption by 30%, but the extra profit was insufficient to warrant a large scale change in the forage base. The reasons for the lower than expected difference in ROA between the farmlets included the better than expected performance of RM, lower than expected summer forage production from tall fescue and the brassica crops in CF, lower than expected DM yields and low consumption of whole crop silage, and greater exposure of the higher stocked CF system to drought in 2006/07. However, the revised forage plan in RM Plus that focussed on grazing crops that were integrated into the pasture renovation program offered promise to increase profit above ryegrass.

ACKNOWLEDGEMENTS

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REFERENCES

Milk production response and feed conversion efficiency to conserved forage crops fed at three levels of grain intake in a sub-tropical environment

D.G. BARBER, A.R. ANSTIS, M.N. CALLOW, E.J. LITZOW

Agri-Science Queensland, DAFFQ, University of Queensland Gatton Campus, LAWES Qld 4343

ABSTRACT

Feed conversion efficiency (FCE) of forage crops in northern Australia is variable and primarily dependant on feed quality. A 20-day split plot feeding experiment with two runs was conducted at Mutdapilly Research Station with 72 and 54 Holstein Friesian dairy cows, respectively, in mid to late lactation. Four conserved forages (corn silage, barley silage, soybean silage and lucerne hay) were assessed for milk yield and composition responses and FCE at three levels of grain intake (0, 3 and 6 kg grain as-fed/cow.d^{-1}). Milk protein concentration increased with increasing grain intake on barley silage. Milk yield and FCE was not significantly increased with increasing grain intake, however there were differences seen between forages. It is concluded that milk yield and FCE is not responsive to short term changes in grain intake when feeding conserved forage diets, particularly if the diet is not balanced for CP intake.

Key Words: Feed conversion efficiency; grain; corn; barley; lucerne; soybean; silage; hay.

INTRODUCTION

Forage crops grown for silage have different quality characteristics to pastures with cereal and legume based forages providing an opportunity to supplement the starch and protein content of the diet respectively. Cereal based silages such as corn and barley are high in starch (>20% DM), while legume silages and hays are high in crude protein (>18%). The objective of this study was to determine the responses in FCE of dairy cows offered two cereal silages (corn and barley) and two conserved legumes (soybean silage and lucerne hay) at three levels of grain intake.

MATERIALS AND METHODS

Two runs of a 20-day split plot feeding experiment consisting of a 10 day adaptation period and a 10 day treatment period were conducted at Mutdapilly Research Station. Run 1 was conducted in November 2008 and assessed two temperate forages (barley silage and lucerne hay) that were offered with three levels of grain intake (0, 3, and 6 kg/cow.d^{-1}) in the dairy. Seventy-two dairy cows (223 ± 15 DIM) were randomly assigned to the six treatments with twelve cows per treatment. Run 2 was conducted in March 2009 and assessed two tropical forage species (corn silage and soybean silage) that were offered with three levels of grain intake (0, 3, and 6 kg/cow.d^{-1}) in the dairy. Fifty-four dairy cows (200 ± 14 DIM) were randomly assigned to the six treatments with nine cows per treatment. Feed intakes and refusals were measured daily. Cows were milked twice daily with milk composition samples taken every second day. Feed conversion efficiency (L milk/kg DM) was calculated as the solids corrected milk yield (L/cow.d-1) divided by the feed consumed (kg DM/cow.d-1). Treatment means were analysed in Genstat using an analysis of variance model (Payne et al. 2007), with forage species as the main plot treatments and grain intake as the subplot treatment. There was no replication of the main plots hence the effect of forage could not be tested. The effect of grain level within a forage was tested if the interaction between forage and grain intake was significant at P<0.05.

RESULTS

Forage intake did not change (P>0.05) with increased grain intake for all treatments. Total and ME intake increased (P<0.001) with increasing grain intake for the corn and soybean silages only. Crude protein (CP) intake increased (P<0.05) with grain intake in all forages. Milk yield was not affected by grain intake (P>0.05) within forage types (Table 1). Milk fat was decreased with grain (P<0.01) on the lucerne hay diet and milk protein was higher (P<0.05) at the highest grain intake on the barley silage diet. There were no significant changes in FCE with increasing grain intake within forages. There was a significant forage x grain intake interaction for milk fat (P<0.01) and protein (P<0.05) concentration in run 1 and for DM and ME intake (P<0.01) in run 2, with an interaction for CP intake (P<0.001) within all forages.
**Table 1:** The effect of increasing grain offered (0, 3 and 6 kg/cow.d⁻¹) on forage, dry matter (DM), metabolisable energy (ME) and crude protein (CP) intake, milk yield, milk composition and feed conversion efficiency (FCE) when fed with barley silage, lucerne hay, corn silage or soybean silage

<table>
<thead>
<tr>
<th>Variable</th>
<th>Barley silage</th>
<th>Lucerne hay</th>
<th>Corn silage</th>
<th>Soybean silage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grain intake (kg DM/d)</td>
<td>0.0 2.5 5.0</td>
<td>0.0 2.5 4.8</td>
<td>0.0 2.7 5.2</td>
<td>0.0 2.7 5.1</td>
</tr>
<tr>
<td>Forage intake (kg DM/d)</td>
<td>14.7 13.9 12.9</td>
<td>17.1 17.7 16.5</td>
<td>11.7 10.7 9.7</td>
<td>12.0 11.7 11.8</td>
</tr>
<tr>
<td>Total intake (kg DM/d)</td>
<td>14.7 16.4 17.9</td>
<td>17.1 20.2 21.3</td>
<td>11.7⁻ 13.4⁻ 14.9⁻</td>
<td>12.0⁻ 14.4⁻ 16.9⁻</td>
</tr>
<tr>
<td>ME intake (MJ ME/d)</td>
<td>146 172 196</td>
<td>172 212 231</td>
<td>114⁻ 141⁻ 167⁻</td>
<td>114⁻ 149⁻ 184⁻</td>
</tr>
<tr>
<td>CP intake (kg DM/d)</td>
<td>1.6⁻ 1.9⁻ 2.0⁻</td>
<td>3.8⁻ 4.3⁻ 4.3⁻</td>
<td>0.8⁻ 1.0⁻ 1.2⁻</td>
<td>2.2⁻ 2.4⁻ 2.6⁻</td>
</tr>
<tr>
<td>Milk yield (L/d)</td>
<td>14.4 16.6 16.9</td>
<td>17.3 20.2 9.0</td>
<td>10.0 11.8 10.5</td>
<td>14.0 14.9 14.9</td>
</tr>
<tr>
<td>Fat (% m/v)</td>
<td>3.98 4.21 4.24</td>
<td>4.46⁻ 4.12⁻ 3.97⁻</td>
<td>4.38 4.63 4.45</td>
<td>4.68 4.70 4.57</td>
</tr>
<tr>
<td>Protein (% m/v)</td>
<td>3.11⁻ 3.23⁻ 3.41⁻</td>
<td>3.40 3.47 3.48</td>
<td>3.48 3.47 3.26</td>
<td>3.22 3.38 3.18</td>
</tr>
<tr>
<td>FCE (L milk/kg DM)</td>
<td>1.10 1.20 1.12</td>
<td>1.19 1.07 0.88</td>
<td>0.85 0.92 1.02</td>
<td>1.11 1.04 1.04</td>
</tr>
</tbody>
</table>

**DISCUSSION AND CONCLUSION**

The short term response in milk yield and FCE was not affected by increasing grain intake within forages, with the lowest FCE levels seen within the corn silage diet. The lower response on the corn silage diet may be due to an insufficient supply of rumen degradable protein (RDP), with increasing starch intake compared with the lucerne and soybean diets. Substitution was minimal across all forages, though the forages used here were of relatively low quality compared with ryegrass pasture and it has been reported that substitution is less for lower quality forages (Waldo et al. 1981, Broderick et al. 2002). It is concluded that milk yield and FCE is not responsive to short term changes in grain intake when feeding conserved forage diets, particularly if the diet is not balanced for CP intake.

**ACKNOWLEDGEMENTS**

We thank the Queensland dairy industry and Dairy Australia for financial support.

**REFERENCES**


Strategies for increasing dairy system productivity while controlling environmental footprint: a common systems research approach in two regions of New Zealand

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ABSTRACT

The first year physical production of dairy farmlet systems designed to achieve high milk production while reducing nitrate leaching in Waikato (non-irrigated) and Canterbury (irrigated), New Zealand, is reported. Two farmlets were compared in each region: one with a lower stocking rate and incorporating inputs that should increase production efficiency and reduce the potential for nitrogen (N) loss via animal cycling, and one with a higher stocking rate representing the predominant trend toward greater intensification. Farmlet design and targets were determined from pre-experimental modeling. The results provide evidence to support the core efficiency concepts embodied in the modeling. They indicate that high pasture intakes, feed conversion efficiency and milk solids production can be achieved in systems with lower stocking rates, and low feed and N fertiliser imports. While initial results are promising, more information is required over several years, including N leaching losses and economic performance, before firm conclusions can be drawn.

Keywords: dairy systems, environmental impacts, nitrogen

INTRODUCTION

The New Zealand Government’s National Policy Statement on Freshwater Management 2011 requires Regional Councils throughout New Zealand to set quality limits for all surface and groundwaters in their regions. Nitrogen (N) is a pressing issue in several important dairy catchments because, on most soil types used for dairying, it can readily leach below the root zone of pasture into receiving waters. To sustain industry growth, future systems must increase productivity while at least holding, or preferably reducing, total N leaching loads.

The key point of focus for controlling N losses from New Zealand dairy systems is N cycling via the grazing animal. Nitrogen intake by grazing cows far exceeds N output in products, with 75 - 90% of N ingested being excreted, mostly via urine patches with N loadings between 500 and 1000 kg N/ha (Whitehead, 1995). These loads are well in excess of the capacity of the pasture in and around the patch to take up the available nitrogen. Much of this N will be transformed to nitrate through nitrification, which can then be readily carried below the root zone by drainage water. Strategies for controlling this loss pathway include: lowering stocking rate to reduce urine N patch deposition by the milking herd and all replacement animals (lower stocking rate = lower replacement animal numbers); standing animals off pasture at times when the risk of N leaching from freshly deposited urine is highest; reducing N fertiliser inputs; using animals of very high genetic merit (Breeding Worth, BW) which partition a higher proportion of surplus N to faeces instead of urine compared to cows of low genetic merit (Woodward et al. 2011); using diverse pasture mixtures that include forage herbs which appear to reduce urinary N concentration compared to perennial ryegrass/white clover pasture (Woodward et al. 2012); manipulating animal diet, for example through the use of tannin-containing feed and supplements; and applying nitrification inhibitors (e.g. Di and Cameron, 2007).

Many of these strategies have implications for management of the key interactions between pastures and grazing animals that drive production efficiency and low costs of production. The individual effects of many of them on potential environmental losses have been investigated, but no research has been conducted in New Zealand to determine the combined effect of several strategies on productivity and environmental outcomes, plus the associated system management requirements and risks.

The objective of the work reported here is to measure whole-system outcomes of different management strategies in two important dairying regions in New Zealand: Waikato, in the North Island, where pastures are not irrigated; and Canterbury in the South Island, where irrigation is used to maintain pasture growth in summer. This paper reports the first year of physical production results from 4 farmlets (2 in Waikato, 2 in Canterbury) initiated in 2011 to address the objective.
MATERIALS AND METHODS

An overview of the systems established in Waikato (DairyNZ Scott Farm, Newstead, Hamilton) and Canterbury (Lincoln University Research Dairy Farm, Lincoln) is provided in Table 1. All 4 systems were designed using the results of pre-experimental modelling to set targets for productivity and environmental outcomes (Burggraaf et al. 2011, Beukes et al. 2011). The core concept adopted in the modelling and the farmlets is production efficiency: for example, through the use of high genetic merit animals that efficiently convert pasture to milk thereby allowing high milksolids production per hectare at a lower stocking rate (and, therefore, fewer total animals and urinary N load). Significant challenges associated with this concept include: achieving very high pasture utilization and per cow pasture intakes, while simultaneously achieving high per-cow milk production; maximising cow reproductive performance; effectively integrating mitigation tools such as nitrification inhibitors; and limiting farm gate N surplus by restricting N fertiliser use and feed imports.

The respective physical production plus profit and environmental targets are shown in Tables 2 and 3. The Waikato experiment began on 1st March 2011 while the Canterbury experiment began on 26th September 2011. A stocking rate contrast is common to both sites, as is the use of relatively high BW animals (see Tables 2 and 3) and a nitrification inhibitor (2 applications in Waikato, between April and September 2011, and one application in April 2012; 2 applications in Canterbury – early April and May 2012). All farmlets are stocked with mixed-age, Holstein Friesian x Jersey cross animals. Cows were dried off by the end of May at both sites, and either retained on the milking platform (Waikato) or moved to dairy support land for winter feeding (Canterbury).

Pastures in both Waikato farmlets are predominantly perennial ryegrass / white clover, although 23% of the area is in a tall fescue / white clover mixture. In Canterbury, high stocking rate efficient (HSE) pastures are all perennial ryegrass / white clover, while about 70% of the low stocking rate efficient (LSE) area is perennial ryegrass / white clover and the rest was sown with a diverse pasture mix including perennial ryegrass, white clover, prairie grass, chicory, plantain and lucerne in autumn 2011. The Canterbury pastures were spray irrigated (lateral sprinkler system) with an average of 20 mm per week from December 2011 to February 2012. At both sites, pasture mass in each paddock was measured weekly (by calibrated visual observation in Waikato and calibrated pasture plate meter in Canterbury), and this information was used to help manage pastures and feeding. Pre- and post-grazing pasture mass data were used to calculate both pasture grown, and pasture consumed.

Table 1: Treatment details for the Waikato and Canterbury farmlet experiments

<table>
<thead>
<tr>
<th>Farmlet name</th>
<th>Waikato</th>
<th>Canterbury</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Current</td>
<td>Efficient</td>
</tr>
<tr>
<td>No. of cows</td>
<td>42</td>
<td>34</td>
</tr>
<tr>
<td>Area (ha)</td>
<td>13.1</td>
<td>13.1</td>
</tr>
<tr>
<td>Stocking rate (cows/ha)</td>
<td>3.2</td>
<td>2.6</td>
</tr>
<tr>
<td>Planned start of calving</td>
<td>1st July</td>
<td>1st July</td>
</tr>
<tr>
<td></td>
<td>High stocking rate efficient (HSE)</td>
<td>Low stocking rate efficient (LSE)</td>
</tr>
<tr>
<td></td>
<td>34</td>
<td>34</td>
</tr>
<tr>
<td></td>
<td>6.75</td>
<td>8.25</td>
</tr>
<tr>
<td></td>
<td>5.0</td>
<td>3.5</td>
</tr>
<tr>
<td></td>
<td>1st August</td>
<td>1st August</td>
</tr>
</tbody>
</table>

In the Waikato experiment, a stand-off pad was used to remove cows from pastures for part of each day.
on the Efficient farmlet from 1st March to early July in 2011 and 2012. Supplementary feed was generally offered in the paddock, apart from when cows were on the stand-off pad in Waikato. Nitrogen fertiliser was generally applied after each grazing in the high stocking rate systems at both sites, but less frequently in the low stocking rate systems. Milk volume was measured at each milking for all cows. Milk fat and protein concentration were measured from herd tests conducted weekly (Waikato) or fortnightly (Canterbury). Nitrate leaching was monitored continuously at each site during periods when drainage water could be collected for analysis of N concentration, using ceramic cup samplers in Waikato, and lysimeters (e.g. Di and Cameron, 2007) in Canterbury. Data for N leaching, farm gate N surplus, and estimated operating profit were not available at the time of writing, therefore this paper presents only physical production information for the first year of each experiment.

**RESULTS**

The actual data reported in Tables 2 and 3 span different periods at the two sites: June-May in Waikato, and October-May in Canterbury. Hence, they are not directly comparable with each other. The comparison between modelled and actual data within each site is also complicated by this asynchrony. Hence, here we concentrate on the apparent differences in physical production between the ‘Efficient’ (Waikato) and ‘LSE’ (Canterbury) treatments, and their respective controls (‘Current’ and ‘HSE’).

**Table 2:** Physical production of the ‘Current’ and ‘Efficient’ farmlet systems in the Waikato for 2011/12 (June – May inclusive) lactation compared to pre-experimental model predictions

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Stocking rate at peak (cows/ha)</td>
<td>3.0</td>
<td>2.6</td>
<td>3.2</td>
<td>2.6</td>
</tr>
<tr>
<td>Nitrogen fertilizer used (kg N/ha)</td>
<td>180</td>
<td>50</td>
<td>142</td>
<td>51</td>
</tr>
<tr>
<td>Pasture grazed directly (t DM/ha)</td>
<td>11.4</td>
<td>10.4</td>
<td>14.5</td>
<td>13.4</td>
</tr>
<tr>
<td>Total pasture conserved (t DM/ha)</td>
<td>3.3</td>
<td>3.4</td>
<td>0.91</td>
<td>1.02</td>
</tr>
<tr>
<td>Total pasture harvested (t DM/ha)</td>
<td>14.7</td>
<td>13.8</td>
<td>15.4</td>
<td>14.4</td>
</tr>
<tr>
<td>Feed consumed (t DM/cow):</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Grazed pasture</td>
<td>3.8</td>
<td>4.0</td>
<td>4.5</td>
<td>5.1</td>
</tr>
<tr>
<td>Concentrate^a</td>
<td>0</td>
<td>0.21</td>
<td>0</td>
<td>0.18</td>
</tr>
<tr>
<td>Pasture silage (home-grown and purchased)</td>
<td>0.93</td>
<td>1.00</td>
<td>0.36</td>
<td>0.38</td>
</tr>
<tr>
<td>Maize silage</td>
<td>0</td>
<td>0</td>
<td>0.15</td>
<td>0</td>
</tr>
<tr>
<td>Total^2</td>
<td>4.73</td>
<td>5.21</td>
<td>5.00</td>
<td>5.66</td>
</tr>
<tr>
<td>Pasture as % total</td>
<td>80</td>
<td>77</td>
<td>90</td>
<td>90</td>
</tr>
<tr>
<td>Concentrate as % total</td>
<td>0</td>
<td>4</td>
<td>0</td>
<td>3</td>
</tr>
<tr>
<td>Cow genetic merit (BW)</td>
<td>60</td>
<td>120</td>
<td>99</td>
<td>183</td>
</tr>
<tr>
<td>% herd entering as heifers</td>
<td>23</td>
<td>17</td>
<td>21</td>
<td>18</td>
</tr>
<tr>
<td>Milksolids production</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Days in milk</td>
<td>223</td>
<td>273</td>
<td>261</td>
<td>278</td>
</tr>
<tr>
<td>Milksolids per cow (kg)</td>
<td>368</td>
<td>460</td>
<td>372</td>
<td>461</td>
</tr>
<tr>
<td>Milksolids per hectare (kg)</td>
<td>1044</td>
<td>1160</td>
<td>1202</td>
<td>1207</td>
</tr>
<tr>
<td>Profit and environment targets</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Operating profit ($/ha)^1</td>
<td>2441</td>
<td>3216</td>
<td>n.a.</td>
<td>n.a.</td>
</tr>
<tr>
<td>Farm gate N surplus (kg/ha)</td>
<td>186</td>
<td>154</td>
<td>n.a.</td>
<td>n.a.</td>
</tr>
<tr>
<td>N leached (kg/ha)^2</td>
<td>56</td>
<td>28</td>
<td>n.a.</td>
<td>n.a.</td>
</tr>
</tbody>
</table>

^a Concentrate = maize grain; ^1 Milk price assumed = $6.05/kg milksolids; ^2 includes estimated leaching from support land used to rear replacement animals plus grow maize silage; n.a. = not available at time of writing

In Waikato, total pasture grown and harvested was lower for Efficient compared to Current (Table 2).
Mean daily pasture intake was 12 kg/cow and 14 kg/cow and for Current and Efficient respectively, and pasture comprised 90% of total diet in both systems. Feed conversion efficiency (FCE) was 74 and 81 kg MS/t total DM intake for Current and Efficient respectively.

Table 3: Physical production of the ‘High stocking rate efficient’ (HSE) and ‘Low stocking rate efficient’ (LSE) farmlet systems in Canterbury for 2011/12 (October-May inclusive) lactation, compared to pre-experimental model predictions (for the whole lactation period)

<table>
<thead>
<tr>
<th></th>
<th>HSE - model</th>
<th>LSE – model</th>
<th>HSE – 2011/12</th>
<th>LSE – 2011/12</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stocking rate at peak (cows/ha)</td>
<td>5.0</td>
<td>3.5</td>
<td>5.0</td>
<td>3.5</td>
</tr>
<tr>
<td>Nitrogen fertilizer used (kg N/ha)</td>
<td>400</td>
<td>150</td>
<td>317</td>
<td>171</td>
</tr>
<tr>
<td>Pasture grazed directly (t DM/ha)</td>
<td>18.3</td>
<td>15.6</td>
<td>16.0</td>
<td>13.3</td>
</tr>
<tr>
<td>Total pasture conserved (t DM/ha)</td>
<td>0</td>
<td>0.43</td>
<td>0.44</td>
<td>1.83</td>
</tr>
<tr>
<td>Total pasture harvested (t DM/ha)</td>
<td>18.3</td>
<td>16.0</td>
<td>16.4</td>
<td>15.1</td>
</tr>
<tr>
<td>Feed consumed (t DM/cow):</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Grazed pasture</td>
<td>3.66</td>
<td>4.45</td>
<td>3.2</td>
<td>3.7</td>
</tr>
<tr>
<td>Concentratea</td>
<td>0.80</td>
<td>0.10</td>
<td>0.08</td>
<td>0.02</td>
</tr>
<tr>
<td>Pasture silage (home-grown and purchased)</td>
<td>0</td>
<td>0.38</td>
<td>0.4</td>
<td>0.4</td>
</tr>
<tr>
<td>Total</td>
<td>4.46</td>
<td>4.93</td>
<td>3.6</td>
<td>4.1</td>
</tr>
<tr>
<td>Pasture as % total</td>
<td>82</td>
<td>98</td>
<td>88</td>
<td>90</td>
</tr>
<tr>
<td>Concentrate as % total</td>
<td>18</td>
<td>2</td>
<td>2</td>
<td>0.05</td>
</tr>
<tr>
<td>Cow genetic merit (BW)</td>
<td>150</td>
<td>180</td>
<td>108</td>
<td>122</td>
</tr>
<tr>
<td>% herd entering as heifers</td>
<td>20</td>
<td>15</td>
<td>24</td>
<td>28</td>
</tr>
<tr>
<td>Milksolids production</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Days in milk</td>
<td>280</td>
<td>277</td>
<td>214</td>
<td>226</td>
</tr>
<tr>
<td>Milksolids per cow (kg)</td>
<td>434</td>
<td>451</td>
<td>392</td>
<td>428</td>
</tr>
<tr>
<td>Milksolids per hectare (kg)</td>
<td>2170</td>
<td>1578</td>
<td>1976</td>
<td>1503</td>
</tr>
<tr>
<td>Profit and environment targets</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Operating profit ($/ha)¹</td>
<td>4,810</td>
<td>4,334</td>
<td>n.a.</td>
<td>n.a.</td>
</tr>
<tr>
<td>Farm gate N surplus (kg/ha)</td>
<td>339</td>
<td>154</td>
<td>n.a.</td>
<td>n.a.</td>
</tr>
<tr>
<td>N leached (kg/ha)²</td>
<td>43</td>
<td>29</td>
<td>n.a.</td>
<td>n.a.</td>
</tr>
</tbody>
</table>

¹ Concentrate = cereal grain; ¹ Milk price assumed = $6.10/kg milksolids; ² for milking platform area only; n.a. = not available at time of writing

In Canterbury, total pasture harvested was only 1.3 t DM/ha less in LSE than HSE, despite 1.5 fewer cows/ha and just over half the fertiliser rate. However, a higher proportion of total pasture harvest was captured via silage conservation in LSE compared to HSE (12% versus 3%). Mean grazed pasture intakes were similar for HSE and LSE (15.0 kg DM/cow/d from 214 days in milk (DIM) in HSE, and 16.8 kg DM/cow/d from 226 DIM in LSE). As in Waikato, grazed pasture comprised around 90% of total diet in both systems. LSE cows produced 9% more milksolids per animal than HSE cows.

DISCUSSION AND CONCLUSIONS

All four systems displayed high levels of production efficiency in this first lactation. The lower-stocked Efficient and LSE systems operated with low N fertiliser inputs relative to benchmarks for their respective regions: average N fertiliser use in 2010/11 was 159 and 247 kg N/ha for Waikato and Canterbury farms respectively (source: Dairybase, DairyNZ; Diane Sutton, pers. comm.). Evidence emerged from both of these systems to support the efficiency concepts modelled by (Beukes et al. 2011) and (Burggraaf et al. 2011). In Waikato, the high BW cows in Efficient ate more pasture each, and
converted this to milk more efficiently, than the cows in Current, allowing similar total MS/ha with a 19% reduction in stocking rate in Efficient compared to Current. In Canterbury, the difference in BW between the experimental herds was less than in Waikato, but the difference in stocking rate was greater. Here, LSE resulted in lower MS/ha compared to HSE, but still performed at a very high level relative to the average performance of farms in the Selwyn district of Canterbury in 2009/10 (1236 kg MS/ha, 384 kg MS/cow, 3.22 cows/ha, source: DairyNZ, 2010). Total pasture harvested per hectare in LSE was 1.3 t DM/ha (8%) less than in HSE, despite 1.5 fewer cows/ha.

The production data reported here cover only one year of a proposed 4-5 year study in each region, and many questions remain to be answered regarding sustainability of the efficiency differences between lower- and higher-stocked systems achieved in the first year. Actual N leaching losses in the first year have not yet been compiled for these treatments. Low N fertiliser inputs, fewer cows, minimal imported feed, and use of nitrification inhibitors should have resulted in relatively low N leaching potential in the Efficient and LSE systems. Further gains could be expected in the Efficient system in the Waikato from use of the stand-off facility, and through the partitioning of more surplus N to faeces rather than urine in the high BW animals used in this farmlet (Woodward et al. 2011). However, this remains to be confirmed from information on faecal and urinary N concentrations and loads, plus analysis of ceramic cup sampler (Waikato) and lysimeter (Canterbury) data, over several years. Additionally, the analysis must be broadened to include all hectares used on the milking platform and support areas to gain a complete picture of environmental footprint.

ACKNOWLEDGEMENTS

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REFERENCES


An economic forage value index for New Zealand dairy farmers

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2 Lincoln University
3 Agriseeds Ltd.
4 PGG Wrightsons Seeds Ltd.
5 Agricom Ltd.
6 Cropmark Ltd.

ABSTRACT

This paper describes a forage evaluation system (www.dairynzfvi.co.nz) that rates perennial ryegrass cultivars according to a forage value index (FVI; $/ha) based on the economic value of seasonal dry matter (DM) production in New Zealand dairy production systems. Further development of the FVI requires: data to calculate performance values for seasonal DM yield for more cultivar x endophyte combinations; performance values and economic values for nutritive value, persistence and grazing traits of cultivars; and information on the effects of interactions between grass and clover.

Keywords: dairy, pasture, traits, economic values

INTRODUCTION

Pasture plant breeding in New Zealand has produced a wide range of commercially-available perennial ryegrass cultivars, many with different endophyte strains. Breeding has definitely changed plant attributes (for example, ploidy, and maturity date), but currently there is no agreed way to gauge the value being delivered to dairy farm businesses as a result of those changes. Farmers must make complex pasture cultivar choices in the absence of independent information on the relative economic performance of different options. The objective of the work reported here was to develop the foundations for a scientifically-based, independent and region-specific forage evaluation system (‘DairyNZ Forage Value Index’, or FVI) that ranks forage cultivars according to their estimated annual economic benefit to dairy farming systems.

MATERIALS AND METHODS

Data on seasonal dry matter (DM) yields of 14 perennial ryegrass cultivar-endophyte combinations were analysed to calculate performance values (PV) relative to a base group of cultivars that had been entered into trials before 1996. Yield data were obtained from three-year National Forage Variety Trials (NFVT, e.g. Easton et al. 2001) and aggregated according to trial location: northern New Zealand, and the rest of New Zealand. Previous analyses showed significant re-ranking of cultivars (based on PV for yield) occurred between these two broad environments. Performance values were then combined with estimated economic values (EV, using the methods described by Chapman et al. 2012) for extra DM grown in five seasons of the year (winter, early spring, late spring, summer and autumn) to calculate an overall forage value index (FVI; $/ha/year) for each cultivar in each of four regions in New Zealand. For presentation, cultivars were ranked and grouped into five bands, from the top 20% performers through to the bottom 20% for each region.

RESULTS

Figure 1 shows an example of the FVI output. Star ratings 5 to 1 relate to the top 20% performers through to the bottom 20% of performers. Index values ($/ha/year) for each star rating are shown in the screen box. The confidence value is calculated from the number of NFVT trials for a cultivar, where a trial within the target region = 1 and a trial outside the target region = 0.5 (minimum = 2 for listing, eg one trial within a region and two outside; maximum shown = 10). Performance values (5 = top 20%; 1 = bottom 20%) for seasonal DM yield are also shown.
DISCUSSION AND CONCLUSIONS

An economically-based FVI is technically feasible. There is substantial variation among cultivars in estimated FVI using the seasonal DM trait. Significant genotype x region interactions in PV and EV are taken into account in the evaluation system. Development of the DairyNZ FVI has exposed significant information gaps that must be filled to ensure that FVI rankings align with relative on-farm performance. These include: lack of DM yield data for all cultivar x endophyte combinations currently being marketed; the need for specific, separate NFVT testing protocols to assess persistence; lack of systematic information on nutritive value traits and grazing efficiency for cultivars; and unknown effects of interactions between perennial ryegrass and other species in pasture mixtures, especially white clover, on relative cultivar rankings.

ACKNOWLEDGEMENTS

DairyNZ Inc. for funding; New Zealand Plant Breeders Research Association for access to NFVT data.

REFERENCE


Intake, crop utilization and nitrogen outputs of cows wintering on swedes at two different allowances in Southern New Zealand

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ABSTRACT

Two swede allowances (8.1 (Standard) or 10.6 (High) kg DM/cow/d) were allocated to dry dairy cows during winter to measure intake and foraging behaviour, and the potential fate of the nitrogen consumed. There was a further allowance of approximately 5 kg DM/cow/d of baleage. Total crop intakes (6.7 to 7.0 kg DM/cow/d) were similar. Crop utilisation declined (P<0.05) at the higher allowance (78% cf 66% on Standard and High allowances, respectively). Cows spent a similar amount of time (4.6 h/d) at the feeding face, but walked further on the High treatment (1.84 cf 3.06 km/d on the Standard and High treatment) to reach shelter. Nitrogen concentration of faeces (1.9 g/kg DM) and urine (4.4 g/l) reflected the high water content of the diet (swedes averaged 11.5 % DM). Calculations of nitrogen and water balances predicted nitrogen outputs similar to the nitrogen intakes, with the small deficit being accounted for by the increased BCS and foetal development.

Keywords: allowance; intake; nitrogen; utilisation; walking.

INTRODUCTION

Wintering cows on forage crops in the South Island of New Zealand reduce the grazing pressure on the milking platform (Judson et al. 2010). These wintering systems, along with the range of allowances used, can impact on nitrate leaching and cow intake. These wintering systems need to be quantified in a systematic way to ensure that farmers are aware of the trade-offs associated with each.

MATERIALS AND METHODS

This experiment at the Telford Farm Training Institute farm (lat. 46.2923 S, long. 169.7299 E), near Balclutha, New Zealand compared the intake and foraging behaviour of non-lactating cows (n=80 per treatment; 550 kg LW) nominally allocated 9 or 11 kg DM/d as swedes (Brassica napus cv Invitation) and approximately 5 kg DM/d pasture baleage. The potential fate of consumed nitrogen was estimated.

Intake was calculated by the difference between the amount of crop offered and that remaining after 24h on 6 separate grazing events as described by Thompson & Stevens (2012). Time on the feeding face and distance travelled were recorded using GPS tracking collars on 7 cows per treatment, recording their position every 5 minutes over 6 days.

The nitrogen concentration of faeces and urine, and the DM concentration of faeces were measured twice on 10 cows per treatment using standard laboratory techniques (AOAC 1990).

Statistical analysis used ANOVA with feed allocation as the treatment effect with each collection time used as replication. A nitrogen and water budget was developed for each treatment and validated against the measured.

RESULTS

While swede allowances were significantly lower for the Standard than the High allowance (Table 1), the crop intakes were similar in both treatments, resulting in lower crop utilisation at the High allowance (Table 1). Supplement intake was higher for the High allowance, but total dry matter and energy intake was not significantly different (Table1). Cows spent a similar amount of time at the feeding face on both treatments, but cows walked further on the High allowance (Table 1). Small variations in the final energy intakes were mostly accounted for by the small differences in body condition score and the extra distance travelled.
Table 1: Allowance, intake utilisation and time at the feeding face, and distance walked of dry, pregnant cows (LW 550 kg) grazing swedes (Brassica napus) at two allowances

<table>
<thead>
<tr>
<th>Crop Allowance</th>
<th>Treatment</th>
<th>Standard</th>
<th>High</th>
<th>LSD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crop allowance (kg DM/cow/d)</td>
<td>8.1</td>
<td>10.6</td>
<td>2.4</td>
<td></td>
</tr>
<tr>
<td>Crop intake (kg DM/cow/d)</td>
<td>6.4</td>
<td>7.1</td>
<td>1.86</td>
<td></td>
</tr>
<tr>
<td>Supplement intake (kg DM/cow/d)</td>
<td>4.6</td>
<td>5.9</td>
<td>1.2</td>
<td></td>
</tr>
<tr>
<td>Total intake (kg DM/cow/d)</td>
<td>11.0</td>
<td>13.0</td>
<td>2.76</td>
<td></td>
</tr>
<tr>
<td>Crop utilisation (%)</td>
<td>78</td>
<td>66</td>
<td>5.2</td>
<td></td>
</tr>
<tr>
<td>Time at feeding face (hr/d)</td>
<td>4.65</td>
<td>4.54</td>
<td>0.98</td>
<td></td>
</tr>
<tr>
<td>Distance walked (km/d)</td>
<td>1.84</td>
<td>3.06</td>
<td>0.15</td>
<td></td>
</tr>
<tr>
<td>Energy intake (MJME/cow/d)</td>
<td>131</td>
<td>147</td>
<td>32.6</td>
<td></td>
</tr>
</tbody>
</table>

The nitrogen concentration of both faeces and urine (1.9 g/kg DM and 4.4 g/l respectively) reflected the high water content of the diet (swedes averaged 11.5% DM). Nitrogen intake averaged 270 and 282 g/cow/d at N concentrations of 25 and 22 g/kg DM for the Standard and High allowances respectively. Calculations of nitrogen and water balances predicted nitrogen outputs of 242 and 264 g/d with 76 and 82% being excreted as urine for Standard and High allowances respectively.

DISCUSSION AND CONCLUSION

The data indicate that a daily allowance per cow of between 8 and 9 kg DM as swedes is adequate to meet the maintenance and pregnancy requirement needs of dairy cows in winter in southern New Zealand, when accompanied by 4 to 5 kg of dry matter as hay or Baleage, with 82% of cows being at a BCS of 5 or greater.

Animal behaviour data indicate that the provision of shelter may be beneficial to cows grazing crops in winter as the High allowance cows walked to and from shelter each day.

Urinary N concentration was lower than values recorded during lactation (e.g. 6-7 g/l, de Klein et al. 2003). The proportion of N excreted as urine was very high for the dietary N concentration recorded when compared to the literature (Carruthers and Neil 1997). This may be due to the high feed water intake coupled with the potentially high cation balance in the diet (supplement DCaD=650) inducing an increase in urinary N output (Nennich et al. 2006). The small deficit between the nitrogen input and output could be accounted for by the increased BCS and foetal development.

ACKNOWLEDGEMENTS

Dairy NZ and MPI Sustainable Farming Fund for funding, Telford Farm Training institute for the cows and site, and farm staff of Telford and technical staff from AgResearch Invermay for assistance.

REFERENCES


Chicory and plantain as feeds for dairy cows in late lactation

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2University of Sydney, Camden, NSW 2006, Australia
3AgResearch, Private Bag 3123, Hamilton 3240, New Zealand

ABSTRACT

Two experiments were conducted to investigate the effect of incorporating either chicory (Cichorium intybus L.) or plantain (Plantago lanceolata L.) into the diet of dairy cows in late lactation on milk production. In the first experiment (conducted indoors), cows were offered 0, 20 or 40% of the diet as herb (either chicory or plantain) with the balance as perennial ryegrass pasture (poor or moderate estimated metabolisable energy (ME) content). In the second experiment, cows grazed outdoors on ryegrass pasture with chicory or plantain offered at 20, 40 or 60% of the diet. In the indoor experiment with poor estimated ME pasture (9.6 MJ/kg DM), cows offered chicory or plantain had 6% greater dry matter intakes (DMI) and produced 19% more milk and 17% more milksolids than cows fed pasture only, but there was no effect of herb proportion in the diet. When pasture estimated ME was moderate (10.5 MJ/kg DM), cows supplemented with chicory or plantain had similar milk and milksolids yields to cows fed pasture only, with similar (outdoor experiment) or reduced (indoor experiment) DMI.

Keywords: chicory; plantain; herb; perennial ryegrass; milk production; milksolids; dairy cow.

INTRODUCTION

Pasture-based dairy farms often face feed shortages during periods of summer/autumn soil moisture deficits, and may require supplementary feed to maintain milk production. Supplementary feeds that can be grazed directly are more cost-effective and less labour intensive than conserved feeds (Dillon 2005). During summer/autumn, the forage herbs chicory (Cichorium intybus L.) and plantain (Plantago lanceolata L.) have greater drought and heat tolerance and can produce greater amounts of grazable feed with superior nutritive characteristics compared with perennial ryegrass (Lolium perenne L.) (Rollo et al. 1998; Moorhead and Piggot, 2009). Chicory can increase milk production (Waugh et al. 1998; Chapman et al. 2008), and while there is a lack of information on plantain, it also produces a highly nutritious feed. The hypothesis tested in the experiments reported here was that cows offered chicory or plantain as a supplement to ryegrass pasture in late lactation would have greater milk production than cows offered ryegrass pasture alone.

MATERIALS AND METHODS

Two experiments were conducted in Hamilton, New Zealand (37°47’S, 75°19’E; 40 m a.s.l.) in 2011 and 2012. In the first experiment, 42 Holstein-Friesian cows in late lactation were housed in an indoor feeding facility containing Calan™ gates and offered ryegrass pasture only, or ryegrass pasture with chicory or plantain (comprising either 20 or 40% of the total diet) in two feeds daily (0800 and 1530 h). In an outdoor experiment, 90 late lactation cows grazed either ryegrass pasture only, or ryegrass pasture and chicory or plantain offered to constitute 20, 40 or 60% of the available diet, with a target dry matter intake (DMI) of 15 kg DM/cow/day. Milk and milksolids yield were measured daily. Dry matter intake was calculated per cow in the indoor experiment by weighing and determining the dry matter content of feed offered and refused; and per treatment group in the outdoor experiment by estimating pre and post grazing herbage mass by cutting 10 (pre) and five (post) 0.2m² quadrats per break to ground level in the herb breaks and using a calibrated rising plate meter in the ryegrass breaks. Feed samples were analysed for herbage nutritive characteristics using wet chemistry. Milk production and DMI data were analysed using REML in Genstat 14.1 (VSN International) as a 2 x 2 factorial design (feed type and proportion of herb).
Table 1: Dry matter intake (kg/cow/day), and milk and milksolids yields (kg/cow/day) of dairy cows fed pasture, or pasture supplemented with different proportions of chicory or plantain during an indoor feeding experiment with pasture of two feed quality levels and an outdoor grazing experiment.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Significance&lt;sup&gt;1&lt;/sup&gt;</th>
<th>SED</th>
<th>Treatment</th>
<th>Proportion</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pasture only</td>
<td>20% chicory</td>
<td>40% chicory</td>
<td>60% chicory</td>
<td>20% plantain</td>
</tr>
<tr>
<td>Indoor feeding experiment</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Poor pasture estimated ME (9.6 MJ/kg DM)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dry matter intake</td>
<td>13.5</td>
<td>14.4</td>
<td>14.5</td>
<td>-</td>
</tr>
<tr>
<td>Milk yield</td>
<td>9.9</td>
<td>11.2</td>
<td>12.6</td>
<td>-</td>
</tr>
<tr>
<td>Milksolids yield</td>
<td>0.83</td>
<td>0.96</td>
<td>1.02</td>
<td>-</td>
</tr>
<tr>
<td>Moderate pasture estimated ME (10.5 MJ/kg DM)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dry matter intake</td>
<td>15.7</td>
<td>15.1</td>
<td>14.9</td>
<td>-</td>
</tr>
<tr>
<td>Milk yield</td>
<td>12.2</td>
<td>11.8</td>
<td>12.6</td>
<td>-</td>
</tr>
<tr>
<td>Milksolids yield</td>
<td>1.01</td>
<td>1.00</td>
<td>1.03</td>
<td>-</td>
</tr>
<tr>
<td>Outdoor grazing experiment</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Moderate pasture estimated ME (10.5 MJ/kg DM)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dry matter intake</td>
<td>15.0</td>
<td>15.5</td>
<td>16.0</td>
<td>14.0</td>
</tr>
<tr>
<td>Milk yield</td>
<td>13.0</td>
<td>12.7</td>
<td>13.3</td>
<td>13.7</td>
</tr>
<tr>
<td>Milksolids yield</td>
<td>1.11</td>
<td>1.07</td>
<td>1.13</td>
<td>1.13</td>
</tr>
</tbody>
</table>

<sup>1</sup> NS, Not significant (P>0.1); *, P<0.1; **, P<0.01; ***, P<0.001.

RESULTS

Table 1 presents the DMI, milk and milksolids yields from cows fed pasture or pasture supplemented with herbs. When estimated metabolisable energy (ME) of pasture was poor (9.6 MJ/kg DM) (Table 2), cows supplemented with herbs had 6% greater DMI (14.4 vs. 13.5 kg DM/cow/day; P < 0.05), and produced 19% more milk and 17% more milksolids (0.97 vs. 0.83 kg MS/cow/day; P < 0.01) than those fed pasture only. When pasture estimated ME was moderate (10.5 MJ/kg DM) (Table 2) however, cows offered herbs had reduced (14.8 vs. 15.7 kg DM/cow/day; P < 0.05; indoor experiment) or similar (outdoor experiment) DMI to cows fed pasture, and similar milk and milksolids production. Increasing the amount of herb in the diet had no effect on milksolids production or DMI.

DISCUSSION AND CONCLUSION

When perennial ryegrass pasture estimated ME was poor, supplementing the diet of dairy cows with chicory or plantain increased milksolids yields by 17%. These results are consistent with (Chapman et al. 2008) and (Hutton et al. 2011) who observed increased milk production from livestock grazing herb/clover pastures compared to those grazing ryegrass-based pastures. The increase in production is likely to be the result of improved DMI and greater estimated ME of chicory and plantain.

Low DM feeds (<15%) can reduce DMI (John and Ulyatt 1987), and therefore potentially milk production. Although chicory and plantain had a low DM content (9.6 to 14.2%; Table 2), feeding the herbs at up to 60% of the diet did not reduce DMI or milk production, and therefore, they can be used in a feed deficit without compromising production.

In conclusion, chicory and plantain are grazeable supplementary feed options for mitigating feed deficit and maintaining, or even enhancing, milk production.
Table 2: Nutritive characteristics of perennial ryegrass, chicory and plantain fed in an indoor feeding and outdoor grazing experiment

<table>
<thead>
<tr>
<th>Nutritive characteristics</th>
<th>Indoor feeding experiment</th>
<th></th>
<th></th>
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<th></th>
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</thead>
<tbody>
<tr>
<td></td>
<td>DM$^1$</td>
<td>ME$^2$</td>
<td>CP$^3$</td>
<td>NDF$^4$</td>
<td>DOMD$^5$</td>
</tr>
<tr>
<td>Poor pasture estimated ME</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chicory</td>
<td>10.5</td>
<td>12.3</td>
<td>20.0</td>
<td>22.7</td>
<td>77.2</td>
</tr>
<tr>
<td>Plantain</td>
<td>9.6</td>
<td>11.8</td>
<td>18.9</td>
<td>31.9</td>
<td>74.0</td>
</tr>
<tr>
<td>Perennial ryegrass</td>
<td>16.1</td>
<td>9.6</td>
<td>20.5</td>
<td>48.7</td>
<td>59.9</td>
</tr>
<tr>
<td>Moderate pasture estimated ME</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chicory</td>
<td>11.2</td>
<td>12.3</td>
<td>19.1</td>
<td>23.5</td>
<td>76.6</td>
</tr>
<tr>
<td>Plantain</td>
<td>11.8</td>
<td>12.0</td>
<td>17.1</td>
<td>30.2</td>
<td>74.7</td>
</tr>
<tr>
<td>Perennial ryegrass</td>
<td>18.6</td>
<td>10.5</td>
<td>20.7</td>
<td>48.2</td>
<td>65.5</td>
</tr>
<tr>
<td>Outdoor grazing experiment</td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Moderate pasture estimated ME</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chicory</td>
<td>10.7</td>
<td>12.5</td>
<td>20.6</td>
<td>22.2</td>
<td>77.9</td>
</tr>
<tr>
<td>Plantain</td>
<td>12.4</td>
<td>11.5</td>
<td>20.4</td>
<td>28.1</td>
<td>72.1</td>
</tr>
<tr>
<td>Perennial ryegrass</td>
<td>21.5</td>
<td>10.5</td>
<td>18.8</td>
<td>45.5</td>
<td>65.7</td>
</tr>
</tbody>
</table>

1 DM, Dry Matter (%); 2 ME, Metabolisable Energy (MJ/kg DM); 3 CP, Crude Protein (g/100g DM); 4 NDF, Neutral Detergent Fibre (g/100g DM); 5 DOMD, Organic Matter Digestibility (%).

ACKNOWLEDGEMENTS

The authors acknowledge the assistance of DairyNZ technical staff and the statistical expertise of Barbara Dow. This experiment was funded by New Zealand dairy farmers through DairyNZ.

REFERENCES


Effects of diet during the first winter on replacement heifer weight gain and body condition score

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ABSTRACT

A study was undertaken to investigate five contrasting winter feeding regimes on replacement dairy heifer bodyweight gain and body condition score, and to determine if compensatory growth can be relied upon in replacement heifer rearing systems. Two indoor treatments were offered either grass silage or grass silage and 1.5kg concentrate. A third treatment offered grass silage and concentrate but animals were retained on an out-wintering pad. The final two treatments offered heifers either 100% kale or 70% kale and grass silage. Results indicate that bodyweight gain of the heifers offered silage only was 0.19 kg/day less than all treatments (0.48 kg/day). There was no difference in bodyweight gain between all treatments after turnout to grass. Results indicate that the concept of ‘compensatory growth’ cannot be relied upon when trying to get replacement heifers to attain target weight at mating start date (MST). The results of the study also clearly indicate that kale can be used as a winter feed and BW gains similar to a silage and concentrate based diet can be achieved from it.

Keywords: Replacement dairy heifer; winter feeding; bodyweight; compensatory growth.

INTRODUCTION

Attaining target bodyweight (BW), particularly at mating start date (MST), is a critical component of any replacement heifer rearing system. (Archbold et al. 2012) has shown that BW of replacement dairy heifers at MST was positively associated with subsequent milksolids yield. Optimum development of replacement heifers is critical and needs to be accomplished at low cost without sacrificing performance. Forage brassicas, such as kale, are considerably cheaper as a winter feed than grass silage and concentrates, which are 2 and 4 times more expensive than grazed grass, respectively. However, cattle often exhibit compensatory growth following nutritional restriction (Ryan et al. 1993). The two objectives of this study were to i) investigate five contrasting winter feeding regimes on heifer BW gain and body condition score (BCS) and ii) determine if compensatory growth can be relied upon in replacement heifer rearing systems.

MATERIALS AND METHODS

One hundred and fifty spring born weanling replacement dairy heifer calves were balanced on the basis of breed (Holstein Friesian; 79% of herd, Jersey × Holstein; 13% of herd, Montbeliarde × Holstein; 9% of herd), age (284 ± 20.3 days), BW (213 ± 26.1 kg) and BCS (2.98 ± 0.215) in a randomised block design. They were then randomly assigned to one of five winter feeding treatments from 23 November 2009 to 25 February 2010 (94 days). The five feeding treatments were: i) indoors offered ad libitum grass silage and 1.5 kg DM concentrate (IC); ii) indoors offered ad libitum grass silage only (SO); iii) outdoors on an out-wintering pad offered ad libitum grass silage and 1.5 kg DM concentrate (OWP); iv) outdoors offered 70% kale and 30% grass silage (70K); v) outdoors offered 100% kale (100K). The IC, SO and OWP treatments were all offered the same silage. The 70K animals were offered baled silage. The forage kale was grazed in situ. Prior to the commencement of the experiment all animals received one Tracesure® bolus to provide iodine, selenium and cobalt supplementation; they had previously been supplemented with Cu. The 100K treatment animals were offered straw for the first week of the study to adjust them to the 100% kale diet. It was intended to offer them no further fibre source after the first week; however, due to continuous frost, 3 bales of silage were offered 5 weeks into the experiment. All animals were offered fresh feed daily; the refusals of the IC, SO and OWP animals were removed and weighed daily. The outdoor animals were offered a fresh allocation of kale each morning by moving a temporary electric fence. Animals were grouped by treatment. During the experimental period all animals were weighed weekly and condition scored every three weeks. All animals were turned out to pasture on 25 February and offered ad libitum grazed grass. All animals were then weighed weekly to the start of the breeding season (15 April) and monthly thereafter; BCS was recorded monthly from turnout. All data were analysed using PROC MIXED in SAS. Animal was used as the experimental unit. Pre-experimental values were used as a co-variate in the model. The data are reported in three periods, PI: the 94 day experimental period, PII: the period of time from turnout to the start of the breeding season and PIII: from after the commencement of the breeding season to 6 September.
The dry matter digestibility (DMD) of the pit silage was 0.70 (±0.20), dry matter (DM) was 0.29 (±0.249) and crude protein (CP) was 0.11 (±0.007). The DMD of the baled silage was 0.70 (±0.25), DM was 0.34 (±0.669) and CP was 0.156 (±0.066). The BW gain during the period when treatments were imposed (PI) was similar for the IC, OWP, 70K and 100K treatments (0.48 kg/day; Table 1). The SO treatment gained less BW during PI (P<0.01) than all other treatments. There was no significant difference between treatments in BW gain throughout PII and PIII (0.75 and 0.83 kg/day, respectively). During PI BCS was lowest (P<0.01) for the 100K animals (Table 1). Mean air temperatures during the experimental period were 2.9°C, 3.6°C and 2.8°C lower than the 10-year average in December (6.1°C), January (5.8°C) and February (5.8°C), respectively.

### DISCUSSION AND CONCLUSION

The lack of difference in BW gain between treatments throughout PII and PIII indicates little, if any, compensatory growth by the SO treatment post turnout. The PI BCS of the 100K animals was probably a consequence of prevailing weather conditions during the experiment. Due to a risk of ill-health, frosted brassicas should not be offered for consumption. The BCS of the animals from 100K treatments may have suffered due to feed restriction during extreme periods of cold weather. However, during PII and PIII there was no effect of winter treatment on average BCS, indicating that the 100K animals compensated.

The concept of ‘compensatory growth’ cannot be relied upon when trying to get replacement heifers to attain target weight at MSD. The results of the study indicate that kale can be used as a winter feed and BW gains similar to a silage and concentrate based diet can be achieved from it.

### REFERENCES


### Table 1: Effects of winter feeding treatment on bodyweight (BW) and body condition score (BCS)

<table>
<thead>
<tr>
<th></th>
<th>IC</th>
<th>SO</th>
<th>OWP</th>
<th>70K</th>
<th>100K</th>
<th>SED</th>
<th>Sig</th>
</tr>
</thead>
<tbody>
<tr>
<td>BW gain PI</td>
<td>0.41a</td>
<td>0.29b</td>
<td>0.52a</td>
<td>0.47a</td>
<td>0.51a</td>
<td>0.037</td>
<td>0.011</td>
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<tr>
<td>BW gain PII</td>
<td>0.68</td>
<td>0.82</td>
<td>0.73</td>
<td>0.78</td>
<td>0.72</td>
<td>0.054</td>
<td>0.536</td>
</tr>
<tr>
<td>BW gain PIII</td>
<td>0.80</td>
<td>0.93</td>
<td>0.81</td>
<td>0.82</td>
<td>0.80</td>
<td>0.027</td>
<td>0.111</td>
</tr>
<tr>
<td>Average BCS PI</td>
<td>3.10ab</td>
<td>3.07ab</td>
<td>3.13b</td>
<td>3.05a</td>
<td>2.97c</td>
<td>0.023</td>
<td>0.009</td>
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<tr>
<td>Average BCS PII</td>
<td>3.15</td>
<td>3.16</td>
<td>3.15</td>
<td>3.22</td>
<td>3.18</td>
<td>0.041</td>
<td>0.757</td>
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<tr>
<td>Average BCS PIII</td>
<td>3.05</td>
<td>3.12</td>
<td>3.10</td>
<td>3.09</td>
<td>3.07</td>
<td>0.031</td>
<td>0.6832</td>
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</table>

IC = indoors offered *ad libitum* grass silage and 1.5 kg DM concentrate; SO = indoors offered *ad libitum* grass silage only; OWP = outdoors on an out-wintering pad offered *ad libitum* grass silage and 1.5 kg DM concentrate; 70K = outdoors offered 70% kale and 30% grass silage; 100K = outdoors offered 100% kale.

abc values in the same row not sharing a common superscript are significantly different.

SED = Standard error of difference.
Effects of potassium, sodium and chloride fertilisers on yield and mineral composition of fodder beet

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ABSTRACT

There is renewed interest in fodder beet (Beta vulgaris L.) as a winter forage crop in New Zealand because dairy farmers are demanding high-yielding, high-quality crops for enhancing animal body condition at the start of the milking season. There is limited information on fodder beet mineral composition and its response to fertiliser application in New Zealand conditions. A field experiment was carried out at Southbridge, Canterbury, New Zealand (43°81'S, 172°25'E) to determine the effects of potassium (K; 150 or 300 kg/ha), sodium (Na; 100 or 200 kg/ha) and chloride (Cl; 240 kg/ha) fertiliser applications on dry matter yield and mineral accumulation in fodder beets. Fertiliser rates did not affect harvested biomass or mineral composition of fodder beet. Mineral concentrations were consistently higher in the shoot than the bulb in all treatments. For example, 65%, 87% and 88% of the total plant K, Na and Cl concentration were in the shoots, respectively. Mineral nutrient composition was adequate for animal nutrition except for phosphorus (P). Mineral element interrelationships were also determined, as they affect the metabolism and performance of dairy cows. The Ca: P and K: (Ca+Mg) ratios ranged between 0.6–4.0 and 2–7, respectively. However, as bulbs were at least 64% of the total dry matter, this may lead to inadequate levels of key nutrient such as P and Mg consumed by animals. Therefore, supplementation of these elements is recommended.

INTRODUCTION

During the past four years, the area in New Zealand annually sown to fodder beet (Beta vulgaris L.) has increased from about 1000 hectares (Chakwizira and de Ruiter, 2009) to 6000 hectares (Gibbs, 2011). This increase has mainly occurred in the South Island and been in response to the demand for feeding non-lactating dairy cows during winter. However, there is limited local knowledge of fertiliser requirements for fodder beet. Literature is dated, and recommendations are often based on overseas studies, other crops (e.g. sugar beet) or crops grown for sugar rather than forage biomass. Previous work in New Zealand has shown fodder beet yielded less dry matter (DM) with lower Na but not K (Stephen et al., 1980). A similar result occurred with sugar beet (Draycott et al., 1970). Fodder beet Cl composition has been shown to increase with Cl application rates (Goh and Magat, 1989). Mineral element interrelationships, such as dietary cation-anion difference (DCAD: K + Na – Cl – S)/100 g of DM; Hu and Kung, 2009) have been reported to affect the metabolism and performance of dairy cows. Imbalances between K and Mg and/ or Ca have also been shown to increase incidences of tetany and/ or milk fever in dairy cows. It is therefore important to determine mineral composition of fodder beet crops.

The objective of this study was to determine the effect of K, Na and Cl fertilisers on fodder beet yield and mineral composition of tissue.

MATERIALS AND METHODS

The experiment was located at Southbridge, Canterbury (43°81'S, 172°25'E) on a Waimakariri sandy loam soil (Jessep, 1990). The paddock had been under pasture between 2005 and 2008, and maize (Zea mays L.) followed by triticale (x Triticosecale) in the 2009-10 season. Soil preparation involved conventional cultivation after deep ploughing. The experiment was a randomised complete block design, with nine fertiliser treatments; consisting of a range of K, Na and Cl application rates (Table 1), replicated four times. Each plot was four rows (1.5 m) wide by 15 m long, with a total experimental area of 0.081 ha. Treatments were applied two days after sowing. ‘Colosse’ fodder beet was planted on 1 November 2010 at a row spacing of 375 mm. A soil test to 150 mm depth showed that the initial soil fertility was adequate, except for K. Basal fertiliser was applied at 250 kg/ha DAP (18:20:0:2; N,P,K,S) and 1.5 kg/ha boron. Nitrogen was applied as urea (46% N) at 100 kg/ha. The crop was managed to minimise the risk of weeds, pests and diseases.

Final DM yield was determined on 27 April 2011 by cutting a 5 m length from two rows (3 m2 quadrat). Two plants were retained for DM partitioning and one plant for tissue mineral assessment. Dry matter samples
were dried in a forced-air oven at 90°C to constant weight. The subsample for tissue analysis was crushed and immediately freeze-dried, before being ground for the analyses at Hill Laboratories, Hamilton, New Zealand. During the experimental period, mean temperature was 14.9°C and total rainfall was 393 mm. An additional 200 mm of irrigation water was applied to ensure no yield constraint.

All statistical analyses were carried out with GenStat v.14 (VSN International). The variation associated with predicted means is given by the 5% Least Significant Difference (LSD0.05). A factorial ANOVA was used. The K, Na and Cl elements were coded as being present or not present, and the treatment structure became a full 2^3+1 factorial. A mixed model fitted with restricted maximum likelihood (REML) (Gilmore et al. 1995) was used, with Na and K as continuous variates and Cl and Gypsum as being present or not present. Nutrient removal was calculated using the DM yield and nutrient concentration data. Nutrient ratios (e.g. Ca/P; g/kg) were calculated from these data.

RESULTS AND DISCUSSION

The fertiliser treatments had no effect on total DM yield; with an average yield of 32.8 t DM/ha (Table 1). This was higher than the range between 11-27 t/ha reported in the literature (Goh and Magat, 1989, Stephen et al. 1980). These differences may be attributed to improved genetic material for the ‘Colosse’ fodder beet compared with the ‘Trestel’ and ‘Monoblanc’ fodder beet used in 1989 and 1980, respectively. The Cl fertiliser may have suppressed yield in this experiment. Crops fertilised with Cl in the presence of K tended to show lower yields (Table 1), caused by an interaction (P=0.042) with K.

The bulbs contained between 64 to 73% of the biomass. Mineral concentrations were consistently lower (P < 0.001) in the bulbs than the shoots (Table 1). For example, the average K concentrations were 14.9 and 27.6 g/kg DM in the bulbs and shoots, respectively. Similarly, Na was 4.3 g/kg DM in the bulbs and 31.6 in shoots.

Mineral concentrations were mostly within the NRC (2001) recommendations for dairy cows that are either in late pregnancy (>240 days) or early lactation (<90 days), except for P (Table 1). The K/ (Ca+Mg) and Ca/P ratios were higher (P < 0.001) in the bulbs than shoots for all the treatments. The average K/ (Ca+Mg) ratios were above the critical levels of 2.2 (Grunes and Welch, 1989). A higher value increases susceptibility to physiological problems, such as hypomagnesaemia (grass tetany) and hypocalcaemia (milk fever) for beef and dairy cattle. Mean P concentration in fodder beets was 1.89 g/kg DM, which is lower than the dietary requirements of 2.2 g/kg DM (Grunes and Welch, 1989). Although the Ca/P ratios were within the recommended range of between 1 and 2 (Guillard and Allinson, 1989), the high concentrations of Ca may induce P deficiency and/or exacerbate the oxalate toxic effect to animals.
Table 1: Total dry matter (t/ha), tissue mineral concentration (g/kg DM) and ratios (equivalence basis) for shoots and bulbs of fodder beet grown under different K, Na and Cl treatments at Southbridge, New Zealand in 2010-11 season

<table>
<thead>
<tr>
<th>Treatments (T; kg/ha)</th>
<th>DM (t/ha)</th>
<th>Na g/kg DM</th>
<th>Cl g/kg DM</th>
<th>K g/kg DM</th>
<th>Ca g/kg DM</th>
<th>K/(Ca+Mg)</th>
<th>P g/kg DM</th>
<th>Ca/P equivalent basis</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Shoots</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T1 (0)</td>
<td>10.2</td>
<td>31.50</td>
<td>25.8</td>
<td>46.30</td>
<td>6.75</td>
<td>2.00</td>
<td>2.73</td>
<td>3.38</td>
</tr>
<tr>
<td>T2 (0+Gypsum)</td>
<td>9.5</td>
<td>29.25</td>
<td>31.5</td>
<td>43.50</td>
<td>5.88</td>
<td>1.88</td>
<td>2.80</td>
<td>3.14</td>
</tr>
<tr>
<td>T3 (240 Cl)</td>
<td>10.9</td>
<td>24.50</td>
<td>29.2</td>
<td>45.80</td>
<td>7.48</td>
<td>1.70</td>
<td>1.95</td>
<td>4.40</td>
</tr>
<tr>
<td>T4 (300 K)</td>
<td>9.8</td>
<td>25.75</td>
<td>35.3</td>
<td>45.00</td>
<td>5.60</td>
<td>1.98</td>
<td>2.52</td>
<td>2.84</td>
</tr>
<tr>
<td>T5 (240 Cl, 150 K)</td>
<td>9.5</td>
<td>25.25</td>
<td>27.7</td>
<td>41.80</td>
<td>5.68</td>
<td>2.18</td>
<td>2.51</td>
<td>2.61</td>
</tr>
<tr>
<td>T6 (200 Na)</td>
<td>12.2</td>
<td>26.75</td>
<td>37.8</td>
<td>40.00</td>
<td>6.23</td>
<td>2.15</td>
<td>2.39</td>
<td>2.90</td>
</tr>
<tr>
<td>T7 (240 Cl, 100 Na)</td>
<td>9.7</td>
<td>28.75</td>
<td>29.0</td>
<td>39.00</td>
<td>4.78</td>
<td>2.18</td>
<td>3.28</td>
<td>2.20</td>
</tr>
<tr>
<td>T8 (300 K, 200 Na)</td>
<td>13.0</td>
<td>26.00</td>
<td>32.8</td>
<td>42.80</td>
<td>6.58</td>
<td>1.85</td>
<td>2.23</td>
<td>3.56</td>
</tr>
<tr>
<td>T9 (240 Cl, 150 K, 100 Na)</td>
<td>7.9</td>
<td>31.00</td>
<td>26.6</td>
<td>43.80</td>
<td>6.03</td>
<td>2.45</td>
<td>3.06</td>
<td>2.46</td>
</tr>
<tr>
<td><strong>Bulbs</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T1</td>
<td>20.9</td>
<td>15.25</td>
<td>3.1</td>
<td>5.60</td>
<td>1.18</td>
<td>1.53</td>
<td>6.48</td>
<td>0.77</td>
</tr>
<tr>
<td>T2</td>
<td>22.0</td>
<td>15.25</td>
<td>4.4</td>
<td>6.00</td>
<td>1.18</td>
<td>1.68</td>
<td>6.41</td>
<td>0.70</td>
</tr>
<tr>
<td>T3</td>
<td>21.8</td>
<td>14.00</td>
<td>4.3</td>
<td>6.18</td>
<td>1.15</td>
<td>1.48</td>
<td>6.15</td>
<td>0.78</td>
</tr>
<tr>
<td>T4</td>
<td>25.1</td>
<td>14.50</td>
<td>4.6</td>
<td>5.00</td>
<td>0.98</td>
<td>1.65</td>
<td>6.50</td>
<td>0.59</td>
</tr>
<tr>
<td>T5</td>
<td>21.4</td>
<td>14.50</td>
<td>4.3</td>
<td>6.23</td>
<td>1.10</td>
<td>1.65</td>
<td>6.37</td>
<td>0.67</td>
</tr>
<tr>
<td>T6</td>
<td>20.8</td>
<td>13.50</td>
<td>4.2</td>
<td>5.10</td>
<td>1.18</td>
<td>1.75</td>
<td>5.39</td>
<td>0.67</td>
</tr>
<tr>
<td>T7</td>
<td>24.5</td>
<td>15.50</td>
<td>4.2</td>
<td>4.68</td>
<td>1.10</td>
<td>1.83</td>
<td>6.33</td>
<td>0.60</td>
</tr>
<tr>
<td>T8</td>
<td>25.5</td>
<td>15.25</td>
<td>5.2</td>
<td>6.00</td>
<td>1.05</td>
<td>1.68</td>
<td>6.70</td>
<td>0.63</td>
</tr>
<tr>
<td>T9</td>
<td>20.8</td>
<td>16.50</td>
<td>4.7</td>
<td>7.05</td>
<td>1.18</td>
<td>1.88</td>
<td>6.72</td>
<td>0.63</td>
</tr>
<tr>
<td><strong>LSD_{0.05}</strong></td>
<td>6.10</td>
<td>4.46</td>
<td>4.59</td>
<td>7.82</td>
<td>1.32</td>
<td>0.31</td>
<td>1.01</td>
<td>0.89</td>
</tr>
<tr>
<td><strong>Treatments*Partitions</strong></td>
<td>3.0-</td>
<td>1.0-</td>
<td>5-16</td>
<td>2.0-</td>
<td>2.0-</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Critical concentrations</strong></td>
<td>6.0</td>
<td>1.5</td>
<td>4.0</td>
<td>3.2</td>
<td>2.2</td>
<td>1-2</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

1 Numbers within parentheses are quantities of nutrients applied in kg/ha followed by symbol for specific nutrient.

2Critical concentrations for dairy cattle production as reported by (Grace et al. 2000) and NRC, (2001) and ratios as reported by Guillard and Allinson, (1989) and Grunes and Welch, (1989).

CONCLUSIONS

Fodder beet crops produced high DM yield, averaging 32.8 t/ha across the treatments. Additional K, Na and Cl fertilisers did not improve DM yield. The plant mineral concentrations, with the exception of P, were adequate for animal production. Bulbs, which contained about 67% of harvested biomass, had consistently lower Ca and P concentrations than those recommended for animal production. This suggests that shoot consumption may not be sufficient to supply these mineral elements to high-producing dairy cows and hence their supplementation is recommended.

ACKNOWLEDGEMENTS

Ballance Agri-Nutrients for financing the project. We also thank the Rakaia Island Dairies who allowed us to undertake the trial on their property.

REFERENCES


The effects of milking interval on indicators of nitrogen utilisation in morning and afternoon milk from dairy cows grazing ryegrass pasture

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ABSTRACT

Environmental considerations require reduced losses of nitrogen (N) from grazing cows, and milk urea-N may be a simple way to monitor losses and evaluate mitigation options. The higher concentration of milk urea-N in afternoon (pm) compared with morning (am) milk may reflect the lower water soluble carbohydrate:crude protein ratio in morning compared with afternoon grass, or the shorter interval between morning and afternoon milking. To separate these effects, cows grazing ryegrass pasture were milked at either 7:00 am and 3:00 pm, giving successive 8 h and 16 h intervals (conventional; CON), or at 7:00 am and 7:00 pm, giving equal 12 h intervals (delayed; DEL). Milk yield was higher in the morning than in the afternoon for CON (13.1 vs 6.7 l/cow), but equal for Del (9.9 l/cow), reflecting the equal intervals. The concentrations of milk urea-N were higher in the pm milk compared with the am milk for CON (5.0 vs 4.1 mmol/l; p=0.006), but the am concentration for Del was higher than for CON (4.9 vs 4.1 mmol/l; p=0.06) and equal to the pm. This suggests that the concentration of this metabolite is affected more by the interval between milkings than by the WSC:CP ratio of the grass eaten during the interval preceding milking. Comparisons among feeding and management regimes using milk urea-N as an indicator for potential N excretion should take into account the intervals between milkings and milk yield.

Keywords: Milk urea nitrogen; water soluble carbohydrate; nitrogen utilisation; ryegrass.

INTRODUCTION

Nitrogen (N) excretion from pasture-based dairy production systems is coming under increasing scrutiny. A higher concentration of water soluble carbohydrate (WSC) in pasture may improve the efficiency of N utilisation in the rumen and reduce the amount of N that is excreted (Pacheco et al. 2007). The concentration of urea-N in morning milk is lower than in afternoon milk (Cosgrove et al. 2007). Given the diurnally high concentration of WSC and WSC:protein ratio in afternoon grass, this may reflect more efficient utilisation of N during digestion of afternoon grass, and less surplus N being excreted the following morning. If milk urea-N reflects short-term changes in dietary WSC or protein, it may be an easily measured indicator of N utilisation and a proxy for urinary-N excretion.

However, there may be an alternative explanation for the diurnal difference in concentrations of milk urea-N. The longer interval between the main bout of grazing following afternoon milking and milk harvest the following morning, together with the greater yield of milk, may allow greater time for clearance of milk urea-N from the udder and for dilution. This paper provides a preliminary report on an experiment to test the comparative effects of feed composition (WSC:protein), and the alignment of feed intake and digestion with timing of milk harvest and sampling, on the concentration of urea-N in milk. Our hypothesis was that the concentrations of milk urea-N in morning and afternoon milk reflect the WSC:protein of feed consumed during the preceding period, rather than the different intervals between successive milking events.

MATERIALS AND METHODS

To test this hypothesis two contrasting milking regimes were imposed on spring-calving cows (n=50, 109 ± 9.1 days-in-milk) grazing annual (Lolium multiflorum) or perennial (Lolium perenne) ryegrasses at Massey University No 4 Dairy (for details see Cosgrove et al. 2007). The timing of milking of cows alternated at 3-d intervals from conventional (CON) at 7:00 am/3:00 pm (8/16 hr intervals) to delayed afternoon milking (DEL) at 7:00 am/7:00 pm (12/12 h intervals), for 5 successive 3-d periods (three of the 8/16 and two of the 12/12), commencing 3 Dec, 2006. Milk samples collected from each cow at each milking were analysed for milk urea-N (using the urease procedure, as described by Pacheco et al. 2007). Milk samples collected from each cow at each milking were analysed for milk urea-N (using the urease procedure, as described by Pacheco et al. 2007). Milk urea-N (mMol/L) was calculated as the molar concentration of milk urea multiplied by 2.

Cows were offered a daily pasture allowance of 54 kg DM/cow/day in two allocations of 0.4 at 8:00 am following the morning milking, and 0.6 at either 4:00 pm (CON) or 8:00 pm (DEL) following the afternoon or evening milking, with the expectation of a dry matter intake of 18 kg DM/cow/day from each treatment.

Samples of the fresh allocation of pasture offered to
cows were hand-plucked to simulate herbage consumed on d 3 of each of the 5 periods and the concentrations of WSC and crude protein (CP) were determined by near infra-red reflectance spectroscopy (feedTECH, AgResearch Grasslands, Palmerston North). The mean concentrations (± s.d.) of WSC in ryegrass offered at 8:00 am, 4:00 pm (CON) and 8:00 pm (DEL) were 193 ± 19, 215 ± 26 and 222 ± 23 g/kg DM, respectively, and the concentrations of CP were 187 ± 18, 177 ± 20 and 154 ± 16 g/kg DM, respectively. The mean WSC:CP ratios were 1.1, 1.2 and 1.3 at 8:00 am, 4:00 pm and 8:00 pm, respectively.

RESULTS

Total daily milk yield (19.8 L/cow/d) was not affected by milking interval, but the distribution of milk yield changed from 6.7 L/cow in the afternoon and 13.1 L/cow in the morning for the CON treatment, to 9.9 and 9.8 L/cow at the am and pm milkings, respectively, for the DEL treatment (Table 1). The concentrations of milk urea-N in the pm were 5.0 and 4.9 mMol/L for CON and DEL, respectively (P=0.93) but in the am were 4.1 and 4.9 mMol/L (P=0.07) for the CON and DEL treatments, respectively (Table 1).

DISCUSSION AND CONCLUSION

If the primary determinant of the concentration of milk urea-N is the concentrations of WSC and CP, and the WSC:CP ratio of the feed consumed between successive milkings, it was expected that the concentration of milk urea-N would be higher in pm milk than in am milk for both milking intervals. The similar am and pm concentrations of milk urea-N when the milking intervals were similar (DEL) suggests that the concentration of this metabolite is affected more by the interval between milkings than by the WSC:CP ratio of the grass eaten during the preceding interval. Comparisons among feeding and management regimes using milk urea-N as an indicator of urinary-N excretion should take into account the intervals between milkings and milk yield. Other factors such as the interval between the period of feed consumption and milking, and ryegrass cultivar may also influence concentrations of milk urea-N.

ACKNOWLEDGEMENTS

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REFERENCES


Table 1: The effect of changing the intervals between milkings from 8/16 h (Conventional; milked at 7:00 am and 3:00 pm) to 12/12 h (Delayed; milked at 7:00 am and 7:00 pm) by delaying the time of afternoon milking from 3:00 pm to 7:00 pm, on the yields of milk at the morning (am) and afternoon (pm) milkings and the concentrations of urea-nitrogen (N) in milk

<table>
<thead>
<tr>
<th>Milking time of day</th>
<th>Milking regime</th>
<th>Conventional (7:00 am/3:00 pm)</th>
<th>Delayed (7:00 am/7:00 pm)</th>
<th>P &lt;sup&gt;1&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk yield (L/cow/d)</td>
<td>am</td>
<td>13.1</td>
<td>9.9</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td></td>
<td>pm</td>
<td>6.7</td>
<td>9.8</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td></td>
<td>P&lt;sup&gt;2&lt;/sup&gt;</td>
<td>&lt;0.001</td>
<td>0.89</td>
<td>LSD&lt;sup&gt;3&lt;/sup&gt;=0.64</td>
</tr>
<tr>
<td>Milk urea-N (mMol/L)</td>
<td>am</td>
<td>4.1</td>
<td>4.9</td>
<td>0.06</td>
</tr>
<tr>
<td></td>
<td>pm</td>
<td>5.0</td>
<td>4.9</td>
<td>0.94</td>
</tr>
<tr>
<td></td>
<td>P&lt;sup&gt;2&lt;/sup&gt;</td>
<td>0.006</td>
<td>0.94</td>
<td>LSD=0.85</td>
</tr>
</tbody>
</table>

<sup>1</sup> P-values of contrasts comparing milking regimes within time of day and times of day within milking regime, respectively.

<sup>2</sup> LSDs are for comparing means within milking regimes and times of day.
The effect of mechanical mulching on kikuyu pasture quality

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ABSTRACT

Kikuyu pasture makes up a large proportion of the pasture available to dairy cows in Northland, New Zealand. The quality of this pasture has been shown to impact milk production during periods of rapid growth in summer and autumn. Mechanical mulching of pastures in autumn increased the soluble carbohydrate content and decreased the neutral detergent fibre content when compared to not mulching. This has positive implications for increasing milk production.

Keywords: kikuyu; mulching; milk; forage quality.

INTRODUCTION

Mechanical mulching of kikuyu during peak growth in summer/autumn is used to prevent the development of a stoloniferous mat, promote green leaf growth and, when combined with drilling or broadcasting Italian ryegrass, improve the quality of feed on offer during the winter/spring months. The hypothesis tested was that mechanical mulching of kikuyu pastures would improve pasture nutritive quality.

MATERIALS AND METHODS

Pasture samples were collected from the Northland Agricultural Research Farm (NARF, Dargaville, NZ) between May 2010 and March 2012. The botanical composition of the pasture ranged from approximately 80% kikuyu (summer/autumn) to 10% (winter/spring). In the preceding autumn, 22 hectares (ha) was drilled with Italian ryegrass seed (IRG) at 20 kg/ha and mechanically mulched to 2 cm (mulched treatment), and 21 ha with IRG at 20 kg/ha (non-mulched treatment). Four paddocks with the highest pasture cover for each treatment were sampled monthly. Samples were bulked and analysed using near-infrared reflectance spectroscopy. Data were analysed with GenStat 14.1 (VSN International 2011) as mixed models with year, month, treatment as fixed effects and sampling date as a random effect.

RESULTS

Neutral detergent fibre was lower and soluble carbohydrate higher in the mulched farmlet (P≤0.05) when averaged over the whole period (Table 1). The differences between treatments were most apparent during the active kikuyu growing periods (January to May). There was a trend for metabolisable energy and digestibility of the pastures to improve with mulching (P=0.1).

Table 1: Mean nutrient content of mulched and non-mulched kikuyu pastures at the Northland Agricultural Research Farm from May 2010 to March 2012

<table>
<thead>
<tr>
<th>Nutrient</th>
<th>Mulched</th>
<th>Non-Mulched</th>
<th>SED</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crude protein (% DM)</td>
<td>21.7</td>
<td>21.3</td>
<td>0.635</td>
<td>0.58</td>
</tr>
<tr>
<td>Acid detergent fibre (% DM)</td>
<td>26.5</td>
<td>27.5</td>
<td>0.692</td>
<td>0.16</td>
</tr>
<tr>
<td>Neutral detergent fibre (% DM)</td>
<td>47.6</td>
<td>49.8</td>
<td>1.084</td>
<td>0.05</td>
</tr>
<tr>
<td>Soluble carbohydrate (% DM)</td>
<td>9.4</td>
<td>7.5</td>
<td>0.883</td>
<td>0.04</td>
</tr>
<tr>
<td>Organic matter digestibility (% DM)</td>
<td>69.1</td>
<td>67.3</td>
<td>1.045</td>
<td>0.10</td>
</tr>
<tr>
<td>Metabolisable energy (MJ/kg DM)</td>
<td>11.1</td>
<td>10.8</td>
<td>0.168</td>
<td>0.10</td>
</tr>
</tbody>
</table>
DISCUSSION AND CONCLUSION

The improvement in pasture quality resulting from mulching in the current trial supports the findings of (Reeves et al. 1996), who manipulated the grazing management of kikuyu to improve pasture quality and subsequent milk production. Unlike temperate pastures which have a fairly constant nutrient content throughout the year, tropical pastures vary greatly (Stobbs, 1973). Mulching pastures in the current work increased the proportion of leaf in the pasture, especially during the summer/autumn period, and this was associated with a decline in NDF content and an increase in soluble carbohydrates. The results demonstrate that in addition to grazing management, mulching kikuyu dominant pastures during autumn and direct drilling Italian ryegrass can increase the quality of pasture offered to dairy cattle in the subsequent season.

ACKNOWLEDGEMENTS

Thanks to the NARF staff and committee for their assistance, Ellett, Hine Rangi and the Northland Dairy Development Trusts and DairyNZ for their financial support.

REFERENCES


Seasonal Pattern of Dry Matter Concentration in Plantain Pasture Mixes

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ABSTRACT

The dry matter (DM) yield, concentration and botanical composition of plantain and ryegrass based pastures was monitored monthly in adjacent paddocks on seven farms in Northland, New Zealand for between 2 and 4 years. Lower DM concentration was observed in winter and spring on both pasture types but the lowest values were observed on the plantain-based pastures. Dry matter concentration values of less than 15% were recorded every month between May and October for the plantain pastures even though total DM yields were higher than the ryegrass pastures. This may impact on DM intake and subsequent milk production in cows grazing pastures with high plantain content.

Keywords: Northland; C4 pastures; dairy

INTRODUCTION

Low pasture nutritive value during summer and autumn has resulted in renewed farmer interest in sowing plantain (*Plantago lanceolata* L.) mixes. Plantain/ryegrass/clover mixes on farms in Northland can have DM concentrations of less than 15%, markedly lower than well-established ryegrass/clover pastures (Piggot 2009). This could restrict DM intake (DMI) of grazing cows and reduce milk production (Cabrera Estrada et al. 2004; John and Ulyatt 1987). Improving feed quality through incorporating new species into existing pasture swards could give economic benefits to farmers who are challenged with sub-tropical pastures (C4), provided cow intake is not restricted. The purpose of this paper is to compare the seasonal variation in DM concentration in plantain-based and ryegrass-based pastures on commercial farms in Northland.

MATERIALS AND METHODS

Plantain-based pastures were established in paddocks on seven farms in the Northland region using a seed mix of plantain, white clover (*Trifolium repens*), red clover (*Trifolium pratense*) and diploid perennial ryegrass (*Lolium perenne*) sown at 2, 2, 3 and 10 kg seed/ha respectively. These paddocks were compared with adjacent paddocks of predominantly perennial ryegrass of varying age (often older). Herbage mass was measured (using the cage technique of Piggot 1997) simultaneously in paired paddocks at monthly intervals. The mean yield of the plantain-based pastures and ryegrass pastures was 19.2 and 14.1 t DM/ha/year respectively. Plantain was the dominant component of the plantain-based pasture, comprising 54-90% of total annual DM yield in year 1 following sowing, declining to 29-60% in year 3. Ryegrass comprised 70-95% of annual DM yield in the ryegrass-based pasture. Red plus white clover content was similar in both pasture types, comprising 5-20% of annual DM yield. More details on the study methods and results can be found in Moorhead and Piggot (2009). The repeated measurements through time were modelled using spline models within the linear mixed model framework as described by (Verbyla et al. 1999). Residual maximum likelihood (REML) in GenStat 14.1 (VSN International 2011) was used to fit these models.

RESULTS

The DM concentration of both pasture types was lowest between May and October and was consistently lower for the plantain-based pastures than for the ryegrass-based pasture (mean difference = 3.86 ± 0.49 %, P<0.001, Figure 1). It is important to note that this is observational data rather than data from a randomised trial so not all of this difference can necessarily be attributed to the composition of the pasture sward. However, for the plantain-based pasture samples, more than 90% were <15% DM between May and July, and more than 60% between March and September (Table 1). In comparison, 65 and 47 % of all the ryegrass/clover samples recorded <15% DM for the same periods, respectively.
Figure 1: Dry matter (DM) concentration of plantain/ryegrass/clover and ryegrass/clover cage cut samples collected between 2001 and 2012. Error bar indicates the average standard error of the difference between DM%. Horizontal line indicates 15% DM threshold.

Table 1: Proportion of ryegrass/clover and plantain/ryegrass/clover monthly cage cut samples collected between 2001 and 2012 with less than 15% dry matter

<table>
<thead>
<tr>
<th>Month</th>
<th>Plantain</th>
<th>Ryegrass</th>
</tr>
</thead>
<tbody>
<tr>
<td>Jan</td>
<td>20</td>
<td>7</td>
</tr>
<tr>
<td>Feb</td>
<td>32</td>
<td>11</td>
</tr>
<tr>
<td>Mar</td>
<td>63</td>
<td>17</td>
</tr>
<tr>
<td>Apr</td>
<td>66</td>
<td>31</td>
</tr>
<tr>
<td>May</td>
<td>90</td>
<td>52</td>
</tr>
<tr>
<td>Jun</td>
<td>96</td>
<td>75</td>
</tr>
<tr>
<td>Jul</td>
<td>97</td>
<td>69</td>
</tr>
<tr>
<td>Aug</td>
<td>81</td>
<td>44</td>
</tr>
<tr>
<td>Sep</td>
<td>75</td>
<td>39</td>
</tr>
<tr>
<td>Oct</td>
<td>55</td>
<td>19</td>
</tr>
<tr>
<td>Nov</td>
<td>23</td>
<td>4</td>
</tr>
<tr>
<td>Dec</td>
<td>16</td>
<td>10</td>
</tr>
</tbody>
</table>

DISCUSSION AND CONCLUSION

Dry matter concentration of ryegrass pastures rarely fell below 15% in the current study, but was below this value in the plantain-based pastures over much of winter and spring. This period generally coincides with reduced pasture growth rates and lower pasture mass, which could restrict pasture allowances. Low DM concentration of pasture could further impact on DMI. Clark and Woodward (2007) suggested that feeding cows pasture with DM concentration less than 15% could reduce DMI and affect milk production. In order to maximise DMI, low DM concentration of plantain-based swards in winter/spring should be considered when allocating pasture to dairy cows and possibly ameliorated by increasing pasture allocation or introducing high DM supplements when this seasonal variation is most apparent.

REFERENCES


Effect of pasture allowance and species diversity on rumen degradability and short-term grazing intake

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ABSTRACT

Pasture allowance and rumen degradation rates have been shown to affect herbage intake and nutrient supply of lactating dairy cows, which ultimately influence milk production. The objective of this study was to compare the effect of allowance and pasture type on dry matter intake (DMI) during the first grazing session (GS) and subsequent impacts on rumen fermentation. Holstein Friesian X Jersey cows in late lactation were assigned to two perennial ryegrass dominant pasture with two pasture allowances. Pasture types were simple and diverse and were offered at high (HA, 17 kg DM cow\(^{-1}\) d\(^{-1}\)) and low (LA, 15 kg DM cow\(^{-1}\) d\(^{-1}\)) herbage allowances. Herbage intake during the first 4hr GS was greater on simple compared to diverse pasture (10.5 vs 7.9 kg Dm cow\(^{-1}\), respectively, \(P<0.05\)). Increasing allowance affected 4hr DmI, with greater DmI at HA compared to LA (9.9 vs 8.5 kg DM cow\(^{-1}\), respectively, \(P\leq 0.05\)). Daily DmI (14.31 kg Dm cow\(^{-1}\)) was not affected by treatments. In sacco Dm disappearance was affected by pasture type, with diverse pasture having greater potential disappearance than simple (84.2% of Dm vs 78.3% of Dm, respectively, \(P<0.05\)). Rumen degradation rate (mean 11.5% hr\(^{-1}\)) was not significantly affected by treatment. Altering pasture diversity and pasture allowance will influence short-term DMI. Results show the benefits of increasing pasture species diversity on improving degradability and nutrient availability to the animal.

Keywords: Pasture allowance, sward type, rumen, intake, in sacco

INTRODUCTION

New Zealand dairy pastures typically consist of perennial ryegrass (\textit{Lolium perenne} L.) and white clover (\textit{Trifolium repens}) species and animal performance on these pastures is often limited by intake. Increasing feed degradability may increase DMI, improving animal production. Chicory and plantain have high organic matter digestibility, contributing to high in sacco degradation rates (Burke \textit{et al}. 2000) and thus forage herbs may benefit traditional pasture swards. This study aimed to compare herbage intake and rate of herbage intake on in sacco rumen degradation in dairy cows grazing simple and diverse pastures at high and low pasture allowances.

MATERIALS AND METHODS

A grazing study was conducted at the Lincoln University Research Dairy Farm from 30 March 2012 to 4 April 2012. Simple mixtures which contained perennial ryegrass (78%) and white clover (3%) and diverse mixtures (58% ryegrass, 6% clover) also containing chicory (4%) and plantain (18%) were sown in January 2010. Forty-eight Holstein Friesian X Jersey cows in late lactation were assigned to simple or diverse pasture swards at high or low pasture allowance (17 and 15 kg DM cow\(^{-1}\) day\(^{-1}\) > 1500 kg DM ha\(^{-1}\) respectively). Pasture mass decline was determined from compressed pasture height measured every 30 minutes for four hours from the start of the grazing session (GS). Dry matter intake was calculated from the difference in pre and post grazing mass as determined by a calibrated rising plate meter. In sacco degradation was recorded using freshly mown pasture samples which were incubated in the rumen of fistulated cows (n = 8) for 2, 4, 6, 8, 24 and 48 hours. Degradation parameters were fitted to a non-linear equation (\textit{Ørskov} and \textit{McDonald} 1979) in Sigmaplot. Means were analysed in GenStat, using ANOVA.

RESULTS

Daily (24 hour) herbage intake was unaffected by treatments (Table 1). Herbage intake during the GS was greater for cows grazing simple compared to diverse pasture (10.5 vs 7.9 kg DM cow\(^{-1}\) respectively) and greater for cows on high compared with low allowance (9.9 vs. 8.5 kg DM cow\(^{-1}\) respectively). No interaction between pasture mix and pasture allowance was observed. Proportion of daily herbage consumed at four hours was unaffected by treatments.

In sacco degradability was greater for diverse compared with simple mixes (84.2% vs. 78.3% respectively Table 2) but was unaffected by high or low allowance (81.8 vs. 80.7% respectively). Soluble fraction (A), potentially degradable fraction (B) and fractional degradation rate (k) were unaffected by treatments.

DISCUSSION

While rates of herbage intake during the GS were affected by pasture allowance and pasture type, DMI
was not altered by treatment. Lack of treatment effects on DMI may have been due to reduced nutritional demands in late lactation and the ability of animals to increase grazing time to maintain a constant daily intake (Bryant et al. 2012). Differences in intake during the GS may have been due to variation in opportunity for selection due to differences in botanical composition and grazing area.

In sacco degradation rate was unaffected by treatments and probably did not influence herbage intake. (Burke et al. 2000) observed faster in sacco degradation rates of chicory and plantain than perennial ryegrass, and lack of degradation rate significance in the current study may have been due to low (<25%) proportions of herb in diverse swards. Proportions of herb may however have been sufficient to alter total feed degradability, with chicory and plantain having high organic matter digestibility as a result of low fibre and high soluble carbohydrates, relative to perennial ryegrass (Burke et al. 2000). The effect of herbage allowance on rumen degradation rates are unlikely to be detected from in sacco studies as allowance tends to alter degradability through intake rate and its effect on mastication and rumination behaviour (Gregorini et al. 2009).

However, cows grazing on diverse pastures may receive greater nutrient and energy supply due to increased selection for a high quality diet and more complete rumen degradation. Similarly, slower rates of herbage intake may also indicate increased mastication or rumination time (Gregorini et al. 2009), enabling greater rumen digestion efficiency.

**CONCLUSION**

Increasing species diversity in pasture swards may increase digestive nutrient supply to dairy cows through increased herbage degradability and slower rate of herbage intake.

**ACKNOWLEDGMENTS**

The authors would like to thank all students and staff at Lincoln University and Lincoln University Research Dairy farm involved. This research was funded by FRST and DairyNZ (DRCX0802).

**REFERENCES**


**Table 1:** Daily and four hour herbage intakes of dairy cows grazing simple (S) and diverse (D) pasture types (PT) at high (HA) and low (LA) pasture allowance (PA)

<table>
<thead>
<tr>
<th>Treatment</th>
<th>SLA</th>
<th>SHA</th>
<th>DLA</th>
<th>DHA</th>
<th>SED</th>
<th>PA</th>
<th>PT</th>
<th>PA x PT</th>
</tr>
</thead>
<tbody>
<tr>
<td>Daily herbage intake (kg DM/cow/day)</td>
<td>13.73</td>
<td>16.03</td>
<td>13.66</td>
<td>13.82</td>
<td>1.579</td>
<td>0.49</td>
<td>0.46</td>
<td>0.52</td>
</tr>
<tr>
<td>4 hr herbage intake</td>
<td>9.27</td>
<td>11.73</td>
<td>7.76</td>
<td>8.05</td>
<td>0.606</td>
<td>&lt;0.01</td>
<td>≤0.05</td>
<td>0.11</td>
</tr>
<tr>
<td>Proportion of intake consumed in 4hr (%)</td>
<td>0.67</td>
<td>0.73</td>
<td>0.57</td>
<td>0.58</td>
<td>0.111</td>
<td>0.68</td>
<td>0.20</td>
<td>0.81</td>
</tr>
</tbody>
</table>

**Table 2:** In sacco rumen degradation parameters within dairy cows grazing simple (S) and diverse (D) pasture types (PT) at high (HA) and low (LA) pasture allowance (PA), using a non-linear model (Ørskov and McDonald, 1979). P = potentially degradable %, A = soluble fraction %, B= slowly degradable fraction %, k = fractional degradation rate (% per hour).

<table>
<thead>
<tr>
<th>Coefficient</th>
<th>SLA</th>
<th>SHA</th>
<th>DLA</th>
<th>DHA</th>
<th>SED</th>
<th>PA</th>
<th>PT</th>
<th>PA x PT</th>
</tr>
</thead>
<tbody>
<tr>
<td>P</td>
<td>77.5</td>
<td>79.0</td>
<td>83.8</td>
<td>84.6</td>
<td>2.08</td>
<td>0.60</td>
<td>&lt;0.05</td>
<td>0.87</td>
</tr>
<tr>
<td>A</td>
<td>23.2</td>
<td>27.7</td>
<td>27.7</td>
<td>31.1</td>
<td>5.77</td>
<td>0.53</td>
<td>0.53</td>
<td>0.94</td>
</tr>
<tr>
<td>B</td>
<td>46.9</td>
<td>45.8</td>
<td>48.5</td>
<td>46.3</td>
<td>9.33</td>
<td>0.86</td>
<td>0.92</td>
<td>0.96</td>
</tr>
<tr>
<td>k</td>
<td>10.2</td>
<td>9.6</td>
<td>13.2</td>
<td>13.0</td>
<td>4.28</td>
<td>0.92</td>
<td>0.50</td>
<td>0.96</td>
</tr>
</tbody>
</table>
Effect of fluctuating water logging in winter on growth of perennial ryegrass

M.V.H. STAINES, J.E. BAKER, L. PASZKUDZKA-BAIZERT, D.L. BENNETT, R.J. MORRIS, P.A. CASSON

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ABSTRACT

An experiment with perennial ryegrass pasture grown in pots was conducted to quantify the effect of fluctuating water logging during winter/spring on pasture growth rate. Two treatments were a well-drained (D) control and a water logging (W) treatment, which closely replicated actual movements in the water table during the wet winter/spring of 2007 in Busselton, Western Australia. The experiment resulted in four pasture harvests, with the 2nd and 3rd harvests covering the 95-day period of water logging. Growth rates differed significantly only for the 3rd harvest: 45 (D) vs 36 (W) kg DM/ha/day (P<0.05). Overall, the effects of fluctuating water logging on growth rates of perennial ryegrass were small and not significant.

Keywords: Fluctuating water logging, perennial ryegrass

INTRODUCTION

Fluctuating water logging in winter is common in dairy pastures in south-western Australia due its Mediterranean climate with high winter rainfall and duplex soils which impede deep drainage. Previous research has shown that pasture species, genotype and soil factors affecting oxygenation are amongst factors affecting the impact of water logging on pasture growth (Rogers and Davies 1973; Eccles et al. 1990; McFarlane et al. 2003). A short-coming of these and other studies is that water logging was often unrealistic in extent and duration. The purpose of our study was to quantify the effect of realistic, fluctuating, water logging in winter/spring on growth of perennial ryegrass.

MATERIALS AND METHODS

An experiment was carried out from early April to late November 2009 with well-established (2 years old) perennial ryegrass growing in pots filled with sandy soil. Pots were 15 cm diameter, 40 cm high, had a fine mesh bottom and were placed on a table with a wire-mesh top to facilitate drainage.

Pots were allocated randomly to two lots of 4 replicates, each with 25 pots arranged in a square. Four random replicates were kept moist but well-drained (D) at all times, thus providing ideal growing conditions. Four random replicates were placed in metal bins (40 cm deep) to prevent drainage and exposed to fluctuating water logging (W) (see Figure 1) during winter/spring to replicate movements in the water table as recorded in dairy paddocks at Vasse Research Centre (VRC), Busselton, Western Australia, during the wet winter/spring of 2007. Water logging (=water level <40 cm below ground level [BGL]) commenced on 29 Jun 2009 and ceased on 2 Oct 2009 and was imposed over a total of 95 days, with a mean water level of 15 cm BGL (s.d. 12.6). Water used for the water logging treatment was brought up to an electrical conductivity (EC) as recorded at VRC in 2007 by adding sodium chloride to tap water (typically 0.18 g/L). Mean final EC was 112 ± 17 mS/m.

Pasture was harvested mechanically to a stubble height of 5 cm in early April and then every time when ryegrass reached the 3-leaf stage till late November. The experiment resulted in four pasture harvests: on 15 Jun (pasture grown prior to the start of water logging); on 17 Aug and 8 Oct (pasture grown almost all during water logging) and on 26 Nov (pasture grown after the finish of water logging). Fertiliser was applied immediately after every harvest (equivalent to 1, 0.2, 0.4, 0.2 kg/ha/d for N, P, K and S respectively). Analyses of variance were used to compare treatment means, with 1 d.f. for the treatment effect and 6 d.f. for the error term.

RESULTS

Pasture growth rate for the four harvests is shown in Figure 2. The only significant treatment difference occurred at the harvest in early Oct, when water logging had a significant adverse effect on pasture growth rate: 45 (D) vs 36 (W) kg DM/ha/day (SEM 1.8, P=0.02). Over the entire experimental period (233 days) the effect of water logging on pasture growth rate was not significant: 52 (D) vs 51 (W) kg DM/ha/d (SEM 1.9, P=0.63).
Our results show that the effect of prolonged but realistic, fluctuating, water logging of perennial ryegrass grown in sandy soils was transient and overall not significant. Rogers and Davies (1973), using a pot trial with 4 pasture species grown in compost, reported that 112 days of severe continuous water logging on ryegrass grown in sandy soil was minimal.

Although the effect of fluctuating water logging per se was small, under practical conditions, water-logged pasture that is being grazed is prone to pugging, which can lead to significant sward damage with reduced pasture production and persistency (Nie et al. 2001; Menneer et al. 2005). Thus, a priority for water logged paddocks remains minimizing pugging damage by reducing grazing time.

REFERENCES


Marginal cost analysis to determine optimal annual ryegrass sowing rates

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ABSTRACT

Replicated field trials demonstrate that annual ryegrass early season growth rates are sowing rate dependant and face a decreasing marginal return (kg yield/kg seed) as sowing rates increase. Yield within each year closely followed second order polynomial relationships with sowing rate (average $r^2=0.95$), and when multiple trials are combined, sowing rate explains the majority ($r^2=0.7$) of yield response. Due to the diminishing marginal return, marginal cost analysis is an economically rational tool to making sowing rate decisions. We demonstrate that depending on substitute feed cost, further profits can be captured by increasing sowing rates of cultivar Winterstar®II from the standard 20 to 30 kg/ha to 35 to 45 kg/ha.

Keywords: annual ryegrass; sowing rate; marginal cost analysis.

INTRODUCTION

Farmers are often advised that an optimal sowing rate for annual ryegrass in pure swards is between 20 and 30 kg/ha, or perhaps to increase sowing rates with expected rainfall/irrigation supply. However, work by (Wynn et al. 2011) and (Veneto et al. 2004) suggests farmers face a decreasing marginal response to sowing rate.

The objectives of this research were to determine the yield response function of annual ryegrass to sowing rate and develop a marginal cost analysis to make informed and profit maximising decisions regarding sowing rates.

MATERIALS AND METHODS

Trials were conducted in 2003, 2009 and 2010 in Ballarat, Victoria. A late maturing tetraploid annual ryegrass (cv ‘Winterstar® II’) was sown in autumn at 10, 20, 30, 40 and 50 kg/ha in a replicated randomized block design (four replicates) and yield determined by complete plot harvesting. Following each harvest, a replacement fertiliser application consisted of 48.0, 4.4, 5.0 and 5.5 kg/ha of N,P,K and S respectively. ANOVA was conducted using Statistix 9 (Analytical Software, 2008) and trend lines fitting by Microsoft Excel (Microsoft, 2007).

RESULTS AND DISCUSSION

Yield results of the sowing rate trials are presented in Table 1.

Table 1: Yield results of sowing rate trials

<table>
<thead>
<tr>
<th>Sowing Rate</th>
<th>Cut 1</th>
<th>Cut 2</th>
<th>Cut 3</th>
<th>Cut 4</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>kg/ha</td>
<td>kg DM/ha</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Date</td>
<td>10/7/03</td>
<td>29/9/03</td>
<td>3/10/03</td>
<td>16/12/03</td>
<td>2003</td>
</tr>
<tr>
<td>10</td>
<td>1813a</td>
<td>2427a</td>
<td>1930a</td>
<td>2363a</td>
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<td>20</td>
<td>2269a</td>
<td>2653a</td>
<td>2035a</td>
<td>2475a</td>
<td>9432ab</td>
</tr>
<tr>
<td>30</td>
<td>2467a</td>
<td>2530a</td>
<td>2030a</td>
<td>2475a</td>
<td>9502ab</td>
</tr>
<tr>
<td>40</td>
<td>2823a</td>
<td>2535a</td>
<td>2097a</td>
<td>2784a</td>
<td>10120b</td>
</tr>
<tr>
<td>50</td>
<td>2699a</td>
<td>2441a</td>
<td>1913a</td>
<td>2391a</td>
<td>9444ab</td>
</tr>
<tr>
<td>CV</td>
<td>31.5</td>
<td>6.2</td>
<td>6.3</td>
<td>11.8</td>
<td>10.4</td>
</tr>
<tr>
<td>Date</td>
<td>7/7/09</td>
<td>8/8/09</td>
<td>28/8/09</td>
<td>16/9/09</td>
<td>2009</td>
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<tr>
<td>10</td>
<td>443a</td>
<td>1245a</td>
<td>1614a</td>
<td>2068a</td>
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</tr>
<tr>
<td>20</td>
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<td>1801b</td>
<td>1765b</td>
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</tr>
<tr>
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<td>1812b</td>
<td>1901a</td>
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</tr>
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<td>40</td>
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<td>2197b</td>
<td>1922ab</td>
<td>1937a</td>
<td>7547c</td>
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<td>50</td>
<td>1819d</td>
<td>2010b</td>
<td>1864b</td>
<td>1869a</td>
<td>7563c</td>
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<tr>
<td>CV</td>
<td>17.6</td>
<td>14.8</td>
<td>10.0</td>
<td>9.1</td>
<td>8.4</td>
</tr>
<tr>
<td>Date</td>
<td>8/7/10</td>
<td>6/8/10</td>
<td>5/10/10</td>
<td>-</td>
<td>2010</td>
</tr>
<tr>
<td>10</td>
<td>115a</td>
<td>862a</td>
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<td>2762ab</td>
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<td>689b</td>
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<tr>
<td>50</td>
<td>936c</td>
<td>1705d</td>
<td>2609b</td>
<td>-</td>
<td>5250b</td>
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<tr>
<td>CV</td>
<td>26.2</td>
<td>7.7</td>
<td>8.9</td>
<td>-</td>
<td>7.69</td>
</tr>
</tbody>
</table>

$P<0.05$, CV = coefficient of variation

The 50kg/ha sowing rate results from 2003 are excluded from the following analysis, as experimental error appears responsible for erroneous results, i.e. first cut yield is not linear with sowing rate, contrary to findings of (Venuto et al. 2004), (Wynn et al. 2011) and subsequent work by PGW Wrighton Seeds.

YIELD RESPONSE

Consistent with previous studies, first cut yield increased linearly with sowing rate in all three years ($r^2$
Averaging 0.98. As the seasons progressed, growth rates converged, presumably due to compensatory tillering at lower sowing rates. By the fourth cut in 2003 and 2009, growth rates were the same for all five sowing rates. These trials confirm sowing rate can manipulate early season annual ryegrass growth rates and increase total yield. The highest sowing rate trialled (50 kg/ha) appears to have marginally reduced late season yields.

To allow comparison of the three trials, data was normalised by subtraction of the applicable 10kg/ha sowing rate yield (Figures 1 and 2). Consistent with (Venuto et al. 2004), sowing rate variation explains almost all within year total yield via second order polynomials (Figure 1) with an average $r^2 = 0.95$. Due to the diminishing marginal return, marginal cost analysis is the most suitable method to decide on how much of this 1.6 tonne/ha yield response is it rational to pursue. The derivative (Equation 1) of the equation in Figure 2 describes the marginal response (kg yield/kg seed) and can be transformed by including seed cost to describe marginal feed cost at any sowing rate between 10 and 50 kg/ha. Figure 3 presents marginal feed cost as a function of sowing rate assuming $3.80/kg seed cost. Fixed costs are excluded as they do not influence short run decisions.

**Equation 1:** Marginal response of yield to seed

\[
\text{Marginal Response} = -1.7988 \times \text{sowing rate} + 96.971
\]

**Figure 1:** Within-year relative total yield response v sowing rate.

**Figure 2:** Relative total yield response v sowing rate. Polynomial fitted to all data points.

Yield response clearly suffers a diminishing marginal return, the rate of which varies slightly between years (Figure 1). When combined (Figure 2), all data points explain a majority of yield response ($r^2=0.7$) by a second order polynomial.

**Marginal cost analysis**

Between the 10 and 50 kg/ha sowing rate, yield differs by approximately 1.6 tonne/ha (Figure 2). In the case of a dairy, the most appropriate marginal revenue is likely to be the supplement cost of energy on a cents/MJ basis and equations should be transformed accordingly.

As an example of how this concept can be used to maximise resource use efficiency and profits, Figure 3 demonstrates that:

- where feed grown has a value of $150/tonne, approximately 40 kg Seed/ha would maximise profits; and
- importantly, unless marginal revenue is very low (i.e. extremely cheap supplement), the use of low sowing rates is sub optimal and will not maximise profits.

In addition, while beyond the scope of this paper, consideration should be given to utilisation and the minor value of nutrient removed in product. Given the importance of short term ryegrasses (Annual and Italian) to dairy systems, further work is warranted to identify the cause of variability in response to sowing rate between years, and define the response curves of other cultivars. Work by the Authors suggests sowing time may explain a large portion of variance; however temperature and water availability will also likely contribute.

The authors also suggest the identified response curve is not be applied to common cultivars as seed sources vary in quality (germination and vigour) and genetic potential for early growth.

**Figure 3:** Marginal feed cost v sowing rate
REFERENCES


A high concordance is possible between methane emissions from individual dairy cows measured by the SF\textsubscript{6} tracer and respiration chamber techniques

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ABSTRACT

Sulphur hexafluoride (SF\textsubscript{6}) tracer and respiration chamber techniques were used to measure the individual methane emissions of 14 lactating Holstein-Friesian cows fed a wheat-based and maize-based diet for 4 weeks each in a crossover sequence. Cows were fed in a well ventilated building and loafed on a pad outside. Lin’s concordance correlation coefficient between the two methods was 0.835. This high concordance means that our implementation of the SF\textsubscript{6} tracer technique can be used to accurately measure the methane yield (g/kg DM) of individual cows.

Keywords: Dairy cows; wheat; maize; methane.

INTRODUCTION

Two techniques are commonly used to determine methane emissions from individual animals, namely respiration chambers and the sulphur hexafluoride (SF\textsubscript{6}) tracer technique. Chambers provide an accurate methane measurement but are expensive to build and operate. The SF\textsubscript{6} tracer technique provides an indirect method for estimating emissions from individual cows and can be used with grazing animals. However, measurement variability has been reported to be greater with the tracer technique (e.g.: Grainger et al. 2007). If the SF\textsubscript{6} tracer technique could consistently give individual cow measurements similar to chambers, it could be used for screening large numbers of animals as required for genetic studies.

The objective of this experiment was to assess the concordance between the enteric methane yield of individual Holstein-Friesian dairy cows determined using a SF\textsubscript{6} tracer technique and by the respiration chamber technique.

MATERIALS AND METHODS

Fourteen multiparous, Holstein-Friesian cows, 169 days in milk, were offered a wheat-based diet for 4 weeks and a maize-based diet for 4 weeks in a randomized crossover experiment at the Department of Primary Industries, Ellinbank, Victoria, Australia (38°14’ S, 145°56’ E). Cows were offered a common amount of lucerne hay (10 kg DM/day), cold pressed canola (2 kg DM/day) and minerals (0.2 kg DM/day) supplemented with either wheat grain (10 kg DM/day) or maize grain (10 kg DM/day). Equal quantities of feed were offered at 0630 and 1530 hours, immediately after milking. Dry matter intake was recorded for each feeding.

Methane yield of individual cows was measured using the SF\textsubscript{6} tracer technique (3 days) and 4 to 6 days later by the respiration chamber method (last 2 days of diet period). Measurements began following at least 16 days of acclimatisation to each diet. During the SF\textsubscript{6} measurement, cows were housed indoors for 6 h per day and spent the remaining 18 h on an outdoor loafing pad. Concentrations of background gases indoors were collected as per (Williams et al. 2011) while those outdoors were collected using one canister on each fence, about 1 m above ground level. Mean daily concentrations of background gases for individual cows were calculated using a time weighted average. Background corrections for individual cows were as per Equation 2 of (Williams et al. 2011).

Concordance analysis using Lin’s concordance correlation coefficient (CCC: 1989; 2000) was carried out on the methane yield data from the 19 data pairs that had similar feed intakes while undergoing methane measurement by both the SF\textsubscript{6} and chamber technique. Lin’s CCC measures the agreement between two variables, in this case the results obtained from the two methods for measuring methane. A paired t-test was used to test for a difference between mean CH\textsubscript{4} emission measured by the two techniques on the same cows and diets.

RESULTS

Lin’s concordance correlation coefficient was 0.835 for the comparison of the two methods used to measure methane yield of individual cows. Mean methane yield determined via the two techniques did not differ ($P = 0.265$) although results from the SF\textsubscript{6} tracer technique were generally numerically higher than those from the respiration chambers (Figure 1).
DISCUSSION AND CONCLUSION

Based on the high concordance between results for individual cows when measured by the SF$_6$ tracer and respiration techniques, we conclude that our implementation of the SF$_6$ tracer technique can be used to accurately measure the methane yield (g/kg DM) of individual cows.

While previous studies have reported similar results (e.g.: Grainger et al. 2007; McGinn et al. 2006), most implemented the SF$_6$ tracer technique within respiration chambers or reported only correlations between the two techniques.

The high concordance between the chamber and tracer techniques for their methane yields found in this study indicates that it is valid to use our implementation of the SF$_6$ technique in a research program to screen a large number of dairy cows to identify a subset of individuals with a genetic predisposition for low methane yield.

ACKNOWLEDGEMENTS

This research was funded by the Department of Primary Industries – Victoria, Dairy Australia, Meat and Livestock Australia, and the Australian Government Department of Agriculture, Fisheries and Forestry under its Australia’s Farming Future Climate Change Research Program. Anthony Hookey, Serge Ziero, Di Mapleson and farm staff (Department of Primary Industries – Victoria) are thanked for their technical support.

REFERENCES


Evaluation of equations to predict dry matter intake and nitrogen use efficiency for dairy cows on pasture feeding experiments

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ABSTRACT

Conducting experiments to measure dry matter intake (DMI) and nitrogen intake is laborious and costly. To assist, equations have been developed to predict DMI and feed efficiency, defined as the ratio of output (e.g. gain or milk yield) to feed consumption, using a few parameters; however, they may not account for all between-animal variation. In this investigation we evaluated the accuracy of existing equations for predicting DMI and nitrogen use efficiency (NUE) (conversion of dietary nitrogen to milk nitrogen) with data derived from a pasture based N balance experiment using 16 animals with either high or low breeding index (BI). Results showed high concordance correlations between predicted and measured NUE and a reduction in correlation for predicted and measured DMI due to the effects of body reserve mobilization. Genetic influences in BI resulted in different energy metabolism, production and body tissue utilisation between the two groups. BI appears to be a good indicator of NUE; however equations may need improvement to account for these divergent components.

Keywords: dry matter intake; nitrogen use efficiency; breeding worth; body reserves.

INTRODUCTION

A major difficulty in nutrition research is measuring feed dry matter intake (kg/cow.d; DMI) and accurately estimating feed efficiency (ratio of output to feed consumption) and nitrogen use efficiency (conversion of dietary nitrogen to milk nitrogen) for individuals. Many prediction equations have been developed to assist with these estimates (e.g. Vadiveloo & Holmes, 1979; NRC., 1996; Heard et al. 2004); however these may not always account for between-animal variation. Long-term experiments involving the measurement of feed intake of cattle are laborious and costly (Archer, 1999). In this experiment we evaluated existing prediction equations in terms of their accuracy for predicting DMI and nitrogen use efficiency (NUE) of dairy cows of high and low breeding index (BI) fed a pasture diet. The applications of this work (i) highlight the potential value of using these equations in future studies, and (ii) shows the need for improvements to account for inaccuracies.

MATERIALS AND METHODS

DMI (kg/day) and NUE (g/g) (measured) data were obtained from a 9 day indoor N balance experiment using 16 cows grouped by BI (High; n=8/Low; n=8) and fed a pasture diet at DairyNZ, Hamilton, New Zealand during the spring of 2010. Details of the experiment have been reported by (Woodward et al. 2011). Predictions of daily DMI (kg/day) were estimated by calculations from (Rattray et al. 2007) by combining ME requirements for maintenance (MJ/day) (0.56 MJ ME/kg W0.75) and lactation (MJ/day) (ME = 1.1 × milk yield (kg/day) × NE/k J K) where NE/k J = (0.376 × fat %) + (0.209 × protein %) + 0.976 MJ NE/litre, and K = (feed ME MJ/ kg DM × 0.02) + 0.4. DMI (kg/day) was then estimated as total ME requirement (MJ/day) divided by feed ME (MJ/kg DM). Predictions of NUE (g/g) were made by dividing feed N (g/day) (DMI (kg/day) × (crude protein % / 6.25) × 10) by milk N (g/day) (milk yield (kg/day) × (protein % / 6.38) × 10). Linear regression and Lin’s concordance test was conducted in Genstat (13th Ed) to evaluate correlations between predicted and measured values, using BI as a group factor.

RESULTS

The average measured and predicted DMI were 15.4 (SEM 0.28) and 15.6 (SEM 0.33) kg DM/cow.day respectively. The average measured and predicted NUE were 0.20 (SEM 0.006) and 0.20 (SEM 0.005) g/g respectively. The concordance correlation coefficient between predicted and measured DMI for all animals was 0.71 however there was a lower correlation for low BI cows (0.42) compared to high BI cows (0.71). Concordance between measured and predicted NUE for all animals was 0.86. Similar to DMI correlations, there was lower accuracy for low BI cows (0.23) and higher for high BI cows (0.85). The relationships between predicted and measured NUE were not driven by a particular animal with a noticeably higher efficiency. Linear regression between predicted DMI and BI had higher significance than between measured DMI and BI (R²=...
0.48; \( P<0.01 \) and \( (R^2=0.26; P<0.05) \) respectively. Similarly, predicted NUE had a stronger relationship with BI \( (R^2 = 0.60; P<0.001) \) than measured NUE \( (R^2 = 0.59; P<0.001; \text{Figure 1}) \), showing that BI was better able to predict estimated DMI and NUE.

**DISCUSSION AND CONCLUSION**

The high concordance between predicted and measured NUE suggests strong power for the use of these equations in the absence of feeding trials. Predictions of DMI account for maintenance and lactation costs, suggesting the reduction in accuracy of these equations may be explained by the effect of body reserve mobilization. BI had a strong influence due to genetic differences between high and low animals in production and body reserve utilization. High BI cows are able to consume more feed and utilise this to partition more energy into milk and use more body reserves for this purpose (Davey *et al*. 1983), whilst other research has suggested a lack of relationship between genetic merit and ME efficiency of feed for milk production (Trigg and Parr, 1981). Our results indicate different maintenance requirements between high and low BI cows. BI was able to reasonably predict both DMI and NUE and with future investigation may provide a proxy for the prediction of NUE and DMI from BI directly; however we may need additional information in equations to account for divergent components (animal variation) which have a large influence on DMI.

**ACKNOWLEDGEMENTS**

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**REFERENCES**


A comparison between wheat or maize grain fed as a high proportion of the diet on milk production and methane emissions from dairy cows

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ABSTRACT

Large amounts of methane (CH$_4$), a potent greenhouse gas, are produced in the rumen of cows as they ferment ingested feed. The Australian dairy herd makes a significant contribution to Australia’s green-house gas emissions. We used a randomised cross-over experimental design in which 14 lactating cows were offered either a wheat-based or maize-based diet for 28 days, after which the grain component of the diet was switched, and the cows offered the other grain based diet for a further 28 days. The effects of these diets on milk production and methane emissions were measured. Milk yield was similar on both diets: 27.8 kg/day for wheat-fed cows and 27.9 kg/day for maize-fed cows. Milk fat % was reduced ($P < 0.01$) by the wheat based diet (2.75% wheat vs. 4.23 % maize) and consequently milk fat yield also declined (0.77 kg/day wheat vs. 1.18 kg/day maize; $P < 0.01$). Methane emissions were significantly ($P < 0.001$) reduced on the wheat based diet (219 g CH$_4$/day wheat vs. 424 g CH$_4$/day maize). These findings indicate that if dairy cows were fed high amounts of wheat grain supplements, the Australian dairy industry could achieve substantial reductions in CH$_4$ emissions. However, such a strategy would negatively impact on production of milk fat and profitability.

Keywords: Dairy cows; wheat; maize; methane.

INTRODUCTION

Methane is a greenhouse gas 21 times more potent than carbon dioxide in terms of its global warming potential, and the dairy herd makes a significant contribution to Australia’s greenhouse gas emissions. When ruminants are fed feed supplements such as crushed wheat, barley, crushed maize or sorghum grain, all of which contain high concentrations of starch, the pH in the rumen may decrease. High starch-low fibre diets affect products of digestion and may lower milk fat concentration, inhibit CH$_4$ production and sometimes cause acidosis. It has been estimated that up to 15% of Australian dairy herds are fed relatively high amounts of grains such as wheat, barley, triticale, maize or sorghum. The starch in maize is known to be more slowly degraded in the rumen than the starch from wheat. However, there is little comparative data available on the effects on milk production and CH$_4$ emissions when cows are fed high amounts of maize or wheat-based supplements.

MATERIALS AND METHODS

We employed a randomised cross-over experimental design in which 14 lactating cows were fed either a wheat-based or maize-based diet for 28 days, after which the grain component of the diet was switched, and the cows fed the other grain for a further 28 days. Eight of the cows were fitted with rumen cannulae (Rumen Cannula, www.rumen cannula.com ). Individual cows were held in pens and offered 10.2 kg DM/day of lucerne hay and 12.2 kg DM/day of a concentrate mix containing 16.3% cold pressed canola, 1.0% molasses powder, 1.0% minerals and 81.7 % of either crushed wheat or crushed maize. Measurements of feed intake, milk production and milk composition were made daily. After 26 days on each diet, cows were transferred to respiration chambers for two days and their CH$_4$ emissions measured using the methods described by (Moate et al. 2011). During these two days, rumen fluid pH was measured continuously in the rumen fistulated cows by intra-ruminal electronic bolus (KB5, Kahne Limited, www.kahneanimalhealth.com) weighted to reside at the base of the rumen. Data analysis was undertaken using a mixed model in which fixed factorial effects were specified for Block by Period, and for Diet (Wheat or Corn) by Cow type (fistulated or non-fistulated). Random effects were specified for Animal, Period within Animal, and Day within Period within Animal.

RESULTS

Cows offered the wheat-based diet ate 9.1 kg DM/day of lucerne hay and 11.5 kg DM/day of concentrate while cows offered the maize-based diet ate more ($P < 0.01$) lucerne hay (10.1 kg DM) and more ($P < 0.01$) concentrate (12.2 kg DM/day). Milk yield was similar on both diets: 27.8 kg/day for cows offered the wheat-based diet and 27.9 kg/day for cows offered the maize-based diet. Milk fat % was reduced ($P < 0.01$) by the wheat-based diet (2.75% wheat vs. 4.23 % maize) and consequently milk fat...
yield was also severely decreased ($P < 0.01$) by the wheat diet ($0.77$ kg/day wheat vs. $1.18$ kg/day maize). There were no differences between the wheat- and maize-fed cows in terms of concentrations in milk of protein, lactose and somatic cells or in yield of milk protein or milk lactose. Methane emissions were decreased ($P < 0.001$) on the wheat-based diet (219 g CH$_4$/day wheat vs. 424 g CH$_4$/day maize). Similarly, CH$_4$ yield was also depressed ($P < 0.001$) on the wheat-based diet (11.1 g CH$_4$/kg DMI vs. 19.5 g CH$_4$/kg). Mean rumen pH (6.1 wheat vs. 6.2 maize) was not affected by diet, but the type of grain did influence the duration rumen fluid pH was below pH 6 ($633$ min/day wheat vs $334$ min/day maize vs., $P = 0.019$) and the area below pH 6 but above the pH vs. time curve ($237$ pH.min wheat vs. $39$ maize pH.min, $P = 0.001$).

**DISCUSSION AND CONCLUSION**

Our findings comparing the effects of either wheat- or maize-based concentrates on milk production and milk composition are consistent with much previous research. However, our finding that CH$_4$ emissions from lactating dairy cows fed a wheat-based diet were almost half the emissions of cows fed maize-based diet is novel. For dairy cows, CH$_4$ abatement of this magnitude has rarely been previously reported in the scientific literature. This research has quantified the effects on milk production and CH$_4$ emissions of feeding high amounts of wheat- or maize-based supplements to dairy cows. We speculate that the duration rumen pH was below 6, and the area below pH 6 but above the pH vs. time curve, may play a role in the mechanism responsible for the observed methane mitigation. It is concluded that the Australian dairy industry could achieve substantial reductions in CH$_4$ emissions by feeding high amounts of crushed wheat grain supplements containing starch which is quickly degradable in the rumen. However, such a strategy would negatively impact on production of milk fat and profitability.

**ACKNOWLEDGEMENTS**

This research was funded by Dairy Australia, Meat and Livestock Australia, the Victoria Department of Primary Industries, and the Australian Government Department of Agriculture, Fisheries and Forestry under its Australia’s Farming Future Climate Change Research Program. This work would not have been possible without the technical work of Anthony Hookey, Serge Ziero, Di Mapleson and other staff at Department of Primary Industries – Victoria, Ellinbank Centre.

**REFERENCES**

Feeding grape marc to dairy cows suppresses methane emissions

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ABSTRACT

Grape marc (the skins and seeds remaining after grapes are pressed to make wine), is currently a waste by-product, but is a substantial resource that could be used by the dairy and beef industries. Grape marc contains high concentrations of crude fat and condensed tannins, both of which can reduce enteric methane (CH$_4$) emissions when fed to ruminants. Large amounts of CH$_4$, a potent greenhouse gas, are produced in the rumen of cows as they ferment ingested feed. The Australian dairy herd makes a significant contribution to Australia’s greenhouse gas emissions. Dairy cows in late lactation were fed a control diet or diets supplemented with either dry grape marc or ensiled grape marc, and effects on milk production and CH$_4$ emissions were measured. Both ensiled and dry grape marc had small negative impacts on production of milk fat, but reduced enteric CH$_4$ emissions by 20%. We conclude that grape marc, when used as a feed supplement for ruminants, has a role to play in CH$_4$ abatement.

Keywords: Dairy cows; grape marc; methane.

INTRODUCTION

Each year, the Australian wine industry produces approximately 200,000 tonnes of grape marc (the skins and seeds remaining after grapes are pressed to make wine). Thus grape marc is a substantial resource which could be used in the dairy and beef industries. There are three different types of grape marc that are currently commercially available. Fresh grape marc is the fresh grape skins and seeds after the grapes have been pressed and it is usually ensiled to prevent it from rotting and becoming mouldy. Ensiled grape marc has good long term stability and is suitable for feeding to ruminant animals. An alternative commercial product is dried grape marc. Grape marc typically contains 100 - 120 g crude fat/kg DM and 10 - 30 g condensed tannins/kg DM. Feeding ruminants with feed supplements high in either fat or tannin has been reported to result in reduced CH$_4$ emissions (Beauchemin et al. 2008; Moate et al. 2011). Enteric CH$_4$ emissions constitute between 5 and 10% of gross energy intake. If CH$_4$ emissions could be reduced, the saved energy could potentially be used to support milk production. Furthermore, CH$_4$ emissions from ruminants, is an issue of global importance because CH$_4$ is a greenhouse gas 21 times more potent than carbon dioxide in its global warming potential. There is no information in the scientific literature concerning the effects on CH$_4$ emissions or milk production when grape marc is fed to ruminants. The objective of this research was to evaluate ensiled and dried grape marc for their potential as feed supplements to support dairy production and inhibit methane emissions from dairy cows.

MATERIALS AND METHODS

An indoor feeding experiment was carried out involving 32 dairy cows in late-lactation (203 ± 72.8 DIM) fed for 18 days on either a control diet (containing lucerne hay, crushed wheat, minerals and molasses), or diets supplemented with either dry grape marc or ensiled grape marc (Table 1). Feed intake and milk production were measured daily. Milk composition (protein and fat) was measured daily over the last six days. Methane emissions were measured over the last 2 days using the SF$_6$ tracer technique.

RESULTS

The concentrations (g/kg DM) of crude protein, acid detergent fibre, neutral detergent fibre, crude fat and bound condensed tannin in the dried grape marc were 131, 477, 507, 142, and 20.1 respectively. For ensiled grape marc, the respective concentrations were 133, 531, 535, 126 and 7.8. The milk volume of cows fed dried grape marc was similar to that from cows fed the control diet, but milk fat yield was reduced by both the dried grape marc and ensiled grape marc (Table 1). Both dried and ensiled grape marc reduced CH$_4$ emissions by approximately 20%.
Table 1: Influence of dried and ensiled grape marc on milk production and methane emissions

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Control</th>
<th>Dried Grape marc</th>
<th>Ensilied Grape marc</th>
<th>SEM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of cows</td>
<td>12</td>
<td>10</td>
<td>9</td>
<td>-</td>
</tr>
<tr>
<td>Feed intake (kg DM/cow.d)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Alfalfa hay</td>
<td>13.2</td>
<td>8.9</td>
<td>8.8</td>
<td>-</td>
</tr>
<tr>
<td>Crushed wheat</td>
<td>3.8</td>
<td>3.8</td>
<td>3.7</td>
<td>-</td>
</tr>
<tr>
<td>Minerals</td>
<td>0.1</td>
<td>0.1</td>
<td>0.1</td>
<td>-</td>
</tr>
<tr>
<td>Molasses</td>
<td>0.2</td>
<td>0.2</td>
<td>0.2</td>
<td>-</td>
</tr>
<tr>
<td>Dry grape marc</td>
<td>0</td>
<td>4.9</td>
<td>0</td>
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</tr>
<tr>
<td>Ensiled grape marc</td>
<td>0</td>
<td>0</td>
<td>4.7</td>
<td>-</td>
</tr>
<tr>
<td>Total Dry Matter intake</td>
<td>17.3</td>
<td>17.9</td>
<td>17.5</td>
<td>-</td>
</tr>
<tr>
<td>Total crude protein intake (kg/cow.d)</td>
<td>2.72</td>
<td>2.64</td>
<td>2.59</td>
<td>-</td>
</tr>
<tr>
<td>Milk (L/cow/d)</td>
<td>14.6 b</td>
<td>15.4 b</td>
<td>12.8 a</td>
<td>0.39</td>
</tr>
<tr>
<td>Fat (%)</td>
<td>4.94 b</td>
<td>3.99 a</td>
<td>4.91 b</td>
<td>0.143</td>
</tr>
<tr>
<td>Protein (%)</td>
<td>3.56</td>
<td>3.52</td>
<td>3.47</td>
<td>0.053</td>
</tr>
<tr>
<td>Fat yield (g/cow.d)</td>
<td>720 b</td>
<td>613 a</td>
<td>608 a</td>
<td>16.3</td>
</tr>
<tr>
<td>Protein yield (g/cow.d)</td>
<td>517 b</td>
<td>540 b</td>
<td>437 a</td>
<td>10.5</td>
</tr>
<tr>
<td>CH₄ (g/cow.d)</td>
<td>470 b</td>
<td>375 c</td>
<td>389 a</td>
<td>8.1</td>
</tr>
<tr>
<td>CH₄ (g/kg DMI)</td>
<td>26.1 c</td>
<td>20.2 a</td>
<td>21.5 b</td>
<td>0.39</td>
</tr>
<tr>
<td>CH₄ (g/L Milk)</td>
<td>35.3 b</td>
<td>26.1 a</td>
<td>35.2 b</td>
<td>1.9</td>
</tr>
</tbody>
</table>

Means in the same row followed by different superscripts differ significantly (P<0.05)

DISCUSSION AND CONCLUSION

For the first time in the scientific literature, we report the effects of feeding either dried or ensiled grape marc on milk production, milk composition and CH₄ emissions from dairy cows. Feeding of both dried and ensiled grape marc to cows in late lactation has only a small negative impact on dairy productivity, but substantially decreases CH₄ emissions. The 20% reduction in CH₄ emissions and methane yield from feeding either dried or ensiled grape marc represents one of the largest reported reductions in emissions from dairy cows in vivo resulting from a nutritional intervention (Beauchemin et al. 2008). More information is needed to identify dietary combinations of grape marc and other feeds that reduce methane emissions while increasing milk production.

ACKNOWLEDGEMENTS

This research was funded by the Department of Primary Industries - Victoria, Dairy Australia, Meat and Livestock Australia, and the Australian Government Department of Agriculture, Fisheries and Forestry under its Australia’s Farming Future Climate Change Research Program. This work would not have been possible without the technical work of Anthony Hookey, Serge Ziero, Di Mapleson and other staff at Department of Primary Industries – Victoria, Ellinbank Centre.

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Effect of ploidy and pasture mass on milk production and nitrogen use efficiency in late summer

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ABSTRACT

Pre grazing mass and ploidy of perennial ryegrass pastures were investigated as immediate strategies that could be used to manipulate dry matter intake (DMI), milk production and nitrogen use efficiency (NUE) by reducing pasture crude protein (CP) content of the diet. Dry matter and N intake and milk production were compared using Friesian x Jersey dairy cows grazing diploid or tetraploid ryegrass at a high or low pasture mass. Dry matter intake was similar for all treatments (15.5 kg DM/cow/d). Crude protein content was affected by ploidy (18.7 vs 21.6% CP tetraploid and diploid respectively, \(P<0.05\)) and mass (18.2 vs 22.2% CP high and low mass respectively, \(P<0.05\)). There was a tendency for milk production to decrease with increasing pasture mass on diploid but not on tetraploid pastures (\(P<0.10\)). Pasture mass did not effect NUE but there was a trend for improved NUE on tetraploid compared with diploid pastures (0.23 and 0.19 respectively, \(P<0.10\)). These results highlight the capability of using tetraploids to improve NUE without negatively impacting milk production.

Keywords: Lolium perenne; Trifolium repens; polyploidy

INTRODUCTION

Animal performance under grazing systems is determined by pasture intake and its nutritive value. While temperate pasture species such as perennial ryegrass typically have high nutritive value, the ability of grazed pastures to meet cow requirements can be limited by the negative relationship between herbage mass and fibre content. Increasing pasture mass above a minimum height can improve intake as animals respond positively to increases in bite depth (Hodgson 1981) or leaf area index (Chacon and Stobbs 1976). However, if bite depth is not limiting then increases in pasture mass may constrain intake through a reduction in quality (Combellas and Hodgson 1979). The desire to graze at increased pasture mass is driven by the need to sustain high leaf area and to reduce urinary N losses by lowering the N concentration of the diet and increasing N use efficiency (NUE). Increasing the regrowth interval, and thereby mass, results in reductions in herbage N content (Bryant et al. 2012). One solution to address the trade-off between pasture mass and pasture quality is through the use of tetraploid varieties (O’Donavan and Delaby 2005). The purpose of this study was to compare DM and N intake and milk production for determination of NUE by dairy cows grazing diploid or tetraploid ryegrass at high or low pasture mass.

MATERIALS AND METHODS

A grazing trial using 48 lactating Friesian x Jersey cows was carried out at Lincoln University Research Dairy Farm between 9 and 18 February 2010. The experiment was two replicates of a 2 x 2 factorial arranged in a completely randomised design (eight separate groups of cows). The factorial combination was two perennial ryegrass ploidy levels (diploid cv Arrow, sown in April 2009 and tetraploid cv. Bealey, sown in 2008) and two pasture masses (high and low, created by altering the regrowth interval prior to the experiment). All pastures were sown with white clover (cv. Kopu II). Botanical and chemical compositions were determined from snip samples cut to grazing height. Milk yield and milk composition were recorded between days 6 to 9. Dry matter intake was calculated from pre and post grazing mass. Mass was determined by a rising plate meter calibrated for each ploidy treatment. Milk use efficiency (NUE) was calculated by dividing N in milk (g milk protein/6.38) by N intake. Group means for pasture and milk variables (8 experimental units) were calculated and analysed by ANOVA with ploidy and mass as fixed terms (Genstat version 12.2).

RESULTS

Pasture variables are presented in Table 1. An interaction between ploidy and mass revealed greater pasture mass accumulation in diploid pastures (54% increase) compared with tetraploids (29% increase). High pasture mass resulted in increased fibre content and reduced crude protein and digestibility (\(P<0.05\)) compare with low mass. Tetraploid pastures contained a lower proportion of clover and lower CP than diploid pastures (\(P<0.05\)).

There was no effect of treatments on DM or N intake (Table 2) when offered at the same allowance. Similarly the concentration of fat (5.35%) and protein (3.95%) in the milk was unaffected by ploidy or mass. However, milk production by cows grazing
the diploid pastures tended to be more sensitive to changes in pasture mass compared to animals grazing diploid pastures \( (P<0.10) \). As pasture mass increased, milk fat, milk protein and total milk solids tended to decline when cows were offered diploid pastures \( (Table \, 2, \, P<0.10) \). Cows grazing tetraploid pastures also tended to have greater NUE than those on diploid pastures \( (0.23 \, vs \, 0.19 \, respectively, \, P<0.10) \)

**DISCUSSION**

The findings of this study show the potential for tetraploids to maintain productivity of dairy cows in mid lactation whilst improving NUE for milk. Increasing pasture mass has been offered as a tool for reducing N losses by reducing the concentration of N in the diet \( (Bryant \, et \, al. \, 2010) \). However, those studies also demonstrated that the reduction in N intake on diploid pastures at higher mass was negatively associated with milk yield in spring \( (Bryant \, et \, al. \, 2010) \). In the absence of reproductive stems as in the spring experiment, the findings from the present study show a similar negative relationship between mass and milk production on diploid pastures. This may be due to the increased fibre content or grazing behaviour constraints due to very high mass or a combination of the two.

The interaction between ploidy and mass for milk production could have been more pronounced had there not been such large differences in clover content. It was expected that tetraploids would result in greater milk production at the same allowance as diploids \( (Castle \, and \, Watson \, 1971; \, O’Donavan \, and \, Delaby, \, 2005) \). However, at clover contents of close to 30% in the diploid pasture here, an advantage in animal performance could be attributed to legume content as shown by \( (Harris \, et \, al. \, 1997) \).

Because there was no effect of ploidy on N secretion in milk, the trend for reduced NUE on diploid pastures can be explained by differences in pasture N content which was likely to be influenced by high clover populations. Typically, diploid perennial ryegrass has poorer feeding value (higher fibre and lower crude protein) at high pasture mass levels as compared with tetraploids \( (O’Donavan \, and \, Delaby, \, 2005) \), however, a greater clover content of high feeding value in diploid pasture in the current study may have confounded the data. In summary, the risk of compromising animal productivity by adopting a low frequency grazing regime to improve NUE has the potential to be reduced by using tetraploid cultivars.

**ACKNOWLEDGEMENTS**

The authors gratefully acknowledge the help of staff at the Lincoln University Research Farm, manager Jeff Curtis and technician, Valerie Walpot. This research was funded by the Foundation for Research Science and Technology and DairyNZ. Contract: Dairy Systems for Environmental Protection (DRCX0802).

**REFERENCES**


Table 1: Pasture characteristics with respect to pre grazing mass, compressed height, botanical and chemical composition as influenced by ploidy level and herbage mass of perennial ryegrass

<table>
<thead>
<tr>
<th>Ploidy Mass</th>
<th>Diploid Low</th>
<th>Diploid High</th>
<th>Tetraploid Low</th>
<th>Tetraploid High</th>
<th>P value</th>
<th>Ploidy</th>
<th>Mass</th>
<th>P x M</th>
</tr>
</thead>
<tbody>
<tr>
<td>Height (cm)</td>
<td>16.8</td>
<td>26.5</td>
<td>18.6</td>
<td>24.6</td>
<td>1.46</td>
<td>NS</td>
<td>**</td>
<td>NS</td>
</tr>
<tr>
<td>Mass (kg DM/ah)</td>
<td>3290</td>
<td>5059</td>
<td>2953</td>
<td>3808</td>
<td>241</td>
<td>**</td>
<td>***</td>
<td>*</td>
</tr>
<tr>
<td>Botanical Composition (% DM)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Leafy</td>
<td>68.1</td>
<td>57.5</td>
<td>91.4</td>
<td>76.4</td>
<td>7.39</td>
<td>*</td>
<td>†</td>
<td>NS</td>
</tr>
<tr>
<td>Stem</td>
<td>3.0</td>
<td>11.0</td>
<td>1.4</td>
<td>12.0</td>
<td>5.48</td>
<td>NS</td>
<td>†</td>
<td>NS</td>
</tr>
<tr>
<td>Clover</td>
<td>27.7</td>
<td>28.3</td>
<td>4.9</td>
<td>8.0</td>
<td>5.60</td>
<td>**</td>
<td>NS</td>
<td>NS</td>
</tr>
<tr>
<td>Dead</td>
<td>1.1</td>
<td>3.2</td>
<td>2.2</td>
<td>2.9</td>
<td>1.60</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
</tr>
<tr>
<td>Chemical composition (% DM)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Crude protein</td>
<td>24.1</td>
<td>19.1</td>
<td>20.1</td>
<td>17.2</td>
<td>1.11</td>
<td>*</td>
<td>**</td>
<td>NS</td>
</tr>
<tr>
<td>Crude fibre</td>
<td>36.8</td>
<td>39.8</td>
<td>42.1</td>
<td>47.0</td>
<td>2.09</td>
<td>**</td>
<td>*</td>
<td>NS</td>
</tr>
<tr>
<td>Soluble carbohydrates</td>
<td>12.4</td>
<td>13.9</td>
<td>11.9</td>
<td>11.3</td>
<td>1.51</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
</tr>
<tr>
<td>Digestibility (OM)</td>
<td>79.3</td>
<td>77.0</td>
<td>77.7</td>
<td>75.2</td>
<td>1.07</td>
<td>†</td>
<td>*</td>
<td>NS</td>
</tr>
<tr>
<td>Energy (MJ ME/kg DM)</td>
<td>12.1</td>
<td>11.9</td>
<td>11.9</td>
<td>11.6</td>
<td>0.16</td>
<td>†</td>
<td>†</td>
<td>NS</td>
</tr>
</tbody>
</table>

Where † \( P<0.10 \); * \( P\leq0.05 \); ** \( P\leq0.01 \); *** \( P\leq0.001 \); SED, standard error of the difference.

Table 2: Dry matter (DM), N intake and milk yield results of dairy cows offered diploid or tetraploid ryegrass pastures at high or low pasture mass.

<table>
<thead>
<tr>
<th>Ploidy Mass</th>
<th>Diploid Low</th>
<th>Diploid High</th>
<th>Tetraploid Low</th>
<th>Tetraploid High</th>
<th>SED</th>
<th>P value</th>
<th>Ploidy</th>
<th>Mass</th>
<th>P x M</th>
</tr>
</thead>
<tbody>
<tr>
<td>DM intake (kg/d)</td>
<td>16.4</td>
<td>15.0</td>
<td>13.8</td>
<td>16.6</td>
<td>1.94</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
<td></td>
</tr>
<tr>
<td>N intake (g/d)</td>
<td>633</td>
<td>459</td>
<td>447</td>
<td>454</td>
<td>70.9</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
<td></td>
</tr>
<tr>
<td>Milk constituents</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Litres (kg/d)</td>
<td>17.0</td>
<td>15.6</td>
<td>16.0</td>
<td>16.1</td>
<td>0.64</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
<td></td>
</tr>
<tr>
<td>Solids (kg/d)</td>
<td>1.60</td>
<td>1.39</td>
<td>1.46</td>
<td>1.53</td>
<td>0.08</td>
<td>NS</td>
<td>NS</td>
<td>†</td>
<td></td>
</tr>
<tr>
<td>Fat (g/d)</td>
<td>922</td>
<td>794</td>
<td>841</td>
<td>869</td>
<td>46</td>
<td>NS</td>
<td>NS</td>
<td>†</td>
<td></td>
</tr>
<tr>
<td>Protein (g/d)</td>
<td>676</td>
<td>593</td>
<td>622</td>
<td>661</td>
<td>40</td>
<td>NS</td>
<td>NS</td>
<td>†</td>
<td></td>
</tr>
<tr>
<td>Fat (%)</td>
<td>5.48</td>
<td>5.11</td>
<td>5.36</td>
<td>5.43</td>
<td>0.27</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
<td></td>
</tr>
<tr>
<td>Protein (%)</td>
<td>4.02</td>
<td>3.80</td>
<td>3.87</td>
<td>4.11</td>
<td>0.18</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
<td></td>
</tr>
<tr>
<td>NUE milk</td>
<td>0.17</td>
<td>0.20</td>
<td>0.22</td>
<td>0.23</td>
<td>0.02</td>
<td>†</td>
<td>NS</td>
<td>NS</td>
<td></td>
</tr>
</tbody>
</table>

Where N use efficiency (NUE) is g milk N/g N intake; †, \( P<0.10 \); SED, standard error of the difference.
A modelling approach to screen grazeable forage options for automatic milking system herds

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ABSTRACT

The main objective of this study was to explore sustainable forage options tailored to automatic milking system (AMS) dairy farming using the Agricultural Production Systems Simulator (APSIM) model. Three basic simulation scenarios were undertaken using forage crops (namely maize, soybean and sorghum) for the spring-summer period. Subsequent crops in the three scenarios were forage rape over-sown with ryegrass. Each simulation (1 year) was run using actual climatic records for the period from 1900 to 2010. Simulated forage yields in maize, soybean and sorghum-based rotations were 28.2, 22.9 and 19.3 t DM/ha, respectively. Results indicate that APSIM can be used to assist in devising preferred grazeable forage options for AMS herds and may provide decision support during climatic uncertainty.

Keywords: forage options; forage rotations; APSIM; AMS; dairy.

INTRODUCTION

One of the challenges to increasing milk production in large pasture-based herds with an AMS is growing increased volumes of grazeable forages within a radius of approximately 1- km of the dairy. This is because increased walking distance is associated with undesirably long milking intervals (e.g. beyond 16 hours; Lyons N, unpubl. data) and reduced milk yield (Jago and Kerrisk 2011). Potential exists to minimize average walking distances if the yield of grazeable forages grown in close vicinity to the dairy can be increased by incorporating a complementary forage system (Garcia et al. 2008). The APSIM model is validated in simulating crop yields under various sowing management strategies (Keating et al. 2003). The main objective of this study was to screen potential combinations of grazeable forage options that could increase forage utilisation.

MATERIALS AND METHODS

The study site (Camden, NSW: 150.70°E, -34.05°S) has vertisol soil and an average annual rainfall of 737.7 mm. Three basic simulation scenarios (with irrigation) were undertaken over the years from 1900 to 2010 using maize, soybean or sorghum during spring (sowing dates in Table 1), with each followed by forage rape over-sown with ryegrass. Forage rape was sown on 15 February, 20 February and 1 May; a day after harvesting maize, soybean and sorghum, respectively. The ryegrass over-sown with forage rape on 28 April and 1 May in maize and soybean treatments, respectively, was planted after one grazing of forage rape, but sown at the same time as forage rape on 1 May in sorghum treatment. Final harvest of forage rape-ryegrass was made one day before sowing the next crop in spring (Table 1). Long term average values of monthly simulated growth rate (kg/ha/day) for each forage were used to calculate total simulated forage yield (Table 1). There were 56 neutral (normal), 29 La-Niña (typically wetter than average) and 26 El-Niño (typically drier than average) years in the time period. Data dispersion among years or differences due to climate was used for risk assessment or probability of not achieving a certain target.

RESULTS

The rotation of grazing maize was the highest yielding of the screened forage options (Table 1). Standard deviations (based on 111 years) indicate that under non-limiting nitrogen fertilizer and irrigation the yield differences between years were minimal. The most critical periods when forage supply may not be available using these rotations were approximately two months immediately after sowing of summer forages and similarly two months after sowing of forage rape. Irrigation requirement increased by up to 18, 16 and 17% in maize, soybean and sorghum-based rotations in El-Niño years compared with neutral years, and decreased by up to 8, 7 and 13% respectively in La-Niña years compared with neutral years.
Table 1: Simulated forage yields (t DM/ha) in rotations of maize, soybean and sorghum sown in summer followed by forage rape over-sown with ryegrass

<table>
<thead>
<tr>
<th>Rotations</th>
<th>Simulated sowing of spring crop</th>
<th>Simulated forage yields (t DM/ha)</th>
<th>Total forages (t DM/ha/yr.)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Maize (M)-based</td>
<td>10 Oct</td>
<td>12.4</td>
<td>15.8</td>
</tr>
<tr>
<td>Soybean (S)-based</td>
<td>15 Oct</td>
<td>9.5</td>
<td>8.3</td>
</tr>
<tr>
<td>Sorghum (Sg)-based</td>
<td>1 Nov</td>
<td>10.2</td>
<td>4.6</td>
</tr>
</tbody>
</table>

DISCUSSION AND CONCLUSION

The APSIM model assisted in identifying preferred forage options to potentially maximise grazeable forage yield in close vicinity of the AMS dairy. This in turn could allow for a reduction in the average daily distance walked by cows, resulting in a reduced incidence of undesirably long milking intervals, which may, in turn, result in increased milk production per cow. Ultimately this may also help to reduce purchased feed and cost of production. Yield variability of the simulated forages in the rotations were minimal between years under non-limiting inputs, but irrigation water requirements were higher in El-Niño years compared with La-Niña and neutral years. Our analyses also indicate that simulation analysis may provide assistance in decision support by identifying optimal periods for forage supply and critical periods when alternative forages are needed. In addition, simulation analysis may provide decision support under climatic uncertainty. Further work should be conducted regarding the ideal proportion of forages and pastures on the wider farm and herd. This would ensure that a more comprehensive understanding of the full system is developed including diet balancing and the need for supplementary feeds.

ACKNOWLEDGEMENTS

We acknowledge funding from Dairy Australia, Department of Primary Industries, NSW, University of Sydney, and DeLaval.

REFERENCES


Comparison of ruminal pH of dairy cows consuming wheat-grain or maize-grain based diets

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ABSTRACT

Measurements of rumen pH in dairy cattle have demonstrated a diurnal pattern in response to feeding. Intra-ruminal boluses were used to measure ruminal pH in eight dairy cows fed a wheat based diet for 4 weeks and a corn based diet for 4 weeks in a randomised cross-over sequence. Boluses were deployed in each cow during the last week on each diet. The mean rumen pH for cows fed a wheat-grain based diet (5.9) was lower ($P = 0.008$) than for cows fed a maize-grain based diet (6.1). The area below pH 6 was 353 pH.min per day for cows fed wheat but only 47 pH.min per day for cows fed maize. Our findings suggest that the mean pH alone does not reveal a lot about rumen fermentation. However, examination of the diurnal patterns of ruminal pH may indicate the mechanisms whereby pH influences digestion, production and health of dairy cows.

Keywords: diurnal rumen pH; intra-ruminal bolus; dairy cattle.

INTRODUCTION

Research has demonstrated a diurnal pattern in rumen pH in response to feeding (Wales and Doyle, 2003). A low nadir in ruminal pH (<5.5) and extended periods of pH less than 6 have been used as indicators of subacute ruminal acidosis (Dohme et al. 2008).

The objective of this work was to measure variation in ruminal pH of dairy cows fed wheat-grain and maize-grain based diets.

MATERIALS AND METHODS

Eight multiparous, Holstein-Friesian cows, fitted with rumen cannula (110 mm internal diameter; Rumen Cannula, www.rumencannula.com), were offered a wheat-based diet for 4 weeks and a corn-based diet for 4 weeks in a crossover sequence experiment at the Department of Primary Industries, Ellinbank, Victoria, Australia (38°14' S, 145°56' E).

Cows were offered a common amount of lucerne hay (10 kg DM/day) and cold pressed canola (2 kg DM/day) supplemented with either wheat grain (10 kg DM/day) or maize grain (10 kg DM/day). Equal quantities of feed were offered at 0630 and 1530 hours, immediately after milking.

Eight pH-recording boluses (KB5, Kahne Limited, Auckland, New Zealand) were deployed after calibration in accordance with the manufacturer’s instructions on the day of insertion into the rumen and floated freely within the rumen. Boluses were deployed in each cow during the last week on each diet and were set to record 1 pH measurement every 2 minutes.

Mean pH, duration below pH 6.0 and area below pH 6.0 were calculated for each cow on each diet. The daily pH pattern was obtained by averaging all records for each cow, for each diet, in 2 minute intervals. Area below pH 6.0, a function of the time and extent to which pH was below 6.0, was calculated as the area bounded by the line of measured pH and the line pH = 6.0. Statistical calculations were by analysis of variance.

RESULTS

Mean ruminal pH of cows fed the wheat-grain based diet was less than that on the maize-grain based diet (Table 1). Diurnal range in ruminal pH was greater in cows fed the wheat diet than the maize diet (Figure 1) and pH was below 6.0 for longer with the wheat than the maize-based diet. The difference between diets was even greater when the area below pH 6 was compared (Table 1).

Table 1: Rumen pH characteristics of cows fed wheat- or maize-based diets, averaged over 46 cow-days of measurement for each diet

<table>
<thead>
<tr>
<th>Diet</th>
<th>Wheat</th>
<th>Maize</th>
<th>SED</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of cows</td>
<td>7</td>
<td>8</td>
<td></td>
<td>-</td>
</tr>
<tr>
<td>Mean pH</td>
<td>5.9</td>
<td>6.1</td>
<td>0.04</td>
<td>0.008</td>
</tr>
<tr>
<td>Mean duration pH below 6.0 (min/day)</td>
<td>906</td>
<td>435</td>
<td>104.5</td>
<td>0.006</td>
</tr>
<tr>
<td>Mean area below pH 6 (pH.min/day)</td>
<td>353</td>
<td>47</td>
<td>28.7</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>
**Figure 1:** Average daily pH pattern for 8 cows fed wheat (- -) and maize(–) based diets, determined from 46 cow-days of measurements for each diet.

**DISCUSSION AND CONCLUSION**

While the means of ruminal pH on the wheat-grain and maize-grain based diets were slightly but significantly different, the pH patterns were markedly different (Figure 1). Wheat has a faster degradation rate than maize (Herrera-Saldana et al. 1990) and this difference is thought to be reflected in the diurnal pattern of ruminal pH.

The pattern of ruminal pH has implications for infrequent or single sampling for pH measurement, and dietary effects differ over the day. Logging ruminal pH at frequent intervals reveals the complete diurnal pattern and shows that mean pH alone will not reveal a lot about rumen fermentation. However, the diurnal patterns of rumen pH suggest quite different rates of rumen fermentation for each diet.

**ACKNOWLEDGEMENTS**

This investigation was part of a project funded by Dairy Australia, Meat and Livestock Australia, the Victoria Department of Primary Industries, and the Australian Government Department of Agriculture, Fisheries and Forestry under its Australia’s Farming Future Climate Change Research Program. This work would not have been possible without the contribution of the technical staff at Department of Primary Industries – Victoria, Ellinbank Centre.

**REFERENCES**


Can diverse pasture mixtures reduce nitrogen losses?
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DairyNZ, Private Bag 3221, Hamilton 3240, New Zealand

ABSTRACT
In March 2012 an indoor trial compared intake, milk yield and composition, and nitrogen (N) partitioning to milk, urine and faeces in dairy cows fed either perennial ryegrass/white clover pasture (Rye) or mixed pasture which also contained chicory, plantain and lucerne (Mix). Dietary N content of the Mix was lower than the Rye pasture (crude protein 15.0 vs 18.6% total DM). Milk yield (12.5 vs 11.3 kg/cow/day; SED=0.2) and the percent of daily N intake allocated to milk (23 vs 15%; SED=1) were higher in cows fed Mix pasture. Urinary N concentration was lower in cows fed Mix (0.26 vs 0.62%; SED=0.02), but volumes were similar so urinary N output from cows fed Mix pasture was half that from cows fed Rye (100 vs 200 g N/cow/day; SED=4). The lower N content of the Mix pasture resulted in only 29% of dietary N in the urine of cows fed Mix compared with 43% (SED=1) in the Rye cows. Use of mixed pastures on-farm could therefore reduce N losses without negative impacts on milk production.

Keywords: dairy cow; mixed pasture; ryegrass; chicory; plantain; lucerne; milk yield; nitrogen partitioning.

INTRODUCTION
New Zealand's dairy industry has been traditionally based on perennial ryegrass/white clover pastures. Only a small proportion of ingested feed nitrogen (N) is removed from the farm system in animal products, with 60-80% deposited in urine and faeces (Waghorn et al. 2007). Urinary N is more volatile than faecal N and is largely in the form of urea which is mineralised to ammonium (NH₃) and nitrate (NO₃). Urinary N is vulnerable to leaching into groundwater and also accounts for about 60% of nitrous oxide (N₂O) emissions from pasture (Pacheco and Waghorn, 2008). Growth of dairying into regions with more extreme climatic and environmental challenges has highlighted a case for using more diverse, mixed pastures in future farm systems. The ultimate aim is to have a diverse forage mix providing a more uniform, year round supply of pasture that persists under normal grazing pressure, moisture stress and insect attack, and at the same time reduces N losses to the environment, while remaining profitable.

MATERIALS AND METHODS
Standard perennial ryegrass (Lolium perenne) white clover (Trifolium repens) pastures and mixed pastures which contained ryegrass/white clover as well as chicory (Cichorium intybus), plantain (Plantago lanceolata) and lucerne (Medicago sativa) were sown in March 2010 at DairyNZ’s research farm in Hamilton. In early March 2012, 16 (8 twinsets) multiparous, late-lactation Holstein-Friesian dairy cows were housed in individual metabolism stalls for 10 days and fed either Rye (51% ryegrass, 17% white clover, 2% other grass, 12% weeds, 18% dead) or Mix (11% ryegrass, 5% white clover, 38% chicory, 28% plantain, 15% lucerne, 1% weeds, 2% dead) pasture. The impact of mixed pasture on dry matter intake (DMI), milk yield and composition, and N partitioning within the cow were measured over the final 5 days. Means, standard error of difference (SED) and the significance (p value) of each variate were analysed including cow twinset as a blocking factor and treatment as a fixed effect.

RESULTS AND DISCUSSION
Mix pasture had lower DM (15.9 vs 19.9%), crude protein (15.0 vs 18.6% total DM) and neutral detergent fibre (31.7 vs 40.1% total DM) contents, but a higher predicted metabolisable energy (ME) concentration (10.9 vs 10.2 MJ/kg DM) than Rye. Cows fed Mix pasture had lower DMI and this, combined with the nutritional differences between pasture diets meant the N intake of cows fed Mix pasture was only 75% of cows fed Rye pasture (Table 1). However predictions using the Cornell Net Carbohydrate and Protein System model (CNCPS v6.1.39) indicated energy and protein intakes of cows on both pasture treatments were above requirements for their level of milk production.

Although estimated daily ME intakes of cows fed Mix and Rye pasture were similar (159 vs 161 MJ/cow/day), milk yield was higher on the Mix pasture (Table 1) which may have been due to differences in efficiency of energy utilisation of the respective diets, or to the estimation of their ME concentrations. Milk protein concentration was also higher from cows fed Mix pasture, so daily milk N output and the proportion of N intake partitioned to milk were higher compared to cows fed Rye pasture (Table 1). Similarly (Woodward et al. 2009) showed that increasing the amount of condensed tannin-containing birdsfoot trefoil in cows’ diets increased partitioning of N intake to milk but this was only due to increased milk yield and not an increase in milk protein concentration.
There were no differences in faecal N concentration in the DM or faecal N output, but cows fed Mix pasture partitioned more of their N intake to faeces than cows fed Rye (Table 1).

The major difference between diets was the lower urinary N concentration from cows fed Mix pasture (Table 1). This decrease could have been due to a number of interrelated factors especially the lower DM content and N concentration in the DM of the Mix pasture. N digestibility was lower in the Mix (61%) than the Rye (68%) pasture, and because the N intake was lower on the Mix pasture, less N was available for milk and urine production. Consequently, urinary N output from cows fed Mix pasture was half that of the cows fed Rye and they allocated a much lower percentage of their N intake to urine (Table 1). Pacheco and Waghorn (2008) showed that as the daily N intake of cows fed pasture (with 85% N rumen degradability and 12 MJ ME/kg DM) is increased above 300 g N/cow/day there is a rapid rise in urinary N excretion, relative to output in milk or faeces. This experiment showed clear opportunities for improving N use efficiency and reducing urinary N output by feeding mixed pasture to dairy cows.

**CONCLUSION**

These results show dairy farmers could include mixed pastures within pasture based systems and reduce N losses without negative impacts on milk production. Substantial gains could be made in farm sustainability provided mixed pastures did not reduce DM yields or increase the cost and complexity of farm management.

**ACKNOWLEDGEMENTS**

Assistance from DairyNZ farm and technical staff and statistical analyses by Barbara Dow were appreciated. Funding was provided by the Ministry of Science and Innovation.

**REFERENCES**


<table>
<thead>
<tr>
<th>Table 1: Measurements of daily intake (DMI), milk yield and composition, nitrogen (N) concentration in faeces and urine, N outputs and partitioning of N intake (% of total N intake) in dairy cows fed either ryegrass-based (Rye) or mixed species (Mix) pasture. Values are the means for each group of 8 cows during the 5 day measurement period.</th>
<th>Pasture Treatment</th>
<th>SED</th>
<th>$P$ value</th>
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<tbody>
<tr>
<td>Measurement</td>
<td>Mix</td>
<td>Rye</td>
<td>**</td>
</tr>
<tr>
<td>DMI (kg DM/cow/day)</td>
<td>14.6</td>
<td>15.8</td>
<td>0.3</td>
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<tr>
<td>Milk yield (kg/cow/day)</td>
<td>12.5</td>
<td>11.3</td>
<td>0.2</td>
</tr>
<tr>
<td>Milkfat (%)</td>
<td>5.33</td>
<td>5.34</td>
<td>0.08</td>
</tr>
<tr>
<td>Milk protein (%)</td>
<td>4.03</td>
<td>3.84</td>
<td>0.04</td>
</tr>
<tr>
<td>Milksolids yield (kg/cow/day)</td>
<td>1.16</td>
<td>1.03</td>
<td>0.02</td>
</tr>
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<td>Feed N intake (g N/cow/day)</td>
<td>350</td>
<td>466</td>
<td>7</td>
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<td>Milk N output (g N/cow/day)</td>
<td>79</td>
<td>68</td>
<td>2</td>
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<tr>
<td>Faecal N concentration (%)</td>
<td>2.83</td>
<td>2.84</td>
<td>0.02</td>
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<tr>
<td>Faecal N output (g N/day)</td>
<td>136</td>
<td>151</td>
<td>7</td>
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<tr>
<td>Urinary N concentration (%)</td>
<td>0.26</td>
<td>0.62</td>
<td>0.02</td>
</tr>
<tr>
<td>Urinary N output (g N/day)</td>
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<td>200</td>
<td>4</td>
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<td>Partitioning of feed N intake (%)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Milk</td>
<td>23</td>
<td>15</td>
<td>1</td>
</tr>
<tr>
<td>Faeces</td>
<td>39</td>
<td>33</td>
<td>1</td>
</tr>
<tr>
<td>Urine</td>
<td>29</td>
<td>43</td>
<td>1</td>
</tr>
<tr>
<td>Retained</td>
<td>9</td>
<td>9</td>
<td>1</td>
</tr>
</tbody>
</table>
Effect of turnip supplementation on grazing behaviour, milk yield and composition in late lactation dairy cows

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ABSTRACT

Although commonly grown as part of a pasture renovation program, turnips (Brassica rapa L.) provide forage for grazing during the summer period, where quantity and nutritive value of perennial ryegrass pasture is insufficient to meet the requirements of lactating dairy cows. Turnips are reported to increase milk yield, but decrease the concentration of milk fat. A study was conducted to investigate milk production response and animal behaviour associated with feeding a pasture based summer diet supplemented with turnips and whole crop silage, compared to a more traditional pasture based diet supplemented with hay and pasture silage. The turnip supplemented diet was associated with an increase (P<0.001) in milk yield from 20.6 to 23.0 kg/head/day. Milk solids and milk protein concentration also increased (P<0.05). There was no difference in milk fat concentration. On average, turnip utilisation was 66% of feed offered, with intake averaging 4.5 kg DM/head/day. Turnips can provide a source of forage to increase milk yield over summer, however consideration needs to be given to the area grown, and provision of NDF supplements to avoid milk fat depression.

Keywords: Turnip; dairy cow; late lactation; milk yield; milk fat; milk protein; grazing behaviour.

INTRODUCTION

The majority of Australian dairy enterprises in southern Australia experience a ‘summer feed gap’, where the nutritive value and quantity of summer pasture is insufficient to meet nutritional requirements of high producing cows (Stockdale et al. 1997). Purchasing supplementary feeds is expensive and adds to cost of production. Home-grown forage crops offer a relatively cheap alternative to traditional supplements such as hay, silage and grain (Stockdale et al. 1997). Traditionally, turnips (Brassica rapa L.) have been grown as a summer crop as part of pasture renovation, rather than specifically to provide forage for grazing (Notman 1994). Turnips are of high yield and quality for summer feeding therefore have potential to be useful as a summer supplementary feed for lactating dairy cows (Moate et al. 1998). This study aimed to investigate milk production response to inclusion of turnips in the diet of late lactation dairy cows.

MATERIALS AND METHODS

An experiment was conducted near Terang in southwest Victoria (142°5’E, 38°16’S) to measure milk production in summer when cows were offered turnips as part of the diet compared to ryegrass pasture with typical forage supplements. The experiment was a two period study; a 21 d covariate period, followed by a 28 d measurement period. Seventy-two Holstein cows in late lactation (> 250 DIM, 558 ± 9 kg LWT, 4.5 ± 0.1 BCS) were offered one of two experimental rations; one a predominantly ryegrass pasture based diet, supplemented with pasture silage and both lucerne and pasture hay (control) and the other a pasture based diet, supplemented with whole crop triticale cereal silage and turnips (turnip). Both treatments were additionally supplemented with concentrate, fed twice daily during milking. The full allowance of turnips (5.5 kg DM/cow per day) was introduced over 10 d, starting at an allowance of 2 kg DM/d.

FEED INTAKE

Intakes of whole crop silage, pasture hay and lucerne hay were recorded daily throughout the experiment. Pasture intake was determined by measuring pre and post grazing mass using a calibrated rising plate meter. Turnip intake was measured by cutting 3 x 1 m² quadrats pre and post grazing. Utilisation of the turnip crop over the grazing period during grazing was measured by cutting additional quadrats at one and two hours into the daily turnip allowance. It was assumed that the full allocation of grain was consumed daily.

MILK PRODUCTION

Milk yield was recorded automatically using ALPRO milk meters for individual cows at each milking. Milk fat, protein, lactose and somatic cell count was determined using standard herd test methods on day 10 of the experimental period.
GRAZING BEHAVIOUR

A time budget was produced for when the cows were grazing turnips, in order to provide information on utilisation over the allocation period. Behaviour of 6 cows was recorded at 5 min intervals on three occasions during the experimental period, for the duration of turnip allocation (generally between 1100 and 1400 hours). Behaviour was recorded in 6 distinct categories; grazing, ruminating, lying, drinking, idle and other.

STATISTICAL ANALYSIS

Milk yield data (measured daily) was analysed using REML, with day and treatment as factors. The remaining data were analysed using ANOVA (Genstat v.9, VSN International). A shewhart chart approach was used to determine when differences in milk volume between the two treatments became significant on a time scale. In this approach the chart shows a signal (significant difference) whenever an average value falls outside set limits (Hunter 1989, Shewhart and Deming 1939), in this case, outside two standard deviations from the mean.

RESULTS

Feed intake

Dry matter intakes (DMI) of feeds are shown in Table 1. Mean DMI of turnips was 4.95 ± 1.1 kg DM/head (90% of the target intake). Total DMI (kg DM/cow/day) on the turnip diet was greater than the control diet. The pasture treatment was offered 3.5 kg DM/head/day of perennial ryegrass pasture and consumed 3.0 kg DM/head/day. Cows on the turnip treatment were offered 3 kg DM/head/day of perennial ryegrass pasture, consuming an average of 2.5 kg DM/head/day.

Table 1: Average intake (kg DM/cow per day), dry matter (DM), crude protein (CP), neutral detergent fibre (NDF) (g/kg DM) and estimated metabolisable energy (MJ/kg DM) of feeds

<table>
<thead>
<tr>
<th>Treatments</th>
<th>Control Kg DM/day</th>
<th>Turnip Kg DM/day</th>
<th>Nutritive Value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>DM</td>
</tr>
<tr>
<td>Pasture</td>
<td>3.0</td>
<td>2.5</td>
<td>447</td>
</tr>
<tr>
<td>Concentrate</td>
<td>5.3</td>
<td>5.3</td>
<td>898</td>
</tr>
<tr>
<td>Pasture Silage</td>
<td>5.3</td>
<td>-</td>
<td>338</td>
</tr>
<tr>
<td>Whole crop silage</td>
<td>-</td>
<td>6.9</td>
<td>547</td>
</tr>
<tr>
<td>Pasture Hay</td>
<td>2.45</td>
<td>-</td>
<td>902</td>
</tr>
<tr>
<td>Lucerne Hay</td>
<td>2.45</td>
<td>-</td>
<td>867</td>
</tr>
<tr>
<td>Turnip</td>
<td>-</td>
<td>5.0</td>
<td>194</td>
</tr>
<tr>
<td>Total</td>
<td>18.4</td>
<td>19.6</td>
<td></td>
</tr>
</tbody>
</table>
DISCUSSION AND CONCLUSION

The estimated utilisation efficiency of turnip recorded was considerably lower than that from other studies where utilisation of between 80% and 95% of available DM has been reported (Moate et al. 1999, White et al. 1999). (Moate et al. 1999) offered turnips to stall fed and grazing dairy cattle for 4 hours (stall fed) and 3.5 hours (grazing) which may have allowed greater intake than observed in the current study. The high utilisation reported by (Moate et al. 1999) reflects the stall fed animals. The cows in this experiment were offered 7.5 kg DM of turnip, with a target intake of 5.5 kg DM and capacity to eat more according to the utilisation rates cited above. The low utilisation observed may indicate that 5 kg DM is the maximum voluntary intake of turnip crops, as suggested by (Moate et al. 1998). However, total feed allowance in both the control and turnip treatments was sufficient to meet both production and maintenance requirements; therefore drive for further consumption of the forage may have been reduced.

Decline in time spent grazing and lower than predicted utilisation may be related to the method of feeding used in the experiment, whereby cows were offered turnips straight after access to the feed pad, where they consumed an average of 6.9 kg DM of whole crop silage (598 g/kg DM NDF) on the feed pad, which potentially reduced capacity for further intake over the allocation period. A longer allocation period may have enabled cows to consume more turnips, following a period of rumination. Gut fill due to consumption of a high NDF feed (such as the whole crop silage) limits intake due to distension of the rumen and slow rate of passage through the gastrointestinal tract. A period of rumination would help alleviate fill, increase rate of passage and allow further intake (Beauchemin and Yang 2005).

The increase in milk production from the turnip system cows can be potentially attributed to two aspects of the diet, NDF and soluble carbohydrate content. Average NDF intake of cows on the turnip rations was lower than cows fed the control ration (Table 1), presumably due to the lower NDF of the turnips relative to the supplements provided in the control system. This would enable increased intake (consistent with observations) and the increase in energy consumption (Table 1). Further, (Moate et al. 1998) report that turnips contain high levels of readily fermented carbohydrates. Potentially, soluble carbohydrates and starch in turnips are likely to result in increased production of propionate and therefore lactose; the major determinant of milk volume (Walker et al. 2004).

The increase in milk yield in turnip fed cows became significant (using a shewhart chart approach (Hunter 1989, Shewhart and Deming 1939) 15 days after turnips were first offered. This delay in response is typical when concentrates or supplements are introduced to the diet, due to changes in rumen microflora and changes to grazing behaviour (Van Soest 1994, Kellaway and Harrington 2004). This ‘lag’ period before the increase in milk production becomes significant highlights the importance of correct agronomy to achieve high DM yields of turnip crops. Low yields and/or insufficient area of crop could prevent a significant response and may limit the economic benefit of growing turnips (Jacobs et al. 2001).

Milk solids production in turnip-fed cows increased by 0.24 kg per cow per day compared with control cows, similar to the responses observed by (Clark et al. 1996, 1997) and (Harris et al. 1998). There is a perception that turnip feeding decreases milk fat concentration (as with other highly digestible supplements) due to the low NDF content and decreased acetic acid production (Notman 1994, 2004).
Moate et al. 1998). This is not confirmed by the results of this study; turnip feeding did not have a significant effect on milk fat concentration. However, the turnip ration contained about 35% NDF, which is unlikely to impact milk fat concentration. The composition of the remainder of the ration should be considered in order to maintain NDF content and avoid milk fat depression. Potentially, the timing of turnip allowance, following access to whole crop silage, may also have helped to provide an NDF “buffer” during turnip grazing.

Turnips can provide feed of adequate nutritive value to increase milk solids production over summer. However, there is a requirement for growing sufficient areas of forage and careful management to ensure high yielding crops, providing sufficient feed to increase maintain milk production and potentially increasing milk protein output.

REFERENCES


Higher sowing rate increases the proportion of annual ryegrass \((Lolium multiflorum)\) in an irrigated mixed pasture with kikuyu \((Pennisetum clandestinum)\)

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Department of Agriculture, Fisheries and Forestry (DAFF)

ABSTRACT

The subtropical environment of Queensland is conducive to the growth of temperate and tropical plant species, but managing both within a mixed pasture to achieve the optimum balance between yield and forage quality is challenging. This study aims to evaluate establishment options of annual ryegrass \((Lolium multiflorum)\) oversown into kikuyu \((Pennisetum clandestinum)\) to increase the relative yield of ryegrass compared to kikuyu. A replicated plot experiment was undertaken in southeast Queensland on an established kikuyu pasture. Twelve treatments were laid out as a complete factorial; the main treatments imposed were a medium and a late maturing ryegrass cultivar, three ryegrass plant densities \((0, 500, 1200 \text{ plants/m}^2)\) and pre-planting application with glyphosate. Results on completion of the sampling period showed ryegrass yield was significantly higher \((P<0.05)\) in swards planted at the highest ryegrass density with 6256 kg dry matter \((\text{DM})/\text{ha}\). Treatments did not differ \((P>0.05)\) in terms of total DM yield because of compensatory growth by kikuyu.

Keywords: kikuyu; ryegrass; oversowing.

INTRODUCTION

A mixed pasture containing the tropical grass kikuyu oversown with annual ryegrass has the potential to produce large amounts of DM yield suitable for milk production throughout the year (Botha et al. 2008). However, during the warmer months in particular the stoloniferous growth habit of kikuyu provides a competitive advantage for light and ground cover compared to ryegrass, which in turn decreases the overall nutritive value of the pasture. This study aimed to increase the yield of ryegrass relative to kikuyu by evaluating a range of establishment options.

MATERIALS AND METHODS

A replicated plot experiment was undertaken at Gatton in southeast Queensland on an established kikuyu pasture grazed by dairy cattle. Twelve treatments were laid out as a complete factorial and replicated three times. Plots were planted on 14 April 2011, the treatments included two tetraploid ryegrass cultivars (medium and late maturing), three target ryegrass plant densities \((0, 500, 1200 \text{ plants/m}^2)\) and pre-planting application with glyphosate \((\text{nil, 0.7 L/ha})\). Plots were mechanically defoliated to a residual height of 5 cm at every 2.5-3 ryegrass leaf stage. In total, plots were defoliated 7 times between June 2011 and 20 December 2011. Subsamples of the harvested material were sorted and dried to determine botanical composition and DM content. Results were analysed by performing ANOVAs for each of the seven individual harvests using GenStat. The range in variance was shown by standard deviation.

RESULTS

Total ryegrass yield on completion of the sampling period was significantly higher \((P<0.05)\) in swards planted at 1200 plants/m² with 6256 kg DM/ha compared to 4563 kg DM/ha for swards planted at the lower density (Table 1). This occurred because the ryegrass yield in the high density swards in July, September and October was significantly greater \((P<0.05)\) than those obtained from the low density swards. Similarly, total sward yields planted at the high ryegrass density in July and September were greater \((P<0.05)\) than total sward yields in the low density swards. There was minimal difference in the total yield at completion of the ryegrass season. On 9 November and 2 December plots with no ryegrass recorded significantly higher \((P<0.05)\) total sward yield. Application of glyphosate and the ryegrass cultivar did not significantly affect ryegrass yield \((P>0.05)\), therefore data are not presented.
Table 1: Dry matter yields of the total sward and ryegrass at each harvest (comparison of means is within harvest date and sward). Different superscript letters indicate significant difference between values ($P<0.05$).

<table>
<thead>
<tr>
<th>Target plant density (plants/m²)</th>
<th>Harvest date</th>
<th>1 Jun</th>
<th>13 Jul</th>
<th>1 Sep</th>
<th>11 Oct</th>
<th>9 Nov</th>
<th>2 Dec</th>
<th>20 Dec</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total sward</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>0</td>
<td></td>
<td>1047</td>
<td>294a</td>
<td>661a</td>
<td>2627a</td>
<td>4451c</td>
<td>2037b</td>
<td>747a</td>
<td>11863</td>
</tr>
<tr>
<td>500</td>
<td></td>
<td>1123</td>
<td>327a</td>
<td>929b</td>
<td>3618b</td>
<td>3919b</td>
<td>1533a</td>
<td>822b</td>
<td>12271</td>
</tr>
<tr>
<td>1200</td>
<td></td>
<td>1136</td>
<td>464b</td>
<td>1224c</td>
<td>3709b</td>
<td>3537a</td>
<td>1395a</td>
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<td>387</td>
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<td>203</td>
<td>82</td>
<td>815</td>
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<td></td>
<td></td>
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<td></td>
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<td>71</td>
<td>285a</td>
<td>1979a</td>
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<tr>
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<td></td>
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<td>168b</td>
<td>684b</td>
<td>2664b</td>
<td>2429</td>
<td>271</td>
<td>10b</td>
<td>6256b</td>
</tr>
<tr>
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<td>33</td>
<td>144</td>
<td>780</td>
<td>495</td>
<td>172</td>
<td>41</td>
<td>1065</td>
</tr>
</tbody>
</table>

DISCUSSION AND CONCLUSION

More than doubling the ryegrass planting rate resulted in the highest ryegrass yield during winter and early spring. By late spring, ryegrass yield between the 500 and 1200 plants/m² were very similar, presumably because the density of ryegrass tillers reached a stable population. Total sward yield did not differ on completion of the sampling period because of the compensatory growth from kikuyu in swards with decreased ryegrass content. Similarly, (Botha et al. 2008) found that the oversowing of ryegrass into kikuyu had no impact on kikuyu production in autumn and summer. Interestingly, pre-planting application of glyphosate and ryegrass cultivar had minimal effect on ryegrass yield, suggesting that the growth of kikuyu was not inhibited sufficiently by the application of herbicide and that both cultivars competed equally with the kikuyu. This study has demonstrated that the yield of ryegrass oversown into kikuyu can be increased by targeting a high initial plant density.

ACKNOWLEDGEMENTS

The authors would like to thank Dairy Australia for making this study possible.

REFERENCES

Ruminal fluid pH patterns and whole tract digestibility of maize-based mixed rations compared to wheat grain and pasture silage fed separately to lactating pasture-fed dairy cows

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ABSTRACT

Feeding high amounts of cereal grain to grazing dairy cows in the dairy can increase variations in rumen fluid pH leading to impaired fibre digestion and reduced milk production. An experiment was conducted in grazing dairy cattle to compare the whole tract digestibility and daily patterns of ruminal fluid pH when offered either a maize-based partial mixed ration (PMR) or wheat grain and pasture silage fed separately (Control). Cows fed PMR had less daily variation in ruminal fluid pH, ruminal fluid pH below 6.0 for fewer hours per day, and a higher mean daily pH compared to Control cows. The more stable daily pattern of ruminal pH of cows fed the PMR diet was not associated with any increase in whole tract digestibility.

Keywords: digestibility; partial mixed ration; rumen fermentation; dairy cow; pasture.

INTRODUCTION

Feeding high amounts of supplements to grazing dairy cows as a mixed ration on a feed pad after milking may offer benefits over traditional supplementation strategies. A recent study in Victoria (Auldist et al. 2012; unpublished data) showed that dairy cows grazing a restricted pasture allowance and offered 12 kg DM/cow/d of PMR containing lucerne, wheat grain, maize grain and maize silage had higher milk production responses than cows offered equivalent amounts of supplementary energy as wheat grain in the dairy and pasture silage in the paddock. These authors suggested that one factor responsible for the increased milk response was that the maize in the PMR provided a source of starch that digested more slowly than the wheat, which may have led to a more stable rumen pH, improved efficiency of digestion in the rumen, and greater whole tract dry matter digestibility (DMD) of the diet. The current experiment was conducted to test these hypotheses.

MATERIALS AND METHODS

An experiment was conducted in spring using 14 rumen-fistulated dairy cows. Dietary treatments (n=7) were: Control, 8kg DM/cow/d freshly cut perennial ryegrass pasture, 8.8 kg DM/cow/d milled wheat grain and 3.2 kg DM/cow/d ryegrass pasture silage; and PMR, 8kg DM/cow/d cut ryegrass pasture and 12 kg DM/cow/d PMR (20% maize grain, 31% maize silage, 37% wheat grain, 12% lucerne hay). Both diets were formulated to provide the same amount of ME. Following a 5-d adjustment period, feed DM intake and faecal DM output was measured daily for 5 d. Average values were used to calculate apparent whole tract DMD for each diet. Ruminal fluid pH was measured via the fistula every 2 h over a 24-h period on the second day of the 5 day measurement period.

RESULTS

Cows offered PMR had ruminal fluid pH that was below 6.0 for less time per d than the Control cows (Figure 1). This did not result in a greater DMD in the PMR cows (72.9%) compared to the control cows (75.7%).

Figure 1: Daily patterns if ruminal fluid pH of cows offered the Control (■) and PMR (□) diets. Data points represent means of 7 cows per diet measured every 2 hours over a 24 hour period.

DISCUSSION AND CONCLUSION

In this experiment, two high supplement diets of differing composition fed in different ways (traditional ‘slug’ feeding vs maize-based PMR) were compared. A proportion of the wheat grain in the PMR diet was replaced with maize grain and maize silage, which is a more slowly digestible source of starch. As expected, there was a higher and less variable ruminal pH (Figure 1) in the PMR cows, possibly due to slower starch degradability and therefore less opportunity for the build up of
volatile fatty acids. In ruminants, fibre digestion is comprised at ruminal fluid pH of below 6.0 (Leddin et al. 2009), therefore, it was expected that there would be an improvement in the DMD of the diet of the PMR cows. However, whole tract DMD in the PMR cows was not greater than the Control cows in this experiment. It is concluded that the increased ruminal pH induced by feeding a maize-based PMR when compared to slug feeding wheat grain was measureable but did not result in a significant effect on DMD.

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Cockchafer Distribution, Species Diversity and Seasonal Abundance in Gippsland, Victoria – Preliminary Findings

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ABSTRACT

Red Headed Cockchafer (RHC) Adoryphorus couloni (Bermeister) is a native pest of ryegrass-based cattle pastures in South Eastern Australia. Detection is often only after extensive plant damage occurs, with the predominant management technique then being to remove and re-sow pasture. Other cockchafers such as African Black Beetle Heteronychus arator (Fabricius) and Black Headed Cockchafer Acrossidius tasmaniae Hope (Aphodius tasmaniae) may occur simultaneously, and the influence of soil characteristics on their distribution is also unknown. Understanding this influence on cockchafer distribution could lead to improved early detection and targeted management of these pests. In a preliminary 2011 study three regions in Gippsland, Victoria were surveyed using manual soil sampling and proximal sensing techniques to investigate any association between soil electrical conductivity (a widely-used surrogate indicator of soil texture, moisture content and/or salinity) and above-ground pasture biomass and the spatial distribution of cockchafer in dairy paddocks; to quantify the relative abundance of each species in the three regions; and to collect preliminary data to determine seasonal distribution of cockchafer life-stages in each region. Results indicated that not all species were found together in all regions, and that a potential link between soil characteristics and cockchafer distribution may exist. It also highlighted that detailed population dynamics studies are a fundamental prerequisite for optimising control on-farm. This research forms part of an ongoing 3-year study (2011-2014).

INTRODUCTION

Red Headed Cockchafer (RHC) Adoryphorus couloni (Bermeister) is a native pest of ryegrass-based pastures in South Eastern Australia, where establishment in dairy systems is costing each affected producer up to $200 000 per year in lost production (Cows, cookies and cockchafers n.d.). Detection usually occurs after extensive plant damage, and anecdotal evidence suggests that soil characteristics, moisture and vegetation may influence RHC distribution and population density, though this has not been quantified. Other pasture pest such as African Black Beetle (ABB) Heteronychus arator (Fabricius) and Black Headed Cockchafer (BHC) Acrossidius tasmaniae Hope (synonym: Aphodius tasmaniae) may also occur simultaneously, and the damage they cause may be confused with that of redheaded cockchafer. Understanding the influence of soil parameters on species distribution could lead to improved opportunities for early detection, surveillance and targeted management of these pests.

A preliminary study in 2011 in three regions of Gippsland, Victoria, surveyed selected farm sites using manual soil sampling and proximal sensing techniques to (i) quantify the relative abundance of each species in the three regions and; (ii) collect preliminary data to determine seasonal distribution of cockchafer life-stages in each region and (iii) explore potential associations between soil electrical conductivity (ECa), above-ground pasture biomass and cockchafer spatial distribution in dairy paddocks.

MATERIALS AND METHODS

Damage reported by growers or consultants in previous seasons was used to select eight properties in East (2 sites), South (2 sites) and West (4 sites) Gippsland, Victoria, Australia for sampling between December 2010 and May 2011.

Soil bulk electrical conductivity (ECa) was measured at all sites using an electromagnetic induction sensor (Geonics EM38, UK) to infer soil texture, salinity and moisture in the soil (Proffitt et al. 2006). This method was used previously to map distribution of other root-feeding pests (Bruce et al. 2009, 2011). The EM38 was operated in horizontal dipole mode to capture information from the 0 – 75cm range subsurface (Proffitt et al. 2006). A Trimble TSCe® data-logger plus a Trimble differential global positioning system (DGPS) recorded geo-located ECa data.

Eighteen 1m² sampling points per site were selected using a response surface sampling design
method in ESAP statistical software (Lesch et al. 2000), which best represented all ECₐ ranges. A 0.25 m² x 0.20m deep turf and soil sample was removed at each sampling quadrat using a shovel and all visible cockchafer life-stages collected during an extensive visual search of the sample. Temporal changes in cockchafer distribution were quantified by sampling in both February and April 2011, in the same 1m² quadrat, for all but one site in West Gippsland. This site was sampled once in May 2011, using the EM38 in its vertical mode where it responds to ECₐ to approximately 150cm depth and in the horizontal mode. On completion of sampling and identification, statistical modelling was undertaken using exploratory data analysis (correlation analysis and linear modelling to examine potential relationships between ECₐ and RHC distribution) for the site sampled in May only.

RESULTS

East Gippsland

No RHC was detected in East Gippsland at either sampling time or site, despite growers and consultants reporting there had been previous infestations. ABB predominated at both sites (Figure 1) although BHC was identified in February and April. Adults were the predominant life-stage of both species in February but only for ABB in April. BHC in April were predominately second instar larvae. There was no clear trend in distribution of either species according to ECₐ values mapped by the EM38 (Figure 2).

South Gippsland

RHC was the most abundant cockchafer species at both sites sampled in South Gippsland (Figure 3). ABB was absent from both sites. Predominant RHC life-stages were second and third instar larvae in February and April respectively. Second instar larvae were the predominant BHC life-stage in April. RHC was predominantly present in the low-medium ECₐ range (11-23 mS/m; Figure 4).

Figure 1: Overall cockchafer species abundance and diversity at one East Gippsland site (Site 1) in February and April 2011. Site 2 data not shown.

Figure 2: East Gippsland site survey showing spatial distribution of African Back Beetle and Black Headed Cockchafer in April 2011. Numbers indicating cumulative number of all life-stages found are superimposed on ECₐ collected using the horizontal dipole configuration.

Figure 3: South Gippsland site survey showing spatial distribution of African Back Beetle and Black Headed Cockchafer in April 2011. Numbers indicating cumulative number of all life-stages found are superimposed on ECₐ collected using the horizontal dipole configuration.
Figure 3: Overall cockchafer species abundance and diversity at Site 3 in South Gippsland in February and April 2011. Site 4 data not shown.

Figure 4: Site 3 survey showing spatial distribution of Red Headed Cockchafer February 2011. Numbers indicating cumulative number of all life-stages found at each quadrat sample point are superimposed on EC\textsubscript{a} collected using the horizontal dipole configuration. Numbers indicate higher abundance of RHC in low-medium EC\textsubscript{a} ranges (11 – 23).

West Gippsland

RHC was the most abundant cockchafer species identified at all four West Gippsland sites (Figure 5), with notable variation in quantity between the sites. ABB was either absent or in very low numbers at all but one site. BHC distribution followed a similar pattern. In May, RHC was found in higher numbers compared to BHC (data not shown) with a wider distribution across sampled paddocks (Figures 6 and 7).
Data Analysis
A linear regression of $y = \sqrt{EM38_{\text{Vertical}}}$ against $x = EM38_{\text{Horizontal}}$ gave $R^2 = 0.50$, indicating that a linear relationship between REMV and EMH existed (Figure 8) of moderate predictive value. A general linear model (GLM) fitted to investigate the relationship between EMH, REMV and RHC count, was found to be a useful indicator of RHC count, based on very low values of EMH and high values of REMV correlating to high values of RHC count, with the opposite also true (Figure 9).

DISCUSSION AND CONCLUSION
There are different management strategies available for different cockchafer species in dairy pastures including cultural, chemical and biological control (Berg 2008). Reports from a recent telephone survey of dairy farmers across the three regions indicated up to 25% of respondents in East Gippsland believed they had seen RHC damage on their farm. In contrast the current study did not detect presence of RHC in any of the east Gippsland sites, indicating that in some regions cockchafer species are being incorrectly identified resulting in implementation of inappropriate and costly control strategies. This study highlights the importance of correct identification of cockchafer species, with the population demographics of cockchafer incidence varying considerably with region and sampling time. Monitoring the temporal life-stage changes provided information about the population dynamics and lifecycle of each species - RHC has a reported two-year life cycle in contrast to the one year lifecycle of ABB and BHC, which has implications for successful management.

Preliminary modelling regarding the usefulness of remote sensing as a monitoring tool for cockchafer infestation suggests that there is a relationship between EM38 and RHC incidence. While the mechanism behind this relationship is not yet clear, the analysis undertaken indicates that the cross-product of the EM38 horizontal and the square-root of the EM38 vertical readings is a useful predictor of RHC count.
With further development this method may provide a pathway for producing a useful RHC monitoring tool. This research is being continued in a three-year collaborative project with GippsDairy, jointly funded by Gardiner Foundation, GippsDairy and DPI Victoria (2011-2014) and a PhD study co-funded by the University of New England and Dairy Australia.

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