Agricultural Research Forum 2012

12th & 13th March

Incorporating the Annual Research Meeting of the

Irish Grassland and Animal Production Association

(38th Research Meeting)

Irish Tillage and Land Use Society

(20th Research Meeting)

Soil Science Society of Ireland

(35th Annual Research Meeting)

Irish Agricultural Economics Society

(12th Annual Research Meeting)

Organising Committee

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Summary of Papers

Presented at the

Agricultural Research Forum 2012

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Held at Tullamore etc

Monday and Tuesday, 12th & 13th March 2012.

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Final Programme Agricultural Research Forum 2012

Monday 12th March 2012	Arrival and Coffee	
	Room D.E. Williams I	**Room D.E. Williams II**
10:30-13:00	**Session 1A Soils, Environment & GHG** Chairperson: Dr Paul Murphy	**Session 1B Animal Reproduction** Chairperson: Dr Dermot Morris
13:00– 14:00	Lunch in Restaurant	
14:00 -15:45	**Session 2A Fertilizer & Nutrient Use** Chairperson: Dr Karl Richards	**Session 2B Animal Nutrition** Dr Karina Pierce
15:45-16:15	Tea: Foyer	
16:15- 18:15	**Session 3A Systems & Economics** Chairperson: Dr Fiona Thorne	**Session 3 B Animal Health and Welfare** Chairperson: Dr Kieran Meade
18:15	Review of conference and proposals for further development (D.E. Williams II)	
20:00	Conference Dinner (DE Williams 1)	

Tuesday 13th March 2012 08:30-10:30	**Session 4 Grassland** Chairperson: Dr Brendan Horan	
10:30-11:00	Coffee: Foyer	
11:00 –13:00	**Session 5A Crops & Forestry** Chairperson: Dr Máirtin MacSiúrtáin	**Session 5B Milk Production & Technology** Chairperson: Mr Tom O'Dwyer
13:00 – 14:15	Lunch in Restaurant	
14:15-16:45	**Session 6A Crops & Grassland** Chairperson: Mr John Spink	**Session 6B Animal Genetics** Chairperson: Dr Alan Fahey
16:00-16:30	Tea -Foyer	

Monday 12th March 2012

Session 1A: Soils, Environment and GHG

Venue **D.E. Williams I**

Chair **Dr Paul Murphy, Teagasc Crops, Environment and Land Use Programme Johnstown Castle, Co. Wexford.**

10-Minute Theatre Presentations & 5-Minute Discussion

Monday 12th March 2012

Session 1B: Reproduction

Venue **D.E. Williams II**

Chair **Dr Dermot Morris, Animal & Grassland Research and Innovation Centre, Teagasc, Mellows Campus, Athenry, Co. Galway.**

10-Minute Theatre Presentations & 5-Minute Discussion

Time	Title & Authors	Page
10:30	Influence of a 50-day dietary restriction on pregnancy per artificial insemination in beef heifers. *M.H. Parr, P. Lonergan, A.C.O. Evans, J.F. Roche, T. Fair, M.A. Crowe, M.G. Diskin.*	**15**
10:45	The effect of genetic merit for fertility traits on regulation of the somatotropic axis in hepatic tissue in Holstein cows. *S. B. Cummins, , S.M. Waters, A.C.O. Evans, P. Lonergan and S.T. Butler*	**16**
11:00	A comparison of the plasma and uterine proteome in cattle: evidence for a dynamic uterine environment. S. Faulkner, M.Mullen, G. Elia, P. O'Boyle, M. Dunn and D. Morris	**17**
11:15	Negative energy balance alters hepatic miRNA expression in dairy cows during the early post partum period. *A. Fatima, C. Seoighe, P. O'Boyle and D.G. Morris*	**18**
11:30	High sperm numbers have detrimental effects on bull sperm during liquid storage. *C. Murphy, A. Shafat and S. Fair*	**19**
11:45	The effect of trace mineral supplementation on the reproductive performance of lactating dairy cattle. *H Watson, ACO Evans and ST Butler*	**20**
12:00	Examination of the factors responsible for differences in circulating progesterone in lactating dairy cows with divergent genetic merit for fertility traits. *S.G. Moore, , S. Scully, M.A. Crowe, A.C.O. Evans, P. Lonergan, T. Fair, and S.T. Butler*	**21**
12:15	Factors associated with fertility outcomes in cows treated with protocols to synchronise oestrus and ovulation in seasonal calving pasture-based dairy production systems. *M.M. Herlihy,, M.A. Crowe, D.P. Berry, M.G. Diskin and S.T. Butler*	**22**
	3-Minute Presentations with one short question	
	The effect of dystocia on subsequent performance in dairy cows. *N. McHugh and D.P. Berry*	**23**

Monday 12th March 2012

Session 2A: Fertilizer and Nutrient Use

Venue **D.E. Williams I**

Chair **Dr Karl Richards, Teagasc Crops, Environment and Land Use Programme Johnstown Castle, Co. Wexford.**

10-Minute Theatre Presentations & 5-Minute Discussion

3-Minute Presentations with one short question

Monday 12th March 2012

Session 2B: Animal Nutrition

Venue **D.E. Williams II**

Chair **Dr Karina Pierce, School of Agriculture & Food Sciencecheck title Veterinary Medicine, University College Dublin, Belfield, Dublin 4**

10-Minute Theatre Presentations & 5-Minute Discussion

3-Minute Presentations with one short question

Monday 12th March 2012

Session 3A: Systems and Economics

Venue **D.E. Williams II**

Chair **Dr Fiona Thorne, Rural Economy and Development Programme, Teagasc Ashtown, Dublin 15**

10-Minute Theatre Presentations & 5-Minute Discussion

Monday 12th March 2012

Session 3B: Animal Health & Welfare

Venue **D.E. Williams II**

Chair **Dr Kieran Meade, Animal & Grassland Research and Innovation Centre, Teagasc, Grange Dunsany, Co. Meath**

10-Minute Theatre Presentations & 5-Minute Discussion

3-Minute Presentations with one short question

Tuesday 13th March 2012

Session 4: Grassland

Venue **D.E. Williams II**

Chair **Dr Brendan Horan, Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork.**

10-Minute Theatre Presentations & 5-Minute Discussion

3-Minute Presentations with one short question

Tuesday 13th March 2012

Session 5A Crops and Forestry

Venue **D.E. Williams II**

Chair **Dr Máirtín Mac Siúrtáin School of Biology & Environmental Science, Agriculture & Food Science Centre, University College Dublin, Belfield Dublin 4**

10-Minute Theatre Presentations & 5-Minute Discussion

Tuesday 13th March 2012

Session 5B Milk Production and Technology

Venue **D.E. Williams II**

Chair **Mr Tom O'Dwyer, Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork.**

10-Minute Theatre Presentations & 5-Minute Discussion

3-Minute Presentations with one short question

Tuesday 13th March 2012

Session 6A Arable Crops and Grassland

Venue **D.E. Williams II**

Chair **Mr John Spink, Teagasc Crops, Environment and Land Use Programme Oak Park Crops Research Centre, Carlow.**

10-Minute Theatre Presentations & 5-Minute Discussion

3-Minute Presentations with one short question

Tuesday 13th March 2012

Session 6B Animal Genetics

Venue **D.E. Williams II**

Chair **Dr Alan Fahey, School of Agriculture & Food Science Veterinary Medicine, University College Dublin, Belfield, Dublin 4.**

10-Minute Theatre Presentations & 5-Minute Discussion

3-Minute Presentations with one short question

Does soil biology hold the key to optimised slurry management?

B.S. Griffiths[1], F. Bourdin[1,2], F.P. Brennan[1], R.E. Creamer[1], J.A. Harris[2], N.J. Hoekstra[1], M.G. Kibblewhite[2],G.J. Lanigan[1], P.A. Massey[1,2], E.L. Moynihan[1,2], M. Pawlett[2], K.G. Richards[1].K. Ritz[2], N.E. Rogers[1,2], R. Sakrabani[2], R.P.O. Schulte[1] and S.F. Tyrrel[2]

[1]Teagasc, Department of Crops Environment and Land-Use, Environment Research Centre, Johnstown Castle, Wexford, Co. Wexford, Ireland.[2]Cranfield University, School of Applied Sciences, Cranfield, Bedfordshire, MK43 0AL,UK.

Introduction

Current agro-environmental challenges can no longer be addressed by single-disciplinary research and mitigation approaches, since individual abatement strategies may well be mutually antagonistic. Instead, an integrated, multi-disciplinary strategy for environmental sustainability in a competitive market-climate is required. This strategy should be based on a solid understanding of the soil processes that are the interface between agriculture, nutrient efficiency, gaseous emissions, water quality, and soil functioning (Harris et al., 2011). Teagasc sought to develop their funded PhD projects (Walsh Fellowships) by initiating a 'cluster' of four integrated research projects between the Teagasc Environment Research Centre, Johnstown Castle and Cranfield University (UK). The cluster sought to understand a range of soil biological processes involved in slurry and nutrient management, including interactions between soil microbial community structure and survival of slurry-based microbial pathogens in soil; the balance between soil and slurry microbial communities in nitrogen dynamics; trade-offs between greenhouse gas and ammonia emissions from applied slurry and the role of soil biology in phosphorus incorporation.

Because of the integrated nature of the cluster projects, the results and discussion will be presented as a review of objectives and outcomes from the cluster. As far as possible the four projects used common methodologies, soils and slurries.

Influence of land use and soil microbial communities on pathogen survival

It is unclear whether edaphic or biotic factors play a dominant role in governing pathogen survival, but we hypothesised that soil biology would be more influential in regulating pathogen decay than soil physico-chemical composition. Twelve soils, selected on contrasting land-use (grassland, arable and wood), soil type and management regime, were characterised physico-chemically for: total exchange capacity, pH, % organic matter (OM), phosphorus; exchangeable cations; % organic C; % C; % N, C/N ratio; % clay; % silt and % sand, and microbiologically by phospholipid fatty acid analysis (PLFA). Replicate microcosms of each soil were individually inoculated with approximately 10^7 cells g^{-1} of commonly occurring slurry bacterial pathogens (*Listeria*, *Salmonella* and 2 *E. coli* strains). Pathogen survival data were collected by counting characteristic colonies on pathogen-specific agar over 110 days at 10°C. Triplicate counts were used to fit exponential decay curves and calculate the average death rate (k) for each pathogen. PLFA profiles were analysed by principal component analysis. Physico-chemical, community and k-values were averaged per soil, and entered into a forward stepwise regression model. Regression analysis showed that microbial community composition provided the best predictor of pathogen survival for 3 of 4 pathogens investigated (Fig. 1).

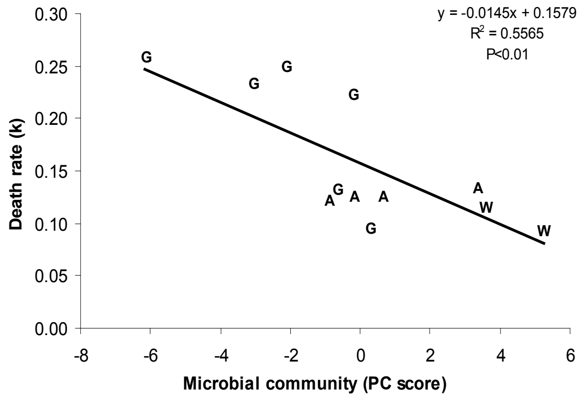

Fig. 1. Death rate of *Salmonella dublin* in grassland (G), arable (A) and woodland (W) soils plotted against microbial community structure.

Communities associated with soils from grasslands were the most suppressive and this was of a general rather than specialist nature, caused by interactions with the total microbial consortium within these soils, rather than with specific microbial groups.

The balance between soil and slurry microbial communities

The pathogen component of land-spread slurry is only a small proportion of its total microbial community. Other microbes present in slurry are potentially important for the mobilisation of nutrients from the slurry OM when applied to soil, but the actual contribution of slurry or soil microorganisms to nutrient cycling is largely unknown. To test this, ammonification and nitrification rates were determined in a 42 day laboratory incubation with 2 x 2 factorial experiment of soil (fresh or irradiated) and slurry (fresh or irradiated), using a standard KCl extraction and chemical determination of NH_4 and NO_3. Results indicated slurry microbes can contribute to soil functions, as seen from the small increase in NO_3 when fresh slurry was mixed with irradiated soil (i.e. no biological activity) but indigenous soil organisms were dominant as seen from the larger changes when fresh soil was present (Fig. 2).

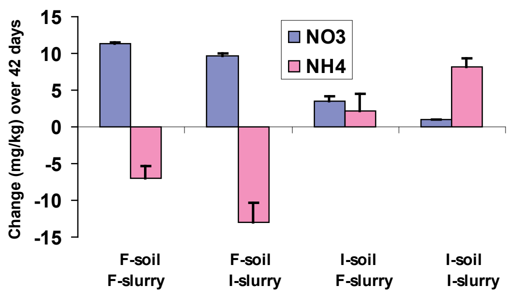

Fig. 2. Change in NH_4 and NO_3 in mixtures of field (F) and irradiated (I) soil and slurry. Bar = s.e. n=5.

Effect of slurry composition, application technique and timing on gaseous emissions

Agriculture in Ireland is the main source of ammonia (NH_3) and contributes 29% of greenhouse gas (GHG) emissions. However, NH_3 abatement strategies to reduce volatilisation of NH_3 might increase N availability and so affect the production of nitrous oxide (N_2O) from these soils. Manure OM is also likely to increase C storage in soils, compared to inorganic fertilisers, but also increases rates of soil respiration, leading to a possible net CO_2 loss from amended soils. It is clear that the fate of slurry OM and N are closely linked and that GHG mitigation strategies need to consider both C and N dynamics concurrently.

To evaluate mitigation options, gaseous emissions of CO_2, NH_3, CH_4 and N_2O from field applied slurry and inorganic fertiliser were determined over a 15 month experimental period in a randomised block design (n=3) following application on four different dates from spring to autumn. Cumulative fluxes for the entire experiment were analysed using ANOVA and the impact of timing of application investigated using a Repeated Measures ANOVA.

CO_2 was the main greenhouse gas emitted from slurry amended soils, regardless of slurry dry matter content or application technique.

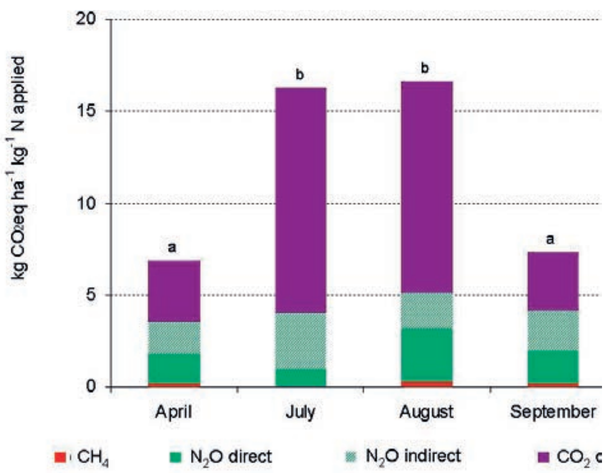

Fig. 3. Cumulative fluxes of GHG over the first three weeks following slurry application. Columns with the same letter are not significantly different, P>0.05.

There was a 55% reduction in GHG emissions by switching from summer to spring application (Fig 3) as soil processes were limited by low temperature and high soil moisture, with no trade-off between NH_3 and N_2O. Slurry application technique and the timing of application are key in NH_3 abatement strategies. Switching from summer to spring application was the best mitigation option reducing both NH_3 and GHG. Spring application reduces gaseous N losses in a period where the N requirement of the herbage is the largest, optimising N fertilisation and reducing the need for a supplementation with mineral N.

Phosphorus incorporation into soil

There is concern about the potential risk that fertilisers pose for water quality as accumulated P at the soil surface is susceptible to mobilisation due to overland flow. Little information is available on the ability of the aboveground or belowground communities to effect the distribution of P in the soil profile.

Experimental mesocosms (27 x 38 x 35 cm) were filled with two soil layers, the lower 30 cm from a low fertility pasture (Morgan's P, 2.4 µg g^{-1}) covered by a top layer, 1 cm, from a high fertility pasture (19.1 µg P g^{-1}). Both soils were sieved to remove earthworms and eggs. Mesocosms were established in a 3 x 2 factorial experiment containing plants (monoculture or a 4 species sward), earthworms (present or absent) and fertiliser (slurry or inorganic). The distribution of P down the soil profile was measured after 18 months (n = 5).

A decrease in labile inorganic P in the 0 – 5 cm layer occurred after the application of slurry but not inorganic fertiliser. Earthworms significantly reduced nutrient concentrations at the soil surface, thus promoting a more uniform distribution of P down the soil profile, but whether this translates into greater P incorporation belowground still remains unclear as there was not an apparent increase at other depths (Fig 4).

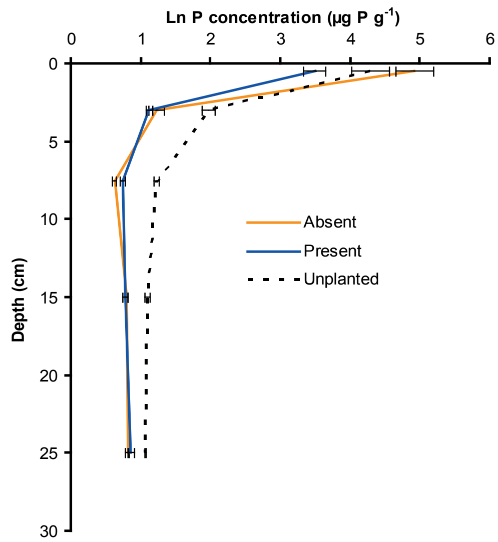

Fig. 4. The distribution of P to a soil depth of 30 cm in the presence and absence of earthworms and an unplanted control with no earthworms. Bar = s.e. n=5.

Conclusions

To manage soils so that their biological communities provide greater services, with less inputs and similar or fewer losses, soil husbandry advice akin to grassland and animal husbandry would be beneficial and offers great potential for improved agricultural management. This cluster has shown the need to incorporate: a suppressive capacity test, maintenance of the soil microbial community, matching timing of farm practice events to soil processes, and consideration of the wider soil biological community, in soil husbandry advice.

Acknowledgements

We acknowledge the Teagasc Walsh Fellowship Scheme and SFI for financial support.

References

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Shifts in bacterial and fungal communities in grassland turfs suggests that fungi contribute to the availability of carbon bonded sulphur

A. Schmalenberger [1,2]
[1]*University of Limerick, Live Sciences, Limerick, Ireland.* [2]*University of Sheffield, Cell-Mineral Research Centre, Broad Lane, Sheffield, UK*

Introduction
Organically bound sulphur such as sulphate esters and sulfonates are the major sulphur (S) compounds in soil ecosystems where sulphate often represents less than 5% of the total S (Autry & Fitzgerald, 1990). As plants almost entirely depend on sulphate as S source, they require microbial S-supply. While some fungi are able to desulfurize sulphate-esters, the use of sulfonates as a S source seems to be limited to a defined functional bacterial guild (Kertesz*, et al.*, 2007; Schmalenberger*, et al.*, 2010). This study investigates whether fungi assist bacteria in sulfonate desulfurization.

Materials and Methods
Freshly sampled grassland turfs (20x15x15 cm) from Woburn Experimental Farm (sandy loam) with dominance of *Agrostis sp.* plants were harvested in October 2008. Oxidation states of S present in the bulk soil (free of major roots) were investigated using the x-ray absorption near-edge spectroscopy (XANES) method (Zhao*, et al.*, 2006). Entire turf samples were incubated in triplicate in growth chambers and watered periodically with de-ionised water (week 1-4) and 0.25X modified Hoagland solution (week 5-8, (Schmalenberger*, et al.*, 2010)) *i)* without S, *ii)* with low molecular weight sulfonate (toluenesulfonate (TS), 0.1 mM S) *iii)* with high molecular weight sulfonate (lignosulfonate (LS), 0.1mM S). The diversity of the bacterial and fungal community was analyzed employing a DNA fingerprinting method (Denaturing Gradient Gel Electrophoresis (DGGE) of bacterial (16S rRNA gene) and fungal (internal transcribed spacer region) housekeeping genes (Muyzer*, et al.*, 1993; Anderson & Cairney, 2004)). DGGE was carried out using a 20-60 % denaturing gradient. The desulfonating bacterial community analysis was based on fingerprinting the *asfA* gene diversity (Schmalenberger*, et al.*, 2008). Correspondence analysis (CA) and permutation tests (Schmalenberger*, et al.*, 2010) were carried out to analyze the fingerprints. Fungal amplicons from the soil samples of all three treatments were grouped into genotypes of witch the ones with more than one member were subjected to sequence identification.

Results and Discussion
XANES analysis clearly identified sulfonates (intermediate form of sulfur) as one of the dominating sulfur forms in this soil. CA biplots of the bacterial and fungal communities and the desulfonating bacterial guild revealed a significant separation of the rhizosphere and the bulk soil samples ($P \leq 0.05$). CA of bacterial and desulfonating bacteria communities identified an effect of the TS application ($P \leq 0.05$) while fungal communities (Fig. 1) in the bulk soil were particularly affected by the addition of sulfonates (LS and TS) in general ($P \leq 0.05$). While the effect of sulfate onto bacterial communities and desulfonating bacterial guilds has been identified before (Schmalenberger*, et al.*, 2010), the effect of sulfonates applied to grassland turfs has not been reported up to date. Sequencing of the most abundant genotypes of the internal transcribed spacer region revealed a dominance of the phylum Ascomycota in the fungal communities. While some sequences identified members of the Glomeromycota, 4 out of 5 genotypes were not closely related to a described fungus (below 90 % similarity).

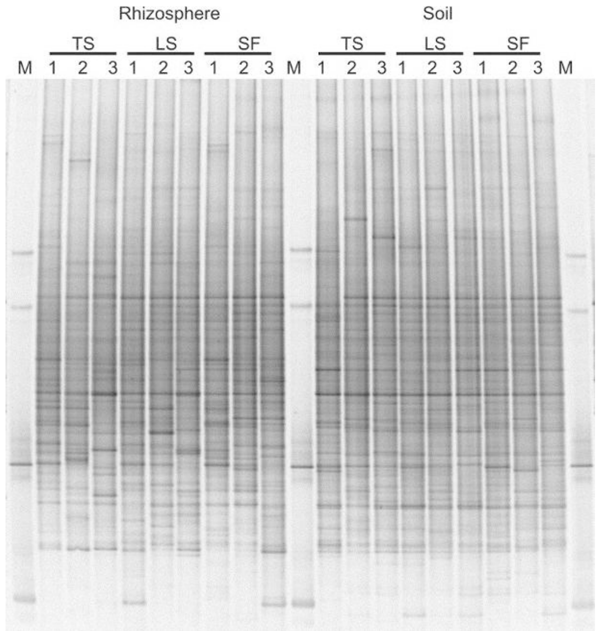

Fig 1: Fungal community DGGE fingerprint of rhizosphere and soil samples from *Agrostis* turfs incubated with toluenesulfonate (TS), lignosulfonate (LS) or without sulphur (SF) in triplicates (1-3) and accompanied by a DNA standard (M).

Conclusions
The results suggest that the fungal community in *Agrostis sp.* rhizosphere is involved in the mobilization and the bio-availability of sulfonates in soil. This might be accomplished directly through the use of TS and LS as a carbon source or indirectly through the support of desulfonating bacteria. However, this needs to be investigated in further detail.

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Losses of nitrate in streamflow from intensive cereal crop catchments in Ireland

A.R. Melland[1]*, P-E. Mellander [1], P. Murphy[1], D.P. Wall[1], S. Mechan[1], O. Shine[1], G. Shortle[1], P. Jordan[1,2]
[1]*Agricultural Catchments Programme, Teagasc, Wexford, Ireland.* [2] *School of Environmental Sciences, University of Ulster, Coleraine, Northern Ireland*

Introduction

Ireland's cereal crop yields are amongst the highest in the world (average 7.5 t ha^{-1} for malting barley and 9 t ha^{-1} for wheat). Whilst these cereal crops constitute only 7% of landuse, government food production targets will require these yields to be substantially increased into the future in part to provide fodder for a planned 50% increase in milk production by 2020 (Anon. 2010). At the same time Water Framework Directive water quality targets must be met. An assessment of streamflow N fluxes and processes of N loss from intensive arable catchments is required to help identify opportunities to increase yields and minimise N losses to waterways.

Materials and Methods

In two benchmark catchments representing contrasting physiographic settings for intensive arable agriculture, experimental monitoring was undertaken to investigate total oxidized nitrogen (TON) losses in stream water over two water years (Wall *et al.* 2011). Arable A catchment in Co. Wexford (11.16 km^2) had predominantly well-drained Typical Brown Earth soils and land use was 45% spring barley. The Arable B catchment in Co. Louth (9.48 km^2) had mainly moderate to poorly-drained soils (Gleyic Luvisols and Surface Water Gleys) and land use was winter wheat and barley (24%) and dairy and beef (47%). Water discharge and chemistry were measured on a sub-hourly basis at stream outlets of each catchment. In-situ calibrated UV sensors collected up to 4464 instantaneous measurements of TON per month. Total oxidised N loads in streamflow were calculated as the product of hourly average concentrations and hourly total discharge. Annual loads were calculated as the sum of sub-hourly loads and time series trends were analysed graphically.

Results and Discussion

In Arable A, TON concentrations were diluted during storms and baseflow concentrations remained relatively stable and below the maximum acceptable drinking water standards of 11.3 mg L^{-1} (Fig.1a). In Arable B, baseflow TON concentrations were lower during summer than winter, and in winter baseflow concentrations were similar to Arable A (Fig. 1b). This seasonal pattern was attributed to disconnection of localised rootzone N sources when water tables dropped and discharge to the surface, that had interacted with these rootzone stores, diminished. Stormflow, i.e. elevated flow closely associated with rain events, dominated streamflow loads of N in both catchments. Annual TON loads exported in streamflow ranged from 15.5 to 32.2 kg ha^{-1} across years and catchments, reflecting an equivalent fertiliser (Calcium ammonium nitrate) N cost of up to €38 ha^{-1} at current prices. Under current regulations most N applications are made during the summer period, when sources were less connected in Arable B. The hypothesized hydrological disconnection may limit N losses in the Arable B environment. The likely environmental impact of the observed N loads, which will vary inter-annually, is unknown and there are currently no environmental standards for N loads in streamflow. However, O'Boyle et al. (2011) suggested a 15% reduction in annual loads could help eutrophic estuaries achieve 'non-problem' status. Nitrogen deficits at the field-scale may further deplete subsoil N stores, and hence loads in streams, over time.

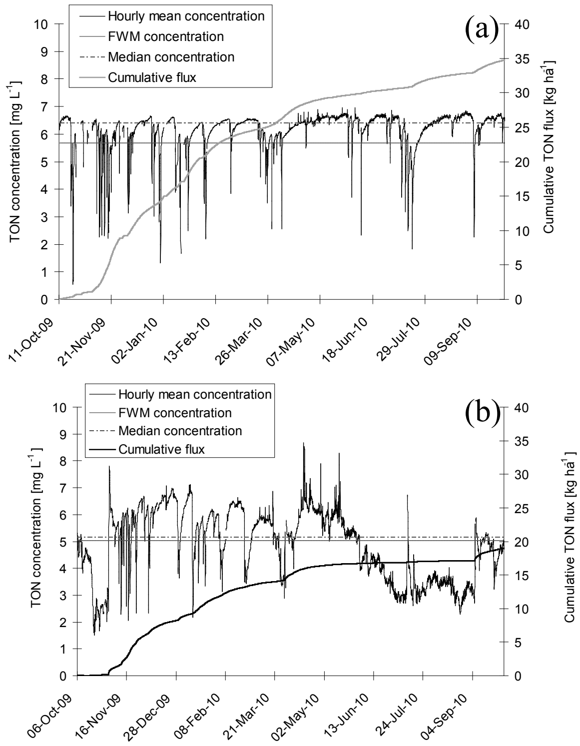

Figure 1. Time series of TON concentration (mg L^{-1}) and cumulative load (kg ha^{-1}) for in Water Year 1 for a) Arable A and b) Arable B. Annual flow-weighted mean (FWM) and median concentrations are shown.

Conclusion

Total oxidized N concentrations were below drinking water standards but the direct downstream impact of observed annual fluxes is not known. Reducing N loads from observed levels would likely require depletion of rootzone and deeper N stores in soils that are connected to the stream during stormflow. Depletion may be achieved over time by reducing application of surplus N to crops.

Acknowledgements

We acknowledge funding from the Irish Department of Agriculture Food and Marine.

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Ecological focus areas: quantifying the contribution of farmland habitats in east Galway to greening measures of the post-2013 Common Agricultural Policy

C.A. Sullivan[1], M. Sheehy Skeffington[2], M. J. Gormally[3] and J.A. Finn[1]

[1]Teagasc Environmental Research Centre, Johnstown Castle, Wexford; [2] Botany and Plant Science, National University of Ireland, Galway [3]Applied Ecology Unit, ,National University of Ireland, Galway

Introduction

Agricultural policy reform in the EU has increasingly incorporated an environmental dimension since the mid 1980's. Proposals for the post-2013 CAP signal even more emphasis on the integration of environmental objectives. In proposals for Greening the CAP, 30% of the direct payments may be linked to ensuring that all farms deliver environmental and climate benefits. 'Ecological focus areas' (EFA's) have been introduced for the first time (COM, 2011), and should comprise 7% of the eligible hectares (excluding areas under permanent grassland) and the examples given include fallow land, terraces, landscape features, buffer strips and some afforested areas. Many Irish farms may already fulfil this requirement but there is a paucity of information on the semi-natural habitat cover on Irish farms. This new emphasis highlights the importance of quantifying the semi-natural habitat diversity of Irish farms. Habitat surveys were carried out in east Co. Galway on 32 lowland farms outside of designated areas to quantify the semi-natural habitat proportions of lowland farms in the context of these EFA guidelines.

Materials and Methods

Thirty two farms were selected randomly from six District Electoral Divisions (DEDs) in east County Galway outside of areas with nature conservation designations. All habitats on each farm were identified according to Fossit (2000) from May to October in 2006 and 2007. These data were digitised and areas and lengths calculated using ArcGIS 9.3.

Results and Discussion

The average surveyed farm size was 39.8 ha (s.e.± 4.6). All farms were dominated by grassland, but a total of 24 habitats were recorded on the 32 farms. Of those, 13 were semi-natural habitats (Figure 1). The average number of habitats on any farm was 10.6 (± 0.6) and the average number of semi-natural habitats was 2.6 (± 0.3). The average cover of semi-natural habitats per farm was 15.2% (± 3.0). Semi-natural grassland (predominantly Wet Grassland) was an important component of the semi-natural habitat cover on the majority of those farms with semi-natural habitats.

The proportion of semi-natural habitat cover varied from 0% to over 60% (Figure 1) with just 9% of the farms having no non-linear semi-natural habitat cover. The percentage cover of semi-natural habitats recorded per farm are illustrated in Figure 1.

Five different types of semi-natural woodland were recorded (excluding woodland with non-native trees such as Broadleaved Woodland) and a range of wetlands such as ponds, marshes and fens were all recorded. Overall, thirteen of the 32 farms (41%) contained <7% of semi-natural habitats.

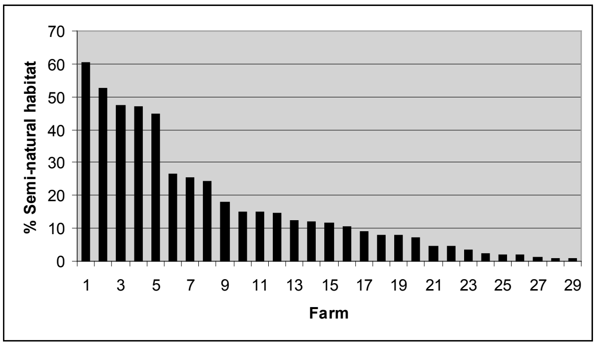

Figure. 1. Proportion of semi-natural habitats per farm. Three farms with no semi-natural habitats are excluded.

Field boundaries also contribute to the ecological focus areas of these farms, but are not included in the above values. Two hundred and eight-six km of field boundaries were recorded on the farms (excluding wire fencing). If each of these features had a width of 1m (a conservative estimate) even farms with no non-linear semi-natural habitats would have landscape features comprising 1.9 to 3% of their area. These values would be at least double in the majority of cases as the majority of field boundaries such as hedgerows would have widths of 2m or more.

Irish farmland has relatively high habitat area and diversity. In a separate study of 50 Irish farms, the mean semi-natural habitat area was 14.3% of the farm area (Sheridan *et al*. 2011). Landscape features such as field boundaries and semi-improved grassland (Sullivan 2010) can complement the area of semi-natural habitat on a farm. If these features are included in 'ecological focus areas', most Irish farms will attain the 7% target area. Reaching this 7% target is possible even for those farms that are dominated by improved agricultural grassland as they often have a high diversity of linear habitats such as hedgerows, earth banks and drainage ditches.

Conclusion

Assuming that these farms are representative of east county Galway then the majority of farms in this landscape type already contain sufficient area of ecological focus areas to satisfy the proposed minimum of 7% as part of the Greening of the post-2013 CAP.

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Effect of dicyandiamide on N_2O and N_2 emissions from slurry amended Irish grassland soils

M. Ernfors[1,2], F. Brennan[1,6], K.L. McGeough[3], R.J. Laughlin[3], C.J. Watson[3], C. Müller[4,5], B.S. Griffiths[1], L. Philippot[6], E. Cahalan[1], K.G. Richards[1,*]

*[1]Teagasc, Johnstown Castle Environmental Research Centre, Co. Wexford, [2]Department of Agrosystems, Swedish University of Agricultural Sciences, Alnarp, Sweden, [3]Agri-Food and Biosciences Institute, Belfast, [4]School of Biology and Environmental Science, University College Dublin, Dublin, [5]Department of Plant Ecology, Giessen, Germany, [6]INRA UMR, Dijon Cedex, France, *Presenting author*

Introduction

Reducing emissions of nitrous oxide (N_2O) from soils is a global research priority. A laboratory study was conducted using three contrasting Irish grassland soils, to improve the understanding of how the nitrification inhibitor dicyandiamide (DCD) affects nitrogen (N) transformations after slurry application. Nitrification inhibitors slow down the microbial conversion of ammonium (NH_4^+) to nitrate (NO_3^-), potentially reducing NO_3^- leaching and the production of N_2O by nitrification and denitrification. The main study objectives were to determine the effects of DCD on (1) net and gross soil N transformations, (2) emissions of nitrous oxide (N_2O) and N_2 and (3) transcript and copy numbers of functional genes involved in nitrification and denitrification (data not presented).

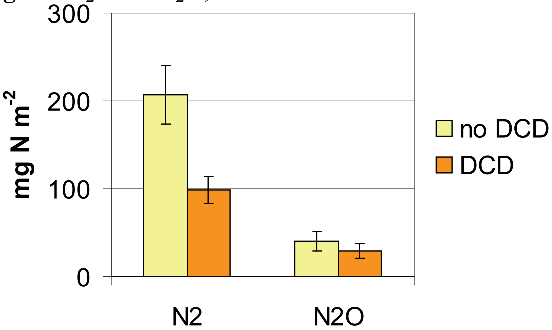
Materials and Methods

Cattle slurry (670 g m^{-2}), with or without DCD (0.44 g m^{-2}) amendment was surface applied to sieved and repacked soil samples of three grassland soils. Nitrogen was applied as NH_4 and NO_3, at rates of 148 and 100 µg g^{-1} soil, respectively, differentially labelled with ^{15}N at an enrichment of 40 atom %, to measure gross N transformation rates. The soil water-filled pore space was 65 % after treatment applications and the samples were incubated at 15 °C. Soil mineral N and/or N_2O/N_2 gas fluxes were determined at 0 h, 2 h, 3.5 h, 5.5 h, 7.5 h, 2 d, 6 d, 10 d, 15 d and 20 d after amendment, using standard methods. Data was analysed by one-way analysis of variance, using SPSS v. 18 software.

Results and Discussion

Without DCD, NO_3 concentrations more than doubled during the incubation, while NH_4^+ decreased and was almost depleted after 20 days (Figure 1). With DCD, mineral N concentrations stayed approximately the same, which indicated a strong effect of DCD on nitrification. Net nitrification, over 20 days, decreased by 89 % ($P < 0.05$) with the addition of DCD. DCD significantly ($P < 0.05$) reduced cumulative emissions of N_2O and N_2 by 27 and 52 %, respectively (Figure 2). Cumulative N_2 rates were 5 fold higher than N_2O with DCD and 3 fold higher without DCD. DCD did not significantly affect the mole fraction of N_2O ($N_2O/(N_2+N_2O)$). The effect of DCD on reducing N_2O emissions has been previously observed. The two fold reductions in N_2 emissions has not been previously reported.

Fig. 2. N_2 and N_2O, cumulative fluxes over 20 days,



averages across three soils. Bars show standard error.

Conclusions

The amendment of slurry with DCD is a useful mitigation measure for reducing N_2 and N_2O emissions in soil. Reduced gaseous emissions from slurry applied to soil could result in increased nutrient availability.

Acknowledgements

This research was funded by the National Development Plan, through the Research Stimulus Fund, administered by the Department of Agriculture, Food and the Marine (RSF 07 719).

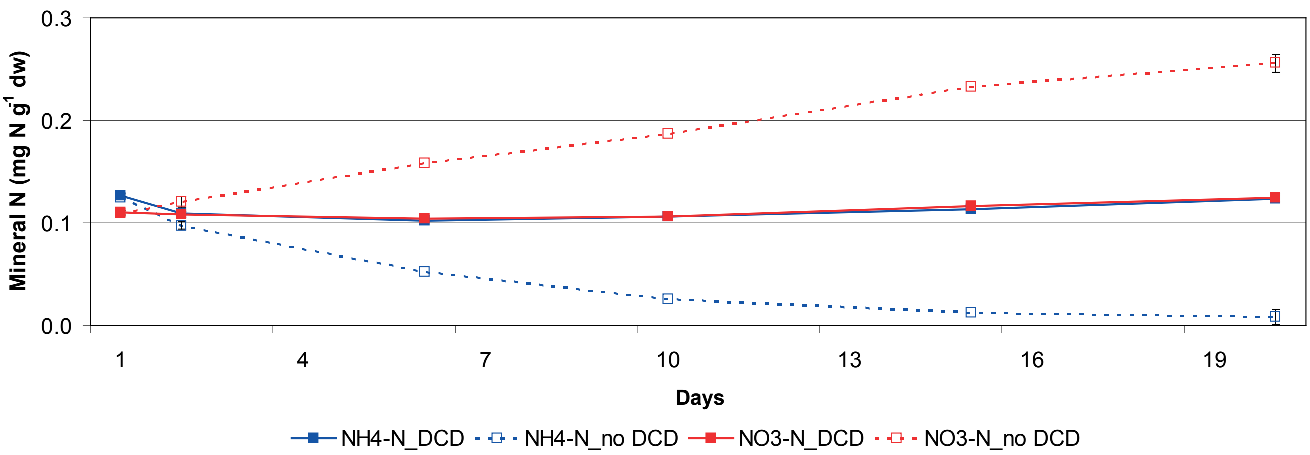


Fig. 1. Soil NH_4^+ and NO_3^- concentrations in microcosms, averages across three soils. Bars show standard error.

The effect of greenhouse gas emissions (GHG) accounting methodology on emissions estimates from dairy systems

D. O'Brien[1, 2], L. Shalloo[1], J. Patton[1], F. Buckley[1], C. Grainger[1] and M. Wallace[2]

[1]Livestock Systems Research Department, Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, [2]School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin 4.

Introduction

Globally, the dairy industry is currently faced with the challenge of increasing production to satisfy growing demand (FAO, 2006), while meeting an international obligation to reduce greenhouse gas (GHG) emissions. This issue has led to an increasing interest in reducing the GHG emission intensity (kg of GHG per unit of milk) of dairy production. However, different methods are used to model GHG emissions from dairy systems, namely Life cycle assessment (LCA) and the Intergovernmental Panel on Climate Change (IPCC) method. The objective of this paper was to compare the IPCC and LCA methodologies in estimating GHG emissions from a grass-based and a confinement dairy system.

Materials and Methods

The input data used to model GHG emissions from the dairy systems investigated in this study were based on the study of Olmos et al. (2009). Holstein-Friesian cows were blocked based on genetic merit, parity, calving date, body condition score and predicted milk yield and assigned randomly from within pairs to either the grass-based or confinement system. Grazed grass was the main feed offered in the grass-based system. Grass silage and concentrate were offered when pasture growth was unable to meet the requirements of the herd. Total mixed ration was fed in the confinement system, which consisted of maize silage, grass silage, barley straw and concentrate.

Greenhouse gas emissions were calculated using a dairy farm GHG model (O'Brien et al., 2011). The model estimates the main GHG emissions: carbon dioxide (CO_2), nitrous oxide (N_2O), and methane (CH_4). The GHG model operates in combination with the Moorepark Dairy System Model (MDSM, Shalloo et al., 2004). The MDSM defines key parameters (e.g. animal feed budgets) required for the GHG model to estimate emissions. The GHG model quantified emissions using the IPCC and LCA methods. The IPCC method only considers GHG from on-farm sources. In contrast, the LCA approach quantifies emissions from all processes associated with dairy production up to the point milk is sold from the farm. Thus, the approach includes emissions from the manufacture of purchased inputs e.g. fuel. Greenhouse gas emissions were estimated in terms of their 100-year global warming potentials (CO_2-eq), which on a weight basis relative to CO_2 was set to a factor of 21 for 1 kg of CH_4 and 310 for 1 kg of N_2O (IPCC, 1996). The main output of the GHG model for both methods was a static account of dairy systems annual GHG emissions, which were expressed, per kg of milk solids (MS). Besides producing milk, dairy farms also produce meat. Thus, GHG emissions were allocated between these products using a physical allocation approach developed by the IDF (2010), where impacts were related to the cow's use of feed to produce milk and meat. Allocation of GHG emissions was also necessary for some concentrate by-products e.g. distillers grain. For these inputs, emissions were allocated based on their relative economic value because a physical relationship could not be established.

Results and Discussion

The GHG emissions of the grass and confinement systems, calculated using the IPCC and LCA methods, are shown in Figure 1. The IPCC results show that GHG emission/kg of MS were, on average, 14.5% lower for the confinement system relative to the grass system. However, the LCA results show that the confinement system increased GHG emission/kg of MS by 18% compared to the grass system. The re-ranking of these two dairy systems GHG emission/kg of MS occurred because the IPCC method excludes emissions associated with farm imports e.g. concentrate. These findings highlight that the most effective dairy system to reduce national emissions could increase global dairy emissions

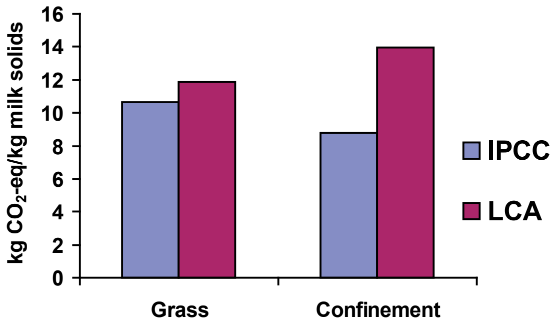


Fig. 1. Greenhouse gas emission of a grass and a confinement dairy system calculated using the Intergovernmental Panel on Climate Change (IPCC) and Life Cycle Assessment (LCA) methods.

Conclusion

This study shows that to reduce GHG emissions per unit of milk, approaches such as life cycle assessment, which consider on and off-farm GHG emissions should be used. Thus, reform of the present IPCC framework is needed to enable quantification of the impact of mitigation strategies on global GHG emissions.

Acknowledgements

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Controls on nutrient losses in overland and subsurface drain flow from Irish grassland

T.G. Ibrahim[1], O. Fenton[1], K.G. Richards[1], R. M. Fealy[2] and M.G. Healy[3]

[1]Teagasc Environmental Research Centre, Johnstown Castle, Co. Wexford. [2]Spatial Analysis Unit, REDP, Teagasc, Ashtown, Dublin 15. [3]Civil Engineering, National University of Ireland, Galway, Co. Galway

Introduction

Food Harvest 2020 focuses on increasing productivity while enhancing the environmental sustainability of agricultural land. In 2015, the dairy sector is expected to expand with the abolition of EU milk quotas. Around 29% of Irish grasslands have poorly-drained soils, and the water table in floodplains or in areas of perched aquifers is often shallow. In these areas, drainage systems may be installed to allow for expansion. Such a move may lead to increased nutrient losses to aquatic ecosystems. Thus, a greater understanding of the controls (fertilizer inputs and hydrological and chemical processes) on nitrogen (N) and phosphorus (P) losses is needed. This study focuses on grassland used for silage, with poorly drained soils, shallow glacial aquifers and a low soil-P index, for a pre- and post-fertilisation period. Such conditions elucidate the "baseline" controls on flow and nutrient patterns in grassland systems.

Material and Methods

The study was conducted from January to April 2009 on four un-grazed plots (Table 1) on a beef farm at the Teagasc Environmental Research Centre, Co. Wexford. Soil and subsoil originate from glacial material. Overland and subsurface drain flow (herring bone drainage) was monitored and water sampled at the bottom of the plots with v-notch weirs and auto-samplers. Water table depth was recorded in piezometers. Samples were analysed for dissolved inorganic nitrogen (DIN), dissolved organic nitrogen (DON), particulate P (PP), dissolved reactive P (DRP) and dissolved un-reactive P (DUP). Soil texture varied from clay loam to sandy loam. Nutrient soil content was similar across plots. Three rainfall events (winter to spring) represented contrasting pre-event and event soil moisture deficit (SMD) patterns (Schulte et al., 2005, Fig. 1), and post- fertilization conditions (Event 7).

Results and Discussion

A decrease in plot size (up to 52.2%, Table 1) and water table depth between Plots 5-6 and Plots 1-2 linked to an increase in runoff coefficients (ratio of total flow versus rainfall for an event, Fig. 2) of 16.9 to 42.5%. Runoff coefficients also increased with increasing amounts of rainfall during and before the events. Subsurface drain flow patterns were more variable, but plots with shallow water table had greater increases in runoff coefficients with wetter pre-event conditions.

Table 1. Plot characteristics

Plot Number	Area (m^2)	Slope (%)
1	7780	3.9
2	7470	4.1
5	4080	4.2
6	4070	5.4

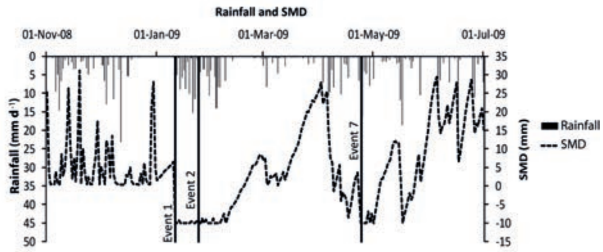

Fig. 1. Rainfall and SMD variations for the study period.

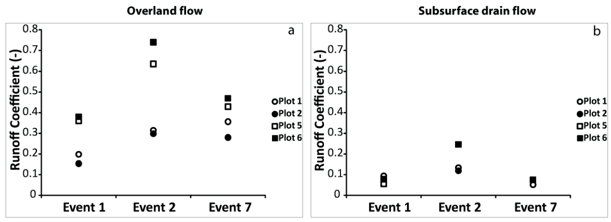

Fig. 2. Runoff coefficients (ratio of total runoff (mm) and rainfall depth (mm)) for the events and plots.

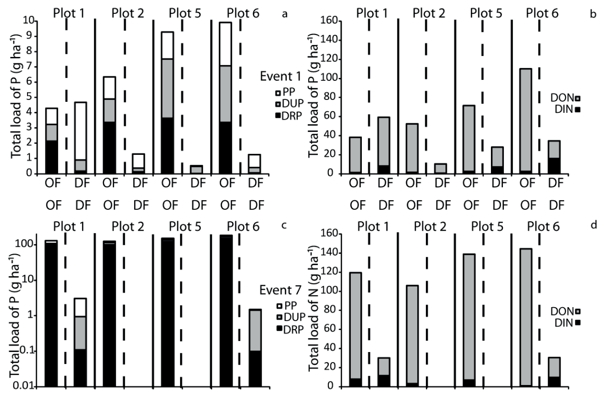

Fig. 3. Loads of nutrient losses in overland flow (OF) and subsurface drain flow (DF) for Events 1 and 7.

Increase in flow induced greater P and N losses. Subsurface drain flow usually generated smaller loads of N and P than overland flow (Fig. 3). For N, this linked with a smaller volume of water generated by the drains. For P, retention in the soil possibly enhanced this process. Nitrogen losses were dominated by DON, but the proportion of DIN was higher in the drains. In overland flow, a shallower water table implied a switch from DRP to DUP-dominated water. In subsurface drains, DUP generally dominated with a shallow water table; otherwise PP dominated. Fertilization resulted in DRP being the dominant P fraction in overland flow.

Conclusions

An integrated assessment of controls on flow and nutrient patterns in hydrologic paths are important when assessing management impacts.

Acknowledgements

We acknowledge the Department of Agriculture and Food Stimulus Fund 07 525 for financial support.

Reference

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The effect of the nitrification inhibitor dicyandiamide (DCD) applied at different times and rates in the autumn on herbage nitrogen uptake in spring

P.J. O'Connor[1, 2], D. Hennessy[1], M. O'Donovan[1] and M.B. Lynch[2]

[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork;* [2]*UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4*

Introduction

Urinary N has a high potential for leaching as the quantity of N excreted exceeds plant requirements. Herbage responses to urinary N normally last for 2-3 harvests (Ledgard *et al.,* 1982). Nitrification inhibitors such as dicyandiamide (DCD) have been shown to reduce nitrate (NO_3^-) leaching (Moir *et al.*, 2007) by slowing the conversion of ammonium (NH_3^-) to NO_3^- in the soil, thereby increasing the quantity of available N in the soil for uptake by herbage in spring. Moir *et al.* (2007) reported that the addition of DCD to urine patches significantly increased pasture N uptake. Selbie *et al*. (2011) observed that DCD (10 kg ha^{-1}) reduced NO_3^- leaching by 45% and N_2O emissions by 70% when applied to dairy cow urine (1000 kg N ha^{-1}) treatments on Irish soils. The objective of this experiment was to investigate the effect of DCD application on N uptake by herbage in spring following the application of DCD on two soil types at different times and rates in autumn.

Materials and Methods

Four experiments were undertaken at Teagasc Moorepark Research Centre, Fermoy Co. Cork, Ireland on two contrasting soil types. The soils were (1) free-draining brown earth at Moorepark (MPK) and (2) a moderate to heavy brown earth at Ballydague (BD). All experiments were undertaken using simulated grazing plots (5m×1.5m MPK; 5m × 1m BD). All experiments were a four factorial arrangement with measurements undertaken over two spring periods. Factors investigated were urine (0 or 1000 kg N ha^{-1}), DCD rate (5 or 10 kg ha^{-1}), urine plus one application of DCD in September, October or November. In all experiments artificial urine (urea and water mix) was used. Dicyandiamide was applied using a walk behind sprayer. Experiment 1 (MPK) and 2 (BD) received no fertiliser N application, while Experiments 3 (MPK) and 4 (BD) received 350 kg N ha^{-1} yr^{-1} in a split application from mid-January to mid-September. Plots were harvested every 4 weeks from February to May (spring period). All fresh samples were weighed and a sub-sample was dried at 40^{0}C for 48 hours. The dried samples were milled through a 1 mm screen and analysed using near infra-red spectroscopy (NIRS) for crude protein concentration. Data were analysed using PROC MIXED in SAS. Data for each experiment were analysed individually.

Results and Discussion

The application of DCD at a rate of 5 and 10 kg ha^{-1} significantly (P<0.01) increased spring herbage N uptake at MPK in Expt 1 by 11 and 15%, respectively, compared to applying zero DCD (Table 1). The application of DCD at a rate of 5 and 10 kg ha^{-1} significantly (P<0.01) increased spring herbage N uptake at BD in Expt 4 by 16 and 18%, respectively, compared to applying zero DCD (Table 1). Urine application significantly (P<0.001) increased spring herbage N uptake in all experiments (Table 1). Applying urine in September significantly (P<0.01) increased spring herbage N uptake compared to October and November urine application at BD in Expt 2 by 14 and 21%, respectively (Table 1). Dicyandiamide increased spring herbage N uptake in Expt 1 and 4; however, DCD's ineffectiveness in Expt 2 and 3 may be due to environmental conditions experienced e.g. high rainfall near application dates leaching DCD beyond rooting zone.

Table 1 The effect of DCD applied following urine applications in September, October or November on spring herbage nitrogen uptake (kg N ha^{-1}).
NS, not significant; **, P <0.01; ***, P<0.001

	Expt 1	Expt 2	Expt 3	Expt 4
	Urine			
Zero Urine	51	45	134	25
Urine	119	65	153	40
s.e.m	3.9	2.9	4.2	1.7
Significance	***	***	***	***
	DCD Rate (kg ha^{-1})			
0	93	60	145	32
5	104	60	150	38
10	110	59	149	39
s.e.m	3.2	2.4	3.4	1.6
Significance	**	NS	NS	**
	Urine application date			
September	114	73	156	41
October	119	63	152	40
November	125	58	150	39
s.e.m	3.9	2.9	4.2	1.9
Significance	NS	**	NS	NS
	Urine application date × DCD rate (kg ha^{-1})			
September 0	106	76	157	34
September 5	104	72	152	43
September 10	113	72	159	44
October 0	114	72	137	37
October 5	122	63	160	44
October 10	127	61	159	40
November 0	121	72	156	37
November 5	133	60	150	38
November 10	135	62	144	43
s.e.m	6.7	5.0	7.2	3.0
Significance	NS	NS	NS	NS

Conclusion

The application of DCD at both rates in Expt 1 and 4 increased spring herbage N uptake compared to when no DCD was applied. Urine application significantly increased spring herbage N uptake in all experiments

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Persistence of dicyandiamide (DCD) in two contrasting Irish soils

E. Cahalan[1, 2], C. Müller[2, 4], M. Ernfors[1, 3] and K. G. Richards[1].
[1] Teagasc, Johnstown Castle, Environmental Research Centre, Co. Wexford. [2] School of Biology and Environmental Science, University College Dublin, Belfield, Dublin 4. [3] Department of Agrosystems, Swedish University of Agricultural Sciences, Sweden. [4] Department of Plant Ecology, Justus-Liebig University Giessen, Giessen, Germany

Introduction
Dicyandiamide (DCD) is a nitrification inhibitor that slows down the conversion of ammonium (NH_4^+-N) to nitrate (NO_3^--N). This has resulted in the reduction of NO_3^--N leaching and nitrous oxide (N_2O) emissions in some studies. There have however been a number of studies in which DCD has been ineffective (Monaghan *et al*., 2009; O'Connor *et al*., 2012). Reasons for the variable efficacy of DCD have been suggested such as soil texture, temperature, moisture and carbon content. As DCD is water soluble it is possible that it can be easily leached from the rooting zone. Knowledge gaps exist as to how the amount of rainfall will impact on DCD persistence in soil. The objective of this experiment was to examine the effect of simulated rainfall on the persistence of DCD in two contrasting Irish soils.

Material and Methods
Intact soil cores were taken from two grassland sites with different soil textures. Johnstown Castle (JC) had a loam texture and Moorepark (MP) had a sandy loam texture. Cores were removed in 150 mm diameter PVC-U pipes that were 300 mm long. The cores were randomly allocated within a growth chamber. Autumn conditions were simulated for the south of Ireland from the 30 year average (12°C daytime, 8°C night time, 12 h daylight and 85% humidity). 60 kg N ha^{-1} as $(NH_4)_2SO_4$ and 20 kg KBr was applied to each core, along with either 0, 15 or 30 kg ha^{-1} DCD. Each core then either received low rainfall (30 year average) or high rainfall (twice 30 year average). 12 treatments were used JC and MP 0L or 0H (0 kg DCD ha^{-1} low or high rainfall), JC and MP 15L or 15H (15 kg DCD ha^{-1} low or high rainfall) and JC and MP 30L or 30 H (30 kg DCD ha^{-1} low or high rainfall). Leachate was collected from each core once per week for 8 weeks and each core was destructively sampled after 10 weeks. Leachate and soil extracts were analysed for DCD using HPLC. Data were analysed used SAS v. 9.1 (Proc MIXED). Factors within the model included soil, rainfall and DCD rate.

Results and Discussion
Up to 21% of the applied DCD was lost through leaching (Figure 1a and b). Soil type did not significantly affect concentrations lost. The level of rainfall affected the load of DCD leached in both soils ($P<0.01$), with high rainfall increasing leaching by 61%, suggesting that in wetter years more DCD would be leached. There was a soil type effect on the amount of DCD remaining in the soil after 10 weeks. There was up to 5 times higher DCD levels found in the JC than in the MP soil ($P<0.01$). Hence, although both soils were incubated at the same temperature and treated the same, degradation rates seemed to vary dramatically. This suggested that soil specific factors influenced the degradation of DCD in soil. Possible reasons for this could have been that the higher carbon content in the MP soil increased the biological activity within this soil. The total DCD recovery (soil and leachate), ranged between 13–65%. The low total recovery of DCD at the end of the study is likely to be due to DCD degradation to the end products NH_3, CO_2 and H_2O.

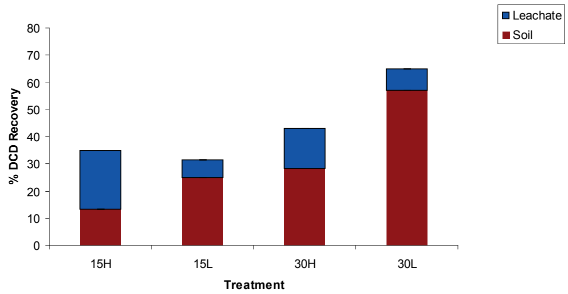

Figure 1a. Soil & leachate DCD recovery in JC soil

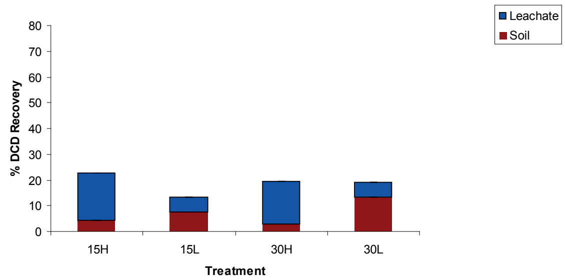

Figure 1b. Soil & leachate DCD recovery in MP soil

Conclusions
Soil type had no effect on DCD leaching but did affect DCD retention in soil. The soil type effect on DCD will affect its efficacy on different sites and helps elucidate the variable agronomic responses to DCD.

Acknowledgements
This research was financially supported under the National Development Plan, through the Research Stimulus Fund, administered by the Department of Agriculture, Food and the Marine (RSF 07 519).

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The effect of the nitrification inhibitor dicyandiamide (DCD) on dairy cow rumen function

P.J. O'Connor[1, 2], D. Hennessy[1], M. O'Donovan[1], M.B. Lynch[2] and E. Lewis[1]

[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork* [2]*UCD School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4*

Introduction

Urinary N has a high potential for leaching (Haynes and Williams, 1993) and urine patches account for approximately 25% of the paddock area over the year (Haynes and Williams, 1993). Hence, urinary N leaching can be a major issue. Moir *et al*. (2007) reported that dicyandiamide (DCD) reduced nitrate (NO_3^-) leaching under urine patches by slowing the conversion of ammonium (NH_3^-) to NO_3^- in the soil, thereby increasing the quantity of available N in the soil. Dicyandiamide applied at a rate of 10 kg ha^{-1} can reduce NO_3^- leaching by 45% and nitrous oxide (N_2O) emissions by 70% under dairy cow urine (1000 kg N ha^{-1}) patches in Irish soils (Selbie *et al*., 2011). Therefore, N emissions from pastures can be significantly reduced by applying DCD to pastures. Recently there has been increasing interest in supplementing animals with nitrification inhibitors, so that the nitrification inhibitor is excreted with the urine and can work directly on the urine patch eliminating the requirement for broadcast application in the field. Ledgard *et al*. (2008) demonstrated that at least 86% of DCD infused into the rumen or abomasum of sheep was excreted in the urine. There is no published research on the effects that the infusion of DCD may have on the rumen function of dairy cows. Rumen parameters such as pH and volatile fatty acids (VFA) are an important factor in relation to animal health, performance and welfare (de Veth and Kolver, 2001). Therefore, the objective of this study was to investigate the effects on dairy cow rumen function of infusing the nitrification inhibitor dicyandiamide (DCD) into the rumen.

Materials and Methods

The experiment took place at the Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork. A Latin square experimental design was used with 2 treatments and 2 periods. Eight non-lactating Holstein-Friesian dairy cows, fitted with ruminal cannulae, were housed in individual stalls. In each period, the animals were offered fresh cut perennial ryegrass pasture daily at a feeding rate of 2.5 times maintenance. Each period lasted 12 days. This composed of a 6-day acclimatization stage and a 6-day treatment and measurement stage. The two periods were separated by a 10-day washout cycle. The two treatments were: (1) Control (CON), 500 ml distilled water daily and (2) Dicyandiamide (DCD), 0.1 g DCD kg lwt^{-1} dissolved in 500 ml distilled water daily. The treatments were pulse-dosed into the rumen daily during the 6-day measurement stage with half the volume dosed in the morning and the remaining half in the afternoon. Rumen measurements took place on days 7, 8 and 11 of each period at 09:00 h and 15:00 h. At these times rumen samples were collected. The samples were strained through three layers of synthetic cheesecloth and frozen for subsequent analysis of lactic acid. The samples were frozen with 50% TCA for subsequent analysis of VFA and ammonia. The data were analysed as a 2x2 Latin square using the mixed procedure (PROC MIXED) of SAS with treatment, experimental period, square, cow and their interactions included in the model.

Results and Discussion

The infusion of DCD into the rumen of dairy cows had no effect on any of the rumen function parameters measured in this experiment as illustrated in Table 1. Rumen parameters examined in this experiment were within the normal range reported for dairy cows offered a pasture diet (Kolver and de Veth, 2002).

Table 1 The effect of DCD compared to a control infusion of distilled water on ammonia, lactic acid, total VFA, concentrations of individual VFA and the ratio of Ketogenic:Glucogenic VFA in non-lactating dairy cows offered a pasture diet.

Item	Con	DCD	s.e.m.[a]	Sig
pH	5.96	5.93	0.06	NS
Ammonia (umol/L)	22.0	20.91	0.99	NS
L-lactic acid (mmol/L)	0.88	1.05	0.22	NS
D-lactic acid (mmol/L)	3.50	3.46	0.45	NS
Total VFA (mmol/l)	121.6	117.2	3.57	NS
Acetic acid (mmol/l)	76.4	73.7	2.33	NS
Propionic acid (mmol/l)	22.2	21.8	0.95	NS
Butyric acid (mmol/l)	16.9	15.9	0.45	NS
Iso acids (mmol/l)	4.35	4.1	0.15	NS
Other acids (mmol/l)	1.77	1.68	0.54	NS
Ketogenic:glucogenic VFA ratio [b]	4.25	4.20	0.11	NS

[a] Standard error of mean
[b] (acetic + butyric) / propionic

Conclusion

The infusion of DCD into the rumen of non-lactating dairy cows is a novel concept to directly apply DCD to urine patches on a grazing sward. Dicyandiamide had no deleterious effect on the rumen function of non-lactating dairy cows as evidenced by no change to the rumen parameters.

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Effect of animal type, diet and temperature on ammonia emissions from bovine slurry during storage

N.M. Rochford[1, 2], G. J. Lanigan[1], S.T.J. Lalor[1] and K. A. Byrne[2]
[1] *Crops, Environment and Land Use Programme, Teagasc, Johnstown Castle, Wexford.* [2] *Department of Life Sciences, University of Limerick, Limerick.*

Introduction

Agriculture is responsible for 98% of Ireland's total ammonia (NH_3) emissions, with land-spreading and housing/storage of these manures contributing the majority of these emissions (Hyde *et al.*, 2003). Currently, national NH_3 inventory calculations do not account for animal type, diet or climatic conditions. The objective of this experiment was to quantify the effect of animal type, diet and temperature on NH_3 emissions from bovine slurry in storage.

Materials and Methods

Slurry was collected separately from two bovine animals of four different age groups: dry dairy cows, dry suckler cows, 13 month steers and 8 month heifers. The animals were fed three different diets ad-lib over a two to three week period or until approximately 200 litres of slurry had been collected. This was then divided up into 25 litre batches and frozen until incubation. The three diets were chosen to represent different C: N ratios of typical Irish livestock diets. Diets were: 1. ad-lib grass silage; 2. 50 % grass silage and 50 % concentrates, and 3. ad-lib concentrates and straw. Slurries were incubated in 5 litre cylinders, at 80 % relative humidity and at temperatures of 5, 10, 15, 20 °C. The experiment was conducted as a randomised block design with four replications. Ammonia emissions were measured on days 0, 5, 9, and 14 of incubation, using a static chamber coupled to an Innova 1412 Photoacoustic Field Gas Monitor (LumaSense Technologies, Inc.). Fluxes were calculated based on concentration accumulation within the chamber over a five minute period. The effects of diet, animal type and temperature and their interactions on cumulative emissions were analysed by Analysis of Variance using Proc Mixed in SAS.

Results and Discussion

Ammonia emissions were significantly affected by animal type ($P<0.001$), diet ($P<0.001$) and temperature ($P=0.05$). All two-way interactions were also significant ($P<0.05$). The effect of the interaction of animal type and diet is shown in Fig. 1. Manure from the older animals fed diets 1 and 2 had the highest emissions. Diet 3 resulted in the lowest emissions, with no significant variation amongst animal type. The effect of the interaction of diet and temperature is shown in Fig. 2. Emissions increased significantly with temperature only in the case of diet 1. The interaction of the effects of animal type and temperature on emissions is shown in Fig. 3. Manure from the older animals had higher emissions compared to the younger animals across all temperatures. However, there was no clear effect of temperature on emissions from each animal type, except in the case of dairy cows at 15 °C, and 8 month old heifers at 20 °C.

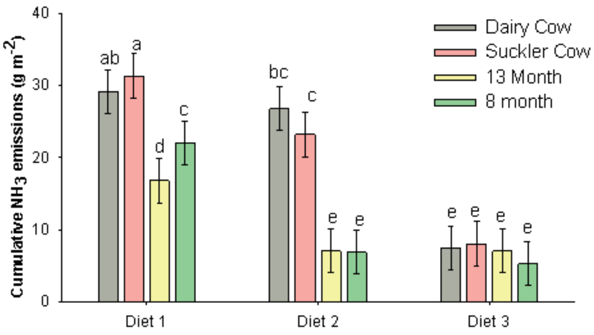

Fig. 1. Effect of diet and animal type on NH_3 emissions from bovine slurry in storage. (Letters indicate differences at $P<0.05$)

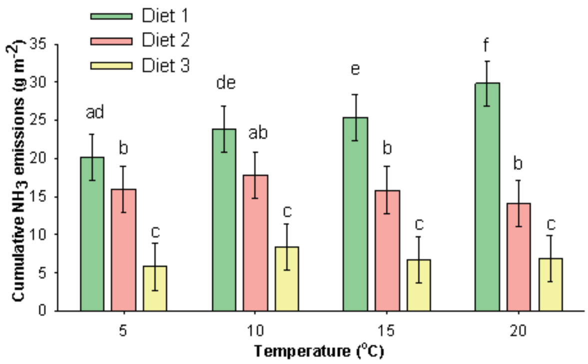

Figure 2 Effect of temperature and diet on NH_3 emissions.

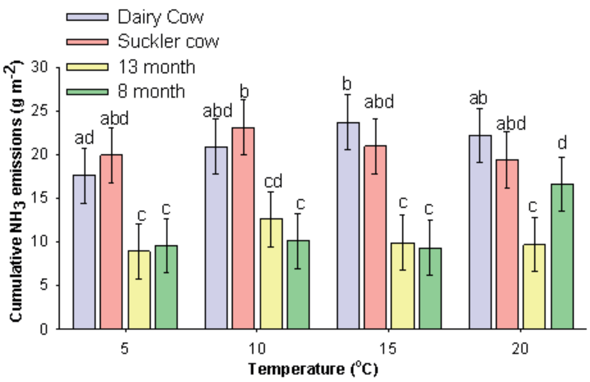

Figure 3 Effect of temperature and animal type on NH_3 emissions.

Conclusions

Animal type, diet and temperature had a significant effect on ammonia emissions during manure storage, indicating that the inclusion of these factors may increase the accuracy of ammonia emission inventory calculations. Further work is required to relate these emissions data to varying manure characteristics and farm-scale housing systems.

Acknowledgements

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Slow delivery of a nitrification inhibitor to soil using a biodegradable hydrogel

E. Minet[1], K.G. Richards[1], D. Rooney[2], C. Breslin[2], C. O'Carroll[2] and L. Gallagher[2]
[1] *Teagasc Environment Research Centre, Johnstown Castle, Co. Wexford, Ireland.* [2]*NUI Maynooth, Chemistry Department, Maynooth, Co. Kildare, Ireland*

Introduction

Reactive nitrogen (N) losses and greenhouse gas emissions from agricultural soils are a source of concern for animal/human health and the environment (Stark and Richards, 2008). A mitigation technique tested with some success is the use of nitrification inhibitors, which can limit N oxidation to nitrate and the formation of other unwanted contaminants (nitrous oxide, methane). However, inhibitors have a limited life-span in soils and repeated soil applications are required to maintain efficiency. A novel approach developed at NUI Maynooth and tested at Teagasc consists of applying a nitrification inhibitor encapsulated in a biodegradable polymeric hydrogel (O'Carroll *et al*. 2010). Although well known in the pharmaceutical industry, this type of slow-release matrix has never been used in an agricultural context. The research objective was to investigate the effect of rainfall rate and soil moisture on dicyandiamide (DCD) soil release from chitosan hydrogel.

Materials and Methods

Chitosan hydrogel was synthesised as small beads (diameter < 2 mm) in a multi-step procedure (O'Carroll *et al*., 2010): i) aqueous solution of chitosan (Sigma-Aldrich) added drop by drop to a solution of DCD + ionic cross-linker (sodium tri-polyphosphate), ii) further polymerisation with a covalent cross-linker (glyoxal), iii) washing in a DCD solution and iv) air-drying.

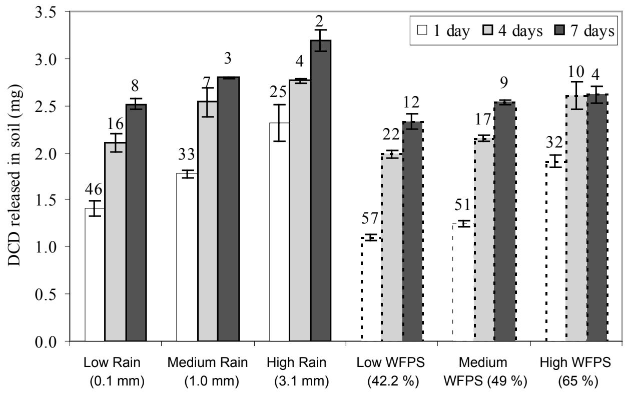
Slow-release of DCD was tested on 6.7 mm-sieved loam soil (Johnstown Castle, Co. Wexford). Each experimental unit (100 ml plastic cup) contained 35 g of dry matter (initial soil moisture content = 30.7 % of dry weight) compacted to 40 ml (19.6 cm^2 cross section) onto which were dropped 20 loaded beads (13 kg DCD/ha). Six treatments were investigated: rainfall rates of 0.1, 1 and 3.1 mm and the corresponding water filled pore space (WFPS) of 42, 49 and 65 %. Samples were incubated at 5 ºC and DCD was destructively sampled on days 1, 4 and 7. The experiment was a randomised block design with 3 replicates per treatment per time point. DCD was extracted from the soil and beads using 2 M KCl, then quantified by reverse-phase HPLC analysis and UV-visible detection (Turowski and Deshmukh, 2004) at 215 nm.

Effects of treatment, time and shelf (blocking factor) on DCD soil release were investigated in a three-way analysis of variance (ANOVA). Bonferroni Post-Hoc tests were used to make pairwise comparisons where significant effects were found.

Results and Discussion

The interaction between treatment and time was not significant ($p = 0.064$). DCD soil-release from chitosan beads significantly increased with time ($p \leq 0.0001$): the amount recovered in soil was the lowest at day 1, followed by day 4 and then day 7 (Figure 1). The rate of DCD release decreased with time. Treatment had a significant effect on DCD soil-release ($p \leq 0.0001$). Pairwise comparisons revealed a significant increase with higher rain ($p \leq 0.0005$). The amount of DCD in soil was greatest at the high WFPS compared to the low and medium WFPS ($p \leq 0.0001$) and there was no difference between low and medium WFPS. The medium and high rainfall treatments had significantly higher ($p < 0.0005$) soil DCD than the corresponding medium and high WFPS treatment. This probably reflected the fact that beads were wet more thoroughly and quickly when water was applied from the top (rain) than when moisture had to diffuse up in the hydrogel.

Figure 1: Mean amount of DCD (in mg ±SE, 3 reps) released in soil by 20 chitosan beads after 1-, 4- and 7-day incubation (5 °C) under varying rainfall rates and WFPS (with corresponding percentages of encapsulated DCD remaining in hydrogel)



The amount of DCD present in beads decreased as the amount of DCD increased in soil (Figure 1): less than 12 % remained encapsulated after 7 days.

Conclusions

The results showed that chitosan hydrogel can delay the soil-delivery of DCD under varying rainfall rates and soil moisture conditions. However, the release process remained fast across all treatments. Further improvements will be needed to delay DCD release over a much longer period of time to be a credible alternative to spray application.

Acknowledgments

The authors thank the Department of Agriculture and Food for funding provided by the Research Stimulus Fund Programme (RSF 07 545).

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The effect of stocking rate on the economic and technical performance and greenhouse gas emissions profile of suckler beef production systems

A.M. Clarke and P. Crosson
Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co. Meath.

Introduction

With EU targets of a 20% reduction in greenhouse gas (GHG) emissions by 2020, agriculture will be required to share the burden of emissions reductions. However, in the context of the targets set out in Food Harvest 2020 for an increase in beef output of 20%, the goal must be to reduce emissions per unit of product produced i.e. to reduce emissions intensity. The objective of this study was to evaluate the impact of increasing stocking rate on the economic and technical performance and GHG intensity of suckler beef production systems.

Materials and methods

For the evaluation of whole-farm system economics and to generate system production profiles, a bioeconomic model of suckler beef production systems, the Grange Beef Systems Model GBSM (Crosson, 2008) was used. The systems of production modelled were based on spring calving suckler calf to beef research farm systems evaluated at Teagasc, Grange. Heifers were finished at 20 months of age whilst males were finished as bulls at 16 months of age. Stocking rate was increased by increasing nitrogen (N) application rates. Eight scenarios representing production systems stocked at between 150 and 220 kg N/ha were evaluated. To model the impact of each scenario on GHG emissions, a suckler beef GHG systems model (BEEFGEM; Foley et al., 2011) was used. This is a single-year, static model which integrates the beef enterprise production profile from GBSM with various GHG emission factors. Direct GHG emissions associated with on-farm activities and indirect GHG emissions associated with purchased inputs and nitrous oxide (N_2O) emissions arising from nitrate leaching and ammonia (NH_3) volatilization are simulated. All the estimated GHG emissions are converted to their 100-year global warming potential carbon dioxide equivalent (CO_2 e) which on a weight basis, relative to CO_2 was set to a factor of 25 for methane (CH_4) and 298 for N_2O.

Results and discussion

Carcass output and profitability increased with increasing stocking rate (Table 1). With each incremental increase in stocking rate, there was a linear increase in the application rate of inorganic N fertilizer. The relative contributions of direct emissions (enteric fermentation, manure management and diesel use), excluding soils emissions, decreased with increasing stocking rate, while emissions from soil and indirect emissions (inputs and indirect N_2O) increased (Figure 1). Overall increasing stocking rate resulted in improved technical and economic performance, however GHG emissions also increased.

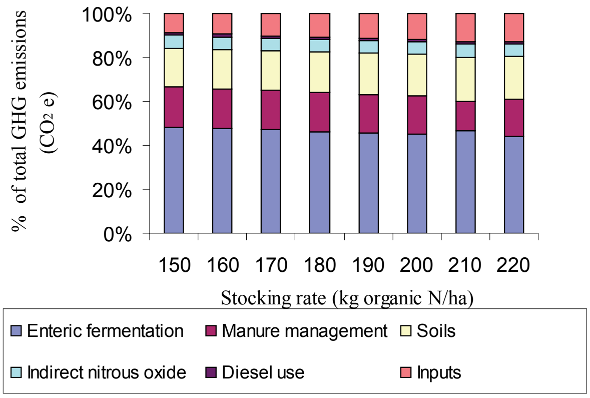

Figure 1: Relative contribution of GHG emission sources

Conclusion

Increasing stocking rate resulted in increased net margin and GHG emissions per kg of beef produced. This highlights the importance of modelling both environmental and economic aspects of sustainability in beef production systems.

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Table 1.Effect of stocking rate on the economic & technical performance & GHG on bull systems of production

Organic nitrogen (kg/ha)	150	160	170	180	190	200	210	220
Farm size (ha)	58.5	54.9	51.8	49.0	46.3	44.0	42.0	40.0
Fertiliser N (kg/ha)	64	81	98	116	136	157	180	204
Carcass output (kg/ha)	410	436	463	489	517	545	570	599
Gross margin (€/ha/yr)	576	630	683	735	790	844	891	943
Net margin (€/ha/yr)	199	228	257	284	313	341	365	390
Direct GHG emissions (kg CO_2 /kg beef)	19.9	20.0	20.2	20.3	20.4	20.5	20.6	20.7
Indirect GHG emissions (kg CO_2/kg beef)	3.4	3.6	3.8	4.0	4.2	4.4	4.6	4.8

Influence of a 50-day dietary restriction on pregnancy per artificial insemination in beef heifers.

M.H. Parr[1, 3], P. Lonergan[2], A.C.O. Evans[2], J.F. Roche[3], T. Fair[2], M.A. Crowe[3], M.G. Diskin[1].
[1]*Animal & Grassland Research & Innovation Centre, Teagasc, Mellows Campus, Athenry, Co. Galway,* [2]*School of Agriculture and Food Science,* [3]*School of Veterinary Medicine, University College Dublin, Belfield, Dublin 4,*

Introduction
It has been hypothesised that follicle development in a period of negative energy balance (NEB), as experienced by the postpartum dairy cow, could be affected by undesirable metabolic changes, and may contain a developmentally incompetent oocyte with an impaired potential to establish a pregnancy (Britt, 1992). It has been established that there was a close relationship between concentrations of non-esterified fatty acids (NEFA) in plasma and follicular fluid in heifers (Jorritsma et al., 2003). To address the potential impact of NEB on oocyte quality, the objective of this study was to establish (i) the concurrent, and (ii) the carryover effects of a 50 day (d) period of dietary restriction on pregnancy per artificial insemination (P/AI) in heifers.

Materials and Methods
A total of 156 reproductively normal, two year old beef heifers with an initial (mean ± SEM) live weight and body condition score (BCS) of 581 ± 4.4 kg, and 3.45 ± 0.05, respectively, were used across four replicates. Heifers were randomly assigned to either a (i) control feed intake group (C, n=68, 1.3 times estimated maintenance energy (M) requirements for 50 d; start = d 0) or (ii) restricted feed intake (R, n=88, 0.65 M for 50 d). Maintenance was calculated from the following equation: (0.091*liveweight) + 8.3 validated by (Mackey et al., 1999). Following the 50-d differential dietary treatment period, all heifers were fed a 2 M diet until the end of the study. Liveweight and BCS were recorded on d 0, 14, 21, 28, 35, 42, 50, 57 and 90. Concentrations of NEFA, beta hydroxy butyrate (BHB), urea and glucose in plasma were measured on d 0, 14, 28, 35, 42, 50, 57, and 90. Oestrus was synchronised using two injections of prostaglandin $F_{2\alpha}$ (PGF2α) administered on d 37 and 48 respectively. Heifers were artificially inseminated (AI) on d 50-52 using frozen thawed semen from one high fertility bull. Pregnancy was determined by ultrasonography 30 d after AI. Following pregnancy diagnosis, all heifers were injected with PGF2α to induce luteoloysis and allow return to oestrus. All heifers were inseminated again on d 93-95 and P/AI was determined 30 d later. Liveweight, BCS and metabolite data were analysed using the Mixed procedure of SAS for repeated measures ANOVA with terms for day, treatment and replicate and their interaction included in the model. Pregnancy per AI was analysed by Fisher's exact chi-square.

Results and Discussion
During the first 50 d of differential feeding, heifers on the R diet lost more weight (70.5 ± 2.8 *v* 5.8 ± 2.1 kg, respectively; P<0.001)) and had greater BCS loss (0.45 ± 0.03 *v* 0.05 ± 0.03 units respectively; (P<0.001)) than heifers on the C diet. In the period whilst heifers were on 2 M, the R heifers gained more weight 79.6 ± 2.5 *v* 49 ± 2.6 kg respectively (P<0.001) and had greater BCS gain 0.38 ± 0.03 *v* 0.18 ± 0.03 units respectively (P<0.001) than heifers on the C diet. A treatment x day interaction was observed for NEFA (P<0.001), BHB (P<0.01) and urea (P<0.05) on d 14, 28, 42 and 50 respectively. Concentration of glucose remained unchanged in both treatment groups. Pregnancy per AI (C: 69%, R: 72%, P>0.05) was similar following AI at d 50. However, following AI at d 93, (C: 64%, R: 80%, (P=0.03), P/AI was lower in C heifers. Although P/AI was lower in C than R heifers following both inseminations, it was in line with previous findings for P/AI in heifers (Parr et al., 2010). Effects were consistent across replicates. Concentrations of NEFA in the R group (Figure 1) were similar to those found in post partum dairy cows (Leroy et al., 2005).

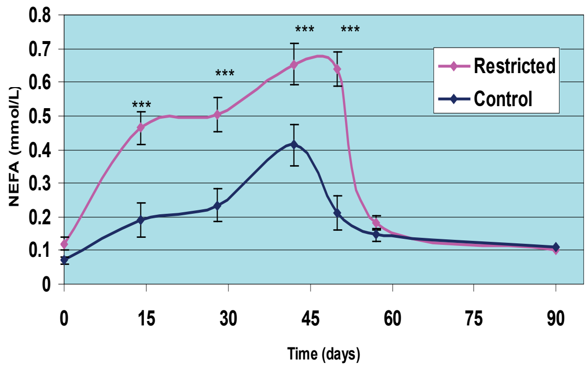

Figure 1. Effect of differential dietary energy intake for 90 d on plasma concentrations of NEFA (± S.E.M.) ***P<0.001.

Conclusions
There was no evidence that a dietary-induced 50 d period of NEB had any concurrent or carryover effects on P/AI in heifers despite an elevation in systemic concentrations of NEFA.

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The effect of genetic merit for fertility traits on regulation of the somatotropic axis in hepatic tissue in Holstein cows

S. B. Cummins[1, 2], S.M. Waters[3], A.C.O. Evans[2], P. Lonergan[2] and S.T. Butler[1]

[1] *AGRIC, Teagasc, Moorepark, Fermoy, Co. Cork.* [2] *School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4.* [3] *AGRIC, Teagasc, Grange, Dunsany, Co. Meath.*

Introduction

The growth hormone/insulin-like growth factor (somatotropic) axis is seen as an important biological mechanism linking nutritional status and reproduction (Lucy, 2001). We previously reported that genetic merit for fertility traits is associated with significant changes in reproductive efficiency, BCS profile and circulating concentrations of IGF-I (Cummins et al., 2011). Cows with good (Fert+) genetic merit for fertility traits had greater circulating concentrations of IGF-I throughout lactation compared with cows with poor (Fert-) genetic merit for fertility traits. The aim of this study was to determine the effect of genetic merit for fertility traits on transcriptional regulation of key genes controlling the hepatic GH-IGF axis during the gestation/lactation cycle

Materials and Methods

A total of 11 cows with good genetic merit for fertility (Fert+) and 12 cows with poor genetic merit for fertility (Fert-) were managed as a single herd under a grass-based system of production. Cows underwent liver biopsy by percutaneous punch technique on d 20 (± 6.7 d) prepartum and on d 2 (± 1.5 d), d 58 (± 3.7 d), d 145 (± 13 d) and d 245 (± 17.1 d) postpartum. Total RNA was isolated and the mRNA expression of growth hormone receptor (GHR 1A and GHRtot), IGF-I, janus tyrosine kinase 2 (JAK2), signal transducer and activator of transcription 5B (STAT5B), suppressor of cytokine signalling 3 (SOCS-3), acid-labile subunit (ALS), and IGF binding proteins (IGFBP1 to IGFBP6) were measured by RT-qPCR. Blood samples were collected coinciding with each biopsy, and circulating concentrations of IGF-I and insulin determined. All data were checked for normality, and transformed if necessary. Mixed models repeated measures analysis were used to compare plasma IGF-I and gene expression data between genotypes. The model included the fixed effects of genotype, time, parity, and their interactions. Cow nested within genotype was included as a random effect. Pre-planned contrasts using the ESTIMATE statement were carried out to compare gene expression data between Fert+ and Fert- cows during three distinct time periods; the dry period (wk -3), early lactation (wk 1 and wk 8), and mid/late lactation (wk 20 and wk 35).

Results and Discussion

During lactation, circulating concentrations of IGF-I were 34% greater in Fert+ cows ($P < 0.01$). Fert+ cows had increased mean expression of *IGF-I* mRNA during the study; however, the differences in *IGF-I* mRNA abundance between Fert+ and Fert- cows was most pronounced at d 145 and d 245. The expression of *IGFBP3* and *ALS* transcripts were similar in Fert+ and Fert- cows for the duration of the study. Fert- cows, however, had greater ($P < 0.05$) expression of *IGFBP2*, *IGFBP4*, *IGFBP5* and *IGFBP6*. There was no effect of genotype on mRNA abundance of *GHR 1A*, *STAT5B*, *JAK2*, or *SOCS-3* ($P > 0.05$).

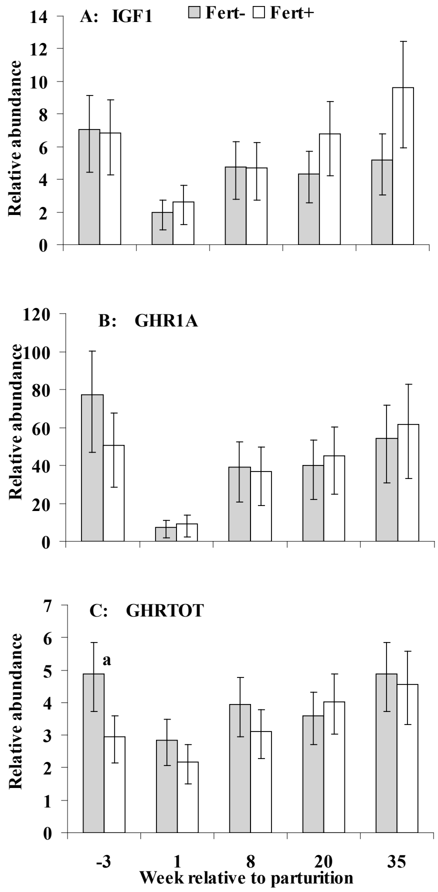

Fig 2. Relative abundance of mRNA in liver for (A) IGF-I, (B) GHR 1A, and (C) GHRtot during wk -3, 1, 8, 20 and 35 relative to parturition in Fert+ and Fert- cows. Vertical bars indicate 95% confidence intervals. (A) IGF-I: IGF-I mRNA abundance was significantly greater in Fert+ cows ($P < 0.05$) over the duration of the study. No genotype × wk or genotype × parity interaction existed ($P > 0.05$). (B) GHR 1A: No genotype, genotype × wk or genotype × parity interaction effects were detected for transcript abundance of GHR 1A ($P > 0.05$). (C) GHRtot: Transcription of GHRtot was significantly greater in Fert- cows ($P < 0.05$) over the duration of the study. *a* denotes differences at $P < 0.1$.

Conclusions

These results demonstrate that genetic merit for fertility traits affects hepatic expression of key genes of the somatotropic axis regulating the synthesis, bioavailability and stability of circulating IGF-I.

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A comparison of the plasma and uterine proteome in cattle; evidence for a dynamic uterine environment

S. Faulkner[1,2], M. Mullen[1], G. Elia[2], P. O'Boyle[1], M. Dunn[2], D. G. Morris[1]

[1] *Animal and Bioscience Research Department, Animal & Grassland Research and Innovation Centre, Teagasc, Mellows Campus, Athenry, Co. Galway, Ireland and* [2] *Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Belfield, Dublin, Ireland.*

Introduction

Early embryo loss is one of the greatest factors affecting fertility in cattle. Prior to implantation the bovine embryo is dependent on uterine fluid for normal growth and development. Uterine fluid has always been considered as a transudate of plasma. Despite this, there is a paucity of information regarding the composition of the bovine uterine proteome. The objective of this study was to identify differences between the plasma and uterine proteome that may play a pivotal role in embryo development and survival.

Materials and Methods

Sample collection was carried out under license in accordance with European Community Directive 86/609/EEC. Uterine flushings (UF) were collected non-surgically from the ipsi- and contralateral uterine horns of cross-bred beef heifers (n=6) on day 7 of the oestrous cycle. Blood plasma (n=4) was collected immediately after flushings and all samples were stored at -80°C until analysis. Samples were albumin depleted using the ProteomeLab™ IgY-BSA spin column proteome partitioning kit (Beckman Coulter, USA) (Faulkner et al., 2011). A total of 50µg of protein from each sample were iTRAQ® labelled prior to separation into 12 fractions using strong cation exchange chromatography. Liquid chromatography (LC) and mass spectroscopy (MS) were performed on each fraction using an Agilent 1100 nanoLC system (Agilent, Germany) and a QSTAR XL mass spectrometer (ABI, USA). MS spectra were automatically taken according to the manufacturers instrument settings for LC-MS/MS analyses. Proteins were identified and quantified using the Mascot Server and an in-house curated version of the IPI protein database for *Bos taurus* (version 3.66, Feb 2011). Proteins were identified with a minimum of 2 peptides at a significance threshold of $P<0.05$. Reporter ion ratios were normalised by summed intensities and quantification was performed by comparing the iTRAQ® protein reporter ion ratios to those obtained from a pooled reference sample. Western blotting was carried out to confirm quantitative MS data. Data were analysed using mixed model ANOVA (PROC MIXED, SAS v 9.1). Student's t-test corrected for multiple testing using the Benjamini and Hochberg correction was used to identify differentially expressed proteins. Proteins with a <10% false discovery rate and a fold-change of ±1.5 or greater were considered to be differentially expressed. Biological processes associated with the differentially expressed proteins were identified using a combination of the PANTHER™ (Protein ANalysis Through Evolutionary Relationships) Classification system and information available in the Uniprot knowledgebase (www.uniprot.org).

Results and Discussion

This is the first study to compare the plasma and uterine proteome in cattle. Thirty-five proteins were higher in UF compared to plasma. Uterine predominant proteins were from 2.5 to 11.3-fold higher in UF. The three proteins present at the highest concentration in UF were triosephosphate isomerase, protein S100-A12 and macrophage migration inhibitory factor which were 11.3, 11.1 and 8.4-fold higher respectively. In contrast, 18 proteins were found to be 1.9 to 10.9-fold lower in UF. The three proteins with the lowest concentration in UF were alpha-2-macroglobulin, apolipoprotein A-I and 50kDa protein (FGG) which were 6.1, 8.6 and 10.9-fold lower respectively. Western blotting confirmed Annexin A1 as a uterine predominant protein and that RBP4 is not different between UF and plasma (data not shown). Annexin A1 was 6.1-fold and 2.9-fold higher in UF as determined by iTRAQ and Western blotting respectively (Fig. 1).

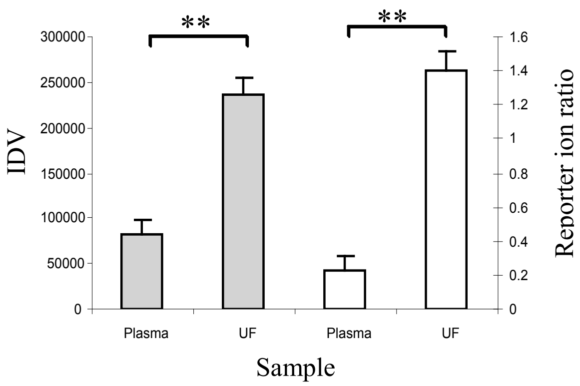

Figure 1. Integrated density value (IDV) (shaded bars) and average reporter ion ratio (open bars) for annexin A1 which were obtained by Western blotting and iTRAQ respectively. Data are presented as least square means and standard errors (** = P<0.01).

Conclusions

The findings of this study indicate that there are many uterine proteins whose concentrations differ significantly from plasma. These proteins are involved in a variety of functions including energy substrate availability, regulation of prostaglandin synthesis, moderation of immune response and reduction of oxidative stress. The concentrations of these proteins appear to be regulated by the uterine endometrium through either selective mechanisms or synthesis and are possibly influenced by environmental factors including the local steroidal mileu. Further studies into mechanisms affecting uterine protein secretions and their impact on embryo development and survival may help to develop strategies to reduce early embryo loss.

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Negative energy balance alters hepatic miRNA expression in dairy cows during the early post partum period

A. Fatima[1,2], C. Seoighe[2], P. O'Boyle[1] and D.G. Morris[1]
[1]*Animal and Biosciences Research Department, Teagasc, Mellows Campus, Athenry, Co. Galway, Ireland and* [2]*School of Mathematics, Statistics and Applied Mathematics, National University of Ireland Galway, Galway, Ireland.*

Introduction

Ribonucleic acid interference (RNAi) is the phenomena where small noncoding RNAs complementary to their target messenger RNA (mRNAs) silence specific genes post transcription. Micro RNAs (miRNAs) are a type of small non coding RNAs, about 19 to 25 nucleotide in length and are important regulators of gene expression in diverse cellular processes such as signal transduction, cell cycle, apoptosis, pluripotency, differentiation, and transformation. Micro-RNAs lead to target mRNA degradation and/or translation inhibition, typically, by base pairing with 3´untranslated regions (3´UTRs) of the target. Increased energy demands to support lactation, coupled with lowered feed intake capacity results in negative energy balance (NEB) in the early postpartum cow. The liver undergoes extensive physiological and biochemical changes in an effort to re-establish metabolic homeostasis and to counteract the adverse effects of NEB which can compromise cow health and fertility. The objectives of this study were: 1) to determine the effect of negative energy balance on the expression of miRNAs in early post-partum dairy cattle liver by performing microarray-based expression profiling, and 2) to investigate the potential role of miRNAs in the regulation of hepatic genes differentially expressed as a result of NEB.

Materials and Methods

An energy balance model of dairy cattle was developed using differential feeding and milking regimes to produce two groups; MNEB (mild negative energy balance) and SNEB (severe negative energy balance) with 6 animals in each group (McCarthy et al., 2010). Total RNA was extracted from frozen liver tissue harvested 11-16 days postpartum, using the Trizol procedure. The Affymetrix Gene Chip miRNAs_2.0 array was used for miRNA expression profiling. All array pre-processing and statistical analyses were performed with the statistical software R (Version; 2.14, www.r-project.org) and Bioconductor packages Affy and puma and quality assessed with the arrayQualityMetrics package (www.bioconductor.org). Differential expression was analyzed using the pumaDE method in the puma package. This method calculates the probability of positive log ratio (PPLR); an estimate of the false discovery rate. The PPLR statistic was then converted into P-like values using the recommended formula in the puma method. A P-like value of <0.05 with fold change of ±1.5 or greater from the puma analysis was set to identify miRNA genes whose expression was significantly up- or down-regulated. Microcosm Targets (www.ebi.ac.co.uk), a web resource for computationally predicted targets of miRNAs, was used to find putative miRNA targets in the 3'UTR regions of differentially expressed genes (mRNAs) in liver tissue from the same animals.

Results and Discussion

This the first study to report the effects of SNEB on liver miRNA expression. In this study ten miRNAs were increased while two were decreased following SNEB (Table1). Of these, miR-31 and miR-296 have been implicated in non-alcoholic fatty liver disease while miR-31 has also been associated with hepatocellular carcinoma. In addition miR-31 also has binding sites in the 3'UTR region of 9 differentially expressed hepatic genes reported previously in these animals. These include lysosomal protein trans membrane 4 alpha (LAPTM4A) and trans membrane protein 41A (TMEM41A), both of which code for proteins involved in metabolic processes of the liver including glycolysis. The results of this preliminary study indicate that miRNAs associated with liver diseases, are significantly up-regulated in the liver of the postpartum dairy cow under SNEB. In a previous study SNEB was reported to cause significant alterations in hepatic gene expression in these animals. This association between differentially expressed miRNAs and differentially expressed genes in the liver of SNEB animals will help to improve our understanding of the mechanisms and pathways involved in the NEB in postpartum dairy cattle.

Table 1: Differentially expressed miRNAs in liver

miRNA	Fold Change	P-like values
bta-miR-185_st	1.50	<0.000001
bta-miR-2328-star_st	1.72	<0.000001
bta-miR-2360_st	1.86	<0.000001
bta-miR-2885_st	1.54	<0.000001
bta-miR-31_st	1.79	<0.000001
bta-miR-2288_st	-1.72	<0.000001
bta-miR-2436-5p_st	1.79	<0.000001
bta-miR-296_st	1.51	0.000005
bta-miR-1281_st	1.70	0.000050
bta-miR-2361_st	1.60	0.000056
bta-miR-2391_st	-1.63	0.000062
bta-miR-2483_st	1.55	0.000169

Conclusions

SNEB affects hepatic miRNAs and their gene targets. Identification of SNPs in either the miRNA seed or the 3'-UTR regions of targets affected by SNEB could lead to a diagnostic test to identify animals susceptible to the deleterious hepatic effects of negative energy balance.

Acknowledgements

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High sperm numbers have detrimental effects on bull sperm during liquid storage

C. Murphy[1], A. Shafat[2] and S. Fair[1]
[1]*Department of Life Sciences, University of Limerick.*
[2]*Department of Physiology, National University of Ireland, Galway.*

Introduction

Due to genomic selection bulls which are in high demand are now entering into artificial insemination (AI) programmes at less than 1 year of age. A typical ejaculate from these bulls will yield 50-150 frozen doses compared to 500-1000 for a mature bull (20 x 10^6 sperm per dose). To maximise the use of young elite sires during a narrow breeding season it is imperative we develop protocols for the use of liquid semen whereby the sperm number per dose can be reduced without affecting fertility. Currently in Ireland, liquid bull semen contains 5 x 10^6 sperm per dose, compared to 2 x 10^6 sperm per dose in New Zealand (Verberckmoes et al, 2005). In addition, liquid semen has a limited lifespan and is not used at greater than 2.5 days post collection. The hypothesis of this study was that 5 x 10^6 sperm per dose is counter productive in terms of the generation of oxidative stress, inhibition of sperm mitochondrial activity as well as the consumption of glucose within the diluent and therefore, reducing the sperm number per dose will allow for liquid semen to be stored successfully for longer duration.

Materials and Methods

Semen was collected from Holstein and British Friesian bulls at a commercial AI centre (5 collections with 3-4 bulls per collection; collection = replicate). Sperm concentration was assessed and the ejaculate was diluted in a 5% egg yolk Caprogen diluent (purged in N gas) to a final concentration of 1 (T1), 2 (T2), 3 (T3), 4 (T4) and 5 (T5) x 10^6 sperm per insemination dose (0.25 mL straws). Semen from each bull was kept separate and each bull was represented in each treatment. Straws were stored at ambient temperature and assessed *in vitro* daily for 6 days (Day 0 = day of collection). On each assessment day, semen was evaluated for progressive linear motility (PLM), viability, oxidative stress, mitochondrial activity and glucose consumption. PLM was assessed using standard procedures. Sperm viability, oxidative stress and mitochondrial activity were examined using the fluorescent probes propidium iodide (PI), CM-H_2DCFDA and rhodamine 123 (R123), respectively, and analysed using flow cytometry (BD-LSR 1; BD Biosciences). Briefly, 1.4 x 10^6 sperm from each treatment were washed twice in phosphate buffered saline (PBS) at 800g for 10 min and incubated at 37°C in the presence of 125 µM CM-H_2DCFDA for 30 min followed by 300 µM PI for 15 min. A final wash was performed in PBS to remove excess stain and 10,000 events were analysed. Mitochondrial activity was analysed as above with the exception of a 15 min incubation at 37°C with 2.5 µM R123. For glucose analysis samples were centrifuged at 8000g at 4°C and the supernatant was removed, frozen at -20°C and analysed later using a commercial glucose assay kit (Megazyme, Ireland). Briefly, samples were diluted 1:2 with distilled water, added to 1 mL of glucose oxidase/peroxidase reagent and incubated at 45°C for 20 min. Absorbance was measured on a spectrophotometer and concentrations of glucose were determined using a standard curve. Data were examined for normality, transformed where appropriate and analysed using repeated measures in SPSS (version 20.0). The model included the main effects of day, treatment and day x treatment interactions. Results are presented as mean ± s.e.m.

Results and Discussion

There was no treatment x day interaction for any of the variables assessed. PLM declined with duration of storage from 95.1 ± 0.68% to 73.8 ± 0.99% for all treatments from Day 0 to 5, respectively ($P<0.001$). There was an effect of day and treatment on percentage live ($P<0.001$) with the highest percentage live in T1 and the lowest in T5 on all days (Day 0: 92.4 ± 0.74 and 67.0 ± 2.96% for T1 and T5, respectively, vs. Day 5: 82.8 ± 2.20 and 58.8 ± 3.56% for T1 and T5, respectively. The percentage of live sperm positive for CM-H_2DCFDA increased in all treatments on each day of storage (Fig. 1; $P<0.001$). There was an effect of treatment ($P<0.001$) with T1 having the lowest percentage of live sperm positive for CM-H_2DCFDA every day and T5 the highest on five days. The percentage of live sperm positive for R123 ranged between 91.6 and 95.8% and was not affected by treatment ($P>0.05$). The level of glucose in Caprogen declined with duration of storage ($P<0.001$), being lowest in T5 and highest in T1 on Day 5 (808.6 ± 23.90 and 964.6 ± 18.90 µg/mL, respectively).

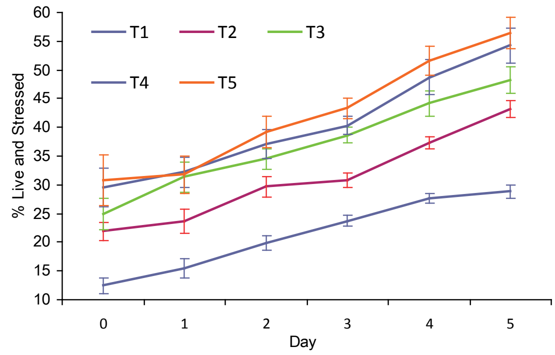

Fig. 1: The percentage of live bull sperm positive for oxidative stress. Semen was stored at a range of concentration from 1-5 million sperm per dose for 6 days post collection; Vertical bars represent ± s.e.m.

Conclusions

Reducing the sperm number per dose reduces the level of oxidative stress and may be beneficial to the prolonged storage of liquid bull semen.

Acknowledgments

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Effect of trace mineral supplementation on the reproductive performance of lactating dairy cows

H Watson[1,2], ACO Evans[2] and ST Butler[1]
[1] *AGRIC, Teagasc, Moorepark, Fermoy, Cork.* [2] *School of Agriculture and Food Science, UCD, Dublin 4, Ireland*

Introduction

Trace mineral deficiencies can arise in pasture-based systems where grazed pasture is deficient or imbalanced in one or more TM and concentrate supplementation is reduced as grass availability increases. The aim of this study was to examine the effects of administering slow release TM boluses at different timepoints on: (i) temporal patterns in blood indicators of trace mineral status; and (ii) effects on reproductive performance in dairy cows in seasonal calving pasture-based systems.

Materials and Methods

This study was a completely randomized experimental design that used 1,381 dairy cows on 5 dairy farms with low levels of concentrate supplementation (<500 kg per cow per year). Within each farm, cows were sorted on the basis of parity and expected calving date, and randomly assigned to one of four treatments: CTRL cows received no TM bolus; DRY cows received TM bolus at dry-off; BREED cows received TM bolus 6 weeks before planned mating start date (MSD); DRY_BREED cows received TM boluses at dry-off and 6 weeks before MSD. Cows were weighed immediately before bolus administration. Cows ≥550 kg received two boluses at the time of treatment, and cows <550 kg received one bolus according to the manufacturers instructions. Each TM bolus contained 30 g Cu oxide, 3400 mg I, 500 mg Se, and 500 mg Co. Blood samples were collected (and plasma harvested) from 10 cows per treatment on each farm at 6 time points between dry-off and 6 weeks after MSD. Plasma samples were analysed for concentrations of Cu, Se and inorganic I (PII). Herd breeding records and ultrasound scanning results at the end of the breeding season were collated. Of the cows initially enrolled, 1311 were retained for analysis of fertility data. Blood TM concentration data were checked for normality, and treatment effects analysed using mixed model repeated measures procedures (SAS Institute Inc., Cary, NC). Treatment, time, treatment × time, parity and farm were included as fixed effects and cow was included as a random effect. Binary reproductive variables were analysed using the Chi-square test.

Results and Discussion

All the herds enrolled in this study were fed concentrate feed for longer than usual in early lactation due to poor pasture availability, thereby increasing the duration of postpartum trace mineral supplementation. PII ($P<0.001$) and plasma Se ($P=0.03$) were affected by TM treatment, but plasma Cu was not ($P>0.5$; Figure 1). PII concentrations were similar to untreated cows at 3 months after bolus administration. Fertility performance data are summarized in Table 1.

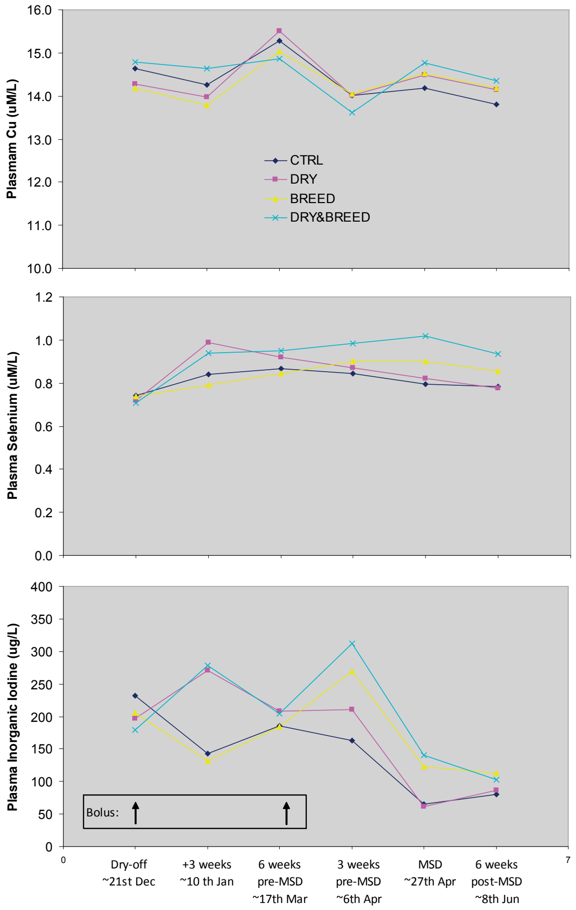

Fig. 1. Temporal patterns of plasma Cu (top), Se (middle) and inorganic I (bottom) in cows administered boluses at different time points.

Conclusions

The results indicate that TM bolus supplementation is unlikely to have a major effect on herd reproductive performance in well managed, low-input pasture-based herds where concentrates are fed until at least 3 weeks before MSD.

Acknowledgements

AllSure boluses were supplied by Animax Ltd.

Table 1. Effects of TM bolus on reproduction variables.

	CTRL	DRY	BREED	DRY_BREED	P-value
n	352	340	335	339	-
21 day submission rate	80.4	82.0	78.5	79.3	0.7
Pregnancy rate to first AI	51.0	52.4	53.3	53.7	0.9
42 day pregnancy rate	66.1	65.9	64.2	70.7	0.3
Final pregnancy rate	86.3	87.0	88.0	87.9	0.9

Examination of the factors responsible for differences in circulating progesterone in lactating dairy cows with divergent genetic merit for fertility traits.

S.G. Moore[1, 2], S. Scully[2], M.A. Crowe[3], A.C.O. Evans[2], P. Lonergan[2], T. Fair[2], and S.T. Butler[1]
[1]Teagasc, Moorepark Animal and Grassland Research and Innovation Centre, Fermoy, Co.Cork. [2]School of Agriculture and Food Science, [3]School of Veterinary Medicine, UCD, Dublin 4.

Introduction
A lactating cow model of fertility has been established composed of two groups of cows with similar genetic merit for milk production traits, but with extremes of good (Fert+) or poor (Fert-) genetic merit for fertility traits. Previous work has indicated that circulating progesterone (P4) concentrations are greater in Fert+ compared with Fert- cows (Cummins et al. 2010). The objectives of this study were to examine corpus luteum (CL) blood flow, hepatic mRNA abundance of genes responsible for P4 catabolism, and metabolic clearance rate (MCR) of P4 in Fert+ and Fert- cows.

Materials and Methods
22 dairy cows with good (n=13, Fert+) or poor (n=9, Fert-) estimated breeding values (EBV) for calving interval (Table 1) were enrolled in the study. The average (± SD) parity and days postpartum at the initiation of the study were 2.7±0.48 and 2.2±0.44, and 61±13 and 62±13, for Fert+ and Fert-, respectively. On the first day of the study, each cow received an i.m. GnRH agonist (10 ug buserelin; Receptal, Intervet Ireland, Dublin), and a CIDR was inserted per vaginum (1.38 g of P4; Pfizer Ireland, Dublin, Ireland). Seven days later, each cow received an i.m. PGF2α injection (25 mg of dinoprost tromethamine; Lutalyse, Pfizer Ireland), and 24 h later the CIDR was removed. Each cow was again administered the GnRH agonist 36 h after CIDR removal.

Table 1. Mean EBV (SD) for milk production and fertility traits of Fert- and Fert+ genotypes.

	Fert-	Fert+	P
Milk BV (kg)	187(114)	248(156)	0.32
Calving Interval BV (days)	3.21(1.4)	-2.55(1.2)	0.0001
Survival BV (%)	-0.65(0.5)	1.82(0.4)	0.0001

Milk yield was recorded twice daily and dry matter intake (DMI) daily starting 4 weeks before sample collection. Blood samples were collected twice daily from d 1 to 7.5 (d 0 = ovulation; confirmed by hormone values) to determine plasma P4 concentrations. On d 7, ultrasonography was used to measure CL volume and the Power Doppler function was engaged to determine CL blood flow intensity (BFI) and blood flow area (BFA). On d 7 pm and d 8 am, prostaglandin F2α was administered to regress the CL. On d 8 am, 2 CIDRs were inserted per vaginum. Liver biopsies were collected on d 9 and hepatic mRNA abundance of genes involved in P4 catabolism was determined by RT-PCR. Genes examined were *AKr1C1, AKr1C3, AKr1C4, CYP2C* and *CYP3A*. On d 10, CIDRs were removed and blood samples were collected from -60 to 660 minutes relative to CIDR removal to measure P4 MCR. All data were analysed using SAS. Mixed model procedures with repeated measures were used where appropriate. Genotype and parity were included as fixed effects. Cow nested within genotype was included as a random effect. The NLIN procedure was used to estimate the decay rate coefficient of P4 for calculating the half-life and MCR.

Results and Discussion
The P4 profile of both genotypes is displayed in Figure 1. From d 1 to 4.5, mean circulating P4 concentrations were not affected by genotype. Circulating P4 started to diverge on d 4.5 and from d 4.5 to 7.5, mean circulating P4 was greater in Fert+ compared with Fert- cows (2.39 vs. 1.97 ng/ml, P = 0.04). On d 7.5, the difference in circulating P4 between Fert+ and Fert- was 0.85 ng/ml (P = 0.01).

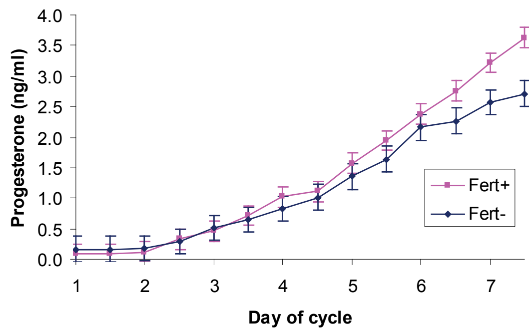

Fig 1. Temporal profile of circulating P4 concentrations from d 1 to 7.5 of the oestrous cycle of Fert+ and Fert- cows.

CL volume and BFI on d 7 were not affected by genotype, but Fert+ cows had greater CL BFA than Fert- cows (2.24 vs. 1.45 cm^2, P = 0.03). Fert+ cows had greater DMI compared with Fert- cows (24.9 vs. 23.4 kg/day, P = 0.03) but there was no effect of genotype on milk yield (30.1 vs. 29.9 kg/day, P = 0.9). Parity did not affect milk yield or DMI. Fert- cows had greater (P = 0.03) abundance of *AKr1C1* mRNA compared with Fert+ cows, but mRNA abundance of the other genes examined did not differ between genotypes. Genotype had no effect on the half-life (37.71 vs. 31.82 minutes, P = 0.31 in Fert+ vs. Fert-, respectively) and MCR of P4 (1.83 vs. 2.34 %/min, P = 0.16 in Fert+ vs. Fert-, respectively). The MCR was lower (1.69 vs. 2.47 %/min, P = 0.03) and P4 half-life tended to be greater (41.3 vs. 29.4 minutes, P = 0.06) in 2nd parity cows compared with 3rd parity cows.

Conclusions
The difference in mean P4 concentrations on d 7.5 appear to be primarily due to greater CL progesterone synthetic capacity rather than differences in MCR. Further work is necessary to explore the mechanisms responsible for greater CL progesterone synthesis in Fert+ cows.

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Factors associated with fertility outcomes in cows treated with protocols to synchronise oestrus and ovulation in seasonal calving pasture-based dairy production systems

M.M. Herlihy[1, 2], M.A. Crowe[2], D.P. Berry[1], M.G. Diskin[3] and S.T. Butler[1]

[1]*Teagasc, Animal and Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork.* [2]*UCD School of Veterinary Medicine, Belfield, Dublin 4.* [3]*Teagasc, Animal and Grassland Research and Innovation Centre, Athenry, Co. Galway.*

Introduction

Herlihy *et al*. (2011) reported that the use of timed artificial insemination (TAI) protocols in seasonal calving cows on pasture-based dairy production systems resulted in both shorter intervals from calving to first service and shorter intervals from mating start date (MSD) to conception. The objective of this study was to further analyse this dataset to identify factors associated with fertility outcomes in cows treated with protocols to synchronise oestrus and ovulation.

Materials and Methods

Lactating dairy cows (n = 1,538) across 8 commercial dairy herds were enrolled in a completely randomised block design study to evaluate synchronisation treatments. Within each herd, cows were divided into 3 calving groups based on days in milk (DIM) at MSD: early (≥ 42 DIM at MSD; n = 1,244), mid (21 to 41 DIM at MSD; n = 179), or late (0 to 20 DIM at MSD; n = 115) Oestrous cycles of cows in the early, mid-, and late-calving groups were synchronised to facilitate insemination after observation of oestrus or TAI at MSD (planned breeding 1; PB1), 21 d (PB2), and 42 d (PB3) after MSD, respectively. For each PB, cows in the relevant calving group were stratified by parity and calving date and randomly assigned to one of the following synchronisation protocols: 1) d −10 GnRH (10 μg i.m. buserelin) and CIDR [Controlled Internal Drug Release, 1.38 g progesterone (P4)] administered; d −3 $PGF_{2\alpha}$ (25 mg i.m. dinoprost); d −2 CIDR removed followed by artificial insemination (AI) at observed oestrus (CIDR_OBS); 2) same as CIDR_OBS, but GnRH 36 h after CIDR removal and TAI 18 h later (CIDR_TAI); 3) same as CIDR_TAI, but no CIDR used (Ovsynch) or 4) untreated control (CTRL). Body condition score (BCS) was recorded at the time of insemination on a 1 to 5 scale (1 = emaciated, 5 = extremely fat) with increments of 0.25 as outlined by Edmonson *et al*. (1989). Cows were classified according to BCS at the time of insemination as ≤ 2.50 (Low), ≥ 2.75 and ≤ 3.00 (Medium) or ≥ 3.25 (High). Prior to assignment to treatment cows were examined by transrectal ultrasonography and the numbers of visible corpora lutea (CL) were counted. To determine conception rates, all cows on synchronisation treatments were scanned at 30 to 32 days post AI. Concentrations of P4 in plasma were determined on the day of AI and 11 days after AI. Cows were categorised according to plasma P4 at d 0 (presumptive oestrus) and d 11 after insemination (high [H] (≥1 ng/mL); low [L] (<1 ng/mL). Only cows with L plasma P4 on d 0 and H plasma P4 on d 11 (LH) were considered synchronised. The following reproductive measurements were calculated and analysed: 21-day submission relative to PB1, PB2, PB3 (binary) and conception at first service (confirmed pregnant by ultrasonography at 30 to 32 days after first AI; binary). The associations between CL status, BCS, DIM and 1) synchronisation rate, 2) 21-d submission rate after PB, and 3) conception at first service for different synchronisation treatments were determined by logistic regression using the GENMOD procedure of SAS; two-way interactions between the effects listed and synchronisation treatment were also evaluated.

Results and Discussion

Presence of a CL at protocol initiation, greater DIM at the onset of synchronisation, and greater BCS at the time of AI were associated with increased likelihood of synchronisation, submission for AI, and conception at first service. Inclusion of a CIDR in the ovulation synchronisation protocol (i.e., CIDR_TAI) increased synchronisation rates in anovulatory anoestrous cows. In the absence of a CL, both CIDR_OBS and CIDR_TAI animals had increased likelihood of conception at first service compared with Ovsynch animals. Low BCS animals treated with CIDR_OBS had increased likelihood of conceiving at first service compared with low BCS animals treated with CIDR_TAI, Ovsynch, or CTRL. Animals < 60 DIM treated with CIDR_OBS and CIDR_TAI had increased likelihood of conceiving at first service compared with Ovsynch. Treatment with CIDR_TAI increased synchronisation rates in cows categorised as low BCS, anovulatory anoestrous, and < 60 DIM compared with both CIDR_OBS and Ovsynch, and increased submission rate compared with CIDR_OBS. Conception rate in cows within these categories, however, was greatest for CIDR_OBS, resulting in minimal differences in actual pregnancy rates between CIDR_OBS and CIDR_TAI treatments, both of which were superior to Ovsynch. Differences between treatments in the response variables investigated were minimal in cows categorised as medium or high BCS, ovulatory and > 60 DIM, indicating that CIDR-based protocols could be targeted at particular cows, and all other cows could be synchronised using Ovsynch.

Conclusion

The results from this study suggest that CIDR-based protocols should be targeted at animals categorised at the time of protocol initiation as low BCS, anovulatory anoestrous or < 60 DIM. The decision to use CIDR_OBS or CIDR_TAI in cows within these categories should be made based on expected heat detection efficiency on the farm versus the management efficiency afforded by using TAI. Strategies to promote cyclicity and greater BCS should lead to improved fertility outcomes in lactating dairy cows treated with protocols to synchronise oestrus and ovulation in seasonal calving pasture-based dairy production systems.

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The effect of dystocia on subsequent performance in dairy cows

N. McHugh[1], J.F. Kearney[2] and D.P. Berry[1]
[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork and* [2]*Irish Cattle Breeding Federation, Bandon, Co. Cork*

Introduction
Dystocia is defined as a calving that requires more assistance than desirable (Meijering, 1984). Dystocia is an economically important trait in the dairy industry as it is associated with approximately 50% of calf mortality cases at birth (Mee et al., 2008; Purfield et al., 2012) but can also have a profound influence on cow performance postpartum. The objective of this study was to quantify the effect of calving dystocia on subsequent cow fertility, milk production, and survival in Irish dairy herds.

Materials and Methods
Calving dates from 972,820 cows totalling 2,034,846 calving events between the years 2002 and 2010 were available from 16,413 dairy herds. Calving to first service interval (CFS) was calculated as the number of days from calving to first recorded service; only calving to first service intervals of between 10 and 250 days were retained. Number of serves (NS) was calculated as the number of inseminations per cow during the breeding season. Only calving intervals (CIV) between 300 and 800 days were retained. Survival (SURV) was defined as whether a cow survived from one lactation to the next. A cow was assumed not to have survived to a subsequent lactation if: 1) no calving record was available for the following lactation, 2) the difference between the cow's last recorded calving date was greater than 800 days from the last recorded calving date of the herd, or, 3) if the cow was slaughtered or died on farm within 400 days of calving. Cows that were recorded as died in the first 50 days (DEAD50) post calving were coded separately. Culling information was available from the cattle movement monitoring system (CMMS) data. In Ireland calving difficulty is scored on a scale of 1 to 4 as follows: no assistance/unobserved; slight assistance; severe assistance or veterinary assistance. In the present study dystocia was defined as severe or veterinary assistance. Only herds that recorded some level of dystocia (1 to 10%) were retained. Average milk yield in the first 60 days post-calving as well as mean milk fat and protein percentage was predicted from a smoothing spline fitted, within lactation, to test-day records using seven knot points. Cows calving less than or greater than 22 months from the median age within parity were excluded from the analysis. Only calving events from parity one to five were retained and herds with no recorded fertility information were discarded. Contemporary group was defined as herd-year-season of calving; only contemporary groups with at least 5 records were retained. Following all edits 65,535 animals remained. The effects of dystocia on subsequent cow performance were determined using a mixed model (ASReml; Gilmour et al, 2011). Fixed effects were parity, age (in months) relative to the median age within parity, the proportion of Holstein and Friesian in each cow, heterosis and recombination loss regression coefficients, dystocia (yes/no) and contemporary group. Cow was included as a random effect.

Results and Discussion
The incidence of dystocia recorded in the present study was 5.15% which is in line with the previously documented dystocia incidence in Ireland (Mee et al., 2008; Mee et al., 2011). The effects of dystocia on fertility, survival and production are summarised in Table 1. The average CFS, CIV and NS were 75.7 d, 397 d and 1.7 serves, respectively. The proportion of cows that survived to the next lactation was 85% and the proportion of cows that died during the first 50 d post partum was 0.6%.

Table 1. Regression coefficients (b; standard error in parenthesis) on the effect of dystocia on cow performance (P <0.01)[a].

Performance	Trait	*b (s.e.)*
Fertility	CFS (days)	0.74 (1.10)
	NS (number)	0.16 (0.04)
	CIV(days)	21.56 (1.32)
Survival	SURV (%)	-0.08 (0.01)
	DEAD 50d (%)	0.01 (0.002)
Production	Milk yield (kg)	-36.13 (21.07)
	Fat yield (kg)	-1.58 (0.88)
	Protein yield (kg)	-1.18 (0.69)

Cows that experienced dystocia had a longer interval to first service which is likely due to a delayed resumption of cyclicity post-calving. Cows that experienced dystocia also required more inseminations and therefore also had longer calving intervals. The probability of the cow surviving to subsequent lactation was also reduced for cows that experienced dystocia (-0.08) compared to cows with no dystocia. The average reduction in milk yield across the first 60 days in milk (-36.13 kg) for cows that experienced dystocia at calving was consistent with a previous study in New Zealand (-42.0 kg; Berry et al., 2007). Similarly fat (-1.58 kg) and protein (-1.18 kg) yield were also reduced in cows that experienced dystocia at calving.

Conclusions
Results from this study clearly show that calving dystocia reduces (P<0.01) milk production, reproductive performance and cow survival and can consequently reduce farm profitability on dairy farms.

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Modelling the fertiliser replacement value of slurry

E. Finneran[1,2], P. Crosson[1] and M. Wallace[2]
[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Co. Meath.* [2]*School of Agriculture and Food Science, Belfield, Dublin 4.*

Introduction

Due to high handling and transport costs, liquid manures have a limited value outside the farm of production (Wilkinson, 1979). Fertiliser replacement value (FRV), calculated as the value of purchased inorganic fertilisers replaced by home produced slurry, is the value most commonly attributed to slurry. The most simplistic calculation of FRV is the sum of purchased fertiliser costs for the quantity of N (nitrogen), P (phosphorous) and K (potassium) contained in the slurry. However, many other factors affect the realised FRV on a given farm including; slurry dry matter and nutrient content, soil nutrient status, crop nutrient requirements, and slurry storage, handling and application methods and timing. Application of slurries must also comply with the requirements of the ND (Nitrates Directive; Dept of Env, 2006). The aim of this study was to model the FRV for cattle slurry, in order to identify the primary drivers of and constraints to achieving higher cattle slurry FRV on Irish farms.

Material and Methods

The Grange Feed Costing Model (Finneran *et al*., 2011) was used to simulate the production of seven feed crops; grazed grass receiving 200 kg N ha^{-1} $year^{-1}$ (GG), a one-cut grass silage system (GS1), a two-cut grass silage system (GS2), a maize silage crop sown under polythene (WCM), a whole-crop winter wheat crop (WCW), a spring barley grain crop (SBG) and a grazed kale crop. All crops were assumed to be grown in a loam soil of index 3 for P and K and index 2 for N for the harvested crops. All production, storage and feed-out costs were included in calculation of total feed costs (TFC; Finneran *et al*., 2011). Two scenarios were simulated for each feed crop. For the baseline scenario (-CS) the full crop nutrient requirement was supplied by purchased inorganic fertilisers. For the second scenario (+CS) cattle slurry was used as a substitute for a proportion of the inorganic fertiliser to meet crop nutrient requirements. Inorganic fertiliser application cost was €45 t^{-1} and slurry agitation and spreading (splash-plate) cost was €2.18 m^{-3}. Slurry N availability to the crop was assumed as 0.25 if applied in spring and 0.05 in any other season (Lalor and Schulte, 2008). P and K nutrient availability factors of 1.0 and 1.0 and the application limits of the ND were assumed. The theoretical 'potential' fertiliser replacement value of average Irish cattle slurry (PFRV) was calculated using Nitrates Directive specifications for nutrient content, and mean 2010 inorganic fertiliser market prices for N, P, and K. The maximum feasible N availability factor of 0.7 was assumed for PFRV calculation (Schröder *et al*., 2007). Modelled fertiliser replacement value (MFRV; blue bars in Fig 1) was calculated as the difference in fertiliser cost between the –CS and +CS scenarios, expressed as € m^{-3} cattle slurry applied under the +CS scenario.

Results and Discussion

TFC was proportionally reduced by between 0.03 (GG200) and 0.15 (GS1) for the +CS scenario relative to the –CS scenario. This was a direct consequence of a total fertiliser cost reduction of between 0.11 (GG200) and 0.55 (WCM) (Table 1).

Table 1. Effect of cattle slurry application (-CS, without cattle slurry; +CS, with cattle slurry) on total fertiliser cost and total feed cost (TFC) and volume of slurry applied (+CS)

	GG200	GS1	GS2	WCM	WCW	SBG	Kale
+CS m^3 applied /ha	12.5	25.0	37.5	50.0	31.3	31.3	37.5
Total fertiliser cost (+CS)/ total fertiliser cost (-CS)	0.89	0.60	0.58	0.45	0.71	0.72	0.48
-CS TFC *(€/1,000 UFL[a])*	66	182	181	171	176	188	157
+CS TFC *(€/1,000 UFL)*	64	155	158	153	166	171	137

[a] UFL = Unité Fourragère Lait

Under a subsequent simulation to represent the slurry N availability factor increasing to 0.70 (due to multi-year slurry application by injection; Schröder *et al*., 2007), MFRV increased to €6.64 m^{-3} for GS1. This indicated a maximum economic efficiency of 0.73. The ND P application limit was the main constraint limiting slurry application volume. Because the available N, P and K contained in 1m^3 of slurry cost €1.20 to apply in inorganic fertiliser form and €2.18 in slurry form, it is clear that the greater application costs associated with nutrient dilute slurry limit the FRV achievable.

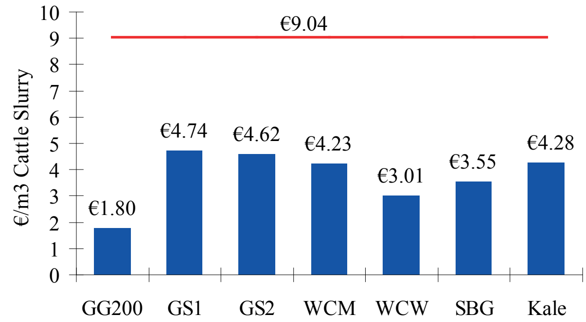

Fig 1. MFRV(€ m^{-3}) (blue bars) and PFRV (red line) for cattle slurry applied to seven common feed crops.

Conclusions

These results show that 1) the Nitrates Directive application limits and 2) the high handling costs associated with slurry are major factors constraining slurry FRV at farm level. Slurry application technologies that improve N availability efficiency from slurry could increase cattle slurry FRV by up to €1.96 m^{-3} if their cost was equivalent to the current cost of splash-plate application.

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Efficiency of CAN, urea, and urea + agrotain (*n*-butyl thiophosphoric triamide) in grassland – relative dry matter yields.

D.L. Antille[1], N. Hoekstra[1] and S.T.J. Lalor[1]
[1]*Teagasc, Johnstown Castle, Environment Research Centre, Co. Wexford, Wexford, Ireland.*

Introduction
In Ireland, CAN and urea-based fertilisers account for *c*.60% of the total fertiliser N applied on managed grasslands (Lalor et al., 2010). Urea-based fertilisers have relatively low cost, high N content and suggested lower susceptibility for NO_3^- leaching and denitrification than CAN (Jordan, 1989). They have, however, higher potential for NH_3 volatilisation resulting in lower yield potential (Watson et al., 1990; Freney et al., 1983). The aim of this work was to determine the relative efficiency of urea, and urea + agrotain compared with CAN in relation to the weather and soil conditions for a range of fertiliser application timings.

Materials and Methods
The experiment used 3 fertiliser treatments (urea (U), urea coated with agrotain [0.48 g kg^{-1}] (UA) and CAN (C)), 3 N-application rates (0 – control, 25, and 75 kg [N] ha^{-1}), and 19 application timings performed once every week from February to April, and once every fortnight from May to September. A complete block design with 4 blocks was used; within each block, application timing was the plot factor resulting in 19 strips so that fertiliser treatment × rate was randomised within the strip. Plots dimensions were 3 m by 1 m marked out on a moderately well drained soil at Teagasc, Johnstown Castle, Wexford, in February 2010. Grass was cut for dry matter yield (DMY) at weeks 4 and 8 after fertiliser application. The data was statically analysed using GenStat 10.1 (2007); this involved ANOVA and the LSD at 5% level to compare the means. The relative yields (RY_{DMY}) of U and UA compared with C were estimated based on Equation [1]:

$$RY_{DMY} = \frac{(F_{DMY} - NF_{DMY})}{(CAN_{DMY} - NF_{DMY})} \times 100 \qquad [1]$$

where: F and NF correspond to DMY of the fertiliser treatment and the control (zero-fertiliser) respectively.

Results and Discussion
Figures 1 & 2 show the relative DMY of U and UA compared to CAN (100%) corresponding to the cuts made at 4 and 8 weeks after fertiliser application, respectively. Overall, there were significant differences ($p<0.05$) in DMY with respect to the timing, the N-application rate and the fertiliser type (except for the second cut made at week 8; $p>0.05$). The interaction timing × fertiliser type was nonsignificant ($p>0.05$) indicating that the differences in DMY encountered between the control (zero-fertiliser) and the treatments were of similar order of magnitude at any given time.

The use of U and UA resulted, overall, in relative DMY values between 7%-11% and between 0%-7% lower compared with CAN. Hence, when comparing U and UA, the use of agrotain improved the agronomic performance of urea-N by *c*.5% across the range of timings and fertiliser rates used in this experiment. By aggregating the data shown in Figures 1 & 2, it can be seen that U and UA performed better than CAN for applications made between the middle of March and early April, and also early May. This effect may be attributed to the particular weather conditions (rainfall and temperature) and soil moisture content recorded in the following 3 days of the fertiliser application. These influenced the magnitude of the N losses from the fertiliser-N applied and the residual N used up by the crop in the period between the first and second cuts.

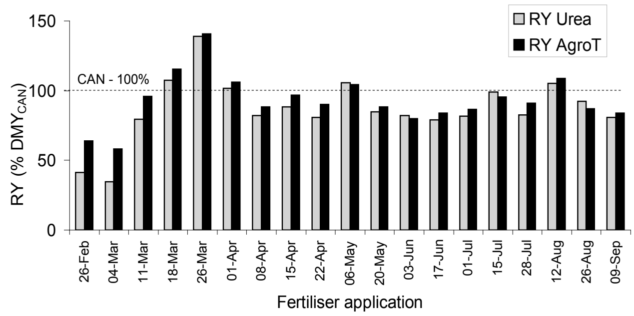

Fig. 1: Relative DMY of U and UA to CAN four weeks after fertiliser application.

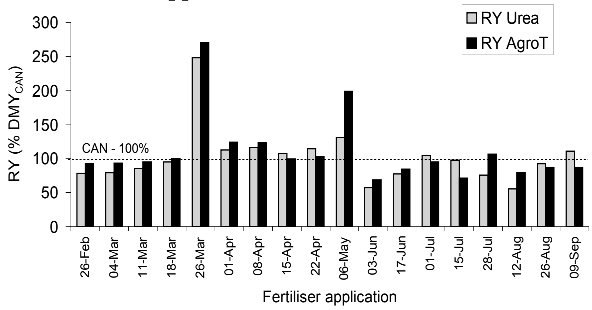

Fig. 2: Relative DMY of U and UA to CAN during the period between four and eight weeks after fertiliser application.

Conclusions
In general, the use of CAN performed marginally better than U and UA regardless of the timing of fertiliser application except for N-applications made between middle of March and early April. Economic analyses are needed to aid the fertiliser choice.

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Soil phosphorus status and sustainable dairy production in Northern Ireland

J.S. Bailey, C. Jordan, J. Mellon and K. Hamill
Agri-Food & Biosciences Institute (AFBI), Agriculture, 18A Newforge Lane, Belfast, BT9 5PX

Introduction

The present decline in fertilizer phosphorus (P) usage across Northern Ireland (NI) (70% since 2003), and the introduction of a maximum farm P surplus of 10 kg P ha^{-1} for derogated farms with manure nitrogen (N) loadings > 170kg N ha^{-1}, will eventually reduce the amount of land enriched with P and contributing to the eutrophication of surface waters. While this is welcome from an environmental stand point, there are concerns that the reduction in P inputs might eventually impair the performance of high yielding cows by reducing the amount of dietary P derived from grass and forages, and thereby undermine the sustainability of the intensive dairy sector. To address this concern, a study was commenced in 2008 to monitor (*inter alia*) nutrient inputs and outputs and the mineral contents of soils, concentrates and herbage, on 12 dairy farms across NI. Data from the first 2 years of this study are presented, here, to show how the concentrations of P in soil and in diary cow diets are linked, and to examine the implications for sustainable dairy production.

Materials and Methods

Twelve dairy farms ranging in size from 45 to 225 ha, and with milk production ranging from 6,500 to 9,500 l cow^{-1}, were selected to provide two from each county, one derogated and one non-derogated. All fields were soil sampled in 2008, and the samples analysed for Olsen-P and mean Olsen-P concentrations per farm determined. Samples of grass were taken from grazed and cut fields 3 times in 2009, analysed for P, and mean annual P concentrations in grazed and cut herbage determined. The average P contents of dairy cow (whole) diets were determined based on: estimates of total dry matter (DM) intake proportionate to milk yield; the known levels and P contents of concentrates offered; and the mean P contents of grass and forage. Regression analysis was used to investigate relationships between soil Olsen-P, grass/forage-P, and the P in whole diets.

Results and Discussion

When mean P concentrations in grazed and cut grass were regressed on soil Olsen-P, curvilinear relationships were obtained revealing a sharp increase in herbage P concentration when soil Olsen-P increased between 20 and 35 mg P l^{-1}, followed by a subsequent levelling off in herbage P concentration (3.7 g P kg^{-1} for grazed grass and 3.4 g P kg^{-1} for cut grass) above an Olsen-P of 40 mg P l^{-1} (Fig 1). Results of previous research suggest that as soil Olsen-P moves beyond 40 mg P l^{-1}, the risk of P losses to water increases significantly (Watson *et al*., 2007). Since there is clearly no animal nutritional advantage in maintaining Olsen-P values above 40 mg P l^{-1} (Fig 1), and given the environmental risk associated with high P soils, there is rationale for advocating a maximum mean Olsen-P level for farmed grassland of < 40 mg P l^{-1}. Currently, it is recommended that Olsen-P is maintained between 16 and 45 mg P l^{-1} for grassland.

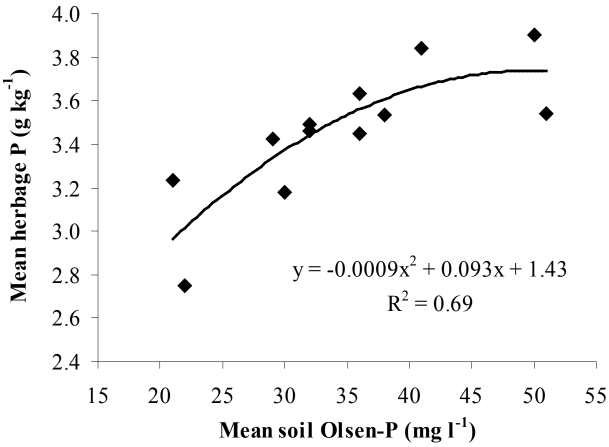

Fig. 1. Mean P content of grazed herbage during the 2009 growing season versus mean soil Olsen-P levels on 12 dairy farms (with quadratic regression curve)

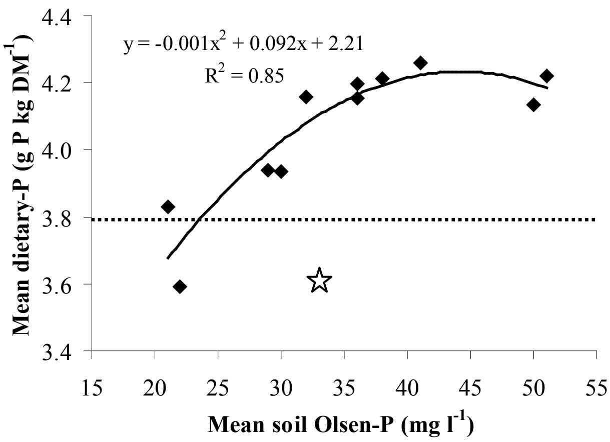

Fig. 2. Mean P concentrations in dairy cow (whole) diets versus mean soil Olsen-P; data for one farm was omitted from the regression analysis (star notation)

On most farms, the proportion of dietary DM intake as concentrates was fairly constant at between 35 and 45% (only in one case was it very low at 16%; see star in Fig 2), and hence the variability in dietary P was largely driven by that in herbage P and hence in soil Olsen-P (Fig 1). When average P contents of dairy cow diets were regressed on soil Olsen-P, the resultant curvilinear relationship suggested that, except when concentrate use was very low, the minimum dietary P requirement of high-yielding dairy cows (3.8g P kg DM^{-1}) (Ferris *et al*, 2010) could be achieved from grass plus concentrates by maintaining a mean Olsen-P of 25 mg P l^{-1} (Fig 2).

Conclusion

For dairy production systems, in which concentrates comprise >35% of DM intake, maintaining mean Olsen-P levels between 25 and 35 mg P l^{-1} should minimise environmental risk without impairing productivity.

Acknowledgements

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Impact of pig slurry amendments to control phosphorus losses in laboratory runoff boxes under simulated rainfall

C.J. O' Flynn[1], O. Fenton[2], P. Wilson[3] and M.G. Healy[1]
[1]*Civil Engineering, National University of Ireland Galway, Co. Galway,* [2]*Teagasc, Environmental Research Centre, Johnstown Castle, Co Wexford,* [3]*School of Mathematics and Statistics, University of St. Andrews, Fife, Scotland*

Introduction

Due to repeated landspreading of pig slurry, land adjacent to pig farms have a phosphorus (P) content which poses a danger of chronic and incidental P losses to the environment. Consequently, there is a shortage of available land on which to spread pig slurry. The addition of chemical amendments to pig slurry in these areas may help reduce surface runoff of P, which may alleviate the problem. The aim of this study was to evaluate the effectiveness of pig slurry amendments in reducing incidental P losses from laboratory runoff boxes under simulated rainfall.

Materials and Methods

Intact P index 4 grassed soil samples, 1 m-long, 0.225 m-wide and 0.05 m-deep, were placed in runoff boxes and pig slurry or amended pig slurry was applied to the soil surface. The following treatments were examined in triplicate: a) a grassed sod-only treatment with no slurry applied b) a grassed sod with unamended slurry (the study control) applied at a rate of 19 kg total phosphorus (TP) ha^{-1} c) grassed sods receiving amended slurry applied at a rate of 19 kg TP ha^{-1}. The results of a laboratory micro-scale study by O' Flynn et al. (2012) were used to select amendments and their application rates to be used in the present study. The amendments examined were: a) commercial grade liquid aluminium sulphate (8% Al_2O_3) applied at a stoichiometric rate of 0.88:1 [Al:P] b) commercial-grade liquid ferric chloride (38% $FeCl_3$) applied at a rate of 0.89:1 [Fe:P] and c) commercial-grade liquid poly-aluminium chloride (PAC) (10% Al_2O_3) applied at a rate of 0.72:1 [Al:P]. The grassed soil was then subjected to three rainfall events (10.3±0.15 mm h^{-1}) at time intervals of 48, 72, and 96 h following land application of slurry. Each event lasted for a duration of 30 min after surface runoff began. Runoff samples for each event were collected at 5 min intervals over this 30 min period. The data was analysed using a general linear model in SPSS.

Results and Discussion

The amendments used in this study all reduced P concentrations in the runoff water compared to the study control (Fig. 1) and resulted in dissolved reactive P (DRP) loads similar (P>0.05) to the soil only treatment (Table 1). Dissolved unreactive P (DUP) loads from all amendments were not significantly different to each other, but were significantly different to the soil only and study control (P<0.05).

Surface runoff of P from soil only was above 0.03 mg P L^{-1}, the median phosphate level above which significant deterioration in water quality may be seen in rivers (Clabby et al., 2008). This indicates that even after chemical amendment, slurry spread on high P index soil still poses an environmental danger. This is because chemical amendment of slurry will only affect the contribution of the slurry to runoff P, but will not affect the contribution of the soil itself. However, the buffering capacity of water means that the concentration of the water in a stream or lake will not be as high as the concentration of runoff.

Runoff samples also underwent analysis for metals, and in all cases were found to be within mandatory limits for surface water intended for the abstraction of drinking water (75/440/EEC).

Table 1. Mean loads (mg m^{-2}) averaged over three rainfall events, for DRP, DUP, total dissolved phosphorus (TDP), particulate phosphorus (PP), and TP

	DRP	DUP	TDP	PP	TP
	mg m^{-2}				
Soil Only	1.91^{ab}	0.44^{a}	2.36^{a}	1.10^{a}	3.46^{a}
Control	4.47^{c}	1.36^{b}	5.83^{b}	5.08^{b}	10.90^{b}
Alum	1.61^{a}	0.73^{c}	2.34^{a}	2.96^{cd}	5.30^{cd}
$FeCl_3$	2.30^{b}	0.78^{c}	3.08^{c}	2.36^{c}	6.34^{c}
PAC	1.79^{ab}	0.82^{c}	2.60^{ac}	1.81^{ad}	4.41^{ad}

[abcd] Means in a column, which do not share a superscript, were significantly different (P<0.05)

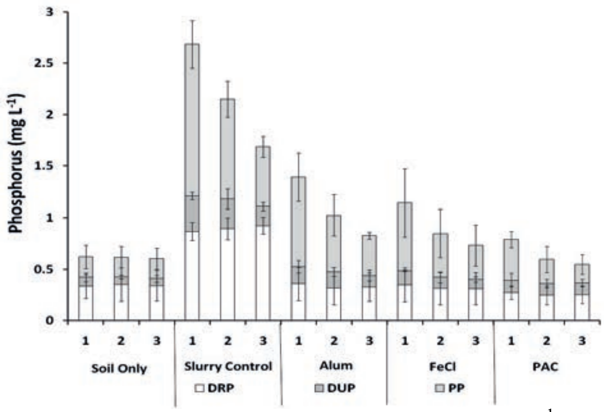

Fig. 1. Flow-weighted mean concentrations (mg L^{-1}) for DRP, DUP and PP in runoff

Conclusions

All amendments examined reduced all types of P losses, but did not reduce them significantly to below that of the soil-only treatment. This indicates that, although incidental losses can be mitigated by chemical amendment, chronic losses cannot be reduced. Although encouraging, the effectiveness of the amendments trialed in this study should be validated at field scale.

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Effect of phosphorus fertilizer application on dry matter yield and P concentration in grass over fourteen years

T. Sheil[1,2], S.T.J. Lalor[1], J. Murphy[1], J. Grant[3] and D. Wall[1]

[1]*Crops, Environment and Land Use Programme, Teagasc, Johnstown Castle, Wexford,* [2]*School of Biological Sciences, Queen's University Belfast, Northern Ireland*, [3]*Teagasc, Ashtown, Dublin 15.*

Introduction

Phosphorus (P) fertilizer is an important nutrient input to optimise grass growth and grass P concentration. Advice for P fertilizer use on grassland in Ireland is formulated to achieve optimum dry matter (DM) yield and herbage P concentration on an annual basis (Coulter and Lalor, 2008). However, the effect of P fertilizer on grass production in different seasons is not well understood. The objective of this study was to investigate the effects of annual P fertilizer application rate on DM yield and P concentration in herbage in different seasons over a fourteen year period.

Material and Methods

The experiment was initiated in February 1995. Two sites with contrasting soil types (sandy loam soil and a clay loam soil) were selected at Teagasc Johnstown Castle, Wexford. Four rates of P fertiliser (0, 15, 30, and 45 kg ha^{-1} yr^{-1}) were applied annually in the spring as 16% super phosphate fertilizer. The treatments were replicated four times at each site in a randomised block design, resulting in 16 plots per site. Phosphorus fertilizer was applied in spring each year. Nitrogen (N) fertilizer was applied in seven equal applications of 40 kg ha^{-1} during the year. Potassium (K) was applied at a rate 120 kg ha^{-1} in February and June each year. Grass was harvested 6-8 times per year between late March and early November with a Haldrup plot harvester. Herbage yield was recorded at each harvest. Grass samples were analysed for DM by drying for 24 hr at 95°C and for total P concentration by the method outlined by Byrne (1979). Soils in all plots were sampled to a depth of 10 cm in autumn in each year. Soil P levels were analysed using Morgan's P extraction method. The effects of P fertilizer, soil P, and harvest number in each year on the herbage DM yield and P concentration were analysed using repeated measures analysis using PROC MIXED in SAS.

Results and Discussion

The P concentration in the herbage was significantly affected by the date of harvest and P fertilizer application rate (P<0.001). The interaction between P fertilizer application rate and harvest date on herbage P concentration was also significant (P<0.001). The mean herbage P concentration at each fertilizer P application rate and harvest date is shown in Fig. 1. The estimated mean herbage P concentration was lower in summer harvests than in earlier or later harvests. The effect of P fertilizer application rate on herbage P concentration was greater with Mar/Apr and Apr/May harvests than in subsequent harvests. As with the herbage P concentration, the DM yield was also significantly affected by harvest date and annual P fertilizer application rate (P <0.001). However, the interaction was not significant in the case of DM yield. The estimated mean DM yield at each fertilizer P application rate for all harvest dates is shown in Fig. 2. The DM yield was estimated to increase by 138 kg ha^{-1} with the application of 15 kg P ha^{-1} yr^{-1} compared with 0 kg ha^{-1} yr^{-1} (P<0.001). There was no significant difference between the 15, 30 and 45 kg ha^{-1} yr^{-1} application rates (P>0.05).

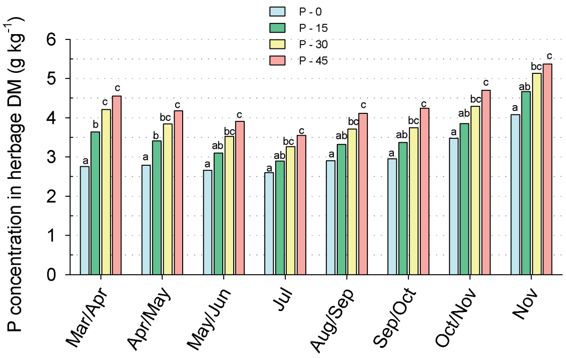

Fig. 1. Effect of annual P fertilizer application rate on mean herbage P concentration at each harvest date. (within a harvest date category, different letters indicate significant differences between rates of fertilizer P application (kg ha^{-1} yr^{-1})).

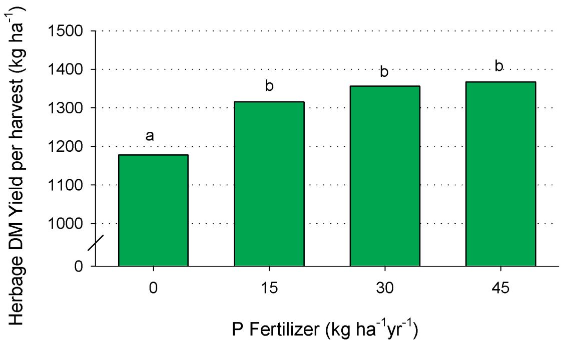

Fig. 2. Effect of annual P fertilizer application rate on mean herbage dry matter (DM) yield across all harvest dates.

Conclusions

Annual application of P fertilizer increased the DM yield and P concentration in herbage over the fourteen years of the experiment. The response to P application was dependent on harvest date in the case of herbage P concentration, but not for DM yield. Further work is required to relate the seasonal response to P fertilizer to the timing of application.

Acknowledgements

Funding from the Teagasc Walsh Fellowship Fund Scheme is gratefully acknowledged.

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The fate of slurry carbon applied to permanent grassland soils

F. Bourdin[1,2], R. Sakrabani[1], M. Kibblewhite[1] and G.J. Lanigan[2]
[1]*Department of Natural Resources, School of Applied Sciences, Cranfield University, Bedfordshire MK43 0AL, UK, [1] Crops, Environment and Land Use Programme, Teagasc, Johnstown Castle, Wexford.*

Introduction

Management effects on grassland C sequestration are poorly understood, particularly on older (~30 years) grasslands, where soil organic carbon may be considered to be in equilibrium. The application of animal manures is considered to be a principle strategy for enhancing grassland carbon sinks. However, it also results in higher soil respiration rates which can, in turn, reduce the total amount of C sequestered. The objectives of this study were to a) assess the proportion of applied slurry C released as CO_2 and b) quantify the effects of applied C on soil respiration in a permanent grassland system.

Materials and Methods

A field-plot experiment (n=3) was carried out on a grassland site, with grass-based (G) and maize-based (M) cattle slurries applied during August 2009 (see Table 1). Maize slurry has a different carbon isotope ratio compared with either grass-based slurry or grassland soils. Therefore, CO_2 arising from mobilisation this substrate can be distinguished from background soil respiration Plots were spread, at a rate of 30 m^3 ha^{-1}, using either splash-plate (SP) or trailing shoe (TS) application to compare both application techniques. The experiment also included control plots (no N applied) and plots fertilised with calcium ammonium nitrate (CAN, 60 kg N ha^{-1}).

Table 1: Characteristics of the soil and of the applied C3 (grass) and C4 (maize) cattle slurries .

	C content (%)	$\delta^{13}C$	DM content (%)	C(gC/kg fresh slurry)
Soil	5.2	-28.2		
C4 slurry SP	42.2	-18.3	3.29	13.9
C4 slurry TS	42.2	-18.3	3.47	14.6
C3 slurry	38.4	-29.8	3.58	13.7

Soil CO_2 flux measurements were taken prior to- and after slurry application, continuing for 30 days post-application using a static chamber coupled to an infra-red gas analyser (EGM-4, PP Systems, Hitchin, Herts, UK). After 30 minutes, gas samples were taken from the chambers by syringe and stored in 12ml exetainers. The carbon isotope ratio's ($\delta^{13}C$) of these samples were subsequently measured by Isotope Ratio Mass Spectrometry (VG Sira 2, Crewe, UK). The effects of treatments were analysed using a general linear model in the statistical package STATISTICA version 9 (Statsoft, Tulsa, Oklahoma) Differences between individual treatments was assessed using Least Significant Difference.

Results and Discussion

The addition of slurry significantly increased the rate of CO_2 emissions ($p > 0.01$) compared to either the control (no fertiliser) plots and/or the inorganic fertiliser (CAN) plots (Figure 1). There were no significant differences between the emission rates for either application technique or slurry type.

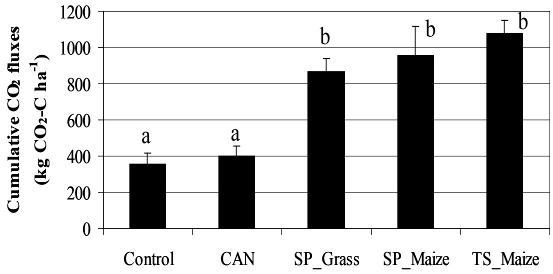

Figure 1 Cumulative soil CO_2 fluxes, over a 30 day period, for grass- and maize-derived slurries as well as for control (no N) and CAN-applied plots.

Upon maize slurry application, both the amount and the $\delta^{13}C$ of respired CO_2 increased, indicating that a large proportion of the increased respiration was slurry-derived. Subsequently, the $\delta^{13}C$ decreased but absolute respiration rates remained high, indicating that the additional C source was enhancing soil heterotrophic respiration. When CO_2 emissions were expressed as a percentage of applied C it was observed that more C was mobilised than had been applied, due primarily to an enhancement of soil heterotrophic respiration.

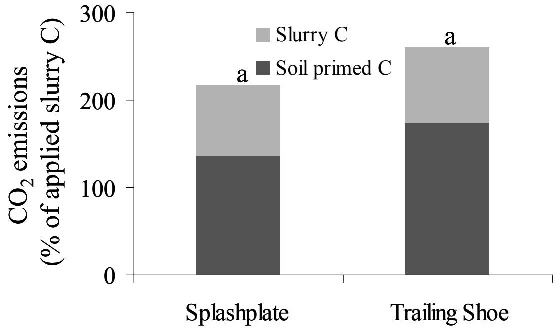

Figure 2 CO_2 emissions expressed as a percentage of applied C for slurry applied by splashplate and trailing shoe and partitioned between slurry-derived CO_2 and soil-derived CO_2.

Conclusions

Older pastures are considered to be in 'C equilibrium' with no net sequestration occurring. This study indicates that the application of animal manures does not enhance soil C. Indeed, the total C efflux is greater that the applied C, principally due to a) de-gassing of CO_2 from the slurry itself and b) enhanced microbial respiration due to the additional of labile C sources.

Acknowledgements

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Evaluation of anaerobically digested cattle slurry as a fertiliser for grass production

S.R. Gilkinson and J.P. Frost
Agri-Food and Biosciences Institute, Hillsborough, Northern Ireland.

Introduction
Anaerobic digestion (AD) results in two products: biogas and digestate. Biogas is a source of renewable energy and due to its economic importance is usually the product that AD plant operators focus on. However, digestate is also valuable, as it contains plant nutrients that can be used as bio-fertiliser to offset the requirement for inorganic fertiliser and associated greenhouse gas emissions from fertiliser production. While AD is a well established technology, particularly on mainland Europe, there is a lack of research data on the fertiliser value of digestate. The nutrient content of digestate depends on the feedstocks used. In Northern Ireland agriculture the greatest quantity organic feedstock available for AD is animal manure, particularly cattle slurry, as cattle dominate the sector. An on-farm digester at AFBI, Hillsborough has been using cattle slurry as the sole feedstock for over 2 years. During this time the total N content of the slurry fed was the same as the digestate removed (mean 3.3 g/kg), but the mean NH_3-N content of digestate (2.10 g/kg) increased from 1.78 g/kg in the slurry fed. The aim of this study was to evaluate digestate as an organic fertiliser for grass production, compared to cattle slurry or inorganic fertiliser.

Materials and Methods
At the start of the growing season digestate from the farm scale digester at Hillsborough (feedstock dairy cow slurry only) and fresh dairy cow slurry were collected in 1 m^3 containers and stored at about 10°C until required. Field plots were laid out on a new re-seed of perennial ryegrass, which had been sprayed with herbicide to remove clover. Plot size was 2 m by 4 m with 0.5 m between plots. Experimental design was a randomised block, with 4 replicates per treatment. Treatments applied were 2 slurry types (digestate and dairy cow slurry) at 35 m^3 ha^{-1} equivalent; by 2 application times before each harvest (early and late) approximately 2 weeks apart; and by 2 application methods, splash plate (SP) and trailing hose (TH) (applied manually). Inorganic fertiliser (CAN) was applied to separate plots at 6 levels of nitrogen. This enabled the nitrogen fertiliser replacement value of the applied organic manures relative to inorganic fertiliser (NFRV) to be calculated. P, K and S were applied to fertiliser plots only, as determined by soil analysis the previous winter. Subsequent herbage analysis indicated adequate supply of P, K and S for all treatments. Treatments were applied 3 times per growing season over 2 years. Mean harvest dates were 18th May, 6th July and 4th September. Herbage mass was estimated by cutting and weighing a 1.5 m wide strip cut from the full length of each plot with a self-propelled plot harvester (Haldrup) to 5.5 cm stubble. Slurry and digestate were sampled at application and herbage was sampled at harvest, for subsequent chemical analysis. Digestate applied contained a mean DM of 57 g/kg, 3.5 g total N/kg and 2.1 g NH_3-N/kg. The values for cattle slurry applied were 73, 3.8 and 2.0 g/kg for DM, total N and NH_3-N, respectively. The data from each harvest were subjected to analysis of variance using Genstat for Windows v12, using year, harvest number and replicate as blocking factors.

Results and Discussion
Total N supplied by slurry was on average 11 kg greater per application than that supplied by digestate (134 *cf.* 123 kg). However, NH_3-N supplied by digestate was 3 kg more than that supplied by slurry (74 *cf.* 71 kg per application). DM yield from digestate only applications *cf.* slurry only applications was significantly higher ($P<0.01$) (Table 1). As a consequence, the NFRV of digestate relative to cattle slurry was 14% greater (0.40 *cf.* 0.35). The average DM yield of herbage per kilo of total N applied was 3.4 kg greater (13%) following digestate application ($P<0.001$) than that following slurry application. However, there was no significant difference ($P>0.05$) in average DM yield per kilo of NH_3-N applied following the 2 manure treatments. This indicates that DM yield was driven mainly by the readily available NH_3-N applied and that it did not matter whether this came from slurry or digestate. Hence the NFRV of slurry and digestate depended on the quantity of NH_3-N applied. Herbage yields that followed late applications of digestate by SP were significantly lower ($P<0.05$) than those that followed late applications by TH (Table 1), but application method did not affect DM yields following early applied digestate. Spring applications of digestate had significantly higher NFRV than applications later in the season (data not presented).

Conclusions
AD improved the NFRV of digested cattle slurry for herbage DM production by 14%, due to higher available N content in digestate. DM yield from digestate applications was affected more by time of application (spring) than by application method.

Table 1: Mean DM yields and NFRV at each harvest as affected by method and time of manure application

				SP digestate		TH digestate		Inter-action	P Value		
DM yield	Cattle slurry	Digest-ate	P Value	early	late	early	late	SED	Method	Time	Inter-action
kg/ha	3474	3646	0.008	3672	3453	3654	3806	138.3	0.092	0.735	0.062
kg/kg total N	26.3	29.7	<0.001	30.2	27.9	30.1	30.7	1.11	0.091	0.308	0.066
kg/kg NH_3-N	49.1	50.0	0.368	49.6	46.4	49.4	51.2	1.92	0.103	0.614	0.070
NFRV	0.35	0.40	0.001	0.38	0.36	0.42	0.42	0.029	0.023	0.789	0.561

Comparison of different methods for obtaining representative samples of cattle slurry

P.B. Berry[1]; S.T.J. Lalor[1]; D.P. Wall[1]; J.P. Quinn[2]; J.P. Frost[3].

[1]Teagasc Johnstown Castle Co Wexford, [2]School of Biological Sciences, Queens University Belfast, [3]AFBI Hillsborough, Co Down.

Introduction

The nutrient content of cattle slurry can be highly variable (O'Bric, 1991). Knowledge of nutrient concentration through laboratory analysis is beneficial for improving the precision with which the fertiliser replacement value of slurry can be incorporated into a farm nutrient management plan (NMP). Obtaining a representative sample of slurry for laboratory analysis can be difficult without complete agitation of the tank due to stratification of slurry in storage. Agitation is usually carried out immediately prior to land spreading. Therefore, the time delay in obtaining results from a laboratory means that these results are used less effectively in a NMP. A reliable method of sampling slurry several weeks before tanks are agitated would be beneficial as results of analysis could be available on the day of slurry application. The objective of this study was to compare pre and post agitation methods of sampling slurry to obtain a representative sample.

Materials and Methods

Seven slatted tanks full of slurry, ranging from approximately 70 to 380 m^3 were sampled within the study: three from the beef farm at Teagasc, Johnstown Castle (JC) and four from dairy and suckler farms in Co. Wexford. Six slurry sampling methods were implemented. Four of the methods were carried out on the slurry tank prior to agitation. These four methods were variations of a 'tube sampler', which consisted of a 2.8 m long open-ended plastic tube with a removable ball stopper at the base attached to a rope running through the pipe. The tube sampler was inserted into the full depth of the tank in all cases. A column of slurry was then extracted from the tank by sealing the base of the tube with the ball stopper by holding the rope taut as the tube sampler was being removed. The four methods that used a tube sampler were: 11A: 11cm diameter tube, inserted at a 45^o angle

11V: 11cm diameter tube, inserted vertically

6A: 6cm diameter tube, inserted at a 45^o angle

6V: 6cm diameter tube, inserted vertically

Two additional methods were used for sampling the slurry after the tank was agitated following normal on-farm procedure. A Bucket and Rope (B&R) method involved collecting a sample of slurry in a bucket lowered into the tank and retrieved by way of a rope attached. Three sub-samples were taken from each agitation point for all the tube sampler and B&R methods. Where tanks had more than one agitation point, sub-samples samples from each agitation point were then bulked resulting in one composite per treatment per tank. As a comparison, sub samples from each tanker load of slurry were collected during emptying of three of the tanks (JC). Samples were analysed in the laboratory for dry matter (DM) total Nitrogen (N), ammonium-N (NH_4-N), total Phosphorus (P) and total Potassium (K). The effect of sampling method on the concentration of DM, N, NH_4-N, P and K in the slurry samples was tested by analysis of variance using Proc Mixed in SAS. Sampling method was included as a treatment factor and tank included as replicated blocks.

Results and Discussion

The range and mean of the concentrations of DM, N NH_4-N, P and K in the slurries are shown in Table 1. The data showed a wide range of DM and nutrient concentrations across the slurry tanks sampled, corresponding to the range that is typically found in slurry in Ireland (O'Bric, 1991). There was no significant difference between pre and post agitation treatments and nutrient concentration ($P>0.05$ in all cases) (Table 1). Therefore the tube samplers could be used to take a representative sample of slurry prior to agitation. There was no significant difference in DM or nutrient concentrations between the different tube sampling methods (diameter or angle). The 6cm sampler might be more practical on farms as its size and weight may make it easier to use than the 11cm tube sampler.

Conclusions

The DM and nutrient concentrations in slurry samples using the tube sampling methods described in this study were not significantly different from the more conventional sampling method using a B&R after agitation. A study with a greater number of replicates would be beneficial to confirm these findings.

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Table 1.Effect of pre and post agitation sampling method on DM and nutrient concentration of cattle slurry samples

Sampling	Pre agitation				Post agitation				
method	11A	11V	6A	6V	B&R	Tanker	s.e.	Range	P value
n	7	7	7	7	7	3			
DM (g kg^{-1})	59.6	60.0	66.4	63.0	67.4	63.2	9.30	16.5-102.8	0.31
N (g kg^{-1})	2.71	2.67	2.79	2.69	3.21	3.37	0.498	0.74-5.43	0.09
NH_4-N (g kg^{-1})	2.14	2.06	2.03	2.02	1.86	2.19	0.324	0.58-3.58	0.32
P (g kg^{-1})	0.65	0.62	0.70	0.65	0.68	0.59	0.099	0.74-5.43	0.24
K (g kg^{-1})	3.41	3.35	3.38	3.36	3.39	3.50	0.325	1.96-4.62	0.96

Nitrogen use efficiency on commercial dairy farms

E. Mihailescu[1, 2], P. Murphy[3], I. A. Casey[2], and J. Humphreys[1]
[1]*AGRIC, Teagasc, Moorepark, Fermoy, Co. Cork;* [2]*Department of Chemical and Life Sciences, Waterford Institute of Technology, Waterford, Co. Waterford,* [3]*Teagasc, Johnstown Castle, Environmental Research Centre, Co Wexford*

Introduction
The Nitrates Directive regulations were implemented in August 2006 in Ireland under Statutory Instrument (SI) 378. These regulations limit the stocking densities and curtail the use of nitrogen (N) on farms. The objective of this study was to examine N balances and N use efficiencies (NUE) on dairy farms following the implementation of the Nitrates Regulations.

Materials and Methods
This study was carried out on twenty-one intensive dairy farms located in the south and east of Ireland. All selected farms were involved in the Dairy Management Information System (DAIRYMIS) programme run by Teagasc, Moorepark Animal and Grassland Research and Innovation Centre. All the farms had a history of accurate record keeping. They were surveyed on a monthly basis during 2010. Stocking density was expressed as the quantity of N excreted by livestock using standard values for annual N excretion for different categories of livestock from the SI relative to the area of the farm used for agricultural production. The N imports (chemical fertiliser, purchased concentrates, and livestock) and N exports (milk and livestock sales) passing the farm-gate were quantified. Biological N fixation was not accounted for as it does not pass the farm-gate (Aarts, 2003). Nitrogen imported in concentrate feeds onto farms was calculated by multiplying the total quantity of concentrate fed by its protein concentration divided by 6.25 (McDonald *et al.*, 1995). Nitrogen in milk exported from farms was calculated by dividing the milk protein concentration by 6.39. Nitrogen exported in livestock leaving the farms was calculated by estimating the total live weight of the livestock sold (or died) from the farms and multiplying by 0.029 for calves and 0.024 for older animals. All N imports and N exports were expressed relative to the utilised agricultural area. The farm-gate balance was the difference between N imports and N exports, whereas N use efficiency was calculated as the ratio between N exports and N imports. The relationship between NUE and N surpluses on all the twenty-one farms were examined using linear regression analysis.

Results and Discussion
The mean stocking rate was equivalent to 183 kg ha^{-1} (s.d. 31.6) of organic N. The results of N balances indicated N surpluses on all the twenty-one farms. There was high variability between farms in terms of N surpluses and N use efficiencies mainly due to variable N imports in fertilizer N (range: 97-297 kg N ha^{-1}) and purchased feeds (range: 6.4-82.2 kg N ha^{-1}) resulting in variable N exports in milk (range: 35.7-88.1 kg N ha^{-1}). Therefore, the farm-gate N surpluses (kg N ha^{-1}) ranged from 73 to 285 with a mean of 196 (s.d. 62.6). Nitrogen use efficiency ranged from 16% to 43% with a mean of 28% (s.d. 5.71). Overall, NUE (R^2 =0.58; P<0.001; s.e. 0.017) decreased with increased N surpluses (Fig.1). In comparison with earlier studies conducted in the mid 1990's (Mounsey *et al.*, 1998) and between 2003 and 2006 (Treacy *et al.*, 2008), stocking density in the present study was lower; 183 kg N ha^{-1} compared with 219 kg N ha^{-1} in the mid 1990's and 202 kg N ha^{-1} between 2003 and 2006.

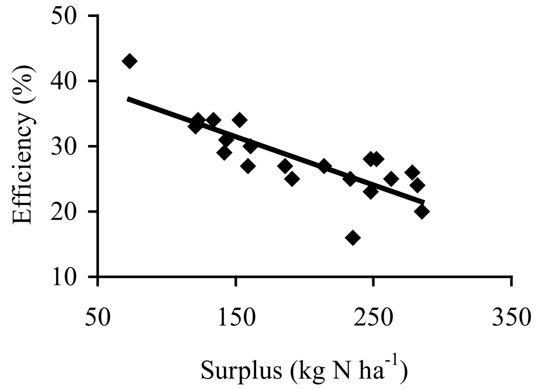

Fig. 1. Relationship between N use efficiencies (Y) and N surpluses (X) on 21 dairy farms in 2010 (R^2 = 0.58; P<0.001; s.e. 0.017)

The mean N surplus in the present study (196 kg N ha^{-1}) was lower than found between 2003 and 2006 (244 kg N ha^{-1}) and in the mid 1990's (304 kg N ha^{-1}). The mean N use efficiency in the current study (28%) was substantially higher than between 2003 and 2006 (19.5%) and in the mid 1990's (17%). This was mostly due to lack of N imports in manure onto the farms in the present study.

Conclusions
The mean N surplus was lower and N use efficiency was much higher than similar previous studies in Ireland indicating that there has been improvement in N use efficiency on dairy farms after implementation of Nitrates Regulations.

Acknowledgements
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Liquid pig manure composition on a small sample of Irish farms

L.M.C. Leliveld[a]*, P. Fiszka[a,b], T. Nolan[a], P.B. Lynch[a], J.V. O'Doherty[b], P.G. Lawlor[a].
[a] *Teagasc, Pig Development Department, Animal and Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork.* [b] *School of Agriculture and Food Science, University College Dublin, Lyons Research Farm, Newcastle, Co. Dublin*

Introduction

Liquid pig manure was traditionally land-spread as a fertiliser. Previous surveys on pig manure composition in Ireland (O'Bric, 1991; McCutcheon, 1997) found high variations in manure composition depending on growth stage of pigs and feeding systems used. In 2006 the Nitrates Directive was enforced in Ireland through the Nitrates Action Programme most recently updated as S.I. No. 610 of 2010. Under this programme the land spreading of liquid pig manure in Ireland is restricted to 170 kg organic N / ha. In the future, further restrictions will also prevent pig manure application at levels exceeding agronomic requirements for P (S.I. No. 610 of 2010). It is not known if pig manure composition in Ireland has changed as a result of these restrictions. Therefore the aim of this study was to assess current liquid pig manure composition on a sample of Irish pig farms in relation to stage of production and feeding system.

Materials and Methods

Manure sampling was performed on 11 commercial farms. At each farm, 5 litre representative samples were taken from different houses and at different time points, resulting in a total of 95 samples. In accordance with sampling methods from previous surveys, the samples were taken from under-slat storage tanks in houses with pigs at different growth stages (pregnant sows: n=14, farrowing sows: n=18, weaner pigs: n=28, finisher pigs: n=25, mixed houses: n=10). The feeding system was recorded for 93 of the 95 samples (dry: n=60, wet: n=33). Each sample was thoroughly mixed and sub-samples were analyzed in a commercial lab, for nitrogen (N), phosphorus (P), potassium (K) and dry matter content (DM).

N content was analyzed by the Total Kjeldahl Nitrogen (TKN) method. P content was analysed using a photometric method. K content was analyzed by microwave digestion followed by an ICP-MS analysis. DM content was analysed by drying in a forced-air drying oven at 70˚C for 72 hours. The data were statistically analyzed using the GLM procedure in SAS, with growth stage and feeding system as independent factors.

Results and Discussion

The survey rendered the following mean values: DM: 48.0 kg/m^3 (SD ± 3.8), N: 2.4 kg/m^3 (SD ± 1.3), P: 1.3 kg/m^3 (SD ± 1.4), K: 2.3 kg/m^3 (SD ± 1.5), and pH: 5.71 (SD ± 0.58). P and K content did not change much compared to previous surveys, but N content seemed to have dropped compared to values obtained from the 16 farms surveyed by McCutcheon (1997). At that time a mean value for N of 6.6 kg/m^3 (4.2 kg/m^3 higher) was found. This lower value for N found in our study may be partly explained by a simultaneous reduction in DM content from the 57.7 kg/m^3 reported by McCutcheon, (1997) to the 48.0 kg/m^3 in this survey. However, the reduction in DM content was not large enough to fully explain the reduction in N content. A further explanation may be due to an increased use of lower protein content diets by pig producers in the interval between studies, however, this needs to be further investigated.

Growth stage and feeding system influenced the pH of liquid manure ($P<0.05$), but not the DM, N, P and K content ($P>0.05$). However, variation was found across farms for DM ($P<0.001$), P ($P<0.05$), K ($P<0.001$) and pH ($P<0.001$), but not N ($P>0.05$). Such variation between farms is line with results from previous manure surveys (e.g. O'Bric, 1991), which stress the importance of farm management to control manure composition.

Conclusions

Despite the small sample size used in the present and previous surveys, this study indicates that the N content of liquid pig manure has decreased. A larger survey would be necessary to confirm this. The high variation between farms stresses the importance of farm management regarding manure composition. Feed system and growth stage alone does not account for the differences in manure composition between farms.

Acknowledgements

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Table 1. Manure composition values. [a, b]: significantly different values ($P<0.05$)

	Growth stage						Feeding system		
	Pregnant sow	Farrowing sow	Weaner	Finisher	Mixed	s.e.	Dry	Wet	s.e.
n	14	18	28	25	10		63	30	
pH	7.57 ^{a}	7.41 ^{ab}	7.08 ^{b}	7.47 ^{a}	7.41 ^{ab}	0.05	7.24 ^{b}	7.56 ^{a}	0.07
DM kg/m^3	74.6	57.7	54.0	50.1	65.3	9.10	63.8	50.5	5.80
N kg/m^3	2.02	2.38	2.44	2.62	2.18	0.23	2.42	2.31	0.15
P kg/m^3	1.93	1.85	1.61	1.35	1.25	0.32	1.76	1.24	0.20
K kg/m^3	1.78	2.49	2.91	2.93	2.51	0.37	2.68	2.64	0.24

RNA-seq analysis of differential gene expression in mild and severe negative energy balance cows

M.S. McCabe[1], S.M. Waters[1], D.G. Morris[2], D.A. Kenny[1], D.J.Lynn and C. Creevey[1]
[1]Animal and Bioscience Research Department, Teagasc, Grange, Dunsany, Co. Meath, [2]Animal and Bioscience Research Department, Teagasc, Mellows Campus, Athenry, Co. Galway

Introduction
Negative energy balance (NEB) is an aberrant physiological state affecting high-yielding dairy cows in the post-partum period where energy requirements for lactation and body maintenance exceed energy intake. The extent of this condition ranges from mild to severe and is of significant economic importance because of its negative impact on cow health and fertility in dairy herds. The role of the liver is central to NEB but the changes in expression of hepatic genes of NEB animals remains incompletely characterised. RNA-seq is the new gold standard for whole transcriptome analysis but so far there are no reports of its application to analysis of hepatic differential gene expression in cattle. We applied RNA-seq technology and bioinformatics/systems biology approaches to total RNA samples that had been previously analysed using microarrays (McCarthy et al., 2010) in order to identify differentially expressed genes (DEG) and their associated pathways in early postpartum lactating dairy cows in either mild NEB (MNEB) or severe NEB (SNEB).

Material and Methods
PolyA mRNAseq Illumina libraries were generated from total RNA. Total RNA extracted from liver as part of the study of McCarthy et al. (2010) was used. In that study liver tissue was harvested from Holstein-Friesian cows in either MNEB (n=5) or SNEB (n=6), at slaughter, 14 days post partum. The libraries were subjected to 36 bp massively parallel single end sequencing on an Illumina GAII. Resulting 36 bp sequencing reads were aligned to the BCM4 *Bos taurus* genome assembly using Bowtie ultra fast short read alignment software. Only reads that uniquely aligned to single locus genes were retained for further analysis. Principal components analysis of variation in numbers of reads was used to see if this variation was associated with MNEB or SNEB. DEseq software was used to identify DEGs with a ≥2-fold change. A gene was deemed to be expressed if the number of reads per gene per animal was ≥4. Biological pathways that were significantly over-represented (p<0.05) among DEGs were identified using the GO-seq software and KEGG pathway annotations.

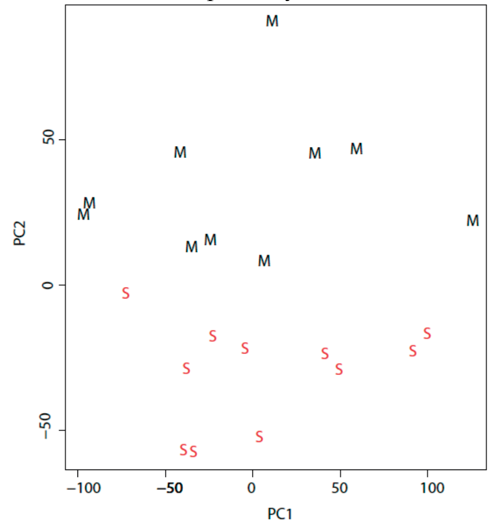

Fig. 1. Scatter plot of 1st and 2nd principal components of read counts in MNEB (M) and SNEB (S) animals

Results and Discussion
An average of 12,833 genes per polyA mRNAseq library was detected as expressed. Of these, 201 DEGs were identified between MNEB and SNEB animals. PCA analysis of variation of gene read counts showed separation of MNEB and SNEB animals on the second principal component. Nine KEGG pathways were significantly over-represented among DEGs (p<0.05) (Table 1). Eight of these pathways were related to fatty acid metabolism and, unexpectedly, included 'steroid hormone biosynthesis', a process which mainly occurs in the reproductive organs rather than the liver.

Conclusions
This study provides a fine scale map of the molecular mechanisms regulating NEB in the bovine liver and has identified potential DEGs that our previous microarray study using the same RNA samples failed to detect.

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R Development Core Team R: (2008) http://www.R-project.org.

Table 1. Biological KEGG pathways over-represented (p<0.05) among DEGs in SNEB cows

Pathway	Pathway name	Overrepresented p value
00140	Steroid hormone biosynthesis	<0.001
03320	PPAR signaling pathway	<0.001
04976	Bile secretion	<0.001
04977	Vitamin digestion and absorption	<0.01
04975	Fat digestion and absorption	<0.01
02010	ABC transporters	<0.01
00592	α-linolenic acid metabolism	<0.01
01040	Biosynthesis of unsaturated fatty acids	<0.05
00830	Retinol metabolism	<0.05

Effect of diet type on the expression of genes regulating ruminal epithelium function of cattle

A.K. Kelly[1], E. O`Shea[1,2], K. Keogh[1,2], R. Prederville[3], A. Cooper[1], S.M. Waters[2], and D.A. Kenny[2]
[1]*School of Agriculture and Food Science, UCD, Belfield, Dublin 4.* [2]*Teagasc Animal and Bioscience Research Department, Grange, Dunsany, Co. Meath,* [3]*Teagasc, Johnstown Castle, Wexford, Co. Wexford.*

Introduction
High concentrate diets increase ruminal volatile fatty acid (VFA) production but also absorptive capacity, compared with forage based diets. Recent evidence indicates that changes in rumen epithelial cell function may mediate improved nutrient absorption. Indeed, fatty acid metabolism, ion transport, and intracellular homeostasis have been identified as the biochemical pathways within ruminal epithelial cells predominantly influenced by diet type. Despite this, there is a dearth of published information on the molecular control of these pathways. The objective of this study was, therefore, to investigate the effect of varying dietary concentrate to forage content on the expression of genes encoding for enzymes involved in the absorption and metabolism of VFA, ion transporters and transcription factors in ruminal epithelial tissue of cattle.

Materials and Methods
This study utilised tissue collected as part of the study of Prendiville et al. (2011). Briefly, in that study, 48 Holstein-Friesian bull calves were assigned to one of three post-weaning dietary regimens *viz.* grazed pasture only (n=17; G); pasture plus 2 kg DM of concentrate (n=16; GC) or ad-libitum concentrate plus 1 kg of straw fed indoors (n=15; C). Animals were slaughtered at eight months of age and ruminal epithelial tissue was harvested from the ventral sac of the rumen, washed in PBS buffer, snap frozen and stored at -80°C. Tissue from 10 animals per treatment was then selected for use in the current study. Total RNA was extracted and 1µg reverse transcribed to cDNA. Primers were designed to amplify specific regions of 25 genes involved in nutrient absorption and metabolism of ruminal tissue. Quantitative real time RT-PCR reactions were performed to measure the relative expression of these genes. *ACTB*, *GAPDH* and $RPLP_0$ were employed as reference genes. All amplified PCR products were sequenced to verify their identity. GenEx 4.3.5 software was used for efficiency correction of the Ct values for all genes, normalisation to reference genes, calculation of quantities relative to the average and natural log transformation of the expression values. Samples of rumen digesta were also collected at slaughter for VFA analysis, determined using gas chromatography. Data were analysed using mixed models ANOVA in SAS with dietary treatment as a fixed effect.

Results and Discussion
Ruminal VFA concentration was greatest for C and similar for G and GC. Acetic acid was highest for G and lowest for C (63.1 *v* 55.3 mol/mol VFA; P<0.05). Conversely, propionic acid concentrations were greatest for C and lowest for G (32.1 *v* 23,2 mol/mol VFA; P<0.05). The ratio of acetic:propionic was highest for G and lowest for C. There was no difference between dietary treatments (P>0.10) for N-butyric, Iso-valeric or N-valeric acids. mRNA expression for Acetyl-CoA-Synthetase was greatest for C, intermediate for GS and lowest for the G treatments. Differences in expression were also detected between treatments (P<0.05) for key genes involved in the ketogenesis pathway *viz*. Acetyl-CoA-Trans, *HMGL*, *BDH1* and *BDH2*. An effect of diet type (P<0.05) was also observed for genes involved in cholesterologenic homeostasis, namely ACAT2, HMGCS2 and ABCA1, with higher expression detected for C compared to GC, which in turn was higher than G. Interestingly, similar dietary effects were also observed for transcription factors PPAR-α and SREBP2 believed to regulate these biochemical events. Moreover, the relative expression values for the ion transporters NHE2, and NHE3 were greatest for C, lowest for G and intermediate for GC.

Table1. Effect of diet on the expression of nutrient absorption genes in ruminal tissue.

Gene	G	GC	C	SEM	Sig.
VFA Metabolism					
Acetyl-CoA-Synthetase	2.66[c]	5.33[b]	9.90[a]	1.04	***
Acyl-CoA-Synthetase	2.02	1.97	2.51	0.3	NS
Acetyl-CoA-Trans	1.74[c]	2.10[b]	3.01[a]	0.25	***
HMGS	3.23	2.03	3.25	0.41	†
HMGL	2.79[b]	7.51[a]	7.50[a]	0.91	***
BDH1	1.67[c]	2.70[b]	4.20[a]	0.36	***
BDH2	2.39[c]	2.83[b]	6.06[a]	0.62	***
ACAT2	1.87[c]	1.93[b]	2.89[a]	0.22	***
HMGCS1	4.68	2.68	4.36	0.91	†
HMGCS2	1.76[c]	5.03[b]	11.63[a]	1.32	***
HMGCL	3.17	3.00	3.71	0.38	NS
HMGCR	16.23	10.67	16.36	3.1	NS
FDFT1	47.54	48.88	35.66	18.7	NS
FDPS	3.68[a]	2.71[b]	4.23[a]	0.39	*
LDLR	3.92[a]	2.46[b]	3.13[a,b]	0.38	*
ABCA1	3.42[c]	5.61[b]	6.02[a]	0.88	*
Ion Transport					
NHE1	3.81	5.57	4.12	1.15	NS
NHE2	3.87[c]	8.88[b]	13.52[a]	1.37	***
NHE3	2.46[c]	5.71[b]	7.45[a]	1.23	***
Transcription Factors					
PPAR-α	6.85[c]	10.16[b]	18.00[a]	2.7	**
SREBP1	2.50[b]	2.54[b]	5.81[a]	0.49	***
SREBP2	1.30[c]	1.82[b]	2.50[a]	0.18	*

†, <0.10; *, <0.05; **, <0.01, ***, <0.01

Conclusion
Consistent with the VFA profiles observed, biochemical pathways involved in ion exchange and VFA metabolism, in particular ketogenesis and associated regulatory transcriptional coordinators (such as PPAR-α, and SREPB) were upregulated in rumen epithelial tissue, in a linear fashion, with increased concentrate allowance. This study provides further evidence for the elucidation of the molecular mechanisms regulating ruminal absorptive metabolism.

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Methane emissions, blood metabolic variables and body composition traits in beef heifers differing in phenotypic residual feed intake

C. Fitzsimons[1, 3], D.A. Kenny[1], M. Deighton[2], A.G. Fahey[3] and M. McGee[1]
Animal and Grassland Research and Innovation Centre, Teagasc, Grange,[1] Dunsany, Co. Meath and Moorepark [2], Fermoy, Co. Cork. [3]School of Agriculture and Food Science, U.C.D., Dublin 4

Introduction
Methane (CH_4) production from enteric fermentation contributes approximately 12% of global green house gas emissions (Hegarty et al., 2007). Residual feed intake (RFI), defined as the difference between actual feed intake and expected feed intake based on maintenance and growth requirements, is a measure of feed efficiency that is independent of growth and body size (Crews, 2005). Selection of feed efficient animals by way of improved RFI has the potential to significantly reduce feed costs in beef production and additionally, due to the positive relationship between intake and CH_4 production, may be a possible mitigation strategy in the reduction of enteric CH_4 emissions (Hegarty et al., 2007). The objective of this study was to characterise productivity related variables and CH_4 emissions in beef heifers differing in phenotypic RFI.

Materials and Methods
Individual dry matter intake (DMI) and growth were measured in 22 Simmental beef heifers, [initial live weight 455 kg (SD = 17.1)] offered grass silage (Dry matter digestibility = 766 g/kg) *ad libitum* for 120 days. Body condition score (BCS), muscularity score, ultrasonically scanned muscle (3rd lumbar vertebrae) and fat (13th rib, 3rd lumbar and rump) depth, skeletal measurements and blood variables (albumin, globulin, total protein, creatine kinase, non-esterified fatty acids, glucose, beta-hydroxy butyrate and triglycerides) were determined. Methane production was estimated using the sulphur hexafluoride (SF_6) tracer gas technique over two 5-day periods on weeks 3 and 11. The residuals of the regression of DMI on average daily gain (ADG) and mid-test metabolic live weight ($LW^{0.75}$), using all animals, were used to compute individual RFI coefficients. Animals were ranked on RFI and assigned to high (inefficient), medium or low groupings. Statistical analysis was carried out using the MIXED procedure of SAS. The model included fixed effects of RFI classification and period and their interaction. Sire was included as a random effect and day of birth was included as a linear covariate. Regression analysis was conducted within period to examine the relationship between RFI and CH_4 using the REG procedure of SAS.

Results and Discussion
Overall ADG and daily DMI were 0.6 kg (SD = 0.07) and 7.8 kg (SD = 0.24), respectively (Table 1). High RFI heifers consumed 9 and 14% more than medium and low RFI heifers, respectively ($P < 0.05$). Body weight, growth, skeletal or composition traits did not differ ($P > 0.05$) between the low and high RFI groups. Concentrations of plasma glucose and urea were higher, and creatinine lower in high compared with low RFI heifers ($P < 0.05$). No interactions between RFI and period were detected for any of the CH_4 related variables measured. Absolute daily CH_4 emissions (g/d) and emissions relative to $LW^{0.75}$ were greater ($P < 0.05$) for high compared with low RFI heifers, with medium RFI animals being intermediate ($P > 0.05$) (Table 1). No differences were detected between RFI groups when CH_4 was expressed relative to DMI. All CH_4 related variables measured were higher ($P<0.001$) in period 1 compared to period 2. The relationship between RFI and CH_4 related variables in period 1 was not significant ($P > 0.05$). Regression analysis in period 2 indicated that a 1-unit increase in RFI was associated with a 25 g/d increase ($P = 0.07$; $R^2 = 0.16$) in CH_4 emissions and a reduction ($P = 0.06$; $R^2 = 0.17$) in CH_4 emissions of 2.5 g/kg DMI. The R^2 obtained for daily CH_4 emissions in period 2 is consistent with the correlation (0.44) obtained by Nkrumah et al. (2006).

Conclusions
This study provides evidence that improving feed efficiency in cattle, by way of improved RFI, will reduce CH_4 emissions while maintaining animal performance.

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Table 1. Productivity traits and enteric methane (CH_4) emissions in beef heifers differing in phenotypic residual feed intake

	RFI Group				Period (P)			Sig. [1]	
Variable	High	Medium	Low	SEM	P1	P2	SEM	RFI	P
Feed intake (kg DM/d)	8.4^a	7.7^{ab}	7.4^b	0.24	-	-	-	*	-
RFI (kg DM/d)	0.52^a	-0.06^b	-0.49^c	0.092	-	-	-	***	-
Mid-test live weight (kg)	483	482	490	18.3	-	-	-	NS	-
ADG (kg)	0.6	0.6	0.6	0.07	-	-	-	NS	-
CH_4 (g/d)	297^a	275^{ab}	260^b	10.3	334	220	10.6	*	***
CH_4 (g/kg DMI)	35	35	36	1.3	40	31	1.4	NS	***
CH_4 (g/kg $LW^{0.75}$)	2.9^a	2.7^{ab}	2.5^b	0.08	3.3	2.1	0.10	*	***

[1]No RFI × Period interaction ($P > 0.1$)

Effects of feeding Bt MON810 maize to sows during first gestation and lactation on maternal and offspring health

M.C. Walsh[1], S.G. Buzoianu[1,3], G.E. Gardiner[3], M.C. Rea[2], O. O'Donovan[3], R.P. Ross[2] and P.G. Lawlor[1]

[1]*Pig Development Department, Animal and Grassland Research and Innovation Centre and* [2]*Food Research Centre, Teagasc, Moorepark, Fermoy, Co. Cork,* [3]*Department of Chemical and Life Sciences, Waterford Institute of Technology, Waterford*

Introduction

Genetically modified (GM) foods are subject to pre-market risk assessment prior to approval for consumption within the EU. However, this type of risk assessment is not considered sufficient to properly evaluate any unintended consequences associated with consumption of GM food by a genetically varied population of humans and animals (EFSA, 2009). Furthermore, there is a lack of long-term cross-generational animal studies conducted with GM feed (Zhang and Shi, 2011). The objective of this study was to examine the trans-generational effects of feeding Bt MON810 maize (GMm) on maternal and offspring health in pigs.

Materials and Methods

Sows (n=24) and their offspring (n=24) were used in a 20-week study. Sows were fed diets containing non-GMm or GMm from service to the end of lactation. Back-fat depth and body weight (BW) of sows were recorded and blood samples were collected at service, on d 56 and 110 of gestation and at d 28 of lactation. Haematological and serum biochemical analyses were conducted on blood samples (Walsh *et al*., 2012). The number of piglets born alive, stillborn and weaned per litter was recorded. Individual BW of piglets was recorded at birth and weaning and average daily gain (ADG) was calculated during the suckling period. At farrowing, the fourth piglet born alive was sacrificed and blood samples were taken for serum biochemical and haematological analyses. Sow BW, back-fat depth, and offspring growth performance, serum biochemistry and haematology data were analysed as a one-factor ANOVA using the GLM procedure of SAS. Sow serum biochemistry and haematology data were analysed using the MIXED procedure of SAS (SAS Inc, Cary, NC) as a repeated measures analysis with Tukey-Kramer adjustment for multiple comparisons. Main effects were obtained using the *slice* option in SAS. Values recorded at service were used as a covariate in the model.

Results and Discussion

Sows fed GMm were heavier on d 56 of gestation (P=0.04) and gave birth to 2.5 more piglets per litter than non-GMm fed sows; however this was not statistically significant. Offspring from sows fed non-GMm tended to be heavier at weaning (P=0.08). Sows fed GMm tended (P<0.10) to have lower serum total protein, and higher serum creatinine and gamma glutamyl transferase activity on d 28 of lactation (Table 1). Serum urea tended to be lower on d 110 of gestation in GMm fed sows and in offspring at birth (P=0.08). Sow haemogloblin (P=0.06), hematocrit (P=0.10) and erythrocyte count (P=0.01) were decreased in response to feeding GMm. Both platelet count (P=0.07) and mean cell haemogloblin concentration (MCHC; P=0.05) were decreased on d 110 of gestation in GMm fed sows however, MCHC tended to be increased in their offspring at birth (P=0.08).

Conclusions

The changes in sow serum biochemistry in response to feeding GMm were not indicative of organ dysfunction Haematological differences between treatments are likely to have been a consequence of increased litter size in GMm fed sows and appeared to be unrelated to GMm exposure. Overall, the effects of feeding GMm to sows during gestation and lactation on offspring serum biochemistry and haematology at birth and BW at weaning were minimal.

Acknowledgements

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Table 1. Effect of feeding Bt (MON810) maize to sows during gestation and lactation on serum biochemistry (n =24).

	Treatment				*P*		
Day	Non-GMm	GMm	Mean	SEM	Treatment	Time	Treatment × Time
Serum total protein, g/L							
d 28 of gestation	75.0	74.0	74.5	1.65	0.65		
d 110 of gestation	73.5	74.8	74.2	1.62	0.58		
d 28 of lactation	75.2	71.9	73.5	1.62	0.10		
Mean	74.6	73.6		1.41	0.63	0.61	0.08
Serum creatinine, µmol/L							
d 28 of gestation	142.6	141.6	142.1	4.13	0.86		
d 110 of gestation	195.6	205.2	200.4	4.13	0.11		
d 28 of lactation	156.1	169.3	162.7	4.28	0.03		
Mean	164.8	172.0		3.15	0.13	0.01	0.09
Gamma glutamyl transferase, units/L							
d 28 of gestation	51.1	55.4	53.1	3.39	0.38		
d 110 of gestation	47.5	47.8	47.7	3.39	0.96		
d 28 of lactation	61.1	70.6	65.8	3.50	0.06		
Mean	53.3	57.9		2.69	0.25	0.01	0.21

The use of a phase feeding regime for finishing pigs between 40 and 120kg

E. Magowan [1] and M.E.E. Ball[1]

[1]*Agri-Food and Biosciences Institute, Hillsborough, Co. Down, N. Ireland*

Introduction

Feed represents approximately 80% of the total cost to rear pigs. Presently the cost to feed pigs is further exaggerated by the fact that raw material costs i.e. cereals and soya, are currently expensive. In order to optimise pig meat sold per kg of feed used, producers often take pigs to heavy slaughter weights (e.g. 120kg) and one diet is usually offered to the pigs throughout the finishing period. However, the nutritional requirements of pigs are reduced as they get heavier. Ideally, to optimise feed use efficiency and reduce nitrogen excretion, pigs should be offered numerous diets across the finishing period to match their nutrient requirements. However, such a feeding regime is impractical without highly sophisticated feeding systems. A compromise may be to offer 2 diets during finish i.e. a phase feeding regime. The aim of this experiment was to compare finishing performance when pigs were offered a two phase or one phase feeding regime between 40 and 120kg using diets with different lysine to digestible energy (DE) ratios.

Materials and Methods

At 12 weeks of age a total of 160 pigs (Tempo x (Landrace x Large white) over two time periods were allocated to one of four dietary regimes based on weight and gender. Pigs were penned in groups of 10 and were offered feed from ACEMO 54 electronic feeders. Individual feed intake was recorded on an ongoing basis between 12 weeks of age and finish (target of 120kg). Pigs were weighted individually at 12, 15, 18 and 20 weeks of age and at finish. Three diets of varying lysine to DE ratio's were used to establish the four dietary regimes. The three diets were simple cereal, soya based diets and had the following lysine to DE ratios 1) 0.70 (CP 180g/kg, DE 13.5MJ/kg, total lysine 9.5g/kg); 2) 0.81 (CP 180g/kg, DE 13.5MJ/kg, total lysine 11g/kg) and 3) 0.59 (CP 167g/kg, DE 13.5MJ/kg, total lysine 8g/kg). The four dietary regimes were 1) Lysine:DE ratio of 0.70 from 12 weeks of age to 120kg; 2) Lysine:DE ratio of 0.81 from 12 weeks of age to 120kg 3) Lysine:DE ratio of 0.70 from 12 to 18 weeks of age and 0.59 from 18 weeks of age to 120kg and 4) Lysine:DE ratio of 0.81 from 12 to 18 weeks of age and 0.59 from 18 weeks of age to 120kg. The hot weight of pigs 45 minutes after slaughter was taken and used to calculate kill out percentage (KO%). The back fat depth of pigs at the P_2 position (65mm from the midline at the level of the last rib) was also taken 45 minutes after slaughter. The effect of dietary regime on average daily gain (ADG), average daily feed intake (ADFI), feed conversion ratio (FCR) and carcass quality (cold weight, KO% and back fat depth) was statistically analysed using Analysis of Variance (Genstat version 10). Twelve week weight was used as a covariate in the analysis for ADG (g/day), ADFI (g/day) and FCR.

Results and Discussion

The 12 week weight of pigs averaged 40.8kg (SEM 0.56) and their finish weight averaged 118kg (SEM 0.71). There was no effect of dietary regime (P>0.05) on the 18 week weight of pigs which averaged 78.5kg (SEM 0.73). The ADG, ADFI and FCR of pigs was similar between 12 and 18 weeks of age (Table 1). However, between 18 weeks of age and finish, pigs offered the two phase regime using lysine to DE ratios of 0.81 reduced to 0.59 had the highest ADFI. They also had an 8% poorer FCR compared with pigs offered the single diet with a lysine to DE ratio of 0.70 from 12 weeks of age to finish. It is noted that the SEM values in relation to FCR between 18 weeks of age and finish are high which may have contributed to the lack of significance observed. On the other hand, the performance (ADG, ADFI and FCR) of pigs offered the two phase dietary regime which used a lysine to DE ratio of 0.70 reduced to 0.59 was similar to that of pigs offered the one diet of 0.81 lysine to DE ratio (Table 1). Furthermore, their ADG and FCR was similar to that of pigs offered the one diet of 0.7 lysine to DE ratio (Table 1). Overall between 12 weeks of age and finish, there was a tendency for ADFI to differ in a similar pattern to that described above but ADG and FCR was similar (Table 1). There was no effect of dietary regime (P>0.05) on KO% (average 74.2%, SEM 0.40) or back fat depth at P_2 (average 14.2mm, SEM 0.48). However, it is noted that all pigs would have incurred penalties due to their back fat depth which was a reflection of their heavy carcass weight.

Table 1 The effect of offering a one or two phase feeding regime varying in lysine to DE ratio

	Dietary regime				
	0.70	0.81	0.70 - 0.59	0.81 - 0.59	SEM
12 to 18 weeks:					
ADG	901	916	889	880	17.3^3
ADFI	2011	2031	2014	1976	40.9^3
FCR	2.27	2.22	2.27	2.27	0.046^3
18 weeks to finish					
ADG	964	972	1012	1012	22.5^3
ADFI	2649^a	2705^{ab}	2808^b	2947^c	48.7^1
FCR	2.62	2.66	2.66	2.83	0.073^3
12 weeks to finish					
ADG	930	941	950	944	14.0^3
ADFI	2329	2361	2401	2458	36.8^2
FCR	2.52	2.52	2.55	2.62	0.044^3

^{1} P<0.001; ^{2} P=0.082; ^{3} P>0.05

$^{a, b, c}$ Numbers with common superscripts are not significantly different (P>0.05)

Conclusions

Adopting a two phase dietary regime using a lysine to DE ratio of 0.70 reduced to 0.59 resulted in similar pig performance between 12 weeks of age and finish compared with using one diet. The '0.59' diet was cheaper and therefore economic savings would have been made adopting this two phase dietary regime. Furthermore, nitrogen excretion would have been reduced due to a reduction in nitrogen input.

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An evaluation of the effects of forage type and feed value, concentrate feed level and protein concentration, and shearing on lamb performance

T.W.J. Keady and J.P. Hanrahan
Teagasc, Animal & Grassland Research & Innovation Centre, Athenry. Co. Galway

Introduction

Results of a previous study at Athenry (Keady and Hanrahan, 2011) showed that increasing maturity of maize at ensilage, the feed value of grass silage (FVGS) and concentrate feed level increased lamb performance. Furthermore, Keady and Hanrahan (2011) concluded that the substitution effect of concentrate, which was linear regardless of forage feed value or type, increased as maize silage and grass silage feed value increased. Finally, Keady and Hanrahan (2011) reported that *ad libitum* concentrate resulted in high levels of lamb performance (growth rate of 267 g/d) similar to that achieved in many situations pre-weaning. The aim of the current study was to evaluate the effects of: (a) forage type and feed value, (b) concentrate feed level and crude protein concentration, (c) *ad libitum* concentrate, (d) shearing and (e) potential interactions on intake and carcass gain of finishing lambs.

Materials and Methods

High and low FVGSs were ensiled on 24 May and 17 June, respectively, precision chopped treated with an inoculant. Maize silage was ensiled precision chopped treated with an inoculant-based additive. Two iso-energetic concentrates were formulated to contain crude protein (CP) concentrations of 180 (HP) and 130 (LP) g/kg DM. The three silages were offered *ad libitum* supplemented with 0.4, 0.8 or 1.2 kg per lamb daily of the HP concentrate. Maize silage was also supplemented with 0.4 kg per lamb daily of LP concentrate. Lambs were also offered *ad libitum* concentrate plus 0.5 kg of the high FVGS daily. Lambs offered the grass and maize silages received 20 and 30 g/d of a mineral/vitamin mixture. Each of the 11 treatments was offered to 24 castrate male Suffolk-X lambs (initial LW 39.0 kg), half of which were shorn, for 54 days at which point all lambs were slaughtered and carcass data recorded. Food intake was recorded daily. All data analysis employed mixed model procedures. Differences among the 22 treatments were partitioned using orthogonal contrasts.

Results and Discussion

The mean DM and starch concentrations of the maize silage were 319 g/kg and 324 g/kg DM, respectively. The mean DM, ammonia N and DMD concentrations for the high and low FVGS were 239 and 262 g/kg; 83 and 84 g/kg N; and 745 and 713 g/kg DM, respectively. The effects of diet on forage intake and carcass gain are presented in Table 1. Lambs offered the maize silage had higher forage intake than those offered the high FVGS, which was greater than those offered the low FVGS. Lambs offered the maize silage had higher carcass gain being significantly higher than those offered the low FVGS. Increasing concentrate feed level reduced forage intake and increased carcass gain. The response to concentrate feed level depended on forage type and feed value. Relative to the grass silage, maize silage increased lamb carcass gain. Concentrate CP concentration did not alter forage intake or performance.

The effects of shearing on forage intake and performance are presented in Table 2. Shearing lambs at housing increased forage intake ($P<0.001$) and kill-out proportion ($P<0.01$), decreased final liveweight ($P<0.05$) and had no effect ($P>0.05$) on daily carcass gain or carcass weight.

Table 2 Effect of shearing on lamb performance

	Treatment			
	Unshorn	Shorn	s.e.	Sig
Forage DM intake (kg/d)	0.59	0.70	0.018	***
Live-weight gain (g/d)	161	170	6.6	NS
Final live weight (kg)	48.1	47.3	0.51	*
Carcass gain (g/d)	90	89	3.3	NS
Carcass weight (kg)	22.5	22.4	0.19	NS
Kill out (g/kg)	465	473	2.5	**

Conclusions

Regardless of diet type, shearing lambs at housing increased forage intake but had no beneficial effects on lamb performance. Relative to the two grass silages, offering maize silage resulted in the highest carcass gain. Response to concentrate feed level depended on forage type and feed value. The level of protein in the concentrate offered with the maize silage had no effect on lamb performance.

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Table 1 Effect of forage type and feed value, and concentrate feed level and protein concentration on lamb performance

		Forage				Linear response to conc			
	Conc (kg/d)	LS[1]	HS[1]	MS[1]	s.e.	Forage	Response	Contrasts	
Forage DM intake	0.4	0.69	0.81	0.96		LS	-0.18 ± 0.04 ***	LSvHS	*
(kg/d)	0.4LP[2]			0.95		HS	-0.29 ± 0.04 ***	MSvGS	***
	0.8	0.60	0.65	0.77		MS	-0.35 ± 0.04 ***		
	1.2	0.49	0.48	0.56					
	Ad-lib		0.14		0.040				
	mean	0.59[a]	0.64[b]	0.77[c]	0.015				
Carcass gain	0.4	15	50	63		LS	94.0 ± 7.6 ***	LSvHS	***
(g/d)	0.4LP[2]			73		HS	73.9 ± 7.6 ***	MSvGS	***
	0.8	82	97	106		MS	60.1 ± 7.7 ***		
	1.2	109	124	123					
	Ad-lib		144		5.4				
	mean	68[a]	90[b]	98[b]	3.43				

[1]LS = Low FVGS, H = High FVGS, MS = maize silage; [2]LP = low protein concentrate

Fat colour, and the colour and tenderness of muscle from Holstein-Friesian, Norwegian Red x Holstein-Friesian or Jersey x Holstein-Friesian cattle raised as bulls or steers

A. McNamee[1], M.G. Keane [1], E.G. O'Riordan[1], D.A. Kenny[2], P.G. Dunne[1] and A.P. Moloney [1]
[1]*Teagasc, Animal and Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath,* [2]*School of Agriculture, Food Science and Veterinary Medicine,, University College Dublin.*

Introduction
Approximately 0.186 of male cattle slaughtered annually in Ireland is represented by animals sired by dairy breeds (DAFF, 2009). Any change in the sire chosen by dairy farmers has relevance therefore to the beef industry. There is an increasing interest within the Irish dairy cattle industry in using alternative dairy sires to the traditional Holstein-Friesian (HF). The objective of this study was to determine the effect on some aspects of beef quality when two such alternative sire breeds, Norwegian Red (NR) and Jersey (JE), were used on HF dairy cows. As there is also increasing interest in the production of male cattle as bulls rather than steers, this factor was also examined.

Materials and Methods
Bulls (n=60) and steers (n=60, castrated at 8 months of age) were reared from 4 weeks of age according to the Grange dairy calf to beef blueprint (Keane *et al.,* 2008) to a mean target weight of 600kg. Animals were slaughtered, within gender, when they reached the target weight. On each slaughter date, animals were transported 144km to a commercial slaughter facility and slaughtered within 1.5 hours of arrival. At 48 hours *post-mortem*, a section of subcutaneous adipose tissue was removed from the *M. longissimus dorsi et thoracis* (LD) close to the 10^{th} rib for colour measurement. The pH of LD was measured and samples were collected for measurement of colour after storage for a further 24 hours at 4°C and for instrumental tenderness (shear force) after ageing in vacuum at 2°C for 14 days. The concentration of haem pigments was measured in LD samples frozen at 48 hours *post-mortem* (Krzywicki, 1982). Colour was measured using a benchtop HunterLab UltraScan XE colorimeter and shear force using a Warner Bratzler shear blade attached to an Instron Univeral testing machine. Data were analysed according to a split-plot design with breed (B) as the main plot and system of production i.e. bulls or steers (G) and all interactions contained in the sub-plot.

Results and Discussion
Liveweight at slaughter averaged 633 and 620 kg for HF bulls and steers, respectively. The corresponding values for NR were 619 and 604 kg and for JE, 572 and 556 kg (sed 6.91, $p<0.05$). Carcass weight averaged 319 and 305 kg for HR bulls and steers, respectively The corresponding values for NR were 315 and 298 kg and for JE, 288 and 264 kg (sed 4.87, $p<0.05$). Meat quality data are summarised in Table 1. Adipose tissue from JE was more yellow ($p<0.05$) than from HR or NR which did not differ and adipose tissue from steers was more yellow ($p<0.05$) than that from bulls. There was no difference between breeds or genders in muscle pH. There was no difference between breeds for muscle lightness or redness or in instrumental tenderness. Muscle from bulls was less red and lighter than muscle from steers ($p<0.05$) consistent with the differences in concentration of haem pigments. Muscle from bulls was less tender than muscle from steers ($p<0.05$).

Conclusion
Under the conditions of this study, there was little difference between breeds in the aspects of meat quality measured and in particular when compared to the effect of slaughtering animals at a constant carcass weight when produced as bulls rather than steers.

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Table 1. Effect of breed and gender on aspects of meat quality

	Holstein-Friesian		Norwegian Red		Jersey			Significance[1]	
	Bulls	Steers	Bulls	Steers	Bulls	Steers	SED[2]	Breed	Gender
Fat									
Yellowness	16.5	18.0	16.5	17.2	17.1	18.5	0.44	*	***
Muscle									
pH	5.60	5.59	5.62	5.58	5.59	5.59	0.021	NS	NS
Lightness	36.1	37.2	36.0	37.0	35.1	36.5	0.62	NS	*
Redness	14.3	15.4	13.7	15.0	14.4	15.3	0.44	NS	*
Haem (mg/g)	8.0	9.8	8.3	9.2	8.3	10.4	0.53	NS	*
Shear force (N)	32.1	26.3	35.3	25.7	31.8	22.3	2.83	NS	*

[1]No breed * gender interactions, [2] √ (2*error mean square/number of observations per mean)

The effect of dietary laminarin, fucoidan with zinc oxide alone and in combination in the diet of the weanling piglet on performance, selected faecal microbial populations and volatile fatty acid concentrations

P. Mc Alpine[1], C. O Shea[1] P. Varley[1] and J.V. O Doherty[1]

[1]Department of Animal Husbandry and Production, *University College Dublin, School of Agriculture, Food Science and Veterinary Medicine, Lyons Research Farm Newcastle, Co Dublin, Ireland.*

Introduction

Pigs are faced with many new challenges during the post weaning period .These abrupt changes disturb the equilibrium in the gut microbiota, making piglets susceptible to enteric pathogens (Alexopoulos et al., 2004) decreased feed intake and decreased daily weight gain (Estrada et al., 2001). Zincoxide (ZnO) inclusion at (2500-3000 ppm) has been extensively used and proven during the first two weeks weaning to reduce the incidence of post weaning diarrhoea. Seaweed extracts such as laminarin and fucoidan (SWE) have been investigated as a potential feed additive in pig diets due to antimicrobial and immunomodulatory properties (Reilly et al., 2008). The aim of this experiment was to determine could the combination of SWE containing laminarin and fucoidan, with ZnO confer beneficial effects on the newly weaned pig.

Materials and Methods

One hundred and ninety two piglets weaned at 24±2 days of age, with an initial live weight of 6.5 kg ± 0.785 kg, were used in the experiment. The piglets were blocked on the basis of initial live weight, and within each pen were assigned to one of the four dietary treatments. The dietary treatments consisted of (T1) basal diet, (T2) basal diet with 6.9 g kg of SWE, (T3) basal diet with 3.1 g kg of ZnO, (T4) basal diet with 6.9 g kg of SWE and 3.1 g kg of ZnO. The diets were offered in meal form for 40 days after weaning. Weaner pigs were observed for clinical signs of diarrhoea during the performance experiment and a scoring system was applied .Faecal samples were collected for VFA and microbiology analysis. The studies were analysed as 2x2 factorial using PROC GLM (SAS, 2006). The statistical model included the main effects of SWE and ZnO concentration, there supplementation and the interaction between SWE and ZnO.

Results and Discussion

There was a significant interaction between SWE and ZnO on feed efficiency and average daily feed intake ($p<0.05$). Pigs offered SWE alone had improved feed efficiency than basal fed pigs; however there was a deterioration in feed efficiency when SWE was added to ZnO in combination. Similarly in average daily feed intake there was no effect of SWE when compared to the basal diet. However when added in combination with ZnO feed intake increased significantly ($p<0.05$).

The supplementation of SWE alone increased the coefficient total tract apparent digestibility(CTTAD) of DM, OM, N, NDF, ash, GE compared with non-SWE supplemented diets; however there was no effect of SWE when added to ZnO in combination. ZnO alone fed pigs had a reduced faecal score throughout the experiment in contrast to pigs offered diets without ZnO supplementation (2.49 vs 2.82 s.e.m 0.117; $P < 0.019$). There was an interaction ($P <0.005$) between SWE and ZnO on faecal E.coli: Lactobacilli ratio in the link period. Pigs offered the SWE alone supplemented diet had lower faecal Lactobacilli: E.coli ratio than pigs offered the basal diet; however there was no effect of SWE inclusion when added to the ZnO diet. These results suggest that SWE supplemented alone was sufficient in improving feed efficiency and reducing ADFI, whilst ZnO inclusion alone reduced the incidence of scouring by maintaining a low faecal score throughout the experiment, yet when the pair are mixed, their combination was not synergistic.

Conclusions

No significant advantages were observed with the combination of ZnO with SWE; however the inclusion of SWE alone had positive effects not only on pig performance but also in reducing faecal E.coli counts, and increasing nutrient digestibility. ZnO inclusion significantly reduced the onset of scouring; however the combination of ZnO and SWE extracts conferred no beneficial effects on newly weaned piglets.

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Table 1: Effects of SWE and ZnO inclusion on ADFI,ADG,FCR, faecal score, dry matter digestibilty (DMD) and faecal Lactobacilli : E.coli ratios over the entire experimental period days 0 – 40

Period	Treatment					Significance		
0-40	T1	T2	T3	T4	s.e.m	SWE	ZnO	SWExZnO
ADFI kg d	0.633	0.605	0.606	0.676	0.021	0.319	0.338	0.034
ADG kg d	0.356	0.374	0.377	0.369	0.017	0.771	0.623	0.447
FCR kg kg	1.82	1.62	1.63	1.84	0.065	0.713	0.845	0.005
Faecal score	2.82	2.58	2.82	2.49	0.117	0.701	0.019	0.691
DMD	0.781	0.862	0.804	0.788	0.006	0.0001	0.0001	0.0001
Lacto:Ecoli	1.62	1.58	1.61	1.28	0.078	0.034	0.08	0.05

A preliminary assessment of near infrared reflectance spectroscopy as a means of assessing the expected intake of perennial ryegrass

G. A. Burns[1,2], P. O'Kiely[2], M. O'Donovan[3], E. Lewis[3], and T. J. Gilliland[4]

[1]*Queen's University of Belfast;* [2]*Animal & Grassland Research and Innovation Centre, Teagasc, Grange;* [3]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark;* [4]*Agri-Food & Biosciences Institute, Crossnacreevy.*

Introduction

National variety evaluation schemes for perennial ryegrass (*Lolium perenne* L.) assess the potential agronomic value of grass varieties for ruminant-based production systems based on seasonal and annual productivity, persistence and nutritive quality (Grogan & Gilliland, 2011). The use of animal production indices would greatly assist in identifying the merits of a variety. However, such indices are often unavailable for evaluation schemes due to the scale and cost of operation required to account for animal variation (Camlin, 1997). The use of near infrared reflectance spectroscopy (NIRS) has been identified as a technique that could rapidly assess the expected intake of a grass variety (Agnew *et al.,* 2004). The near infrared spectra contain information on the underlying chemical composition of forage samples thereby providing the opportunity to predict their expected intake. This research was undertaken as a preliminary assessment of the ability to assess expected intake by NIRS.

Materials and Methods

A herbage sample was randomly selected from each of 18 perennial ryegrass dominant paddocks at Teagasc Moorepark. The paddocks had between 18 and 48 cows grazing with unrestricted access to grass. An assessment of dry matter intake (kg DM per cow per day) was made using the n-alkanes marker technique (Mayes *et al*., 1986; Dillon and Stakelum, 1989). Each grass sample was dried and milled prior to being scanned on a NIRsystems XDS in duplicate between 1100 – 2500 nm, and averaged. A standard normal variate detrend scatter correction and 1,4,4 derivation were applied to the spectra prior to a modified partial least square regression as described by Burns *et al*. (2012) being carried out to relate the spectra to the measured intake. Water soluble carbohydrate (WSC) concentration and *in vitro* dry matter digestibility (DMD) were assessed as described by Burns *et al*. (2012). Correlations were carried out between each of these two traits and dry matter intake (GenStat v.14.0).

Results and Discussion

The NIRS calibration model provided a disappointing estimate of expected intake (R^2 = 0.467; Figure 1) which can partially be attributed to error associated with the n-alkanes technique. Agnew *et al*. (2004) were able to develop a calibration model to predict the short term intake (kg DM per hour) of ryegrass dominant swards with a higher degree of accuracy (R^2 = 0.76). In part, the latter can be attributed to the larger calibration set (n = 203) that likely encompassed more variation (relative standard deviation = 27 %) than the current study (RSD = 9 %) and had a larger range in intake values. No significant correlation was found between intake and *in vitro* DMD or WSC. This may also reflect the small size of the current dataset. The n-alkanes technique provides a medium term assessment of intake (kg DM per cow per day) which may allow a wider array of factors to affect the intake. Thus, a larger calibration set that encompasses more variation in intake is required. Variety evaluation schemes normally involve mechanical harvesting which causes different sward morphology to that when grazed. Thus further study into the effect of management on the robustness of calibration models would also be required prior to implementing intake indices into national variety evaluation schemes for perennial ryegrass.

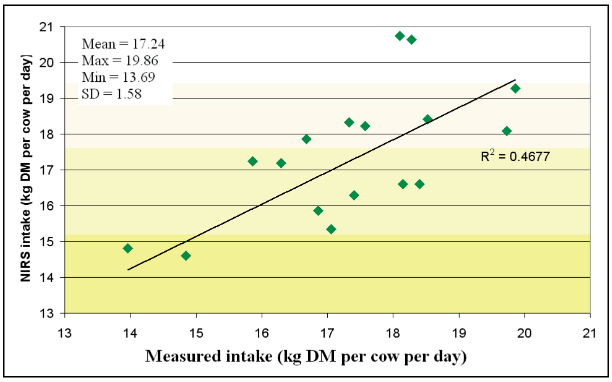

Fig 1. Scatter graph comparing the measured intake (unrestricted) as assessed by the n-alkanes technique (x-axis) to the expected intake predicted by NIRS (y-axis).

Conclusions

Following this preliminary study, an expansion of the calibration set to extend the range of intake figures is required before NIRS could be used to assess the expected intake of perennial ryegrass varieties on the Irish national variety evaluation scheme.

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Post-weaning growth and carcass traits of bulls and heifers from first-parity beef suckler cow breed types

M. McGee and D. Minogue
Teagasc, Animal & Grassland Research and Innovation Centre, Grange, Dunsany, Co. Meath.

Introduction

Sourcing cow replacements from within the suckler herd (rather than from the dairy herd) in Ireland has resulted in a reduction in proportion of dairy ancestry in cows and consequently reduced milk yield and calf weaning weight (McGee *et al.,* 2005; Minchin and McGee, 2011). Milk yield is an important determinant of lifetime live weight performance in spring-calving calf-to-beef systems where no creep feed is offered to calves pre-weaning (Murphy *et al.*, 2008). The objective of this study was to compare the post-weaning growth and carcass traits of progeny from Limousin × Holstein-Friesian (LF), Limousin × Simmental (LS), Charolais × Limousin (CL) and Charolais × Simmental (CS) beef suckler cows.

Materials and Methods

Data were collected from 108 progeny of spring-calving (mid-March) first-parity, LF, LS, CL and CS cows, bred to four Blonde d'Aquitaine sires. Cows and calves were grazed together for the first grazing season following which they were weaned gradually and housed indoors (November) in slatted floor pens. They were offered grass silage (DMD ~73%) *ad libitum* plus 2 (bulls) or 1 (heifers) kg/head daily of a barley-based concentrate. At the end of the first winter (March) they were turned out to pasture and rotationally grazed for 114 (bulls) or 205 (heifers) days. Following housing, bulls were gradually introduced to barley-based concentrates *ad libitum* plus ~1 kg grass silage DM/head daily until slaughter 85 days later (~18.5 months of age). Prior to housing heifers were offered concentrates at pasture for 16 days, then housed and offered grass silage *ad libitum* plus 4.6 kg concentrates/head daily, until slaughter 63 days later (~20.5 months of age). Live weight was recorded regularly and after slaughter, carcasses and kidney + channel fat were weighed and carcasses were graded for fat and conformation. Data were analysed using the GLM procedure of SAS. The model contained fixed effects for dam genotype, gender, genotype × gender and sire of calf. Birth day was included as a covariate.

Results and Discussion

Progeny from LF were 52 kg heavier at weaning than CL, with LS and CS being intermediate ($P<0.001$) (Table 1). Live weight gain (ADG) post-weaning did not differ ($P>0.05$) between breed type. Consequently, breed differences in live weight post-weaning, predominantly reflected differences in their pre-weaning growth, which was mainly due to differences in milk yield between the cow breed types (Minchin and McGee, 2011). Carcass weight of LF was, numerically, 6 kg heavier than LS and CS and 16 kg heavier than CL ($P>0.05$), which is consistent with previous findings using dairy and beef crossbred cows (Murphy et al., 2008). Carcass conformation score was lowest for LF and highest for CL. Carcass fat score did not differ ($P>0.05$) between breed type. Bulls were significantly heavier at weaning and had a higher carcass weight per day of age, greater kill-out proportion and carcass conformation score and, lower carcass fatness than heifers. The magnitude of some differences between genders partly reflected contrasts in production system.

Conclusions

Weaning weight and ADG from birth to slaughter was greater for LF than CL with breed types having Simmental ancestry being intermediate, but carcass weight per day of age did not differ between breed types. Performance of bulls was superior to heifers.

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Table 1: Growth and carcass traits (s.e.m.[1]) of progeny from Limousin × Holstein-Friesian (LF), Limousin × Simmental (LS), Charolais × Limousin (CL) and Charolais × Simmental (CS) cows

	Cow breed type (B)						Gender (G)			
	LF	LS	CL	CS	s.e.m.	Sig[2]	Male	Female	s.e.m.	Sig.[2]
Live weight (kg)										
Weaning / Housing	317^a	283^b	265^c	284^b	5.7	***	295	279	4.0	**
At grass - 8 d post-turnout	377^a	338^{bc}	320^c	345^b	7.0	***	364	326	5.1	***
Housing	545^a	506^{bc}	484^c	513^b	8.7	***	506	518	6.0	
Slaughter	649^a	627^{bc}	606^c	636^{ab}	10.0	*	679	580	7.0	***
Carcass weight (kg)	371	365	355	365	6.7		408	319	4.7	***
Kill-out proportion (g/kg)	572	581	586	573	3.6	**[3]	603	553	2.5	***
Carcass conformation (1-15)	9.2^a	10.5^{bc}	10.7^c	10.1^b	0.23	***	11.3	9.0	0.16	***
Carcass fat (1-15)	7.1	6.9	6.5	6.7	0.31		6.1	7.5	0.22	***
Kidney+channel fat (g/kg carc.)	19^a	16^b	16^b	18^{ab}	1.0	*	11	23	0.7	***
Daily live weight gain (kg)										
First indoor winter period	0.61	0.54	0.56	0.60	0.032		0.67	0.48	0.022	***
Pasture	1.26	1.20	1.20	1.22	0.034	*[3]	1.38	1.06	0.023	***
Indoor finishing period	1.31^a	1.52^b	1.52^b	1.54^b	0.067	*	2.00	0.95	0.045	***
Weaning-slaughter	0.93	0.96	0.95	0.98	0.021		1.16	0.75	0.015	***
Birth-slaughter	1.03^a	0.99^{ab}	0.96^b	1.00^{ab}	0.016	*	1.13	0.85	0.011	***
Carcass weight /day of age (kg)	0.63	0.62	0.60	0.62	0.011		0.73	0.51	0.008	***

[1] Maximum s.e.m. [2] *$P<0.05$, **$P<0.01$, ***$P<0.001$ [3] B × G interaction, $P<0.05$

Green Biorefinery – investigating the nutritive value of the separated press-cake fraction

J. McEniry, C. King and P. O'Kiely
[1]*AGRIC, Teagasc, Grange, Dunsany, Co. Meath*

Introduction

The need to develop alternatives to non-renewable fossil-based resources has stimulated an interest in plant biomass to provide energy, chemicals and materials. An essential component of the 'Green Biorefinery' concept is the initial fractionation of green biomass into a fibre-rich press-cake and a nutrient rich press-juice. The viability of such a process will depend on identifying a range of suitable applications for the separated fractions. This study investigated the estimated nutritive value of the separated press-cake fraction from a range of grass silages and assessed their potential as a feedstuff for ruminants.

Materials and Methods

Triplicate plots of each of two common grass species, perennial ryegrass (PRG; *Lolium perenne* L. var. Gandalf) and cocksfoot (*Dactylis glomerata* L. var. Pizza), were grown in field plots (20 m^2; 125 kg N/ha) and harvested at three sequential dates (12 May, 9 June and 7 July; Harvests 1 to 3; n = 27 plots) in the primary growth. At each harvest date, the appropriate plots were precision-chopped and 6 kg samples were ensiled in laboratory silos. After 100 days ensilage, representative silage samples were fractionated into press-juice and press-cake fractions. Briefly, this process involved hydrothermal conditioning (3 water + detergent: 1 silage mixtures at 60ºC for 30 minutes) followed by mechanical dehydration using an hydraulic press (4.5 Mpa). Representative silage and press-cake samples were analysed for dry matter (DM) concentration, while dried milled samples were used for the determination of neutral detergent fibre (NDF), crude protein (CP) and ash as previously described by Purcell *et al*. (2011). Dry matter digestibility was determined by the pepsin-cellulase method as described by Aufrere and Demarquilly (1989). Data were analysed as a split-split plot design using the Proc MIXED procedure of SAS, V9.1.2, and accounting for replicate blocking.

Results and Discussion

On average, there was an increase ($P<0.001$) in herbage DM and NDF concentrations with advancing harvest date (Table 1). This was accompanied by a decrease ($P<0.001$) in herbage DMD and CP concentration, reflecting the general decrease in plant leaf to stem ratio and the increasing cell wall content as the plant matured. On average, the cocksfoot silages had a lower ($P<0.05$) DMD and a higher ($P<0.05$) CP and ash concentration than the PRG silages.

Ash and CP concentrations were lower ($P<0.001$) in the press-cake fraction than in the original silage, while the opposite ($P<0.001$) was the case for DM and NDF concentrations. Fractionation removed a large portion of the herbage soluble and mineral content (>0.60 of the N and ash compared with the starting silage), with the final press-cake fraction being high in fibre and low in digestibility. The press-cake fraction prepared from the Harvest 1 silages can be compared with poor quality grass silage (<650 g/kg DMD) and may have some potential for animal maintenance; however this material would have to be supplemented to make up for its relatively low CP concentration. In contrast, the DMD of the press-cake fractions at the late harvest dates were similar to straw (513 and 458 g/kg DMD for Harvests 2 and 3, respectively) suggesting that any potential of the press-cake fraction as a feedstuff for ruminants is gone at later harvest dates.

Conclusions

The final press-cake fraction was high in fibre and low in digestibility and CP. The press-cake fraction prepared from the early harvest silage may have some potential for animal maintenance, but this potential decreased with advancing harvest date.

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Table 1 Chemical composition of silages and separated press-cake fractions

Grass species	Harvest	State	DM (g/kg)	DMD (g/kg)	NDF (g/kg DM)	CP (g/kg DM)	Ash (g/kg DM)
Perennial ryegrass	1	Silage	149	783	512	158	110
Perennial ryegrass	1	Press-cake	307	650	873	46	36
Perennial ryegrass	2	Silage	204	661	628	113	86
Perennial ryegrass	2	Press-cake	324	521	919	36	31
Perennial ryegrass	3	Silage	220	552	658	101	72
Perennial ryegrass	3	Press-cake	333	468	886	43	34
Cocksfoot	1	Silage	146	732	535	170	108
Cocksfoot	1	Press-cake	262	599	821	62	39
Cocksfoot	2	Silage	208	634	610	125	98
Cocksfoot	2	Press-cake	324	505	868	55	35
Cocksfoot	3	Silage	209	446	685	109	104
Cocksfoot	3	Press-cake	382	449	906	45	46
		s.e.m.	13.7	22.6	19.0	5.12	2.8
		Sig.	*	NS	NS	NS	*

DM = dry matter; DMD = dry matter digestibility; NDF = neutral detergent fibre; CP = crude protein; s.e.m. = standard error of the mean (relates to three-factor interaction); * = P<0.05, NS = not significant.

Effect of feed restriction and subsequent compensatory growth on the weight of non-carcass parts of Holstein Friesian bulls.

K. Keogh[1,2], S.M. Waters[1], A.K. Kelly[2] and D.A. Kenny[1]
[1]*Animal and Bioscience Research Department, Animal and Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany Co. Meath;* [2]*School of Agriculture Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin 4.*

Introduction
The compensatory growth (CG) phenomenon is commonly exploited by cattle producers to reduce the overwintering costs of beef cattle (Keane and Drennan, 1994). The objective of this study was to examine the effect of compensatory growth potential, following a period of restricted feed allowance, on the relative growth of various non-carcass parts, including highly metabolic organs such as the liver and gastrointestinal tract (GIT), of young bulls during early re-alimentation.

Materials and Methods
Holstein Friesian bulls (n=60) with a mean (SEM) age of 479 (15) days and bodyweight 370 kg (35) were blocked according to weight, age, sire and pre-trial live weight gain into one of two groups: (i) restricted feed allowance for 125 days (RES; n=30) followed by *ad libitum* access to feed for 55 days or (ii) *ad libitum* access to feed throughout (ADLIB; n=30). The first 125 days was denoted as Period 1 and the subsequent 55 days, Period 2. All animals were offered a total mixed ration diet consisting of 70% concentrate and 30% grass silage on a DM basis. Diets were fed individually, with the proportion of feed required based on each animals own individual bodyweight; bodyweight was determined on a fortnightly basis. During Period 1 RES were managed to achieve a target mean daily growth rate of 0.5 kg/day. At the end of this period, 15 animals from each treatment were slaughtered and the weight of a number of non-carcass parts measured. All remaining animals were slaughtered at the end of Period 2. This coincided with the period of peak re-alimentation (Hornick et al., 2000). Measurements taken at each slaughter point included the weight of the head, liver, kidneys, gall bladder, lungs, kidney and channel fat (KCF), reticulo-rumen (empty), spleen, omasum, abomasum and entire intestines (full). All non-carcass parts data were expressed on a kg per kg bodyweight basis (kg/kgBW). Data were statistically analysed using the Mixed procedure of SAS with terms for diet and period, as well as their interaction included in the model, as appropriate.

Results and Discussion
Average daily gain (ADG) for Period 1 was 0.5 kg/d for RES and 1.8 kg/ for ADLIB treatment. During re-alimentation (period 2) an ADG of 2.5 and 1.4 kg/d was observed for the RES and the ADLIB groups. This resulted in differences in bodyweight of 156 and 74kg between RES and ADLIB at the end of periods 1 and 2, respectively. Treatment x period interactions were evident for liver, omasum and reticulo-rumen, with greater organ weight observed for ADLIB compared to RES during period 1, but not for period 2. Intestines, and KCF were heavier, while head was lighter for ADLIB compared to RES treatment across periods. No effect ($P > 0.10$) of either dietary treatment or period was evident for the remaining non-carcass parts examined *viz.* lungs, gall bladder, kidneys, spleen and abomasum.

Conclusions
The results of this study suggest that a number of metabolically active organs including liver and components of the GIT reduce in size following a period of reduced feed intake. This may lead to a reduction in overall maintenance energy requirements while feed is scarce. The study also provides evidence that subsequent compensation of these tissues occurs at a faster rate upon re-alimentation.

Acknowledgements
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Table 1. Effect of treatment (T) and period (P) on the weight of non-carcass parts of Holstein Friesian bulls (kg/kgBW).

	RES		ADLIB			Significance		
	Period 1	Period 2	Period 1	Period 2	SEM	T	P	T*P
Head	0.0366	0.0343	0.0323	0.0316	0.0006	*	***	NS
Liver	0.0096^a	0.0147^b	0.0134^b	0.0131^b	0.0004	***	**	***
Lungs	0.0065	0.0071	0.0061	0.0058	0.0003	NS	NS	NS
Gall bladder	0.0009	0.0009	0.0008	0.0008	0.0001	NS	NS	NS
Kidneys	0.0023	0.0025	0.0026	0.0025	0.0001	NS	NS	NS
KCF	0.0075	0.0102	0.0113	0.0150	0.0006	***	***	NS
Reticulo-rumen	0.0169^a	0.0219^b	0.0196^b	0.0208^b	0.0006	***	NS	*
Spleen	0.0015	0.0018	0.0018	0.0018	0.0001	NS	NS	NS
Intestines	0.0436	0.0533	0.0480	0.0538	0.0019	**	NS	NS
Omasum	0.0095^a	0.0137^b	0.0144^b	0.0124^b	0.0005	*	*	***
Abomasum	0.0082	0.0090	0.0078	0.0080	0.0005	NS	NS	NS

[a,b] Within row values are different ($P < 0.05$). *P<0.05; **P<0.01; ***P<0.001; NS = P>0.05

Effect of feeding Bt MON810 maize for 31 days on the intestinal microbiota of weanling pigs

S. G. Buzoianu,[1,3] M.C. Walsh,[1] M. C. Rea,[2] O. O'Sullivan,[2,4] P. D. Cotter,[2,4] R. P. Ross,[2,4] G.E. Gardiner[3] and P. G. Lawlor[1]

[1]*Teagasc, Pig Development Department, Animal and Grassland Research and Innovation Centre and* [2]*Food Research Centre, Moorepark, Fermoy, Co. Cork;* [3]*Department of Chemical and Life Sciences, Waterford Institute of Technology, Waterford; and* [4]*Alimentary Pharmabiotic Centre, University College Cork, Cork.*

Introduction

Since their release on the market in 1996, genetically modified (GM) crops have been a source of controversy. Concern has been expressed by consumers regarding the potential for negative effects on health arising from GM plant consumption. The role of the intestinal microbiota in host health is well recognised (Hooper, 2004). Therefore any effect that a GM crop may have on the intestinal microbiota may greatly influence animal or human health. Our objective was to assess the effect of feeding a GM Bt maize-based diet for 31 days on intestinal microbiota using the pig as a model for humans.

Material and Methods

Eighteen pigs were weaned at ~28 days, and allowed a 6 day acclimatization period during which they were fed a non-medicated, non-GM diet. Following acclimatisation (day 0), pigs were blocked by weight and litter and assigned to treatments [either isogenic or Bt maize at 39% (weight/weight) of the diet for 31 days; n=9]. In accordance with international guidelines, (ILSI, 2007) the maize varieties were grown in neighbouring plots in the same season to avoid differences in chemical composition due to environmental and seasonal variation. Faecal samples were obtained on day -1 and 30 of the study and ileal and caecal digesta were obtained at slaughter on day 31. *Enterobacteriaceae*, lactobacilli and total anaerobes were enumerated in faecal and digesta samples by culturing on selective media. Relative abundance of bacterial populations in the pig caecum was investigated using high-throughput 16S rRNA gene sequencing. Normally distributed data were analysed as a one-way ANOVA using PROC GLM of SAS. Non-normal data were analysed using the Kruskall Wallis non-parametric test within the NPAR1WAY procedure of SAS. For faecal bacterial counts, day -1 values were used as a covariate in the model.

Results and Discussion

No treatment effects were observed for faecal, ileal or caecal *Enterobacteriaceae*, *Lactobacillus* or total anaerobe counts obtained by culturing ($P > 0.05$; data not shown). High-throughput 16S rRNA sequencing revealed no significant treatment differences between the major bacterial phyla in the pig caecum (Fig. 1). However, compared to pigs fed the isogenic maize-based diet, pigs fed the Bt maize-based diet had higher caecal abundance of *Enterobacteriaceae*, *Helicobacteraceae*, *Helicobacter* and *Bacteroides* ($P < 0.05$; Table 1). Bt maize-fed pigs also had lower abundance of fibre-fermenting bacteria (*Prevotella, Ruminococcus, Eubacterium, Faecalibacterium, Fibrobacter, Clostridium, Bacteroides* and *Butyrivibrio*) when these were analysed as a group ($P < 0.05$; Table 1). However, these changes were not associated with any health effects. As the Bt maize had a lower enzyme-resistant starch content, which is fermented in the hind gut, the differences in caecal microbiota are believed to have occurred due to this.

Table 1. Effect of feeding a Bt or isogenic maize-based diet for 31 days on the relative abundance of caecal bacterial taxa in weanling pigs†

	Isogenic	Bt	95% CI	P
Family				
Enterobacteriaceae	0.1	0.7	0.2-2.6	0.01
Helicobacteraceae	0.04	0.2	0.02-0.4	0.002
Genus				
Helicobacter	0.04	0.2	0.14-0.4	0.002
Bacteroides	0.05	0.1	0.09-0.11	0.01
Fibre degrading bacteria*	22.0	13.0	8.0-18.0	0.03

†Median values (% of the total bacterial population)
CI – confidence interval
*Sum of *Prevotella, Ruminococcus, Eubacterium, Faecalibacterium, Fibrobacter, Clostridium, Bacteroides* and *Butyrivibrio.*

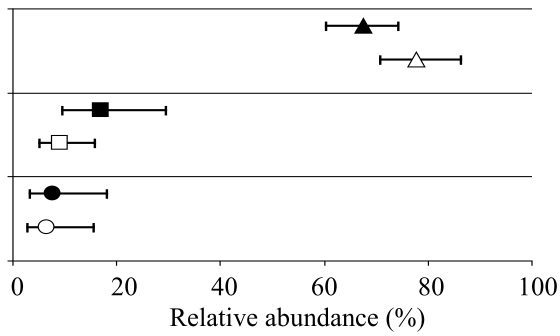

Fig. 1. Effect of feeding a Bt (open symbols) or isogenic (closed symbols) maize-based diet for 31 days to pigs on the mean relative abundance of major caecal phyla Firmicutes (▲,△), Bacteroidetes (■,□) and Proteobacteria (●,○). Data are presented as medians (symbols) and the 95% confidence interval (whiskers).

Conclusions

GM Bt maize has little influence on porcine major caecal bacterial groups. The differences observed are not believed to have major clinical significance and were not associated with any health effects. These results indicate that Bt maize is well tolerated by the host. Due to similarities between the porcine and human intestinal microbiota, a similar response would be expected in humans.

Acknowledgements

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Bioeconomic modelling of alternative replacement heifer policies for suckler beef production systems

P. Crosson and M. McGee
Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co. Meath.

Introduction

There are a range of strategies used by farmers to generate replacement breeding heifers for the suckler cow herd. The predominant approaches are to (1) breed replacements from within the cow herd or (2) purchase replacement heifers from either suckler or dairy herds. The objective of this study was to use a bioeconomic model of suckler beef production systems to investigate the effects of replacement policy on the technical and economic performance of suckler calf to beef production systems.

Materials and Methods

To evaluate technical and financial performance, the Grange Beef Systems Model (Crosson, 2008) was used. This is a whole-farm budgetary simulation model which simulates the primary farm activities that occur on suckler beef farms. The systems of production modelled were suckler calf to beef systems using late-maturing continental cow breed types. Stocking rate was 210 kg organic N per hectare and mean calving date was 15 March. The key assumptions used in this analysis are presented in Table 1.

Table 1. Assumptions used in the replacement heifer policy analysis for suckler beef production systems.

Land area	40	ha
Beef price (R3)	375	€/kg
Fertiliser (CAN) price	270	€/t
Concentrate price	210	€/t
Weaning weight[1]	303	kg/head
Carcass weight[1]	357	kg/head
Replacement calf (4 weeks of age)	250	€/head
Maiden heifer (12 months of age)	800	€/head
Pregnant heifer (24 months of age)	1621	€/head

[1]Mean of steers and heifers

Progeny were finished as steers and heifers at 24 and 20 months of age, respectively. Five scenarios representing alternative replacement strategies were evaluated; purchasing replacement heifers at 1 (PUR1), and 12 (PUR12) months of age, purchasing pregnant heifers at 24 (PUR24) months of age, immediately prior to calving and, breeding replacements from within the suckler herd to calve at 24 (BRED24) and 36 (BRED36) months of age. In the purchased heifer scenarios PUR1 and PUR12, 0.2 and 0.1, respectively, replacement animals in excess of that required were purchased to provide for mortality, selection and reproductive failure. In these scenarios, age at first calving was 24 months of age. The sensitivities of the scenarios to purchase price, beef price and pre-weaning live weight were evaluated.

Results and Discussion

For the scenarios where replacements were purchased, cow numbers, cattle sales and output increased, whilst the number of replacements purchased decreased as age at purchase increased (Table 2). Net margin per ha was 19% lower for PUR12 relative to PUR1 and a further 31% lower for PUR24 with this decrease in margins largely owing to increasing replacement heifer purchase costs. In general, profitability was lower where replacement heifers are bred from within the herd mainly arising from lower numbers of cattle finished relative to the purchased heifer scenarios. BRED24 resulted in a greater number of cows calving, increased output and increased profitability relative to BRED 36. All scenarios were very sensitive to beef price. PUR24 was also sensitive to purchase heifer price with the remaining scenarios showing lower levels of sensitivity to this parameter. The sensitivity of scenarios to pre-weaning live weight gain was intermediate between the beef and purchase price.

Conclusions

As a result of lower purchase and rearing costs, purchasing replacement heifers at 1 month or 12 months of age was more profitable than purchasing pregnant heifers at 24 months of age or breeding replacement heifers from within the herd. However, the most appropriate replacement strategy for individual suckler beef farms will also depend on factors such as the ability to source suitable heifers for breeding, specific herd health risks, and labour and facility requirements associated with each option.

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Table 2. Effect of replacement policy on technical and financial performance of suckler calf-to-beef production systems

Scenario[1]	PUR1	PUR12	PUR24	BRED24	BRED36
Cows calving (number)	59.6	62.3	67.5	65.7	59.1
Replacement heifers purchased (number)	14.3	13.7	13.6	-	-
Cattle sold (number)	55.7	58.3	63.1	47.0	42.2
Live weight output (kg/ha)	1,022	1,070	1,158	923	830
Carcass weight output (kg/ha)	567	593	642	511	459
Profitability (€/ha)					
Gross output	2,042	1,943	1,821	1,921	1,720
Gross margin	1,013	923	772	866	693
Net margin[2]	485	392	240	325	159
Net margin sensitivity (+/- €/ha)					
Purchase price (+/- 10%)	8.8	24.2	54.2	-	-
Beef price (+/- 10%)	201.7	192.0	234.2	184.6	165.9
Pre-weaning LWG (+/- 10%)	36.8	47.9	61.3	31.2	35.3

[1]PUR1, PUR12 and PUR24; purchase of replacement heifers at 1, 12 and pregnant heifers at 24 months of age, respectively. BRED24 and BRED36; home-bred heifers calving at 24 and 36 months of age, respectively. [2]Excluding owned land and labour.

Modelling the economics of dairy calf to beef production systems

A. Ashfield[1, 2], P. Crosson[1] and M. Wallace[2]
[1]*AGRIC, Teagasc, Grange, Dunsany, Co. Meath;*
[2]*School of Agriculture and Food Science, UCD. Dublin*

Introduction
Despite its importance to the Irish economy, the profitability of Irish beef farms remains low with an average net margin for non-breeding cattle farms in 2010 of €304 ha^{-1} and -€185 ha^{-1} excluding subsidies (Hennessy et al., 2011). The objective of this study was to determine the effect of breed, gender and price changes on the profitability of grass based dairy calf to beef systems. The analysis was carried out using the Grange Dairy Beef Systems Model (GDBSM).

Materials and Methods
The GDBSM is a whole-farm systems, static, single-year deterministic simulation model (Ashfield et al., 2011). Production systems modelled were based on three breed groups which represent the progeny of Holstein/Friesian dairy cows bred to Belgian Blue (BB), Aberdeen Angus (AA) and Holstein/Friesian (FR) sires. The model can simulate three genders, bulls, steers (S) and heifers (H), and a range of finishing ages from 15 to 30 months of age depending on breed and gender. Dietary components consist of grazed grass, grass silage and concentrates. The model consists of four sub-models; farm system, animal nutrition, feed supply and financial. The GDBSM was used to model grass-based finishing for AA H finished at 19 months of age and grass silage and concentrate-based finishing for BB H finished at 21 months of age and AA S, FR S and BB S finished at 24 months of age. The production systems modelled operated at a stocking rate of 170 kg organic nitrogen per ha. Scenarios were subjected to a 10% increase and decrease in calf, beef, concentrate and fertiliser price. Base parameters are shown in Table 1.

Results and Discussion
Table 2 presents the physical and financial results for the scenarios modelled. The heifer systems had the largest grazing area with AA H 40% and BB H 17% greater than BB S with all steer systems similar. Consequently, AA H had 53% and BB H 21% less silage area than FR S with all steer systems similar. The proportion of grazed grass in the diet was 45%, 12%, 4% and 2% higher than BB S for AA H, BB H, AA S and FR S, respectively. Total number of animals finished was 42% and 22% greater for AA H and BB H, respectively, than the steer production systems. Despite the heifer systems having a lower carcass weight relative to steer systems, carcass output ha^{-1} was 2% and 9% higher for AA H and BB H than FR S, respectively, due to the larger number of animals finished. Largest carcass output ha^{-1} was for BB S which was 9% greater than FR S. The heifer systems had the highest gross margin (GM) with AA H 43%, BB H 35%, BB S 31% and FR S 10% higher than AA S. This resulted in the net margin (NM) for AA H being 183%, BB H 117%, BB S 127% and FR S 42% higher than AA S. Price sensitivity was a function of the quantity of given inputs used and outputs produced and therefore, beef price, concentrate price and fertiliser price changes had the largest effect on BB S, FR S and steer systems, respectively.

Table 1. Input parameters used in the GDBSM

Area farmed (ha)	50
AA heifer calf price (€ head^{-1})	110
BB heifer calf price (€ head^{-1})	110
AA steer calf price (€ head^{-1})	186
FR steer calf price (€ head^{-1})	95
BB steer calf price (€ head^{-1})	186
Beef price (€ kg^{-1})	3.57
Concentrate price (€ t^{-1})	290
Calcium ammonium nitrate (€ t^{-1})	309

Conclusions
The most profitable system was AA heifers slaughtered at 19 months of age. The results show that maximising the proportion of grazed grass in the diet is an important driver of profitability. Beef price had a large effect on net margin per hectare.

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Table 2. Physical, financial and sensitivity results for the five scenarios studied by the GDBSM

	BB S[1]	FR S[1]	AA S[1]	BB H[2]	AA H[3]
Grazing area (ha)	30	31	31	35	42
Silage harvest (ha)	33	32	32	25	13
Proportion grazed grass in diet (%)	51	52	53	57	74
Number finished	103	103	103	125	146
Carcass weight (kg head^{-1})	352	322	323	287	230
Carcass output (kg ha^{-1})	724	662	664	719	672
Gross margin (€ ha^{-1})	908	764	695	940	991
Net margin (€ ha^{-1})	382	238	168	365	475
Sensitivity (impact on net margin ha^{-1})					
Calf price (+/- 10%)	44	22	44	32	37
Beef price (+/- 10%)	262	228	235	244	221
Concentrate price (+/- 10%)	59	62	54	53	28
Fertiliser price (+/- 10%)	11	11	10	8	7

[1]Belgain Blue (BB), Holstein/Friesian (FR) and Aberdeen Angus (AA) steer slaughtered at 24 months of age, [2]BB heifer slaughtered at 21 months of age, [3]AA heifer slaughtered at 19 months of age.

The effect of stocking rate and calving date on the milk production performance of Holstein-Friesian dairy cows

B. McCarthy[1], K.M. Pierce[2], L. Delaby[3], A. Brennan[1] and B. Horan[1]
[1]*Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork,* [2]*School of Agriculture, Food Science & Veterinary Medicine, University College Dublin, Belfield, Dublin 4,* [3]*INRA, AgroCampus Ouest, UMR 1080, Production du Lait, F-35590 Saint-Gilles, France.*

Introduction
The removal of milk quotas will have a major impact on the Irish dairy industry. The Food Harvest 2020 report sets a target for a 50% increase in milk production by the year 2020 (DAFF, 2011). Stocking rate (SR), traditionally expressed as cows/hectare (ha), is the main driver of milk production in grass-based systems (Macdonald et al., 2008). McCarthy et al. (2011) reported that for a SR increase of one cow/ha, milk production per cow is reduced by 8% whereas milk production per ha is increased by 20%. Calving date (CD) also affects production and profitability in grass-based systems through its effect on the alignment of herd demand to grass supply (Dillon et al., 1995). The objective of this study was to investigate the impact of SR and CD on milk production of Holstein-Friesian (HF) dairy cows over a two year period.

Materials and Methods
Two hundred and seventy six HF dairy cows (138 in both 2009 and 2010, respectively), comprising of two strains of HF (North American and New Zealand) were randomly assigned within strain to one of two mean CD treatments, to establish two groups of dairy cows: Early calving (mean calving date: 12th of February) and late calving (mean calving date: 25th of February). Animals within each CD were then randomly allocated to one of three SR treatments, low (2.51 cows/ha), medium (2.92 cows/ha) and high (3.28 cows/ha). Cows were turned out to grass in early February with SR treatments managed separately and CD treatments within each SR managed similarly. Different grazing intensities were imposed on each SR, with target post-grazing residual heights of 4.5-5.0, 4.0-4.5, and 3.5-4.0 for the low, medium and high SR respectively. Herbage allowance (HA) and herbage removed was measured using the method of Delaby and Peyraud (1996). Concentrate supplementation and artificial fertiliser application was the same for each SR, however late calving treatments received less concentrate. Milk yield was recorded daily and milk composition weekly. Dietary details were analysed using mixed models in SAS. Milk production data were analysed using covariance analysis, with a model that included the effects of year, parity, strain, CD, SR, their interactions and covariates. Milk production per ha was calculated by summing the milk produced from each paddock within each treatment and dividing by the area of the paddock to give the yield per ha. Yield per ha was analysed using variance analysis with the effects of year, block, SR and CD in the model.

Results and Discussion
The low SR had the highest daily HA (17.7 kg dry matter (DM)/cow), the medium SR was intermediate (14.5 kg DM/cow) and the high SR had the lowest HA (12.2 kg DM/cow). Stocking rate had a significant effect on total milk production per cow and per ha and on milk composition (Table 1). As SR increased by 31% (2.51 vs. 3.28 cows/ha), milk yield per cow decreased by 12.4%, whereas milk yield per ha increased by 17.4%. Lactation length decreased as SR increased (289, 283 and 280 days for the low, medium and high SR, respectively). Calving date had no effect on total milk production per cow or per ha (Table 1) however; the late calving treatments had a shorter lactation length (289 vs. 279 days) compared with the early calving treatments. Consequently, the late calving treatments had a higher daily milk yield ($P < 0.001$) than the early calving treatments despite receiving less concentrate ($P < 0.001$; 423 vs. 464 kg DM/cow) and silage (115 vs. 157 kg DM/cow) supplementation.

Conclusion
The results indicate that although CD had no effect on total lactation performance, adjusting mean CD can be an effective strategy to reduce supplementary feed requirements at increased SR in early lactation.

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Table 1: Effect of stocking rate and calving date on milk production performance

	Stocking rate (SR)				Calving (CD)			*P*-values	
	Low	Medium	High	s.e.[1]	Early	Late	s.e.	SR	CD
Milk yield per cow (kg)	5597^a	5045^b	4975^b	60.2	5234	5184	48.4	<0.001	0.470
MS[2] yield per cow (kg)	433^a	392^b	389^b	4.6	409	401	3.7	<0.001	0.133
Milk yield per ha (kg)	13,399^a	14,215^a	15,717^b	371.7	14,402	14,486	303.5	<0.001	0.840
MS yield per ha (kg)	1060^a	1113^a	1255^b	29.2	1155	1131	23.8	<0.001	0.473
Milk composition									
Fat (g/kg)	41.4^a	42.4^b	42.7^b	0.29	42.6	41.8	0.24	0.007	0.015
Protein (g/kg)	36.1^a	35.5^b	35.6^b	0.14	35.9	35.6	0.11	0.004	0.061
Lactose (g/kg)	47.0^a	46.0^b	46.4^c	0.13	46.6	46.3	0.09	<0.001	0.051

[1]s.e. – standard error, [2]MS = milk solids (fat + protein)

Characteristics, intentions and expectations of new entrant dairy farmers entering the Irish dairy industry through the New Entrant Scheme

R. McDonald[1,2], K. Pierce[2], R.M. Fealy[3] P. Savage[4] and B. Horan[1]

[1]*Animal and Grassland Research and Innovation Centre, Teagasc Moorepark, Fermoy, Co. Cork.* [2]*School of Agriculture & Food Science, University College Dublin, Belfield, Dublin 4.* [3]*Spatial Analysis Unit (RERC), Teagasc Kinsealy, Co. Dublin.* [4]*Department of Agriculture, Fisheries, and Food, Agriculture House, Kildare St., Dublin 2*

Introduction

In advance of EU milk quota abolition in 2015, the Irish government has decided to allocate ¼ of the annual 1% increase in milk quota between 2009 and 2015 on a permanent basis to new entrants to dairying. Two hundred and thirty new entrants have successfully received 200,000 litres of milk quota in the initial 3 years of the scheme. The objective of this study was to describe the farm and farmer characteristics of new entrant dairy farmers setting out in the Irish dairy industry in terms of their location, planned production system characteristics, intended operational scale and expected profitability based on an analysis of successful applications to the Irish New Entrant Dairy Scheme (DAFF, 2009).

Materials and Methods

All successful quota applications included a detailed 5 year business plan, detailing existing resources, planned capital investment, equity, predicted income and expenditure over the next 5 years, stock flow and source of capital finance for each year of the plan. Data for the 230 applicants were divided into key variables and analysed to determine the regional, age, experience, educational and off-farm income effects on intentions and expectations of the dairy farm.

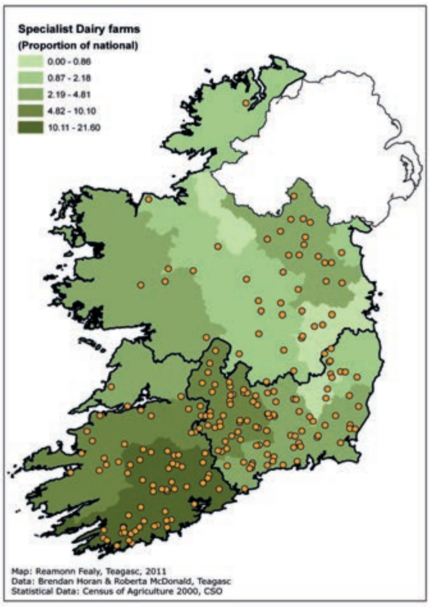

Figure 1. Regional distribution of new entrant dairy farms overlapping the distribution of existing specialised dairy farms

The collated information was analysed using chi-square (PROC FREQ) and generalized linear model (PROC GLM) procedures (SAS, 2006). Address data of the entrants was geocoded to enable GIS mapping of the geographical distribution of new entrants (Figure 1).

Results and Discussion

The results of this study indicate that a young and highly educated group of new farmers are using the New Entrant Scheme to enter the Irish dairy industry with the majority converting from beef and mixed enterprise farms. Ninety-three percent of new dairy entrants have at least two years of formal 3rd level agricultural education and intend to expand to a herd size of 70 cows producing 655kg MS/ha as relatively large scale and efficient milk producer's post EU milk quota abolition.

There was no significant effect of region, dairy experience or education on the expectations and intentions of new entrants. Younger and specialised dairy entrants have fewer owned resources, an increased reliance on additional borrowing and substantial expectations for the productive capacity of their potential farm businesses, when compared to older entrants or those with alternative income sources (Table 1). The average age of new farmers is 36 years with 81% of all new entrants located in the south of Ireland. As a result quota abolition is likely to result in an increased regional bias of milk production in Ireland

Table 1 A summary analysis of the expectations of new entrants to the Irish dairy industry (2009-2011)

	Average	s.e
Total Land (ha)	58.08	
Cow numbers	70.2	1.55
Stocking Rate (LU/ha)	1.74	0.039
Milk solids/ha (kg MS/ha)	655	17.6
SFP received (€)	18,576	1128.4
Capital Borrowed (€)	88,165	5651.3
Total Expenditure (€)	188,681	8417.1
Expected profit per litre (€)	0.05	0.007
Exp. profit per hectare (€)	422	50.7

Conclusions

Applicant age and availability of existing resources have a significant impact on business plans and expectations of new dairy farms. The results provide a further indication that quota abolition is likely to result in an amplified polarisation of milk production and increased production intensity in traditionally intensive milk producing areas in the south of Ireland.

Acknowledgements

The authors wish to acknowledge the participating new entrant dairy farmers for their assistance and the financial support of Allied Irish Bank for this research.

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The value of the Irish sport horse brand within the United Kingdom market

K. D. Hennessy[1] & M. Lambkin
[1]*College of Health Sciences, UCD,* [2]*College of Business and Law, UCD*

Introduction
In the past Irish horses achieved top prices in foreign markets. "... all else being equal, a horse of Irish origin will invariably find a purchaser at a substantially better price than that of any other country", Coyne (1902). Current evidence however suggests that the competitive and market position of the Irish sport horse (ISH) has slipped over time. The objective of this study was to compare the competition and market performance of the ISH with the KWPN (Dutch Warmblood, the leading international sport horse studbook).

Materials and Methods
The international show jumping (SJ) market is the highest value target market for ISH studbook progeny. Studbook world rankings for show jumping are published annually by the World Breeding Federation for Sport Horses (WBFSH). A poor show jumping ranking by the ISH studbook may be linked to low market place prices. The UK sport horse market was chosen as the test market as it is the biggest export market for the ISH (38% of sales) Hennessy and Quinn (2007), the UK does not have a strong performing domestic sport horse studbook, and it is easily accessible to continental studbooks. An online survey was conducted (using Surveymonkey) of UK based sport horse dealers. Respondents were asked to (a) rate the brand reputation on a Likert type scale (from 1 very poor to 5 very good), (b) indicate the relevance of the WBFSH rankings (from 1 not relevant to 5 very relevant), (c) provide a breakdown of horses that they currently owned (market share) and (d) indicate the average prices they had paid for each brand of horse. Respondents were also asked to provide a reason as to why they would pay a price premium for their chosen brand. 140 responses were received, 117of which were usable. All data was reduced to binary level by combining categories. For variables that were assessed using the Likert-type scale, a code of 1 was given for high ratings (4 or 5) and the code of 0 applied to low / medium ratings (1, 2 or 3). For data recorded as numbers, a code of 1 was applied to the top number and a code of 0 to the remaining numbers. Chi-square analysis was applied using 2 x 2 cross tabulations to assess the relationships between measures. Sample representation was similar to the findings of Crossman (2006) on price, Moore-Coyler (2004) on regional representation and the British show jumping database on brand representation.

Results and Discussion
Table 1. Brand prices and WBFSH SJ rankings

	Mean price (SD)	WBFSH rankings			
		2008	2009	2010	2011
ISH	£3,743 (4.6)	11(1)	11(2)	9(6)	9(5)
KWPN	£7,571 (9.4)	1(49)	1(46)	1(49)	1(48)

The average price paid by respondents for ISH horses was £3,743 in comparison to an average price of £7,571 paid for KWPN horses, representing a significant difference (P< .005). A review of WBFSH rankings for show jumping in recent years (Table 1) showed a limited representation of ISH horses in the top 200, hence low rankings for the studbook (11th and 9th). In comparison the KWPN studbook had a very high representation of horses in the top 200 and the studbook has been the top ranked studbook for several years.

Table 2. Relationships between brand reputation and market performance

	ISH Brand reputation		P value
	High	Low	
Market share	22/74 (30%)	38/43(88%)	<.05
Top price	17/52 (32%)	19/23 (83%)	ns
Relevance of rankings	29/76 (38%)	23/44 (52%)	ns
	KWPN Brand reputation		P value
	High	Low	
Market share	19/71 (27%)	40/41 (98%)	<.001
Top price	14/47 (30%)	23/25 (92%)	<.05
Relevance of rankings	41/73 (56%)	34/42 (81%)	<.001

Relationships were found between a high brand reputation for the KWPN and (1) a high market share for the brand, (2) a top price paid for the brand and (3) a high relevance of the WBFSH rankings (Table 2). These findings are supported by a high regard for brand management practices (rigorous selection and provision of extensive information on pedigree and performance), as reasons for paying a price premium for the KWPN.
A relationship was found between a high brand reputation for the ISH and a high market share. However, no relationship was found between brand reputation and top price or a relevance of the WBFSH rankings. Limited reference was made to performance in the respondent's reasons for paying a price premium for the ISH brand.

Conclusions
The results of this research highlight the importance of studbook performance in show jumping. A high KWPN brand reputation is linked with a high relevance of the WBFSH rankings (KWPN is the top ranked studbook) and a high brand value. Such success is underpinned by highly regarded brand management practices.
ISH purchasers tend to have less concern for WBFSH rankings and are a lower value clientele. Hence the ISH is not a serious contender within the more lucrative show jumping market. Only a brand strategy focused on improving the show jumping performance of the ISH will underpin an improvement in the overall value of the brand.

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Effects of production system and the influence of concentrate supplementation during the first season at pasture for dairy bred bulls

[1]R. Prendiville, [2]P. French and [1]E.G. O' Riordan
[1]*Animal and Grassland Research and Innovation Centre, Teagasc, Grange and* [2]*Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark.*

Introduction
Pre-decoupling of support premia, bull beef production was generally less profitable than well managed steer beef, mainly due to the higher premium earning capacity of steers. Currently, there is growing interest in rearing males as bulls due to the inherent efficiencies of improved feed conversion efficiency and growth rate (Steen, 1995). A range of dairy bull beef production systems are currently being employed commercially but, some markets perceive that meat quality of bulls deteriorate with age. The objective of this experiment, at the Johnstown Castle Research Centre, was to investigate the production performance of bulls in 15 month (15MO), 19 month (19MO) and 22 month (22MO) production systems and also the influence of concentrate supplementation during the first season at pasture.

Materials and Methods
One hundred and eighty spring born Holstein-Friesian and Jersey × Holstein-Friesian weaned male calves arrived on-site in May 2010 at ~12 weeks of age and were assigned to a 3 production systems (15MO, 19MO and 22MO of age at slaughter) × 2 concentrate feeding levels (2 kg/head/day (HC) or 0 kg/head/day (LC) at pasture during their first grazing season) factorial arrangement of treatments. Data were available from 141 animals; 47, 46 and 48 bulls in the 15MO, 19MO and 22MO production system, respectively. During the first season (183 days) the HC calves received 310 kg of concentrate DM/head. Pre-grazing herbage yields averaged 1033 kg DM/ha (8.4cm) with a mean post-grazing height of 4.8 cm. Animals were housed on 12 November 2010. Bulls on the 15MO production system were finished on an *ad-libitum* concentrate diet over a 207 day (s.d. 13.6) period (from housing to May-June). During the winter period, animals on the 19MO and 22MO production systems were offered silage *ad-libitum* (730g/kg DMD) supplemented with 1.5 kg concentrate DM and were turned out to pasture 3 March 2011. Bulls on the 19MO production system were housed after a 100 day period at pasture and finished on *ad-libitum* concentrates over a 100 day period. Animals on the 22MO production system were pasture grazed for 200 days and subsequently finished indoors on *ad-libitum* concentrates. Animals were group fed during the finishing period. Concentrates were offered daily and their weights recorded. The concentrates offered consisted of 800 g/kg barley, 140 g/kg soya bean meal, 40 g/kg molasses and 20 g/kg minerals. Animals were weighed fortnightly throughout the study. Carcasses were graded for conformation and fatness according to the European Union Beef Carcass Classification Scheme (Commission of the European Communities, 1982). Data were analysed using the Generalized Linear Model (Proc GLM) statement of SAS. Fixed effects for production system, feeding level during the first season at pasture and genotype were used to analyse the data. Least square means was used in the procedure to compare the difference between the production systems and feeding level for the first season at pasture.

Results and Discussion
Estimated individual concentrate DM intake for the finishing period was estimated to be 1.6, 1.6, 1.2, 1.3, 1.4 and 1.5 tonne for the 15MO HC and LC, 19MO HC and LC and 22MO HC and LC animals, respectively. Slaughter weight was highest ($P<0.001$) for 22MO bulls, lowest with 15MO and 19MO intermediate (Table 1). Carcass weight followed a similar trend ($P<0.001$). Kill out proportion was similar across all treatment groups. Carcass conformation score was greater ($P<0.05$) for 22MO bulls compared to 15MO and intermediate for 19MO. Fat classes were highest for 22MO bulls, lowest with 15MO with 19MO being intermediate ($P<0.01$). Bulls on HC had greater slaughter weights and carcass weights compared to LC ($P<0.001$). No difference in kill out proportion, carcass conformation score or fat class was observed between the feeding level groups.

Conclusion
Results to date indicate that greater slaughter weights, carcass weights and fat classes were achieved in mature dairy bull beef production systems. Current results also show greater carcass weights for animals supplemented with concentrates during the first season at pasture. However, the concentrate supplementation required for the additional carcass weight may be uneconomical.

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Acknowledgements
Financial support from Dawn Meats is gratefully appreciated.

Table 1: Performance and feeding level of dairy bred bulls in 15 month, 19 month and 22 month production systems.

	Production System					Feeding level			
	15 month	19 month	22 month	s.e.[1]	P-value	HC	LC	s.e.	P-value
Slaughter weight (kg)	455^a	577^b	621^c	7.1	<0.001	566	536	5.8	<0.001
Carcass weight (kg)	236^a	302^b	334^c	4.1	<0.001	299	282	3.4	<0.001
Kill out proportion (g/kg)	520	524	525	2.4	0.380	524	521	2.0	0.321
Conformation score (1-15)	4.83^a	5.20^{ab}	5.30^b	0.150	<0.05	5.07	5.16	0.12	0.582
Fat class (1-15)	4.93^a	6.53^b	7.24^c	0.170	<0.01	6.20	6.27	0.14	0.735

[1]weighted standard error of the mean

Bulls from the beef cow herd: effect of system of production on growth and carcass characteristics

E.G. O'Riordan, M. McGee, A.P. Moloney and P. Crosson
Animal and Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co. Meath, Ireland

Introduction
Males produced as bulls are inherently more efficient for beef production than steers of similar breed, age, reared and slaughtered in the same way and, if slaughtered at a younger age have a potentially lower environmental footprint (O'Riordan et al., 2011). As grazed grass, is considerably cheaper than conserved forage or concentrates (Finneran et al., 2011), increasing the proportion of grazed grass in the diet may increase profitability of bull beef systems. As there is little published information on grass-based production systems for weaned late-maturing bulls from the beef cow herd, this study aimed to determine growth and carcass characteristics for such bulls in three contrasting production systems.

Materials and Methods
One hundred and eighty weaned Charolais and Limousin sired suckler bulls were purchased at livestock marts at approximately 8-months of age during October and November 2010. They were vaccinated as a prophylactic measure against respiratory disease, treated for the control of ecto- and endo-parasites and acclimatised to slatted floor accommodation and grass silage plus 2 kg/head concentrates daily. In early December animals were assigned to a 3 (systems of production - PS) × 3 (slaughter weights - SW) factorial arrangement of treatments balanced for birth date (early-March), live weight (370 kg) and sire breed. There were 20 animals per treatment, which were allocated to four pens of five animals. The three PS were: 1) *ad libitum* concentrates (860 g/kg rolled barley, 60 g/kg soya bean meal, 60 g/kg molasses and 20 g/kg minerals/vitamins) plus 1.5 kg grass silage dry matter (DM) daily until slaughter (AL), 2) grass silage *ad libitum* plus 1.5 kg concentrate daily for 120 days followed by AL until slaughter (SAL), or 3) grass silage *ad libitum* plus 1.5 kg concentrate daily for 120 days, followed by 100 days grazing and then, AL until slaughter (GAL). A 3-week period was allowed for animals to adjust to the AL concentrate diet. The three target SW for each system were 670, 720 or 790 kg live weight. Forage and concentrate intakes were recorded daily and live weight at approx. 3-week intervals. On reaching the treatment mean target live weight, animals were slaughtered and carcass weight, conformation and fat score were recorded. Data were analysed using the GLM procedure of SAS. The model contained fixed effects for PS, SW, their interactions and sire breed of the animal. Initial live weight was included as a covariate.

Results and Discussion
By design, PS had no effect (P>0.05) on total weight gain, slaughter or carcass weight and these variables increased (P<0.001) at each SW (Table 1). Mean slaughter age was 1.7 and 3.1 months older, respectively, for SAL and GAL compared to AL. There was a PS × SW interaction (P<0.001) for average daily gain (ADG) during the final finishing phase whereby ADG did not differ between systems at the first SW, but was higher for GAL than AL and SAL at the second SW and, highest for AL and lowest for GAL at the final SW. For the entire feeding period, ADG at the lightest and heaviest SW was greater for AL than SAL, who in turn was greater than GAL (P<0.001), but at the medium SW, ADG was greater for AL compared to SAL and GAL, which did not differ. Kill-out proportion differed (P<0.001) between the three PS, being highest for SAL and lowest for GAL. Carcass conformation score was lower (P<0.05) for GAL than AL or SAL, which did not differ. There was a PS × SW interaction (P=0.05) for carcass fat score, whereby fat score increased with SW for GAL, but not for the other two PS. Kill-out proportion and carcass conformation score increased up to the second SW only (P<0.001).

Conclusions
With the possible exception of the light SW for GAL (fat score, 6.1), carcasses produced had adequate level of fatness and were, thus, suitable for the marketplace. The choice of system will be largely determined by production economics.

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Table 1. Effect of system of production and slaughter weight on bull growth rates and carcass traits

	Production system (PS)			Slaughter weight (SW)				Significance		
	AL	SAL	GAL	670	720	790	s.e.m.	PS	SW	PS×SW
Total weight gain (kg)	308	305	310	248	303	372	6.5		***	
ADG on *ad lib* conc (kg)	1.58	1.78	1.66	1.83	1.67	1.51	0.049	*	***	***
ADG overall (kg)	1.50	1.23	1.05	1.23	1.23	1.32	0.028	***	*	***
Slaughter age (months)	16.1	17.8	19.2	16.2	17.6	19.2	0.15	***	***	
Slaughter weight (kg)	726	722	728	666	721	790	6.5		***	
Carcass weight (kg)	414	417	409	373	412	456	4.1		***	
Kill-out proportion (g/kg)	570	577	562	560	572	577	2.6	***	***	
Conformation score (1-15)	10.3	10.3	9.7	9.4	10.3	10.7	0.16	*	***	
Fat score (1-15)	8.2	7.6	6.9	7.3	7.6	7.8	0.17	***	*	P=0.05

The probability and cost of rain damage to hay-making in Ireland

E. Finneran[1,2], P. Crosson[1], M. Wallace[2]
[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co. Meath;* [2]*School of Agriculture and Food Science, Belfield, Dublin 4.*

Introduction
Feed costs constitute approximately 0.75 of total variable costs on beef farms and therefore, must be minimised for a given level of output to ensure margins are maximised (Finneran, 2011). Although grass silage is the predominant winter feed on Irish farms, grass conserved as hay has the potential to be produced at lower cost, primarily due to lower plastic and handling costs. However, given the longer wilting period required to successfully conserve hay, there is a greater risk of rain damage when compared to grass silage production. The economic cost of rain damage to hay can range from zero, where the hay is conserved successfully without rain, to greater than 1.00 of the crop value, when a rotted crop must be chopped back into the field (Rankin and Undersander, 2000). Rainfall causes losses of dry matter (DM) by leaching of water soluble carbohydrates and leaf shatter, resulting in a decline in conserved feed dry matter digestibility. Re-wetting also delays baling, increases tedding costs and re-starts respiration. Furthermore, baling of hay <800g DM kg^{-1} leads to increased losses due to heating and moulds (Rankin and Undersander, 2000). The aim of this study was to quantify the probability and costs of rain risk to hay-making in Ireland using a historical daily rainfall dataset.

Material and Methods
The Grange Feed Costing Model (Finneran et al., 2011) was used to simulate five crop outcomes corresponding to alternative rainfall events during the wilting period: 1) Good hay baled within 6 days with less than 0.1mm rain. 2) Moderate hay baled within 8 days with between 0.1 and 6.0 mm rain. 3) Moderate baled silage baled on day 5 following between 6.0 and 20.0 mm rain. 4) Poor baled silage baled on day 6 following greater than 20.0 mm rain. 5) Good baled silage baled without rain, following a 48 hour wilt. Daily rainfall data recorded at Birr from the years 1956 to 2008 (Met Eireann, 2010) were used to determine the probability of each of the rainfall states occurring during the wilting period. The level of rainfall determined the crop outcome, when the swath was mown on a random day in the months of May to September. DM losses were simulated, based on experimental data from seven published studies, collated by Finneran (2011) (Table 1). Hay was baled at 820 and silage at 340g DM kg^{-1}. All storage and feed-out costs were included in calculation of total feed costs. This included the capital cost of the hayshed which was applied to all crop states, including the baled silages.

Results and Discussion
The best months for hay conservation were May and June, which exhibited equal probability of 0.19 that good or moderate quality hay could be conserved. This probability was 0.18, 0.17, and 0.15 in the months of July, September and August, respectively. Total feed cost following rain damage was 1.38 (moderate hay), 1.51 (moderate baled silage) and 1.85 (poor baled silage) times the cost of good hay (Fig 1). The probability values in Fig 1 show the probability of each crop outcome when the sward was mowed on a random day in June with the intention of conserving hay. The fifth column in Fig 1 represents the good baled silage benchmark crop state. The TFC of this crop is less than that of moderate hay, despite the baled silage cost including the fixed cost of the hayshed for storage of hay which was not made.

Table 1. Calculation of hay and baled silage mechanical harvesting and rain-related DM losses between mowing and baling (g 100g^{-1})

	Good Hay	Moder-ate Hay	Moder-ate Baled Silage	Poor Baled Silage
Conditioner mowing	1.5	1.5	1.5	1.5
Tedding *(1% per*	5.0	7.0	5.0	7.0
Baling *(1.2x1.2m bales)*	2.5	2.5	1.5	1.5
Respiration	5.0	6.0	5.0	7.0
Rain losses *(includes leaching, leaf shatter and additional respiration due to re-wetting)*	0.0	4.0	8.0	15.0
Total DM losses from mowing to baling	4.0	21.0	21.0	32.0

Data Sources: See Finneran, (2011). DM = dry matter

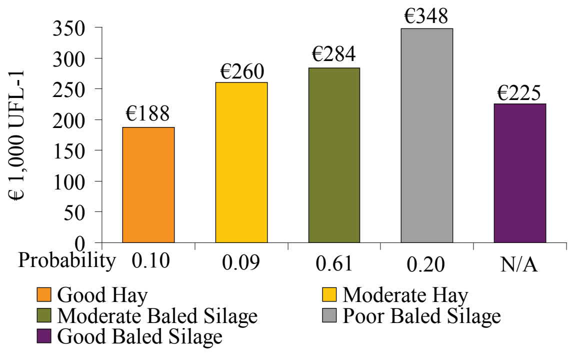

Fig 1. Total feed cost (€ 1000 UFL^{-1}) and probability of four possible crop states arising when a perennial ryegrass sward is mowed on a given day in June with the intention of conserving hay, and good baled silage conserved from the same sward.

Conclusions
The results quantify the relative cost of grass conserved as silage or hay following alternative rainfall events. Based on the rainfall data used in this study, the most probable outcome from a sward mown for hay is a feed crop 1.26 times the cost of good baled silage. The gross value of a potential 'rain – proof' technology for conserving hay has been calculated to be €37 1000 UFL^{-1}. Finally, this study has identified a simulation methodology capable of calculating an economic value for an accurate 7 day weather forecast.

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Economic performance of dairy calf to beef production systems finishing Holstein-Friesian bulls at 15, 19 and 22 months of age

R. Prendiville, E.G. O' Riordan and P. Crosson
Animal and Grassland Research and Innovation Centre, Teagasc, Grange.

Introduction
With the impending abolition of milk quotas in 2015, it is anticipated that dairy cow numbers will increase substantially in Ireland. This, together with the targets set out for both the dairy and beef sectors in the Food Harvest 2020 report (Food Harvest 2020), will result in a greater proportion of male dairy calves available for beef production. Currently, increased emphasis is placed on bull beef production. The aim of this study was to evaluate the economic performance of dairy-beef production systems finishing Holstein-Friesian bulls at 15 (15MO), 19 (19MO) and 22 (22MO) months of age.

Materials and Methods
Performance data were available for 49 spring born bulls; 18, 15, and 16 bulls in the 15MO, 19MO, and 22MO production systems, respectively. This study was conducted at the Johnstown Castle research centre and animal performance details have been described by Prendiville et al. (2012). Animals were at pasture for the first season and housed in November. Bulls on the 15MO production system remained indoors and were finished on an *ad-libitum* concentrate diet over a 207 day (s.d. 13.6) period (from housing to May-June). Animals on the 19MO production system were turned out to pasture for 100 days in the second season, housed and finished on *ad-libitum* concentrates over a 100 day period. Bulls on the 22MO production system were pasture grazed for 200 days and subsequently finished indoors on *ad-libitum* concentrates. Economic analysis incorporated animal inventory and valuation, biological performance and fixed and variable costs associated with production. Labour cost and land charge were not included in the analysis. Beef price and concentrate price were assumed to be €3.50/kg beef carcass and €245 per tonne, respectively. Calves were assumed to be purchased at 3 weeks of age for a purchase price of €140. Animal mortality was 5% from arrival to slaughter with 3% of this occurring at the calf rearing stage. Pasture was supplemented with 2 kg of concentrate per head for the first grazing season. Production systems were evaluated per head and per hectare (ha) with stocking rate set at 165 kg organic nitrogen (N) per ha. Sensitivity analyses were carried out on calf price, concentrate price and beef price by varying these prices by +/-10% to the baseline scenario.

Results and Discussion
Due to the differences in carcass weight, output value per head was greatest for bulls in the 22MO, intermediate for 19MO and lowest for the 15MO (Table 1). However, per ha the results were opposite with 15MO highest and 22MO lowest. Variable costs, on a per head basis, were greatest for bulls in the 22MO, intermediate for 19MO and lowest for 15MO. However, the opposite occurred when expressed per ha. Concentrate costs represented 0.75, 0.63 and 0.62 of the total variable costs for 15MO, 19MO and 22MO production systems, respectively, on a per head basis. Gross margin per head and per ha was lowest for 15MO. Gross margin per head was highest for 22MO while gross margin per ha was highest for 19MO. Fixed costs were highest for 22MO arising from the second winter housing requirement for this system. Thus, net margin per head and per ha was highest for 19MO, lowest for 15MO and intermediate for 22MO. Sensitivity analyses showed that margins were highly sensitive to calf price, beef price and concentrate price.

Conclusions
Results to date indicate that systems of bull beef production utilising pasture in the second season are more profitable than the 15MO bull production system. Where housing for a second winter is required, fixed costs per head are substantially increased and net margin is reduced. Results also indicate that profitability in dairy-beef production systems are highly sensitive to changes in concentrate and beef prices. Calf price had a lower impact; however, it is noteworthy that calf prices have been subject to very significant volatility in the 2010 to 2011 period.

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Acknowledgements
Financial support from Dawn Meats is gratefully appreciated.

Table 1. Economic performance of dairy calf to beef systems finishing bulls at 15, 19 and 22 months of age.

	15 month		19 month		22 month	
Animal units per ha	3.95		2.97		2.38	
Profitability (€)	Per head	Per ha	Per head	Per ha	Per head	Per ha
Output value	759	3001	987	2931	1094	2601
Variable costs	666	2634	696	2067	790	1879
Gross margin	93	367	291	864	304	722
Fixed costs	161	637	162	481	267	634
Net margin	-68	-270	129	383	37	88
Sensitivity (+/- 10%)						
Calf price	10.46	41.35	10.52	31.24	10.54	25.06
Concentrate price	22.37	88.44	19.45	57.76	21.78	51.78
Beef price	26.50	104.77	33.01	98.02	37.53	89.23

Productivity changes on Irish dairy farms between 1996 and 2010.

E. Kelly[1,2], L. Shalloo[1] and M. Wallace[2]
[1]*Livestock Systems Research Department, Animal and Grassland Research and Innovation Centre, Teagasc Moorepark, Fermoy, Co. Cork,* [2]*School of Agriculture, Food Science & Veterinary Medicine, University College Dublin, Belfield, Dublin 4.*

Introduction

The Food Harvest 2020 report states that dairy output is expected to increase by 50% by 2020. If this increase in milk output is to be achieved in a profitable fashion it will need to happen in tandem with increases in efficiency at farm level (Kelly et al., 2011a). The objectives of this study were to measure the total factor productivity (TFP) change of a sample of Irish dairy farms over the period 1996-2010 and to investigate key factors associated with differences in productivity. TFP is defined as an index of output which is divided by an index of input including all factors of production (Fried et al., 2008).

Materials and Methods

Productivity change was calculated with TFP Malmquist indexes using the non parametric Data Envelopment Analysis method. TFP change can be decomposed into efficiency change, which is the change in technical efficiency over time and technical change which is the change in technology use over time. A Malmquist index of greater than one indicates positive TFP growth whereas a value of less than one indicates a TFP decline. A value of one indicates no change. Productivity was measured using data from the National Farm Survey between 1996 and 2010. To be included in the analysis each producer had to be included in the sample for at least two years in a row. Inputs included in the analysis were land (ha), herd size, labour units, concentrate (kg), fertiliser (kg) and other direct costs and overhead costs (€) with output including milk volume and the value of other crop and livestock sales. All monetary values were deflated to 1996 levels based on Central Statistics Office agricultural price indexes. The productivity results were generated in the first stage analysis using DEAP software Coelli (1996). In a second stage analysis to identify factors associated with productivity changes a number of explanatory factors were regressed on the Malmquist index using PROC Reg of SAS 2006, (SAS Institute Inc., Cary, NC 33).

Results and Discussion

Productivity growth over the 14 year period was 10% or on average 0.7% per year. Increases in technical change due to technology changes had the largest contribution to the productivity increases in TFP indicating that producers with the greatest levels of technological uptake had greater levels of productivity. Technical efficiency change reduced which was driven by declines in scale efficiency. This may suggest that constraints to expansion such as quota and land which was found by Kelly et al., (2011b) were contributing to reduced technical efficiency change.

Table 1: Average productivity changes 1996-2010

Variable	Mean	St. Deviation
Efficiency change	0.998	0.108
Scale efficiency change	0.996	0.072
Technical change	1.009	0.044
TFP[1] change	1.007	0.122

[1]Total Factor Productivity Change

Similar to Kelly et al., (2011a) key management factors were associated with differences in productivity with greater productivity generated on farms that had a lower percentage of land rented ($P<0.1$). Higher quota quantity increased technical efficiency change ($P<0.1$) Increasing milk price was associated with reduced technical efficiency ($P<0.001$) but increased technical change. Increased subsidy percentage of gross output was also associated with a decline in productivity change ($P<0.01$).

Conclusions

There was a positive productivity growth on Irish dairy farms between 1996 and 2010 which was mainly driven by technology changes. Increased productivity was associated with reduced percentage of land rented and with greater levels of quota. Milk price and increased subsidies were also associated with productivity changes.

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Table 2: Determinants of technical efficiency change, technical change and TFP[1] change

	Efficiency change	SE[2]	Technical change	SE	TFP change	SE
Intercept	1.075***	0.036	0.894***	0.029	0.974***	0.045
Milk Price (cents/litre)	-0.429***	0.073	0.416***	0.058	-0.047	0.093
Subsidies % output	0.000***	0.000	0.000	0.000	0.000***	0.000
Quota (litres)	0.000*	0.000	0.000	0.000	0.000	0.000
Land Rented %	-0.014	0.013	0.018*	0.010	-0.033*	0.016
R-Squared	0.014		0.023		0.004	

[1]Total Factor Productivity Change, [2]Standard error, Significance superscript-Proc Reg SAS (2006), *** <0.001, **0.001-0.01, *0.01-0.05, +0.05-0.1,

Irish sport horse market requirements

K. D. Hennessy[1] & K. M. Quinn[2]

[1]Centre for Sports Studies, UCD School of Public Health, Physiotherapy and Population Science, [2]UCD School of Agriculture and Food Science

Introduction

The sport horse market place is a changing environment with an increasingly competitive landscape and changing consumer demand. Many attributes combine to dictate a horses' utility in the market place. It is important that breeders of Irish sport horses (ISH) are aware of the market place requirements. The objective of this study was to identify the most important attributes within the Irish sport horse market place.

Materials and Methods

Dealers are very influential within the market place, with 20% of the purchasers buying 51% of the horses at sport horse auction (Hennessy and Quinn, 2005) hence their opinions and actions strongly influence the market. A postal questionnaire was conducted with a total of 302 responses received from Irish sport horses dealers. Respondents were asked to rate the importance of each of nineteen sport horse related attributes (from 1 not important to 5 very important). To identify the most important attributes, data analysis involved testing for significant differences between attributes by sequentially pairing attribute results and running the Wilcoxon Signed Rank Test on each pairing.

Results and Discussion

Soundness was significantly more important to sport horse dealers than any other attribute. This is not surprising as a horse's utility is dependent upon its soundness. A horse that is unsound is of little use or value. The next most important attributes were conformation, movement and temperament. They were not significantly more important than each other but all three were found to be significantly more important than the remaining attributes including: pedigree related attributes (breed of sire, sire, breed of dam, dam family), bio-attributes (gender, height, colour), performance related attributes (animal's own performance or that of its siblings) or experience related attributes (hunt / competition). Soundness, conformation, movement and temperament are attributes that are not recorded in a sales catalogue where as most of the remaining attributes are. Therefore these findings reinforce the findings of Hennessy and Quinn (2006), that catalogue recorded variables have a small impact the decision to purchase and that other attributes that are not captured in the sales catalogue maybe more important in the purchase decision making process.

Conclusions

A horse's soundness, temperament, conformation and movement are more important in the purchase decision making process than the horse's pedigree or performance. It would seem that a decision to buy maybe based on an assessment of the fundamental health, temperament and conformation attributes and that performance and pedigree attributes are of lesser importance. Sport horse breeders need to be aware of the importance of soundness, conformation, movement and temperament and that breeding for performance should not be to the detriment of these most important market requirements.

Acknowledgements

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Table 1. Significant differences in importance between sport horse attributes in the market place

	Medi	Conf	Move	Pres	Temp	Train	Br.	Sire	Br.	Dam	Sib P	Hgt	Col	Br	Comp	Hunt	Reg	Perf	Gend
Soundness	5	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***
Conformation	5	xx	NS	*	NS	***	***	***	***	***	***	***	***	***	***	***	***	***	***
Movement	5		xx	***	NS	***	***	***	***	***	***	***	***	***	***	***	***	***	***
Presence	5			xx	NS	NS	***	***	***	***	***	***	***	***	***	***	***	***	***
Temperament	5				xx	***	***	***	***	***	***	***	***	***	***	***	***	***	***
Trainability	5					xx	***	***	***	***	***	***	***	***	***	***	***	***	***
Breed of sire	4						xx	NS	NS	NS	***	NS	***	***	***	***	***	NS	***
Sire	4							xx	*	NS	***	NS	***	***	***	***	***	NS	***
Breed of dam	4								xx	NS	***	NS	***	***	***	***	***	NS	***
Dam Family	4									xx	***	NS	***	***	***	***	***	NS	***
Sibling Performance	3										xx	***	***	***	***	***	***	***	***
Height	4											xx	***	***	***	***	***	***	***
Colour	3												xx	NS	***	***	NS	***	NS
Broken	3													xx	***	***	NS	***	NS
Comp Exp	3														xx	***	***	***	***
Hunting Exp	2															xx	***	***	***
Registration	3																xx	***	NS
Performance	4																	xx	***
Gender	3																		xx

NS = Not significant, *** = P<.001, ** = P< .01, * = P< .05

Factors associated with selling price and live weight of Italian calves

I. Bazzoli[1], D.P. Berry[2], M. De Marchi[1], M. Penasa[1], A. Cecchinato[1] and G. Bittante[1]

[1]Department of Animal Science, University of Padova, Italy. [2]Animal & Grassland Research and Innovation Center, Teagasc, Moorepark, Fermoy, Co. Cork.

Introduction

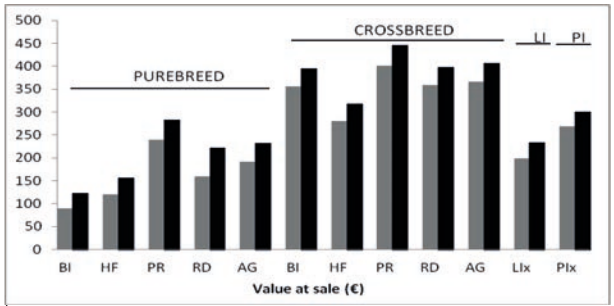
The sale of surplus calves from dairy farms represents a valuable source of income for dairy farmers. In Italy, two distinct destinations for Italian calves exist, veal production and beef production. Knowledge of the factors associated with animal price and live-weight can provide valuable information to producers on the cost-benefit of alternative breeding and management strategies. The objective of this study was to quantify the animal factors including breed type, age, and gender associated with calf price per kg, overall value, and live weight in calves from the Trento province.

Materials and Methods

Data were available from the Breeders Federation of the Trento province (northern Italy) on 37,781 calves collected from 468 farms between June 2002 and May 2011. Calves were weighed at collection, using weighing scales, and then transported to a central location where one qualified technician attributed a price per kg and overall value (i.e., price multiplied by live-weight) to each calf and decided if the animal should be destined for veal or beef production. The following morning calves were transported to producers outside of the Trento province. Information recorded on each calf included calf price (€/kg), live weight (kg), value (€ per calf), date of birth, date of sale, gender, and destination (veal or beef). Data were also available on the sire and dam breed of each animal. Breed type, as defined in this study, consisted of 12 breeds or breed crosses namely purebred calves from Italian Brown (BI), Holstein-Friesian (HF), Simmental (PR), Rendena (RD) and Alpine Grey (AG) sires and dams, and crossbreds to Belgian Blue (BB) sires from each of the purebred dams; crosses to Piemontese (PI) and Limousin (LI) sires were grouped separately. Only calves with known dam and sire breed, sold between 7 and 60 days of age, and weighing between 30 and 120 kg were retained. Furthermore only animals from herd-years with at least 5 calves were retained. Factors associated with calf live-weight, price, and value were quantified using a fixed effects linear model.

Results and Discussion

The vast majority (i.e. 82%) of calves sold were males, and half the calves were sold between 15 and 25 days of age. The correlation between live-weight and price was 0.46 and between live-weight and value was 0.64; both correlations were different (P<0.001) from zero. Herd-year was included (P<0.001) in all models. Male calves were heavier (P<0.001) than females (67 kg vs. 63 kg) and sold for a greater (P<0.001) value (€292 vs. €252). The association between gender and live-weight, price and value (Figure 1), however, differed (P<0.0001) by breed. PR male purebred calves were heaviest (69.6 kg) while BI purebred females were lightest (59.4 kg). Calves destined for beef production were, on average, heavier (69 kg; P<0.001) and received a greater (P<0.001) price and value at sale (€4.60 per kg and €291), compared to those destined for veal production (62 kg live-weight; €3.90 per kg and €253). However, the association between destination and live-weight, price and calf value also differed by breed (P<0.001). The majority of beef crossbreed and calves from dual purpose dam breeds were destined for beef production while the majority of purebred calves from dairy dams were destined for veal production system. The association between age at sale and live-weight differed by breed (P<0.001); age was not associated with either calf price or calf value but both price and value increased (P<0.001) at a decreasing rate with live-weight. The association between age and live-weight of calves at sale differed by breed type (P<0.0001). Live weight, price and value of calves at sale varied by month of sale due to different supply and demand of calves during the year. Calf price was lowest during the autumn and winter months, when many calves were sold. Calves sold in June were heaviest (66 kg) and received the greatest price and value (€4.60 per kg; € 291) while those sold in December were lightest (64 kg) and received the lowest price and value (€4.00 per kg; € 259) at sale.



[1]BI= Italian Brown; HF= Holstein Friesian; PR= Simmental; AG= Alpine Grey; RD= Rendena; [2] PIx=crossbreed Piemontese sire and any of the 5 breeds of dam; LIx= crossbreed Limousin sire and any of the 5 breeds of dam; Crossbreed= Belgian Blue sire and each breeds of dam.

Fig. 1. Least squares means of calf value for different breed[1] and breed crosses[2] by gender (male=black bars; female=grey bars).

Conclusions

Several animal level factors were associated with calf live-weight, price and value and the solutions obtained for these factors will be useful for inclusion in both bioeconomic models and decision support tools to aid in research and day-to-day farm management.

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The influence of catalogue recorded variables on foal prices.

E. Fardy[1] & K. D. Hennessy[2]
[1]UCD School of Agriculture and Food Science, [2]Centre for Sports Studies, UCD School of Public Health, Physiotherapy and Population Science

Introduction
The demand for sport horses tends to be responsive to changes in household income. In economic boom times, with greater disposable incomes, trade tends to be stronger and more vibrant. The EU Equus Conference (2001) reported a positive correlation between the number of horses per captia and mean consumption levels. Previous work by Hennessy and Quinn (2006) during the economic boom reported that male foals with family performance history, by fashionable sires achieved the best prices. The purpose of this study was to identify the most influential catalogue recorded variables on foal prices at auction between 2007 and 2011 and compare the results with those of Hennessy and Quinn (2006).

Materials and Methods
Results of all sport horse foals sold through Goresbridge sales complex (Ireland), between 2007 and 2011 were analysed (531 records) and compared against the results of a similar study conducted on foal sold at auction between 1999 and 2004. Eleven independent variables based on sales catalogue information, were analysed using a multiple regression model (SPSS version 18). The independent variables were binary coded and included: sex (male =1, female = 0), breeding recorded (yes = 1, no = 0),sire popularity (> 300 registered foals = 1, < 300 registered foals = 0), breed of sire (foreign bred (FB) = 1, not FB = 0), dam sire (Irish Draught (ID) = 1, not ID = 0), dam performance (yes = 1, no = 0), dam family performance (yes = 1, no = 0), foal performance (yes = 1, no = 0), sibling performance (yes = 1, no = 0) , breed recorded (yes = 1, no = 0) and star rating of the stallion in the ISH stallion studbook (yes = 1, no = 0). All variables within each data set were tested for multi-collinearity using SPSS linear regression collinearity diagnostics. No collinearity was evident between the variables (VIF < 1.77 for all variables). A linear regression analysis was performed on each data set using the 'enter' method (SPSS version 18) where the log sale price was the dependent variable and the catalogue variables were the independent variables.

Results and Discussion
The mean prices achieved by foals at auction ranged from €3,077 (±SEM 225) in 2007 down to €951 (±SEM 80) in 2010, a 69% difference in value, Figure 1. Seven of the eleven variables were found to have a p value of < 0.05 for at least one of the focus years, Table 1. The variables included in a multiple regression model for each year returned an R^2 square adjusted value ranging from 0.241 to 0.507, indicating that between 24% and 51% of the variability in the price of sport horse foals horses was explained by these variables. The most consistently influential variables were the breed of sire, with foals by foreign bred stallions consistently achieving significantly higher prices than foals by any other breed of sire and sex, with male foals consistently achieving higher prices than female foals. This was followed by sire popularity, those foals whose sire had more than 300 registered foals achieved significantly higher prices than foals whose sire had less than 300 registered foals.

Conclusions
The findings of this research highlights the importance of the sire in achieving a higher than average price at foal sale. His importance is manifested through his breed (FB) and popularity (>300 registered foals). His influence is sustained during an economic downturn whereas the influence of other variables (dam & dam family performance) are not as consistently influential**.**

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Table 1: The influence of catalogue recorded variables on foal price at auction

	1999-2004 (Hennessy & Quinn, 2006)		2007		2008		2009		2010		2011	
Mean price (SEM)	Range in annual means €1,759–€2,479		€3,086 (225)		€1,602 (130)		€1,542 (119)		€951 (80)		€1,394 (92)	
R^2 adjusted	0.279		0.353		0.244		0.331		0.507		0.241	
Predictor variable	p	Beta	p	Beta	p	Beta	p	Beta	p	Beta	p	Beta
Sex	<.001	.167	<0.05	.208	<.001	.289	<.001	.456	<0.05	.255	<0.05	.181
Breeding recorded	n/a		ns		ns		n/s		ns		ns	
Sire breed	<.001	.105	<.001	.501	<.001	.336	<.001	.343	<.001	.752	<0.05	.181
Sire popularity	n/a		<.001	.283	<.001	.231	ns		<.001	.600	<0.05	.187
Sire approval	n/a		ns		ns		ns		ns		ns	
Dam sire breed	n/a		ns		ns		ns		ns		<0.05	.204
Dam perform	<0.05	.06	<0.05	.124	ns		ns		ns		ns	
Damfamily perform	<.001	.144	<0.05	.150	ns		ns		ns		<0.05	.242
Sibling perform	<0.05	.06	<0.05	.033	ns		ns		ns		ns	
Foal perform	<0.05	.07	ns		ns		ns		ns		ns	
Sire Star Rating	n/a		n/a		n/a		n/a		n/a		ns	

Factors associated with the concentration of Immunoglobulin G in the colostrum of Irish dairy cows

M. Conneely[1, 2], D.P. Berry[1], I. Lorenz[2], M.L. Doherty[2], and E. Kennedy[1]

[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork.* [2]*School of Veterinary Medicine, University College Dublin, Dublin 4.*

Introduction

With the impending abolition of milk quotas in 2015 and 50% of dairy farmers intending to expand (O' Donnell et al., 2009), the number of dairy calves born in the coming years is expected to rise. Efficient colostrum management programmes are crucial to ensure the health and productivity of these calves, and provision of good quality colostrum is fundamental (McGuirk et al, 2004). Currently, however, there is a lack of published data on the colostrum quality of Irish dairy cows. Furthermore, few studies have examined the factors associated with the colostrum quality of cows in seasonal, grass-based systems such as those that exist in Ireland. The objective of this study was to determine the factors associated with the IgG concentration in the colostrum of Irish dairy cows.

Materials and Methods

Fresh colostrum samples were collected from 642 spring-calving dairy cows of varying breed and parity from four Teagasc Moorepark research farms from January to May 2011. Each cow was milked by machine at the next scheduled herd milking time following calving. Colostrum was collected in a steel churn, the weight was recorded and a 100ml sample of colostrum was obtained and frozen at -20^{o}C until analysis. The IgG concentration was determined using an ELISA method *(Bovine IgG ELISA Kit Cat. No. 8010, Alpha Diagnostic International, San Antonio, TX, USA)*. Information recorded from the cows included time and date of birth of the calf; sex, weight and breed of the calf, whether the calf was born alive or stillborn, presentation of the calf (normal, posterior, breech, leg-back, head -back), degree of calving difficulty on a 1 to 5 scale (1= no assistance, 5= veterinary intervention). Other information available included time interval from calving to subsequent milking, cow body weight measured up to 14 days post-calving and body condition score (scale 1 to 5; Edmonson et al., 1989) measured within 14 days of calving, length of dry period, cow EBI, breed fraction, and level of heterosis and recombination. Factors associated with colostrum IgG concentration were determined using a fixed effects model in PROC GLM in SAS (SAS, 2009). Only factors associated (P<0.05) with colostrum IgG concentration were included in the final model. The final model included lactation number, time from calving to milking, weight of first milking colostrum and length of dry period.

Results and Discussion

The mean concentration of IgG in the colostrum was 111.8mg/ml and ranged from 13.3 to 255.6mg/ml. In total, 95.5% of the samples in this study contained >50mg/ml IgG, which is considered to be an indication of high quality colostrum (McGuirk et al, 2004).

Colostral IgG concentration was positively associated (P<0.01) with lactation number. Cows in later lactations produced colostrum with higher IgG concentration than those in earlier lactations even after adjustment for differences in milk yield at the time of milking Least square means for colostral IgG concentration (mg/ml) were 95.4 (SE 41.6), 110.2 (SE 11.6), 116.5 (SE 11.6), 114.4 (SE 12.1) and 123.7 (SE 12.0) for cows in their first, second, third, fourth and fifth and above lactations, respectively. Colostral IgG concentration was negatively associated (P<0.001) with time interval from calving to milking. Least square means for colostral IgG concentration (mg/ml) were 120.3 (SE 4), 126.8 (SE 5.4), 118.5 (SE 5.6), 103.4 (SE 5.7), 108.7 (SE 8.2), 92.7 (SE 8.6) and 92 SE 12.3) for samples collected between hours 0 - 3, hour 3 - 6, hours 6 - 9, hours 9 - 12, hours 12 - 15, hours 15 - 18 and hours 18 - 21 post-calving, respectively. Colostral IgG concentration was associated (P<0.05) with dry period length. Least square means for colostral IgG concentration (mg/ml) were 99.4 (SE 14.1), 107.6 (SE 10.9), 92.6 (SE 13.8) and 134 (SE 14.8) for cows that had a dry period length of less than 8 weeks, between 8 and 16 weeks, between 16 and 24 weeks, and over 24 weeks, respectively. IgG concentration decreased (P=0.05) by 1.19 mg/ml (SE 0.061) per kilogram increase in the colostrum weight. This information will enable farmers to make more informed choices regarding the cows they choose as the source of colostrum for newborn calves, thus maximising the efficiency of their colostrum management programmes and ultimately improving calf health across the Irish national herd.

Conclusions

The increase in IgG concentration as time interval from calving to milking decreased implies that colostrum should be collected from the cow as soon as possible post-calving in order to maximise colostral IgG concentration. While cows in later lactations produce colostrum of a higher IgG concentration than cows in earlier lactations, farmers should not be encouraged to automatically discard colostrum from first lactation animals as it may be of very good quality. A more useful criterion on which to base selection of colostrum for feeding is the weight of colostrum produced at the first milking, because as the weight of colostrum produced decreases concentration of IgG increases. Dry period length should be maintained between 8 and 16 weeks to optimise colostral IgG concentration.

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Welfare of dairy heifers out-wintered on wood chip or rubber surfaces compared to indoors on slats

L.A. Boyle[1], R.W. Huijser van Reenen[2], K. O'Driscoll[3], F.J.C.M. van Eerdenburg and F. Buckley[1]
[1]*Animal & Grassland Research & Innovation Centre, Moorepark, Fermoy, Co. Cork.* [2]*Faculty of Vet. Sci., University of Utrecht, The Netherlands.* [3]*Animal and Bioscience Research Dept., Grange, Co. Meath*

Introduction
In spite of their importance in determining future production levels, replacement dairy heifers are often kept (indoors) on fully slatted (FS) floors which are associated with welfare problems (Livesey et al., 2002). Boyle et al. (2008) reported behavioural improvements in yearling heifers out-wintered on a wood chip (WC) pad compared to animals kept indoors in rubber matted cubicles. Out-wintering on a rubber surface (RS) is a potentially more economical and less labour intensive alternative. This study compared the welfare of replacement dairy heifers out-wintered on either a WC or RS with that of animals kept indoors on slats.

Materials and Methods
The study was conducted from 17/11/10 (d0) to 11/02/2011 (d91). 90 heifers were blocked into 9 groups according to breed (Jersey, HF, Norwegian Red and crosses of same), weight/BCS and age (av. age 271d at start) and assigned to 1) WC out-wintering pads (OWP) (n=3); 2) RS (MaxGrip flushing mat™ EasyFix™) OWP (n=3); or 3) FS concrete pens (n=3). On WC and RS the space allowance for lying was 5.65 m^2 /head and heifers fed from an adjacent concrete area (2.31 m^2/head). FS heifers had 1.8m^2 each. All animals had *ad lib* access to grass silage of 70% DMD mixed with maize and concentrates. On d0 and d87 the hardness of the sole (Shore D scale) of the outer claw of the hind foot was assessed using an analog durometer (ASTM D2240; Qualitest International Inc., Richmond Hill, Ontario, Canada).. Five areas on the LHS of each animal were scored for dirtiness (as per Boyle et al., 2008). Dirt scores and BCS were recorded at d0, d42 and d87. Two trained observers observed each group for 20mins/day for 3d/wk. All occurrences of grooming, agonistic, play and sexual behaviour were recorded. TinyTag™ data loggers were used to measure lying behaviour during 2×24hr periods (mean used in analysis). Group feed intakes were recorded 1d/wk. Heifers were weighed un-fasted weekly. Data were analysed using proc mixed of SAS taking repeated measures into account and using Tukey's test for multiple comparisons.

Results and Discussion
Heifers kept indoors in FS pens had the hardest hooves at the end of the experiment (35.3 [FS] *vs.* 32.9[WC] and 30.87 [RS] s.e.m. 0.8; P<0.001). The hooves of heifers that were outdoors were exposed to more moisture which reduces hoof hardness. Dirt scores increased over time in all treatments (P<0.001). However, both FS and WC heifers had lower dirt scores (2.88 and 3.01 respectively) than RS heifers (3.29 s.e.m. 0.101; P<0.05). This may have been because it was difficult to clean the rubber surface when the water froze during a particularly cold period. RS and WC heifers performed more play behaviour (Table 1) which is a positive welfare indicator, and likely because of the larger space allowances as well as the surer surfaces underfoot. Over time, levels of agonistic behaviour reduced in all treatments (P<0.001) reflecting establishment of the dominance hierarchy. There was no difference in overall daily lying time, but FS heifers had longer, and hence fewer, lying bouts than WC or RS animals, per 24hr period. This behavioural pattern is consistent with discomfort while lying. Neither feed intake (FS: 214.3kg, RS: 218.8kg and WC: 212.9kg s.e.m. 4.19; P=0.596) nor ADG over the 91 day trial period (FS: 0.81kg, RS: 0.86kg, WC: 0.81; s.d. 0.033; P=0.397) differed between treatments. However, FS heifers had higher BCS than RS and WC heifers (FS: 3.24, RS: 3.15, WC: 3.16; s.e.m. 0.026; P<0.05].

Conclusions
The only discernable differences between the RS and WC OWP was that heifers were dirtier on the former indicating that this is viable alternative to WC OWP. Deviations in patterns of lying and low levels of play point to welfare problems for the heifers in fully slatted pens. Nevertheless the fact that FS heifers had shelter meant that they were in better body condition. Furthermore, while the implications of hoof hardness for susceptibility to bruising and penetration with stones requires further investigation, softer hooves are a potential risk factor for lameness and hence a potential disadvantage associated with out-wintering.

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Table 1. Effect of winter accommodation on (selected) behaviours of yearling dairy heifers during a 12 week trial

Behaviour	WC OWP	RS OWP	FS	s.e.	Treatment	Time	T*T
Agonistic (no./20min.)	6.67	6.61	7.81	0.755	0.231	<0.001	=0.089
Play (no./20 min.)	1.81[a]	2.03[a]	0.47[b]	0.077	<0.001	<0.0001	<0.001
Total time lying (hh:mm:ss)	13:54:09	13:28:26	13:35:32	00:10:34	ns	<0.001	<0.001
Lying bout duration (hh:mm:ss)	00:52:48[a]	00:53:42[a]	01:01:53[b]	00:01:25	<0.001	<0.001	<0.001-
No. lying bouts (hh:mm:ss)	16.23[a]	15.56[a]	13.51[b]	0.527	<0.001	<0.001	<0.05

WC OWP= Wood chip out wintering pad; RS OWP=Rubber surface OWP; FS=Fully slatted floor indoors; ns=non-significant

Temporal trends in bulk milk antibodies to *Neospora caninum* in a subset of Irish dairy Herds

E. O' Doherty [1 2], R. Sayers [1], D. Berry [1] & L. O' Grady [2]

[1] *Animal & Bioscience Research Department, Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork, Ireland.* [2]School of veterinary medicine, UCD Veterinary Sciences Centre, University College Dublin, Belfield, Dublin 4, Ireland

Introduction

Neospora caninum is a protozoan parasite with canines acting as definitive hosts and cattle as incidental hosts and is one of the major causes of bovine abortion worldwide (Dubey et al., 2007). Infection with *Neospora caninum* can lead to serious economic losses in dairy herds (Chi et al., 2002) and there is little published data on the prevalence of *Neospora caninum* in Irish dairy herds. An objective of this study therefore was to establish the herd level prevalence and incidence of *Neospora caninum* in Irish dairy herds. Bulk milk sampling was chosen as a convenient method of achieving this. (Wapenaar et al., 2007) An additional objective was to examine the association between prevalence and incidence of *Neospora caninum* and sampling date and calving season.

Materials and Methods

A total of 500 herds were randomly selected from the Irish Cattle Breeding Federation (ICBF) database and invited to participate in this study. Herds were selected within strata of herd size (31 to 65 cows, 66 to 99 cows, and >99 cows) and geographical location (county; n=26). A total of 312 were eventually recruited to the study on a voluntary basis. Bulk milk samples were collected from each herd over the 2009 lactation (March, June, August and November). Antibodies to *Neospora caninum* were detected using a commercially available indirect Enzyme linked Immunosorbent Assay (ELISA) [Sensitivity (Se) 99%; Specificity (Sp) 96% with a within-herd prevalence of 10-15% (Svanova, Sweden)]. Results were reported as a pp value and a positive cut-off of ≥0.20 applied as per kit instructions. The true prevalence (the apparent prevalence corrected for test Se and Sp) and incidence (the number of previously negative herds that became positive) of *Neospora caninum* at each sampling time point was calculated using *Survey toolbox* (www.auvet.com.au) (Cameron, 1999). Data on the calving season of study herds was also collected. Herds in which the entire herd calved in spring were classified as spring calving herds (n=266) and herds in which the entire herd did not calve in spring were classified as non spring calving herds (n=43). Logistic regression in PROC GENMOD (SAS, Version 9.1, USA) was used to examine the association between the prevalence and incidence of *Neospora caninum* and sample date and calving season.

Results and Discussion

The apparent prevalence of *Neospora caninum* was 7%, 5%, 3%, and 12% in March, June, August and November, respectively. The true prevalence of *Neospora caninum* in March, June, August, in November, and the incidence of the disease between March and June, June and August, and August and November are shown in Fig.1.

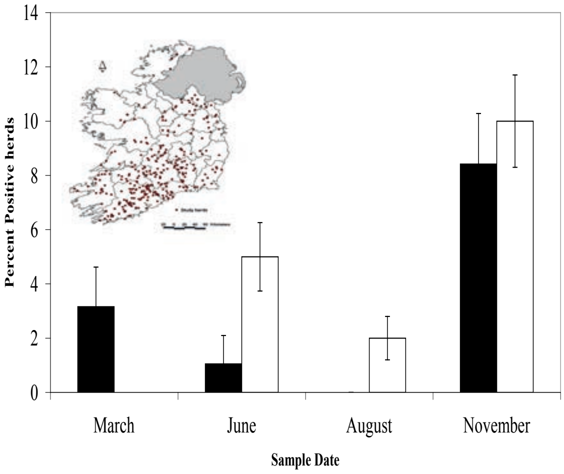

Fig. 1. True prevalence (■) and Incidence (□) of *Neospora caninum* in study herds. (Inset: map of study herd location)

There was a significant association between *Neospora caninum* prevalence and sample date (p=0.0002) as well as between incidence of *Neospora caninum* and sample date (p=0.0003) with the highest number of herds positive at the final sampling time point in November. There was also a significant association between incidence of *Neospora caninum* and calving season (p=0.04) with an increased incidence in non-spring calving herds between March and June and in spring calving herds between August and November, periods when these herds enter late lactation. As some animals positive to *Neospora caninum* only demonstrate a positive antibody response in late lactation, the increase in incidence at these times point was an expected finding as was the increase in prevalence of *Neospora caninum* in spring calving herd in November. (Dubey et al., 2007).There was no association between *Neospora caninum* prevalence and calving season (p=0.10).

Conclusions

There is a need to create further awareness of the economic consequences of infection of *Neospora caninum* in Irish dairy herds and to create awareness around the implementation of suitable control programmes. Results from the current study show that testing of spring calving herds for the presence of neospora positive animals should ideally take place in November due to a higher probability of detection.

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The influence of 'Acid-Buf' mineral supplement on pig welfare during mixing and an out-of-feed event

K.O'Driscoll[1], D. Lemos Teixeira[4], D.M. O'Gorman[3], Stephen Taylor[3] and L.A. Boyle[4]
[1]*Animal and Bioscience Research Department, Grange, Dunsany, Co. Meath* [3]*Celtic Sea Minerals, Carrigaline, Co. Cork* [4]*Pig Production Development Unit, Moorepark, Fermoy, Co. Cork*

Introduction
Pigs in modern production systems typically experience multiple stressors during their lifetime, which can have a negative impact on their health, behaviour and welfare. Acute stressors can increase aggression (O'Connell et al., 2005), physiological stress (Merlot et al., 2004), and performance of harmful behaviours such as tail-biting (Robert et al., 1991). Acid-Buf mineral supplement has a high bioavailability of Mg, which could ameliorate these effects. This study investigated whether 'Acid-Buf' could improve the welfare of growing pigs during two stressful events: mixing of unfamiliar pigs, and a 21h out-of-feed event.

Material and Methods
At weaning (4wks) male and female piglets (n=448) were managed in single sex groups of 14 and assigned to either 'Control' or 'Acid-Buf' diets on the basis of live-weight and back-test scores. At 8wks 7 pigs/pen were mixed with 7 of the same sex and diet from another pen: CL male, AB male, CL female and AB female (n=4 of each). Pigs were managed in this group for a further 9wks. After mixing the behaviour of pigs in each pen was recorded continuously for three hours using a time lapse video recorder. The no. of pigs standing was counted using scan sampling at 10 min intervals. The recordings were also observed continuously for the no. and duration of aggressive interactions and the no. of pigs involved in each bout of aggression. At 16wks pigs were subjected to an out-of-feed event for 21h whereby feed was removed from all feeders at 12:00 and replenished at 09:00 the following day. Behavior observations were carried out by direct observation between 09:00 -10:00 and 15:00 - 16:00 on the day of and day after the out-of-feed event. Each pen was observed continuously for 8×2 min observation periods during each hour. Incidences of aggressive (head-knocks, bites, and fights) and harmful (tail, ear and nose biting, and belly nosing) behaviors were recorded. Salivary cortisol was collected at 10:00 the day before, 08:00, 10:00, 12:00 and 16:00 the day of, at 10:00 for 2 days after the mixing day and out-of-feed event, and analysed by enzyme immunoassay. Skin lesion scores were recorded the day before and after mixing and the out-of-feed event. Data were tested for normality, transformed if necessary, and analysed using SAS (Proc Mixed).

Results and Discussion
Fewer Acid-Buf pigs tended to be standing during the 3 h after mixing than control (49.8 ± 2.6 % v's 51.5 ± 2.6 %; $P = 0.08$). Moreover, although there was no effect of Acid-Buf on the total duration, or duration of bouts of agonistic behaviour after mixing, fewer Acid-Buf pigs were involved in each bout of aggression (Table 1). Acid-Buf pigs also tended to have lower cortisol concentrations (1.67 ± 0.10 ng mL^{-1}) than control pigs (1.81 ± 0.10 ng mL^{-1}; $P = 0.08$). These results indicate a reduction in stress at mixing associated with Acid-Buf supplementation. The duration of bouts and the overall duration of agonistic interactions was longer in male than female pens (Table 1). There was also an interaction between sex and diet on cortisol levels ($P < 0.05$); female Acid-Buf pigs had lower cortisol concentrations (1.51 ± 0.12 ng mL^{-1}) than female control pigs (1.91 ± 0.13 ng mL^{-1}; $P < 0.05$), whereas there was no difference between control and Acid-Buf males (1.70 ± 0.12 *v's* 1.82 ± 0.13 ng mL^{-1}; $P = 0.87$). During the out-of-feed event there was no effect of Acid-Buf or sex on harmful behavior or salivary cortisol concentrations, or of Acid-Buf on agonistic behaviour. However Acid-Buf pigs had lower skin lesion scores than control ($P < 0.05$). Male pigs were more aggressive than females ($P < 0.05$), and tended to have higher skin lesion scores ($P = 0.07$). There also tended to be an interaction between sex and recording time, with female pigs having a more defined circadian rhythm of salivary cortisol secretions ($P = 0.1$)

Conclusions
Acid-Buf reduced activity and the number of pigs involved in aggressive interactions, and lowered salivary cortisol levels after mixing. Moreover, supplemented pigs had lower skin lesion scores after being deprived of feed. These results imply that Acid-Buf supplementation has the potential to ameliorate the negative effects of acutely stressful events. However, the effects appeared to be more significant for female pigs than male. Further research investigating it's effects in mixed sex pens is warranted.

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Table 1. Agonistic behaviour of pigs fed a control diet or supplemented with Acid-Buf during 3 hours after mixing

	Diet		Sex		Diet	Sex
Behaviour	Control	Acid-Buf	Male	Female		
Aggressive interactions (no)	74.4 ± 4.4	88.5 ± 4.4	79.9 ± 4.4	83.0 ± 4.4	NS	NS
Interaction duration (mm:ss)	00:23 ± 00:03	00:16 ± 00:03	00:26 ± 00:03	00:12 ± 00:03	NS	0.001
Total duration (mm:ss)	28:14 ± 03:38	23:08 ± 03:38	34:27 ± 03:38	16:55 ± 03:38	NS	0.01
No. of pigs involved/interaction	2.13 ± 0.39	2.08 ± 0.34	2.13 ± 0.42	2.08 ± 0.29	0.05	0.05
Duration × no. pigs involved (hh:mm:ss)	1:19:28 ± 00:13:48	0:58:30 ± 00:13:48	1:36:16 ± 00:13:48	0:41:42 ± 00:13:48	NS	0.01

There were no statistically significant diet × sex interaction. NS = Non Significant

The Bovine Viral Diarrhoea (BVDv) experience on 14 Irish suckler beef farms

J. O' Shaughnessy[1, 2], J.F. Mee[3], M. Doherty[2], P. Crosson[1], D. Barrett[4], A. Woods[1] and B. Earley[1]
[1]AGRIC, Teagasc, Grange, Dunsany, Co. Meath, [2]School of Veterinary Medicine, UCD, Belfield, Dublin 4, [3]AGRIC, Teagasc, Moorepark, Fermoy, Co. Cork, and [4]Department of Agriculture, Food and the Marine, Sligo Regional Veterinary Laboratory, Doonally, County Sligo.

Introduction

BVDv is a *pestivirus* which is endemic in the cattle population and is responsible for a wide range of clinical syndromes, among which include the deleterious effects of the virus on immune function and reproductive performance. A previous Irish study found the individual animal and herd level prevalence of BVDv-positive cattle to be 0.6% and 25%, respectively (O' Neill et al. 2009). The objective of the study was to determine the individual animal and herd level prevalence of BVDv-positive cattle on 14 Irish suckler beef farms and to document the potential impact this virus may have on farm profitability.

Materials and Methods

Farms participating in the Teagasc-Irish Farmers Journal beef technology transfer programme (http://www.teagasc.ie/advisory/better_farms/beef/) were used in this study (O'Shaughnessy et al., 2012). Given the widespread interest amongst farmers in BVD, the programme management team recommended that these farmers screen their herds for BVDv. However, only 14 of the 16 participants screened their herds in 2010 (February-December) for the presence of BVDv using RT-PCR on ear biopsies performed at Enfer Diagnostics. Ten farms screened all stock, with the other four farms screened one of the following categories; 1) all breeding stock, 2) replacement heifers and calves, 3) newborn calves 4) spring calving cows and their calves only (autumn calving herd were not screened due to farmer reluctance, thus potentially influencing BVDv herd prevalence) . Veterinary account information, sought with the permission of each participating farmer, was retrieved from their respective veterinary practice. Veterinary account information was analysed for antibiotic spend and the number of calls to sick calves.

Results and Discussion

26 out of 2,652 cattle screened for the presence of BVDv were found to be BVDv-positive, with virus-positive animals being found on 7 out of 14 farms screened farms (range 1-10 per positive herd). The overall prevalence of BVDv-positive cattle was 0.98% (range 0-3% per herd, range 0.6-3% per positive herd). The mean age of BVDv-positive cattle was 7 months old (range 3 weeks-18 months old), with 3 cattle < 1 month old, 12 cattle between 1 and 6 months old and 11 cattle > 6 months old. A total of 432 cattle were screened on the farm with ten virus-positive cattle (prevalence 2.3%). This herd had started vaccinating for BVDv in 2008 pre-breeding, with the BVDv-positive calves being born from September 21st –November 15th 2009 (representing 8% of the August 2009-April 2010 calf crop). Calves were diagnosed as BVDv-positive in February 2010. Upon identification as BVDv-positive, all ten animals were isolated, with nine being slaughtered on July 6th 2010, realizing an average €254 each, this figure represented approximately 40% of the market value of non-diseased stock of similar age (CSO 2010). One of the BVDv-positive animals on this farm died of pneumonia in March 2010. There was a large decrease in antibiotic spend on calves during the corresponding period twelve months later, when no BVDv-positive animals were present on the farm, despite an increased number of calvings in that period (Table 1).

Conclusions

The high prevalence of BVDv in these Irish suckler beef herds was a surprising finding and contrasts with what has previously been reported in the Irish literature. An example of a farm with a high BVDv prevalence has been illustrated, demonstrating the potential effects this virus may have at farm level. Although this was a small study, it does however, serve to highlight the need for a wider study to be conducted on the potential impact of BVDv in Irish suckler beef herds.

Acknowledgements

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O' Neill, R., B. Wilson, C. Regan, E.Connaghan & J. Mooney (2009) *Irish Veterinary Journal,* 62**,** 679-683.

Table 1. The number of veterinary calls to sick calves, antibiotic spend and number of calvings on the farm with ten BVDv-positive cattle.

	21st Sept. 2009- 6th July 2010 (A*)	21st Sept. 2010- 6th July 2011 (B**)	[1]Percentage increase/decrease
Vet. calls to sick calves (no.)	12	10	-17
Total antibiotic spend (€)	1302	696	-47
Antibiotic spend on calves (€)	972	637	-34
Calvings (no.)	82	115	+40

[1] The percentage increase/decrease between the period when BVDv-positive calves were born and were present on the farm until slaughter and the corresponding period twelve months later. ((A-B) ÷ A) × 100. * Period of time that ten BVDv-positive animals were born and present on the farm until slaughter. ** Corresponding period twelve months later

The effect of road transport and a 12 hour mid-journey rest period on the physiological responses of bulls

B. Earley[1] and A.D. Fisher[2]

[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co. Meath and* [2]*Faculty of Veterinary Science, University of Melbourne, Australia.*

Introduction

There is limited scientific data on the physiological recovery of bulls after long durations of transport and in particular when given access to a 12 hour (h) mid-journey rest period during transport. Transport conditions have the potential to alter the biological responses of animals. The objective was to investigate effect of a 9 h road transport followed by a 12 h mid-journey rest period and a subsequent 9 h road journey on the welfare of bulls as assessed through physiological concentrations of blood variables.

Materials and Methods

Thirty bulls, continental breed crosses from crossbred suckler dams, (mean live weight 486, s.d. 57.0 kg) were assigned by live weight to one of two treatments, transport (T) (n=15) and control (C) (n=15) on day (d) 0. The T bulls were assigned to 3 pens on the transporter at a spatial allowance of 1.3m^2 and transported by road for 9 h (435 km) after which, they were unloaded and returned for a 12 h mid-journey rest period to the housing environment and had *ad libitum* access to hay and water. On completion of the 12 h rest period, the bulls were re-loaded on the transporter and transported for a further 9 h journey (435 km) by road, rested on the transporter for 2 h before unloading, and returned to 3 pens (n = 5 bulls/pen) and had *ad libitum* access to grass silage supplemented with 2 kg barley/soybean concentrate and water for a 24 h recovery period. The C bulls (n=15) were moved on d 0 to three novel straw bedded pens (5 bulls/pen) in the housing environment and had access to hay and water during the duration of the 'experimental transport' period and had *ad libitum* access to grass silage supplemented with 2 kg barley/soybean concentrate, water, and no hay for the 24 h period coinciding with the 24 h 'post-transport' recovery period. The bulls were weighed, blood sampled and rectal temperature was taken before (-0.25 h), immediately after, the first 9 h journey, the 12 h rest, the second 9 h journey, and during the 24 h post-transport recovery period. Haematology profiles were measured as described by Earley and Crowe (2002). All data were analyzed using the PROC MIXED procedure of SAS (version 9.1; SAS Institute, Inc.) with time relative to transportation as a fixed effect, animal and group as random effects; baseline values for each variable were included as covariates.

Results and Discussion

There was a significant effect of treatment × time ($P<0.0001$), treatment ($P=0.002$) and time ($P<0.0001$) for live weight. Bulls transported for the first 9 h journey had a mean (s.e.) live weight loss of 6.2 (± 0.44) %, regained 3.1 (± 0.17) % during the 12 h rest period, lost 4.0 (± 0.59) % during the second 9 h journey, and had an overall live weight loss of 4.0 (± 0.60) %. The mean (s.e.) % live weight change for controls at the corresponding time-points was 2.7 (± 0.37), 1.21 (± 0.39), 1.11 (± 0.27) and 1.6 (± 0.40) %, respectively. During the 24 h recovery period live weight was regained to pre-transport values in all treatments. The mean rectal body temperature for control and transported bulls was similar throughout the study and ranged from 38.7 (± 0.12) to 39.2 (± 0.10) ^{o}C. There was a treatment × time interaction ($P<0.0001$), no effect ($P>0.05$) of treatment, and an effect of time ($P<0.0001$) for neutrophil % (Table 1). The induction of a stress response was confirmed by the findings of blood neutrophilia in control and transported bulls. White blood cell (WBC) number was greater ($P<0.05$) in control compared with transported bulls at the end of the 24 h recovery period. There was no treatment × time interaction ($P>0.05$), no effect ($P>0.05$) of treatment, and an effect ($P<0.007$) of time for haematocrit % indicating that the changes in neutrophil % were not related to dehydration and haemoconcentration.

Conclusion

Control bulls showed similar changes in physiological responses to transported bulls. Twenty four hours in recovery with access to feed and water was sufficient for many of the blood variables to recover to pre-transport concentrations.

Reference

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Table 1. Haematological variables pre and post-transport in control and transported bulls (n = 15 bulls/treatment).

Variable and Treatment	Pre-transport	Post 9 h transport	Post 12 h mid-journey rest in a lairage	Post 9 h transport by road + 2 h rest on transporter	Post 4 h rest in lairage	Post 12 h rest in lairage	Post 24 h rest in lairage	Pooled s.e.
Neutrophil (%)								
Control	25.3^{a}	31.9^{bx}	32.7^{b}	28.2^{by}	35.8^{b}	36.9^{b}	32.3^{b}	1.57
Transport	20.8^{a}	49.1^{by}	34.9^{b}	41.1^{by}	34.3^{b}	37.7^{b}	32.0^{b}	1.57
Haematocrit (%)								
Control	32.9^{a}	33.9^{b}	32.8^{ab}	32.9^{ab}	33.8^{ab}	33.5^{ab}	32.7^{ab}	0.60
Transport	33.5^{a}	34.8^{b}	34.3^{ab}	34.1^{ab}	34.7^{ab}	34.5^{ab}	33.6^{ab}	0.60
WBC ($\times10^3/\mu$L)								
Control	9.9^{a}	10.5^{x}	10.1^{ab}	10.7^{ab}	11.1^{b}	11.6^{b}	15.9^{bx}	0.29
Transport	9.4^{a}	12.7^{by}	11.1^{b}	11.2^{b}	11.5^{b}	11.2^{b}	12.3^{aby}	0.29

^{ab}Within a row, Lsmeans not having a common superscript differ significantly ($P<0.05$); ^{x,y}Within a column, Lsmeans not having a common superscript differ significantly ($P<0.05$).

The effect of housing system during pregnancy on locomotor ability and claw lesions of sows in farrowing crates

J.A. Calderón-Díaz[1, 2], J. O'Doherty[2] and L. Boyle[1]
[1]Pig Production Dept., Teagasc, Moorepark Research Centre, Fermoy, Co. Cork, [2]Dept., of Animal Science, University College Dublin, Belfield, Dublin 4

Introduction

Concerns about animal welfare have resulted in a partial ban on gestation stalls in the EU from 2013. However, there are indications that claw lesions (CL) are more prevalent in loose than in stalled sows (Gjein and Larssen, 1995). CL are thought to be a major cause of lameness when loose housed sows are kept on concrete slatted flooring without bedding (Schulenburg *et al.,* 1986). The aims of the study were to determine: 1) the effect of housing system during pregnancy on locomotor ability of sows prior to farrowing; 2) the prevalence and severity of CL prior to farrowing and at weaning and 3) the association between CL and locomotor ability.

Materials and Methods

A total of 85 multiparious (range in parity 2-7; mean 3.26) crossbred Large White × Landrace sows were used. Forty-two sows were housed individually in gestation stalls (S) on concrete (1/3 slatted at rear) and 43 sows were housed loose (L) in a single group and fed by an electronic sow feeder during pregnancy. L sows had solid concrete floored lying bays and fully slatted roaming areas. On day 110 of pregnancy (d-5) sows were transferred to farrowing crates on one of 2 floor types: tri-bar (TB) steel (n=25 L and n=23 S) or super coated plastic (SC) (n=18 L and n=19 S). Locomotor ability was scored according to Main *et al*. (2000) on d-5. While sows were lying in the farrowing crate on d-5 and just prior to weaning (d28) the hind claws were inspected for CL: 1) heel overgrowth and/or erosion (HOE); 2) heel sole crack (HSC); 3) white line (WL) damage; 4) wall cracks (WC) and 5) dew claw injuries (DCI). These were scored according to severity using a modified version of a scale developed by FeetFirst™ (Zinpro Performance Minerals, Minnesota, USA) Data was analyzed using SAS. PROC MIXED was used to investigate the relationship between CL and housing system. The model included housing (L *vs*. S), period (d-5 *vs.* d28), floor (TB *vs.* SC) and their interactions. Locomotor ability was analyzed using PROC LOGISTIC. The model included housing and HOE, HSC, WL, WC and IDC as covariates.

Results and Discussion

All the sows had at least one CL. S sows had higher scores for WL and DCI (P<0.01) while HOE scores were higher for L sows (P<0.01; Table 1). HOE, WL and DCI scores increased, whereas HSC scores decreased between d-5 and d28 reflecting a predominately negative impact of housing in farrowing crates on claw health. There was no interaction between floor type in the farrowing crate and housing system during pregnancy (P>0.05). However, floor type had an effect on HSC (2.62 TB vs. 1.35 SC, ± 0.26 P<0.001) and DCI (4.75 TB vs. 5.38 SC, ± 0.22 P<0.05). L sows had a lower odds of being scored 0 or 1, and a higher odds of being scored 2 or ≥3 for locomotory ability (P<0.05; Table 2). Loose sows can move around and are exposed to aggression on slatted floors which probably contributes to their higher locomotor scores. There was no significant relationship between lameness and any of the CL (P>0.05). This is in disagreement with Anil *et al.* (2007) who showed an association between lameness and WL in the lateral claw. This could be explained by the fact that we did not analyse the medial and lateral claws separately.

Table 2. Odds ratios for the effect of housing (Loose vs. Stall) on locomotor ability score in sows prior to farrowing

Score	Odds ratios	95% CI
0-1	0.42	0.067 - 0.439
2	1.49	0.894 - 5.564
>3	2.37	1.471 - 21.570

CI= Confidence interval

Conclusions

Claw lesions are common in sows irrespective of gestation housing system. Although sows confined in stalls had higher severity scores for white line damage and dew claw injuries loose housed sows were more likely to be lame prior to farrowing. This has implications for sow welfare when we switch to loose housing in 2013 as lameness could become more of a problem. Housing in the farrowing crate had a negative impact on claw health of sows.

Acknowledgements

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Table 1. Effect of housing system during pregnancy and period on claw lesion scores of sows

	Housing				Period				Housing x Period
Claw lesion	Loose	Stall	SEM	P value	d-5	d28	SEM	P value	P value
HOE	8.31	7.36	0.25	0.008	5.94	9.73	0.24	<0.0001	0.713
HSC	1.86	2.12	0.27	0.482	2.29	1.68	0.23	0.035	0.478
WL	3.15	3.99	0.22	0.007	2.65	4.48	0.19	<0.001	0.99
WC	4.93	5.02	0.32	0.848	4.92	5.03	0.29	0.749	0.058
DCI	4.55	5.59	0.22	0.001	4.29	5.85	0.21	<0.001	0.019

HOE=heel overgrowth and/or erosion; HSC=heel sole crack; WL=white line damage; WC=cracks in the wall; DCI= dew claws injuries

Association between season and somatic cell count for cows in Irish and UK dairy herds

S.C. Archer[1,2], F. Buckley[2], F. Mc Coy[2], W. Wapenaar[1], and M.J. Green[1]
[1]*University of Nottingham, School of Veterinary Medicine and Science, Sutton Bonington Campus, Sutton Bonington, Leicestershire, LE12 5RD, United Kingdom;* [2]*Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland*

Introduction

Seasonal increase in bulk milk somatic cell count (SCC) is of economic importance to milk processors because of decreased production efficiency, and shelf life of products, and to producers through financial penalties. For Irish dairy herds, bulk milk SCC was highest in autumn (Berry, 2006), but this occurred during summer for UK dairy herds (Green, 2006), indicating the importance of accounting for stage of lactation in order to identify times of the year that are associated with increased cow SCC, to target further investigations.
The aim of this study was therefore to describe association between time of year, and SCC at the cow level for Irish and UK herds. In particular, to identify trends, that may be masked by the effects of stage of lactation and milk yield at the herd level.

Material and Methods

Milk recording databases were provided by the Irish Cattle Breeders Federation, and National Milk Records, UK. The study populations were 7,551 Irish dairy herds, with 10,181,545 records from 860,563 cows taken between 2005 and 2009, and 2,128 UK dairy herds, with 6,772,182 records from 474,669 cows taken between 2004 and 2006. Samples of 497 Irish, and 200 UK herds were taken at random. Four-level linear models for natural logarithm of test day SCC were developed in MLwiN 2.22, using data from herds in the first samples; random effects structure accounted for clustering of cows within herds, parities within cow, and recordings within parity. The models corrected for stage of lactation, milk yield, composition, parity, and herd size; built by backward stepwise elimination of terms from a saturated model. Factors remained in the model if $p \leq 0.05$. Biologically plausible interactions, and herd level random were assessed. Model fit was assessed by inspection of residuals at each level for normality, and by using fixed effects to predict cow SCC for the herds used for model development. Predictions were repeated for further random samples of 493 and 200 Irish and UK herds that were not used for model development, to determine if the results could be generalised.

Results and Discussion

Following adjustment for the confounding influence of stage of lactation, associations between cow SCC and calendar month were larger and more variable from February to August, and in December, for the Irish compared to the UK herds (Figure 1). This was opposite to the trends observed in bulk milk SCC for Irish herds.
At the cow level, increased SCC and variability in SCC indicate that February to August is a key time for the occurrence of new intra-mammary infections, and some of these may become chronic, and contribute high bulk milk SCC later in the year, that is a problem for Irish dairy industry. It is therefore important to monitor rates of new infections, and cures based on individual cow SCC during summer, and take farm specific action, regardless of bulk milk SCC. However, further work is needed to demonstrate the legacy of new infections from the spring and summer, and their contribution to bulk milk SCC later in the year, as well as target rates.

Model fit was acceptable. Fixed effects from the final models were as good at predicting separate data, as they were at predicting that used for parameter estimation, indicating the results can be generalised to other Irish and UK dairy herds.

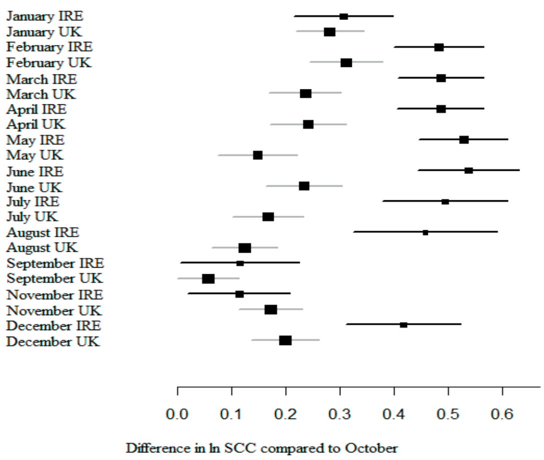

Figure 1. Model coefficients (and 95% confidence intervals) for calendar month (ln = natural logarithm)

Conclusions

Monitoring new intra-mammary infection rate during spring and summer is recommended as part of the national CellCheck program in Ireland.

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Leukocyte profiles of cows with claw horn disorders

K. O'Driscoll[1] and B. Earley[1]
[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co. Meath*

Introduction
Claw horn disruption (CHD) in dairy cows weakens the integrity of the hoof, results in lesions ranging in severity from mild haemorrhages to ulcers, and can cause lameness and pain (Pastell *et al.,* 2010). Although cows with ulcers are normally clinically lame, cows with severe haemorrhaging do not always display impaired locomotion. Thus identification of cows that are in need of hoof trimming, pain relief, or at risk of developing secondary disorders is difficult. Information about the immune status of cows afflicted with CHD could be useful to determine whether these cows could be at risk of development of secondary disorders, and also identify potential biomarkers that could be used to identify cows at risk of developing CHD. The study objective was to examine the haematology profiles of cows with sole ulcers (the most severe pathology associated with CHD), and of cows with moderate and severe haemorrhaging, with sound cows.

Material and Methods
Study 1: Cows from the Moorepark research farms were locomotion scored after milking once weekly. Cows that were considered clinically lame in a hind limb (obvious impairment of one or more hind limbs) had their hind hooves examined. Five parameters (spine arch, tracking, head-bob, ab/aduction, speed) were scored using a 5 point scale, then the sums of the scores added to obtain an overall score (O'Driscoll et al., 2009). 12 clinically lame cows were identified as having at least one ulcer, and no other disorder. These cows were paired with a cow that had good locomotion and no disorders. Cows were matched as closely as possible with their pair using days in milk (DIM), liveweight, body condition score and diet.
Study 2: Cows from the Moorepark herd were locomotion scored and underwent hoof examination at 111 ± 23 DIM. Cows (n = 41) were assigned to 3 categories on the basis of haemorrhage score; 1 = no/minimal haemorrhage, 2 = moderate haemorrhage; 3 = severe haemorrhage (Table 2). Cows were otherwise healthy. Blood samples for both studies were taken on the morning of hoof scoring. Total leukocyte, neutrophil (N) and lymphocye (L) counts were

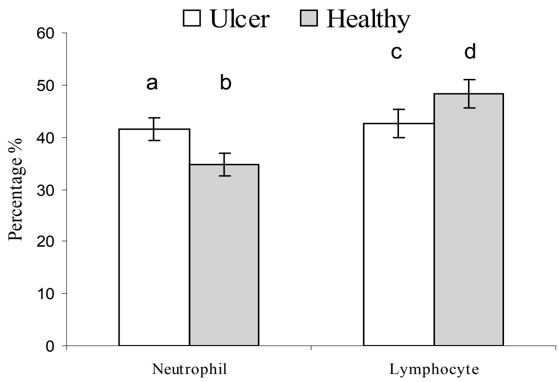

Fig. 1. Neutrophil % and lymphocyte % of cows with a sole ulcer and healthy cows*

determined within 3 hours of blood collection from K_3EDTA anti-coagulated blood (6 mL) using an automated haematology analyzer (ADVIA 2120, Bayer Healthcare, Siemens, UK) equipped with software for bovine blood. All data were log transformed if necessary and analysed using the PROC MIXED in SAS v9.1.

Results and Discussion
Study 1: Cows with ulcers had higher locomotion scores (Mean ± se) than sound cows (13.5 ± 0.54 *v's* 6.7 ± 0.54; $P < 0.001$). There was no difference in total leukocyte counts, neutrophil count, lymphocyte count, or monocyte count, eosinophil or basophil count or %.. Cows with ulcers had higher neutrophil % ($P < 0.05$) and tended to have a lower lymphocyte % ($P = 0.1$) than healthy cows. Ulcer cows and a higher N:L ratio (1.04 ± 0.1) than healthy cows (0.76 ± 0.1; $P = 0.05$).
Study 2: Although all haemorrhage scores in each category were different from each other ($P < 0.001$ for all) there was no effect of category on locomotion score (Table 1) or on the haematology variables.

Conclusions
Cows that were clinically lame with sole ulcers had a leukocyte profile indicative of systemic inflammation and stress. A similar pattern was not evident in study 2. It is possible that that only CHD severe enough to cause clinical lameness, and thus a sickness response, affects leukocyte profiles.

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Table 1. Leukocyte profiles (Lsmeans ± s.e) of cows with no/mild haemorrhages (1), moderate haemorrhages (2) and severe haemorrhages (3)*

Category	1 (n = 10)	2 (n = 20)	3 (n = 11)	*P*-value
Haemorrhage score	2.1 ± 1.5[a]	13.6 ± 1.4[b]	34.8 ± 1.5[c]	<0.001
Locomotion score	7.4 ± 0.6	8.4 ± 0.6	8.2 ± 0.6	0.19
WBC count (10^{-3} cells/µL)	8.24 ± 0.74	9.01 ± 0.52	8.40 ± 0.74	0.64
Neutrophil count (10^{-3} cells/µL)	3.09 ± 0.42	3.42 ± 0.30	3.39 ± 0.42	0.80
Neutrophil %	37.2 ± 2.3	37.7 ± 1.6	39.0 ± 2.3	0.84
Lymphocyte count (10^{-3} cells/µL)	3.8 ± 0.4	4.2 ± 0.3	3.8 ± 0.4	0.53
Lymphocyte %	42.6 ± 2.9	40.0 ± 2.5	42.6 ± 2.7	0.65
N:L ratio	0.87 ± 0.11	0.85 ± 0.08	0.91 ± 0.11	0.91

*Lsmeans not having a common superscript [ab] differ significantly ($P<0.05$); [cd] tend to differ ($P < 0.1$)

Effect of dairy cow treatment (for parasitic diseases) with nitroxynil, oxyclozanide and levamisole on residues in milk, cream, skim-milk and skim-milk powder

C. Power[1,2], B. O'Brien[3], M. Danaher[4], A. Furey[2], Y. Bloemhoff[3], R.Sayers[3] and K. Jordan[1]

[1] *Teagasc, Food Research Centre, Moorepark, Fermoy, Co. Cork;* [2] *Cork Institute of Technology, Cork;* [3]*Teagasc, Animal and Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork;* [4] *Teagasc, Food Research Centre, Ashtown, Dublin*

Introduction

Liver fluke, roundworm and lungworm are parasites that can cause disease in food producing animals (Knubben-Schweizer *et al*., 2010). Anthelmintic drugs are widely used in veterinary medicine for protection or treatment of animals against parasitic disease. Nitroxynil is active against mature and immature liver fluke. Levamisole is administered to control nematode parasites and oxyclozanide is mainly utilized in the treatment of the adult stages of liver fluke, and has been shown to be active against rumen fluke (Paraud *et al*., 2009). The use of anthelmintics in dairy cows may result in residues occurring in milk and dairy products. Therefore, the objective of this study was to investigate the presence of residues of both nitroxynil and a combination drug containing levamisole and oxyclozanide in milk and a variety of milk products, both fat based, such as cream, and defatted such as skim-milk powder.

Materials and Methods

Six lactating dairy cows had nitroxynil administered to them subcutaneously using 1.5 ml of Trodax 34% per 50 kg live weight. Milk samples were taken, twice daily for 16 days and later at weekly intervals for up to 58 days post-treatment. All samples were stored at -20˚C prior to analysis. Samples were subsequently thawed and pooled into 6 independent aliquots, each, containing milk from three cows between Days 1-9 (Period 1), 10-15 (Period 2) and 16-28 (Period 3). For the levamisole and oxyclozanide combination treatment, six Friesian cows weighing between 400 and 500 kg were treated with the maximum dose (150 mL for animals 300 kg and over) of Toloxon. Milk samples (50 mL) were subsequently taken from the cows twice daily, over a 5 day period, and the samples were frozen (-20°C) until analysis. Samples were subsequently thawed and pooled into 2 independent aliquots, each containing milk from three cows between Days 1-5. In both drug administration trials, a 50 ml milk sample was collected from each cow prior to treatment, as a control. Pooling of milk samples was necessary to generate sufficient sample volume for duplicate separation and milk powder manufacture. Each milk was separated into skim milk and cream fractions, and the skim milk was processed to milk powder using a bench-top laboratory-scale spray dryer. Milk, cream and powder samples were analyzed using the procedure described by Whelan *et al.* (2010) for nitroxynil and Whelan *et a*l. (2011) for levamisole and oxyclosanide. Analysis was completed in duplicate and all duplicates were consistent. Data was managed in Excel and all results are shown.

Results and Discussion

In all cases, the majority of the residue was partitioned into the skim-milk fraction, survived powder processing and was detected in the final powder. Average nitroxynil residues measured in the skim-milk were 459±0.05, 169±50 and 15±5.6 μg/L, for Periods 1, 2 and 3, respectively. In cream, the values were 13.3±3.78, 5.5±1.84 and 0.53±0.18 μg/L, respectively. These results show that ≥95% of the drug partitioned into the skim-milk fraction. Furthermore, approximately 88% did not degrade during the spray drying process and was transferred to the powder. Residues of oxyclozanide and levamisole (days 1-5) are shown in Table 1. Average concentrations of oxyclozanide and levamisole in cream were 0.24±0.042 and 0.15±0.014 μg/50 mL, respectively and in skim-milk were 4.4±0.98 and 39±0.0.49 μg/L, respectively. The study showed that >95 and 97% of oxyclozanide and levamisole residues transferred into the skim-milk fraction. When powder was manufactured from the skim milk, >90% and >96% of oxyclozanide and levamisole did not degrade and was transferred to the powder.

Conclusions

The results showed that residues of nitroxynil, levamisole and oxyclozanide will be present in milk after administration, will be partitioned with the skim-milk and will be present in a subsequent powder product. Thus, sufficient caution must be exercised with regard to withdrawal periods to ensure avoidance of risk to public health.

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Table 1. Migration of oxyclozanide and levamisole from whole milk into cream, skim-milk and powder made from the skim-milk by spray-drying (milk samples from days 1-5)

Residue	μg/50 ml cream (%*)	μg/litre skim (%)	μg/kg powder (%)
Oxyclozanide (sample 1)	0.27 (3.1)	5.11 (96.9)	55.0 (90.9)
(sample 2)	0.21 (4.6)	3.73 (95.4)	40.0 (90.2)
Levamisole (sample 1)	0.14 (1.6)	38.6 (98.4)	445.0 (97.8)
(sample 2)	0.16 (2.5)	39.3 (97.5)	449.0 (96.9)

* Based on the expectation of 85 g of powder being produced from 1 litre of milk.

Herd health problems on 16 Irish suckler beef farms

J. O' Shaughnessy[1, 2], J.F. Mee[3], M. Doherty[2], P. Crosson[1], D. Barrett[4], L. O' Grady[2] and B. Earley[1]
[1]*AGRIC, Teagasc, Grange, Dunsany, Co. Meath,* [2]*School of Veterinary Medicine, UCD, Belfield, Dublin 4,* [3]*AGRIC, Teagasc, Moorepark, Fermoy, Co. Cork, and* [4]*Department of Agriculture, Food and the Marine, Sligo Regional Veterinary Laboratory, Doonally, County Sligo.*

Introduction

There have been few international and no published Irish studies documenting herd health control practices and their association with herd health status in suckler beef herds. Herd health problems such as calf diarrhoea and calf pneumonia can significantly reduce the profitability of a suckler beef enterprise (Gunn and Stott, 1998). The objective of this study was to assess animal health control practices associated with herd health status on sixteen Irish suckler beef herds over a two year period (1st January 2009-31st December 2010).

Materials and Methods

Sixteen farms participating in the Teagasc-Irish Farmers Journal BETTER farm beef technology transfer programme (http://www.teagasc.ie/advisory/better_farms/beef/) were used in this study. Participation in the programme was voluntary, with farms being invited to join the programme based on two main criteria; 1) farm location in Ireland and 2) suckler beef cow herds with a predominantly spring calving pattern. Suckler beef farms from the following geographic areas of Ireland entered the programme; south east (N=4), mid west (N=3), midlands (N=3), north west (N=2), north east (N=2) and south west (N=2). The herd was the epidemiological unit used in this study. The mean (s.d.) herd size, stocking rate and farm size was 68 cows (27.6), 2.0 LU/ha (0.3) and 64.3 adjusted hectares for cattle (21.6), respectively. Cows of predominantly Limousin, Charolais, Simmental and Belgian Blue genotypes accounted for 50%, 21%, 17% and 5%, respectively, of all recorded dam breeds on these farms. Charolais, Limousin and Belgian Blue were the breeds of sire used in 35%, 29% and 26% respectively, of all recorded calves. Two questionnaires were designed; 1) a veterinary questionnaire to collect information on the nature and extent of animal health control advice and services provided by the veterinary practitioner and an identification of herd health problems from the practitioners servicing each individual farm, and 2) a farmer questionnaire to collect information on farm background, potential risk factors for animal health problems and farmer-implemented animal health control practices. Considering the size of the farmer questionnaire, it was deemed prudent to post it to farmers on average one month in advance of visits, thereby allowing participants time to fill in some basic questions. Farms and veterinary practices were visited between January and March 2011 when questionnaires were fully completed by the respondents. Descriptive statistics were used to quantify the various variables in the questionnaires including husbandry and management variables and herd health problems using SAS (version 9.1; SAS Institute, Inc.).

Results and Discussion

Results from the farmer questionnaire indicated that 88% of farms had emergency caesarean surgery performed on farm in the study period (prevalence of 2%, range of 0-8% per herd) while 63% and 38% of farms experienced at least one animal mortality due to calf pneumonia and calf diarrhoea respectively. 19% of farmers stated that they did not have individual calving pens, with a further 38% reporting that they cleaned and disinfected calving pens after more than five calvings. 27% of respondents relied solely upon observation of suckling by the calf to ensure adequate colostral intake, while 50% of farmers used a pre-calving calf diarrhoea vaccine and 44 % of farmers reported using respiratory vaccines on calves under three months of age.
The most common health problems identified by the sixteen veterinary practitioners surveyed were dystocia, calf pneumonia and calf diarrhoea (Figure 1). These data support the findings of the farmer questionnaires. The majority (94 and 75%, respectively) of veterinary practitioners responded that they routinely advised these clients on vaccination protocols and calf health. In addition, a minority of practitioners (38%) responded that they routinely advised these clients on pre-calving management of breeding stock.

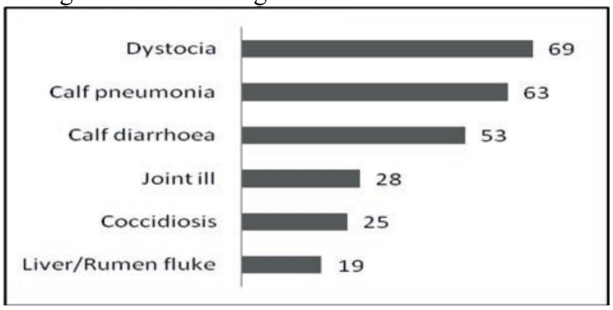

Figure 1. Health problems (% of 32 herd-years) identified by veterinary practitioners in the veterinary questionnaire on 16 BETTER beef farms in 2009 and 2010

Conclusions

Dystocia, calf pneumonia, and calf diarrhoea, in that order, were the primary herd health issues in these Irish suckler beef herds. As a result of the study, a herd health calendar has been produced for each farm. This calendar advises farmers on best animal health management practices throughout the year, on a monthly basis. In addition, changes have been made on some of the farms to improve housing and calving facilities. This small, yet detailed, study provides a basis for practical herd health management control strategies and could serve as the focus for future work in herd health research in suckler beef enterprises in Ireland.

Acknowledgements

The support of industry stakeholders, the Agricultural Trust, ABP Ireland, Dawn Meats and Kepak Group, for the Teagasc/Farmers Journal Better Farm Programme is gratefully acknowledged.

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The change in immunoglobulin G concentration over the first six milkings in Irish Holstein-Friesian dairy cows

M. Conneely[1, 2], D.P. Berry[1], I. Lorenz[2], M.L. Doherty[2] and E. Kennedy[1]

[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork.* [2]*School of Veterinary Medicine, University College Dublin, D4*

Introduction

Provision of adequate immunoglobulin G (IgG) to newborn dairy calves is crucial to ensure their health and productivity (DeNise et al, 1989). The milk produced by the cow for a number of days post-calving has a higher IgG content than whole milk (Foley et al, 1978). However, it may be insufficiently high to ensure adequate absorption by the newborn calf, and as such may not be suitable for feeding at the first feed following birth if the dams own colostrum is not available. The objective of this study was to quantify the change in colostrum IgG concentration with each successive milking post-calving up to the sixth milking.

Materials and Methods

The study was undertaken between 15 January and 30 April 2011 at Teagasc Moorepark Research Farm. The study population consisted of 98 Holstein-Friesian dairy cows; 20 cows of first, second, third, and fourth parity and 18 cows of fifth or greater parity. Post-calving, each cow was milked by machine at the next herd milking times (08:30 and 15:30). Samples were taken for the first six milkings post-calving. Colostrum was collected in a steel churn, the weight was recorded and a 100ml sample of colostrum was obtained and frozen at -20^{o}C until analysis. Information recorded from the cows included time and date of calving, sex of calf, weight and breed of the calf, whether the calf was born alive or stillborn, presentation of the calf (normal, posterior, breech, leg-back, head-back) and degree of calving difficulty on a 1 to 5 scale (1= no assistance, 5= veterinary intervention). Other information available included time interval from calving to subsequent milking, cow body weight measured up to 14 days post-calving and body condition score (scale 1 to 5; Edmonson et al 1989) measured within 14 days of calving, length of dry period, cow EBI, breed fraction, and level of heterosis and recombination.

The IgG concentration was determined using an ELISA method *(Bovine IgG ELISA Kit Cat. No. 8010, Alpha Diagnostic International, San Antonio, TX, USA)* Factors associated with colostrum IgG concentration were determined using mixed models in PROC MIXED (SAS, 2009); cow was included as a repeated effect and a first order autoregressive covariance structure with heterogenous variances was assumed among records within cow. All the aforementioned variables were considered as possible fixed effects in the model. Of particular interest was the association with colostrum IgG level of the number milkings post-calving and associated interactions. The repeatability of IgG concentration was also quantified using mixed models with cow included as a random effect.

Results and Discussion

Only milking number and parity were associated ($P<0.05$) with colostrum IgG levels. Across all animals, IgG concentration decreased post-calving; apart from the fourth milking versus the sixth milking, mean IgG concentration at the different milkings were different ($P<0.05$) from each other. Across all animals the least square means (IgG mg/ml) were 117.2 (SE 4.9), 50.3 (SE 2.7), 26.3 (SE 1.6), 17.7 (SE 1.4), 12.31 (SE 1.1) and 16.9 (SE 1.7) for milking one to six, respectively.

However, the association between milking number and IgG levels differed ($P<0.05$) by parity (Figure 1).Older parity animals produced colostrum with a higher IgG concentration at the first milking, but for all parities, only the colostrum from the first milking had an IgG concentration above the threshold of 50mg/ml IgG which is used to classify colostrum as good quality (McGuirk et al, 2004) .With the exception of parity 2 animals, the proportional decline to the second milking relative to first milking was 54 to 56%; the proportional decline in second parity animals was 64%. The decline in IgG concentration from first to second milking was greatest in second and fifth or greater parity animals (82.2 mg/ml and 80.5 mg/ml, respectively). The repeatability of IgG levels was 0.12.

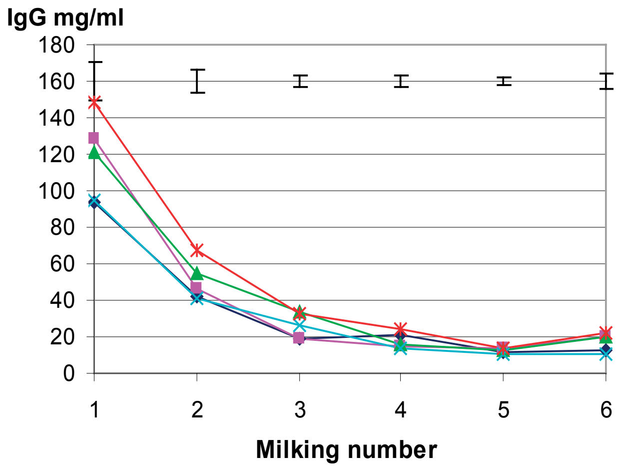

Figure 1. IgG levels for different milkings post-calving for parity 1 (blue), 2 (pink), 3 (green), 4 (turquoise) and 5+ (red); mean 95% confidence interval represented by error bars.

Conclusions

Only the colostrum obtained from the cow at the first milking post-partum is suitable to feed to newborn calves at the first feed following birth, regardless of the parity of the cow.

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Effect of including a disinfectant in the rinse water of a milking machine wash programme

D. Gleeson[1], B. O'Brien[1] and K Jordan[2]
[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co Cork;*
[2]*Teagasc Food Research Centre, Moorepark, Fermoy, Co Cork*

Introduction
Cleaning and disinfection of milking equipment is an essential part of milk production to maintain a high standard of hygiene. The addition of a disinfectant/sterilizer in the final rinse water of a milking machine wash programme may be recommended where the microbial count of a farm water supply is considered unsatisfactory. The addition of chlorine to the final rinse water may have benefits in sterilizing internal milking equipment surfaces. However, it may result in the formation of a residue Trichloromethane (TCM) in milk (Resch and Guthy, 2000). Peracetic acid (PA) has similar antimicrobial properties to chlorine and anecdotal evidence suggests that the substitution of PA in the final rinse water will also reduce/eliminate TCM residues. An alternative biocide disinfectant product used in the disinfection/sterilization of public areas is now promoted for the cleaning of milking equipment. The objective of this study was to determine the effect of these sterilizing agents on bacterial numbers and TCM residues in milk.

Materials and Methods
Four treatments involving different disinfectant product type and usage rate were compared with respect to bacterial numbers in milk, on plastic surfaces and TCM residue in milk. The treatments applied: (a) Chlorine (Sodium Hypochlorite) (5 mL/16 L); (b) PA ('Serpent') at a rate of 11 mL/16 L; (c) PA ('Serpent') at a rate of 21 mL/16 L; (d) Biocide ('Aerocare') at a rate of 1.1 L /16 L. A 30 unit milking plant was rinsed with clean water (16 L per milking unit) immediately after the main detergent wash cycle. An additional rinse cycle (16 L per milking unit) incorporating the disinfectant treatments were carried out two hours prior to am and pm milking. Each treatment was applied for one week at two time periods. Within each week, day 1 and 2 was used as control measurement days (no sterilizing agent applied) and for days 3, 4 and 5 the disinfectant treatment were applied. Two milk samples (100 mL) were taken from the milk line, at each milking occasion, the first as the first milk appeared after the start of milking and the second after 3 rows of cows were milked. Milk samples (n=160) were analyzed for total bacterial counts (TBC), thermoduric bacteria and TCM residues (n=80). For bacterial and TCM results, the log of the ratio between pre and post plant disinfection for each individual treatment were compared using mixed procedures of SAS. The internal plastic surface of claw-pieces (n=128) were swabbed before and after plant disinfection, to measure TBC. Swab data were analyzed using paired Student t-tests.

Results and Discussion
All disinfectant products resulted in a significant reduction in milk TBC ($P<0.01$) (Table 1). Chlorine reduced levels of thermoduric bacteria after disinfection ($P<0.01$). The levels of thermoduric bacteria present prior to disinfection were low for both PA treatments (<75cfu) and this may account for no significant reduction in thermoduric counts being observed after disinfection. The biocide disinfectant foamed during plant circulation to an unsatisfactory extent. All disinfectant products resulted in milk TCM levels within the acceptable target level of 0.002 mg/kg. However, chlorine had significantly higher ($P<0.01$) TCM levels after plant disinfection. The inclusion of PA in the rinse cycle did not eliminate TCM. High numbers of bacteria are present on claw-piece internal plastic surfaces after detergent cleaning (Gleeson *et al*. 2011). The inclusion of either PA or chlorine in the rinse water reduced TBC on plastic surfaces ($P<0.01$).

Conclusions
All disinfectant treatments evaluated resulted in significant reductions in milk TBC. The lowest bacterial numbers on plastic surfaces were observed with PA. PA may be used at lower usage rates and as an alternative product to chlorine which was associated with higher levels of TCM. The biocide product is not suitable for the cleaning of milking equipment due the foaming effect of the product during wash circulation.

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Table 1. Effect of including a disinfectant/sterilizer in the final rinse water of a milking machine wash programme on total bacterial counts (TBC) in milk and on plastic surfaces, thermoduric numbers and TCM residues in milk

	No of samples		Chlorine 5ml/16L	Peracetic Acid-11ml/16L	Peracetic Acid-21ml/16L	Aerocare 1.1 L/16 L
TBC (cfu)	16	Pre	2,667	2078	2,593	1,468
	24	Post	1,528	1,154	1,389	963
		P-value	0.003	0.005	0.004	0.003
Thermoduric (cfu)	16	Pre	299	65	75	159
	24	Post	115	114	47	100
		P-value	0.007	0.047	0.117	0.123
TCM (mg/kg)	8	Pre	0.001	0.001	0.001	0.001
	12	Post	0.002	0.001	0.001	0.001
		P-value	0.010	0.817	0.817	0.731
TBC-plastic (cfu)	16	Pre	203,250	200,667	176,500	116,000
	16	Post	57,000	1,750	7,500	38,000
		P-value	0.006	0.002	0.01	0.21

Effect of different post-grazing sward height on early lactation dairy cow performance

E. Ganche[1,2], M. O'Donovan[1], L. Delaby[3], T.M. Boland[2] and E. Kennedy[1]

[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy Co Cork;* [2]*School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4 and* [3]*INRA, UMR Production du Lait, 35590 St Gilles, France*

Introduction

With the upcoming abolition of milk quotas in 2015 and a 50% increase in milk production by 2020 targeted by the Food Harvest 2020. Irish grass-based dairy enterprises need to explore new strategies to increase milk production per hectare. The contribution of grazed grass in the diet of the lactating dairy cow is maximised through early spring turnout post-calving. This target is challenged by low spring grass supply. Grazing to a very low post-grazing sward height (PGSH; 2.7cm) during the two first grazing rotations improved pasture utilisation but substantially compromised dairy cow milk production during this period (Ganche *et al.*, 2011). Low PGSH needs to be compared to current recommendations (4cm; McEvoy *et al*., 2008) to assess the differences in production performance. This study aimed to establish the implications of different PGSH in spring on dairy cow performance during early lactation.

Materials and Methods

Ninety (27 primiparous and 63 multiparous) spring calving Holstein Friesian dairy cows were balanced on calving date (13 February; s.d. 17.7 days), lactation number (2.1; s.d. 1.05), previous lactation (first 37 weeks) milk yield (4591; s.d. 682.7 kg), bodyweight (BW; 482, s.d. 57.8 kg) and body condition score (BCS; 2.92, s.d. 0.141) in a randomised block design, with animals randomly assigned pre-calving to one of three (n=30) PGSH treatments: 2.7 cm (severe - S), 3.5 cm (moderate – M) or 4.2 cm (lax – L) from February 14 to April 24, 2011. Fresh herbage was allocated daily. Herbage mass (HM; >2.7 cm) was calculated twice weekly by cutting two strips per grazing treatment. Pre and post-grazing heights were measured daily using a folding pasture plate meter.details The differences in PGSH were achieved by ensuring a 3 kg DM define /cow/d difference in daily herbage allowance (DHA) between treatments. All animals were supplemented with 3.4 kg of concentrate DM/d throughout the experiment. Grass DM intake (GDMI) was measured using the *n*-alkane technique (Dillon and Stakelum, 1989) during week 5 (March 12-18) and week 9 (April 11-16) of the experiment. Pasture utilisation was calculated for each grazing rotation from the pre-grazing yield seems an incorrect word? relative to the post-grazing yield. Milk yield was recorded daily; milk composition, BW and BCS were measured weekly. Data on Animal variables were analysed using covariate analysis and the PROC MIXED statement of SAS with terms for parity, treatment and the interaction of parity and treatment. Days in milk and pre-experimental values of what? were used as covariates in the model.

Results and Discussion

During the first two grazing rotations the L treatment had higher pre-grazing HM (+120 kg DM/ha; $P<0.01$) and pre-grazing sward height (+0.60 cm; $P<0.001$) when compared to the S and M treatments (956 kg DM/ha and 6.40 cm, respectively).Were S and M the same? Mean DHA (>2.7 cm) was 7.7, 10.0 and 12.1 kg DM/cow and mean PGSH was 2.7, 3.5 and 4.2 cm for the S, M and L treatments, respectively. Average total DMI was lowest for the S animals (13.3 kg DM/cow; $P<0.001$) when compared to the mean total DMI of the M and L animals, which did not differ significantly (15.1 kg DM/ha). Increasing PGSH from 2.7 to 3.5 to 4.2 cm resulted in a linear increase ($P<0.001$) in milk yield (22.5, 23.6 and 25.1 kg/cow/d, respectively data in Table) and protein yield (750, 807 and 857 g/d, respectively). As a result, milk solids yield increased with PGSH ($P<0.001$; Table 1). Severe grazing depressed ($P<0.01$) both cumulative milk yield (-160 kg/cow) and milk solids yield (-17 kg milk/cow), when compared to the M and L treatments which performed similarly (1538 kg milk/cow and 124 kg milk solids/cow). The severe decrease in production reflected the high level of restriction placed upon the animals in the S treatment as they were offered a very low DHA to achieve the desired PGSH. The quantity of grass utilised (>2.7 cm) was, however, maximised ($P<0.001$) by grazing to 2.7 cm (918 kg DM/ha) when compared to 3.5 cm (779 kg DM/ha) and 4.2 cm (764 kg DM/ha).

Table 1. Effect of post-grazing height (PGSH) on animal performance during the early lactation period

	PGSH treatment[1]				
	S	M	L	SED	*P*
Milk yield, kg/d	22.5[a]	23.6[b]	25.1[c]	0.51	0.001
Milk fat, g/kg	43.9[a]	46.8[b]	45.9[b]	0.91	0.015
Milk protein, g/kg	33.1[a]	34.1[b]	34.0[b]	0.35	0.022
Milk lactose, g/kg	46.8	46.9	47.0	0.22	0.636
Milk solids yield, kg/d	1.75[a]	1.91[b]	2.00[c]	0.046	0.001
End BW, kg	442[a]	451[ab]	464[b]	7.3	0.019
End BCS	2.71[a]	2.80[b]	2.87[b]	0.041	0.004

[1]PGSH: S (2.7 cm), M (3.5 cm), L (4.2 cm)
[a-c] Means within a row with different superscripts differ

Conclusions

Grazing to 2.7 cm physically restricted cows from grazing further into the sward thereby lowering dry matter intake GDMI? which consequently resulted in substantial milk and milk solids production losses. Grazing cows to a lax PGSH (4.2 cm) in early spring resulted in reduced grass utilisation and no significant increase in cumulative milk and milk solids production when compared to grazing to 3.5 cm. This study concludes that grazing swards to 3.5 cm in early spring will satisfactorily achieve a balance between pasture utilisation and dairy cow production performance.

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Relationship between meteorological factors and grass growth in spring in the south of Ireland

C. Hurtado-Uria[1, 2], D. Hennessy[1], L. Shalloo[1], L. Delaby[3] and D. O Connor[2]

[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork;* [2]*Cork Institute of Technology, Bishopstown, Cork;* [3]*INRA, UMR 1080, Production du Lait, 35590 St. Gilles, France*

Introduction

Ireland has conditions that favour grass growth throughout most of the year, with a 300 day grazing season achieved in the south, providing a competitive advantage in offering a cheap feed source to beef and dairy cattle. Grass growth is highly seasonal with little growth over the winter period due to low temperatures and low levels of solar radiation. Peak grass growth occurs in late spring and early summer, followed by a decline in the late summer and autumn. The climate in Ireland is influenced by the westerly winds and the proximity of the ocean, resulting in a temperate humid climate. Meteorological conditions influence grass growth over the course of the growing season, particularly radiation, temperature and rainfall (Burke *et al*. 2004), as a result there are variations in grass growth within and between years. The objectives of the study were to determine the meteorological factors having the greatest influence on growth of perennial ryegrass (*Lolium perenne* L.) in spring from 1982 to 2010 at Teagasc Moorepark.

Material and Methods

Daily data for the spring period from 1982 to 2010 at Teagasc Moorepark (January to April, weeks 1 to 17, 300 observations) were converted into average weekly data. The meteorological data analysed included minimum, maximum and mean air temperatures (°C), soil temperatures at 50 and 100 mm (°C), sunshine hours (h), solar radiation (MJ/m^2), rainfall (mm), calculated evapotranspiration (ET) with Hargreaves's formula (mm) and calculated day length (h). Weekly grass growth was measured using the methodology described by Corral and Fenlon (1978). A regression analysis of weekly meteorological factors and weekly grass growth rates was performed in SPSS with the meteorological factors as the independent variables and grass growth as the dependent variable. The stepwise option was chosen to enter the significant variables at the 5% level and to remove at the 1% level. Data was also used to investigate the start date of grass growth; grass growth was considered to have actively commenced when it was 10 kg DM/ha/day.

Table 1. Regression analysis results of weekly meteorological variables and weekly grass growth.

Variable	B	t	F test	R^2	Error
ET	35.32	13.41			
Soil temp 100 mm	7.90	7.14	235.09	0.70	17.54
Max air temp	-4.74	-4.02			

B is the unstandardized coefficients of the variables
t and F are significant at the 0.001 level (***)

Results and Discussion

The meteorological factors having the greatest effect on spring grass growth were ET, soil temperature at 100 mm and maximum air temperature with an R^2 of 0.70 (Table 1). The three variables showed a positive relationship with grass growth (Figure 1). Temperature affects many physiological and growth functions of perennial ryegrass, including photosynthesis, respiration, spring growth, heading date and senescence. It took an average of 64 days from 1st January for grass growth rates to reach 10 kg DM/ha/day or greater over the 29 years; the maximum number of days required were 113 days in 1986, and the minimum was 36 days in 2008. Grass growth occurs provided soil temperatures are not lower than 5°C.

Conclusions

Evapotranspiration, soil temperature at 100 mm and maximum air temperature were the factors with the greatest influence on grass growth at Moorepark in the January to April period over the years 1982 to 2010.

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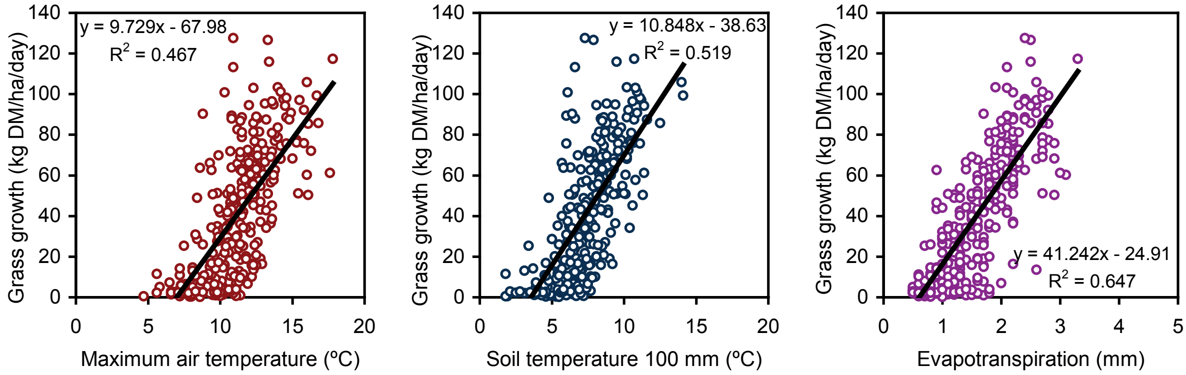

Figure 1. Relationship between grass growth and maximum air temperature, soil temperature at 100 mm and evapotranspiration in spring at Moorepark from 1982 to 2010.

Effect of perennial ryegrass *(Lolium perenne)* cultivar on the leaf, pseudostem, true stem and dead proportions of the sward over a grazing season

M. Beecher[1, 2], E. Lewis[1], T. Boland[2], M. McEvoy[1], M. O'Donovan[1] and D. Hennessy[1]
[1]Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork; [2]School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4

Introduction

Increasing the proportion of grazed grass in the dairy cow diet is a key component of Irish dairy farm profitability (Shalloo, 2004). Selecting the correct cultivar is of major importance due to its potential influence on both sward and animal productivity (Gowen *et al.,* 2003). For the majority of the year the grass plant is in the vegetative state, but for a period of the year it is in the reproductive state. The morphology of the plant changes during these periods. The leaf is comprised of the leaf blade (L) and pseudostem (PS). During the reproductive phase the true stem (S), which has a low feeding value, emerges from the PS. The aim of this study was to determine the change in L, PS, S and dead (D) proportion from May to October in four perennial ryegrass cultivars. This study was part of a wider study examining the effects of cultivar on sward and animal performance.

Materials and Methods

Immediately prior to grazing, herbage morphological composition was determined on four monoculture grazing swards. The grass cultivars were: Bealey (intermediate tetraploid), Astonenergy (intermediate tetraploid), Spelga (intermediate diploid) and Abermagic (intermediate diploid). Swards were grazed by dairy cows to a 4 cm post-grazing height. The area for each cultivar was subdivided into 4 replicates, each measuring 361 m^2. Grass samples were taken once in each replicate in each rotation, from May to October, with eight rotations completed during this period. Grass samples were cut to ground level using a scissors and the vertical structure of the sward was preserved. The samples were divided into two portions: >4 cm and <4 cm stubble height. The >4 cm section was manually separated into L, PS, S and D material. The dry matter (DM) content of each fraction was determined by drying at 40°C for 48 h. Data (L, PS, S and D proportion expressed on a DM basis) were analysed using PROC MIXED in SAS with terms for replicate, rotation number, cultivar and the interaction of cultivar and rotation number.

Results and Discussion

There was a cultivar × rotation interaction (P<0.001) for all four morphological fractions. In mid May Astonenergy had a higher (P<0.05) proportion of L than Abermagic. At the same time Astonenergy had a lower (P<0.05) S proportion compared to Abermagic and Spelga. At the start of June Astonenergy had a higher (P<0.01) proportion of L than Bealey and Spelga. At this time both Astonenergy and Abermagic had a lower (P<0.01) proportion of S than Bealey and Spelga. At the end of June Astonenergy had a higher (P<0.05) proportion of L and lower proportion of S than the three other cultivars. At the end of July, Astonenergy had a higher (P<0.05) proportion of L than Bealey. From mid August onwards for L proportion and from mid July onwards for S proportion there were no significant differences between the cultivars. High L and low S content is desirable as L is usually more digestible than S. Lewis et al. (2011) found that cows grazing Astonenergy spent more time with a low rumen pH (<pH5.2) in the April-June period which appear to be driven by the higher L proportions as reported here, reflecting reports of Astonenergy being highly digestible (DARD, 2010).

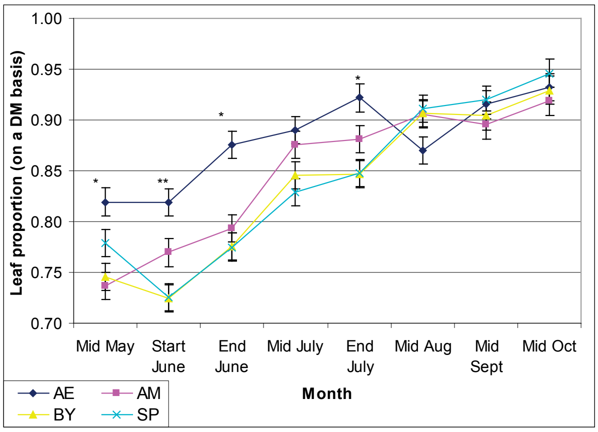

Fig 1. Leaf proportion (expressed on a DM basis) for four cultivars during eight grazing rotations

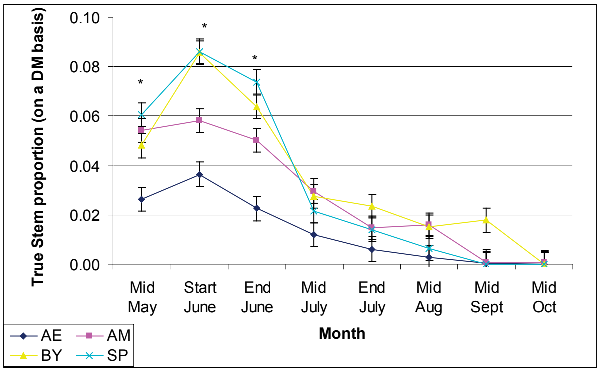

Fig 2. True stem proportion (expressed on a DM basis) for four cultivars during eight grazing rotations

Conclusions

The results show that changes in sward morphology occur during the reproductive phase and differences exist between cultivars. Therefore cultivar selection and management of the grazing sward particularly in early summer are important in maintaining sward and animal performance. Future work should examine if differences exist between cultivars and morphological fractions in terms of organic matter digestibility, which is a key determinant of nutritive value.

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Cultivar influences milk production of grazing dairy cows

M. McEvoy[1], M. O'Donovan[1], J.P. Murphy[1] and L. Delaby[2]

[1]*Animal and Grassland Res. And Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork;* [2]*INRA UMR Production du Lait, St. Gilles, France*

Introduction

Perennial ryegrass is considered one of the most important forage grass species used in temperate ruminant animal production. In such regions, milk production can be achieved in an economic and cost effective manner by maximizing the proportion of fresh grass in the diet of the animal. Grass based ruminant production systems tend to target calving or lambing to coincide with the onset of grass growth and thus, maximize animal production from grazed grass. Plant breeding has largely focused on increasing annual DM yield. While this is an important trait, it fails to define the ultimate value of a grass cultivar, which is its potential to improve animal performance (Reed, 1994). The objective of this study was to quantify the difference in milk performance of lactating dairy cows offered 4 different perennial ryegrass cultivars.

Material and Methods

Four cultivars of perennial ryegrass were sown as monocultures in a split plot design. The cultivars included 2 tetraploids: Bealey (heading date 24th May) and Astonenergy (31st May) and 2 diploids: Spelga (22nd May) and Abermagic 28th May). Cultivars were sown in 2009. In March 2011, 24 cows were blocked and randomly assigned to one of four groups. Each group was then assigned to one of the four cultivars in a 4×4 latin square design. Two latin squares were completed between March to end of July. The first latin square (spring period) began in mid-March and ran for 56 d, divided into 14 day periods. Animals were offered 16 kg DM herbage and 1 kg DM concentrate cow^{-1} d^{-1}. In May, a further 4 cows were blocked and assigned randomly to one of the four groups and the second 4×4 latin square was completed over 84 days, divided into 21 day periods (summer period). Concentrate was removed and animals were offered 17 kg herbage DM cow^{-1} d^{-1}. Area was adjusted daily to ensure correct allocation of herbage. The final 5 days of each period was used for measurement, with the preceding days used to adapt cows to the cultivars. Milk yield was recorded daily, milk composition was determined from a morning and evening sample for 3 consecutive days. Data were analysed using Proc Mixed in SAS. The model included latin square, period and cultivar. Cow was included as a random effect.

Results and Discussion

Pre-grazing sward height was similar across cultivars (9.0 cm). Table 1 presents the milk performance results of the study. There was no interaction between cultivar and season for any parameter, however there was a tendency towards an interaction for protein composition ($P=0.07$). Cultivar had a significant effect ($P<0.001$) on milk yield, Bealey and Astonenergy had higher milk yields (28.7 kg cow^{-1} d^{-1}), than Spelga and Abermagic (-1.4 kg cow^{-1} d^{-1}). Cultivar did effect milk fat ($P<0.05$) and protein ($P<0.001$) content. Milk fat was higher for Bealey and Abermagic (43.4 g/kg) than for Astonenergy and Spelga (41.7 g/kg). Daily milk solids yield was higher for Bealey and Astonenergy (2.17 kg cow^{-1} d^{-1}), than for Spelga and Abermagic. There was a significant effect of season on milk yield and composition ($P<0.001$). Milk yield, fat, lactose content and milk solids was higher in spring than summer, as a result of stage of lactation of the animal, and milk protein was higher in the summer than spring due to the quality of the herbage on offer.

Conclusions

Results from this study show that choice of ryegrass cultivar can influence the milk performance of spring calving dairy cows. The differences observed would go unnoticed if these cultivars were only evaluated in cutting plots. Therefore, these results support the need for testing grass cultivars under animal production trials. Such trials would be beneficial to farmers as it would present them with information on potential improvements in production which could be achieved when selecting cultivars for reseeding.

Acknowledgements

The authors wish to acknowledge Moorepark farm staff.

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Table 1. Differences in milk performance of grazing dairy cows offered perennial ryegrass monocultures in the spring and summer period

	Bealey	Astonenergy	Spelga	Abermagic	SE	P-value Cultivar	P-value Season
Milk yield (kg/d)	28.5^a	28.8^a	27.2^b	27.3^b	0.47	0.001	0.001
Milk fat (g/kg)	43.3^a	41.7^b	41.6^b	43.4^a	0.82	0.05	0.001
Milk protein (g/kg)	33.4^a	33.4^a	32.8^b	33.6^a	0.33	0.001	0.001
Milk lactose (g/kg)	46.7	46.6	46.9	46.7	0.21	NS	0.001
Milk solids (kg/d)	2.18^a	2.15^a	2.02^b	2.08^b	0.04	0.001	0.001

SE=standard error

A comparison of two pasture-based dairy production systems for a wetland drumlin soil in the Border Midlands West Region of Ireland.

D. Patton[1, 2], K.M. Pierce[2], B.Horan[1].
[1]*Animal and Grassland Research and Innovation Centre, Teagasc Moorepark, Fermoy, Co. Cork;* [2]*School of Agriculture, Food Science & Veterinary Medicine, University College Dublin, Belfield, D4.*

Introduction
The objective of Irish dairy production systems in the absence of milk quotas will be to increase milk solids (MS; fat plus protein) production by maximising productivity per unit of available feed (McCarthy et al., 2007). In future, land availability on existing dairy farms will limit milk production expansion and additional new dairy enterprises may emerge outside of the traditional milk production regions on more marginal soil types as entrepreneurial producers move to avail of larger land blocks and potentially lower land costs. Many studies have focused on the potential of increased stocking rates (traditionally measured as cows per hectare; SR) (Macdonald et al., 2008) and increased feed supplementation to increase productivity within pasture systems, however, few studies have focused on the implications of such systems specifically within soil types such as those found in the Border Midlands West (BMW) region. The objective of this experiment was to compare the biological performance of two pasture based systems of milk production differing in overall stocking rate and feed supplementation level on a wetland drumlin soil.

Materials and Methods
Physical performance data were obtained from 120 animals (60 per feed system,) on a 4 year (2008-2011) systems comparison study at Ballyhaise College, Co. Cavan. Animals were randomly allocated to one of two feed systems (FS) based on calving date, genetic potential (Economic Breeding Index; EBI) and parity. Once randomised, all animals remained on the same FS for the duration of the experiment. The two feed systems being evaluated were: a low cost enclosed system (HG) and a high pasture utilisation open system (HI). The HG system had a stocking rate of 3.1 cows per ha, a concentrate input of 542kg per cow. The HI system had a stocking rate of 4.6 cows per ha, a concentrate input of 864 kg per cow. Cows were turned out to pasture in early February with SR treatments managed separately. All cows were inseminated, using artificial insemination, over a 13-week period, starting in late April and ultrasonographic examination was used to determine pregnancy rates. Milk yield was recorded daily during the study with concentrations of fat, protein and lactose determined in one successive evening and morning sample of milk each week. Animal production data for the measurement period were analysed using Proc MIXED of SAS (SAS, 2006). Feed system, year and parity were included as fixed effects in the final model. Chi-square analyses were used to identify differences in pregnancy rates.

Results and Discussion
Feed system had a significant effect on all yield variables (Table 1). The HI system produced more milk per cow, similar fat composition, lower protein composition and higher milk solids (fat plus protein) production per hectare. The higher total lactation milk and milk solids yield per cow and per hectare achieved with the HI group is expected, given the large increase in energy supply with this system. Similarly, the higher protein composition of the HG treatment is consistent with increased grazed grass utilisation. Feed system had no significant affect on any of the reproductive performance parameters. The overall level of reproductive performance within this study was low with only 53% of animals confirmed pregnant in 42 days and 80% confirmed pregnant after a 13 week breeding period. Neither FS produced sufficient winter feed resulting in a feed deficit of 451 and 1,317 kg DM per cow for the HG and HI systems, respectively (equivalent to a winter forage deficit of 39% and 90%, respectively).

Table 1. Effect of feed system on milk production and reproductive performance

System of Production	HG	HI	se	P.value
Production per cow				
Milk (litres)	4,649	4,865	52.9	**
Milk solids (kg)	377	391	4.4	*
Milk composition				
Fat (g/kg)	45.6	45.8	0.40	ns
Protein (g/kg)	35.7	35.0	0.15	***
Production per ha				
Milk (litres)	14,084	22,228	214.4	***
Milk solids (kg)	1,144	1,786	17.6	***
Fertility performance				
Preg. to 1st serve (%)	38	43		ns
42day calving rate (%)	51	55		ns
Empty rate (%)	21	19		ns

*=P≤0.05, **= P≤0.01, ***= P≤0.001, ns = non-significant, se = standard error

Conclusions
While the overall success of the systems of milk production being investigated on this study must be considered in terms of a complete financial appraisal, the results demonstrate that the inclusion of supplements, with a concomitant increase in SR, can significantly increase the productivity of grazing dairy systems in the BMW region.

Acknowledgements
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Effect of re-growth interval on tissue turnover on a perennial ryegrass sward under a cutting regime

G. Tuñon[1,2], D. Hennessy[2], E. Kennedy[2], N. Lopez Villalobos[1], P. Kemp[1] and M. O'Donovan[2]
[1]*Massey University, Palmerston North, New Zealand.*
[2]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland.*

Introduction

The timing of defoliation can have an impact on sward production and quality. Traditionally the decision to graze a sward has been based on rotation length, sward height and/or herbage mass (Mayne *et al.*, 2000). The use of the three leaf stage as an indicator of when to graze results in optimum persistence, production, utilisation and quality of temperate swards (Fulkerson and Donaghy, 2001). Perennial ryegrass (PRG; *Lolium perenne* L.) plants comprise of three green leaves, and as new leaves are produced older leaves senesce. The aim of this study was to quantify the effects of three re-growth intervals (two, three and four weeks) on tissue turnover of a PRG sward under a cutting regime.

Materials and Methods

A three-year old PRG sward was divided into 12 plots (3 m × 5 m) set out in four blocks of three plots. There were three re-growth interval treatments - two, three or four weeks, and the experiment was under taken from 1 April to 16 September 2009. At the beginning of each re-growth period 20 PRG tillers were marked with a ring of coloured plastic coated wire at 10-cm intervals along two 1 m transects in each plot (Hennessy *et al.*, 2008). The length of each green leaf was measured weekly throughout the re-growth period. The youngest leaf present on the tiller on the day of each weekly measurement was marked using Tipp-ex™. The number of leaves produced during each week of re-growth was recorded. This information was used to determine leaf appearance rate (LAR; number of leaves/tiller/day). Leaves were identified by the order in which they appeared and their stage of development, i.e. L1 was the expanding leaf at marking, L2 was the youngest/first fully expanded leaf, L3 the second fully expanded leaf and L4 was the third fully expanded leaf at marking. Mean leaf extension rate (LER; mm/tiller/day) was calculated as the mean daily increase in length (mm) of leaves expanding during the measurement period, including the length of new leaves appearing during the period. All sward measurements were analysed using SAS. Analysis of variance was performed with a mixed model including the fixed effects of treatment and month, the interaction treatment by month and the random effect of plot.

Results and Discussion

Differences between LER for the 2-week treatment compared to the other two treatments were greater in the June to September period than in the April to May period (p <0.001), resulting in a significant interaction between month and treatment (Table 1). The number of leaves appearing per tiller during the re-growth period was always least for the 2-week treatment (p <0.001; Table 2). Tillers harvested every three weeks produced three leaves in each regrowth period from June to the end of the experiment. The tillers in the 4-week treatment had more than three leaves in June, July and August, and less than three in April. At anyone time a PRG plant will have only three green leaves, so additional leaves produced will senesce. During the second half of the experiment the number of new leaves per tiller was greater by 0.26 and 0.28 for Week 1 and Week 2, respectively (p <0.001), compared to the first half of the experiment.

Table 1. Leaf extension rate from Week 1 to Week 2 of re-growth.

Trt	Month						sem†	Trt mean	P
	Apr	May	Jun	Jul	Aug	Sept			
2 wk	8.1	6.8	7.7	9.4	8.5	7.6	0.82	8.0[a] ±0.49	
3 wk	7.3	9.4	9.5	13.0	10.1	13.5	1.10	10.5[b] ±0.55	*
4 wk	7.5	7.5	12.5	12.6	11.5	10.3	1.10	10.3[b] ±0.58	

P = probability *** p <0.001; †sem = standard error of the mean

Table 2. Number of leaves appearing during the re-growth period Week 1 to Week 2 of re-growth.

Trt	Month						sem†	Trt mean	P
	Apr	May	Jun	Jul	Aug	Sept			
2 wk	1.4	1.9	2.0	2.0	2.0	2.0	0.15	1.9[a] ±0.11	
3 wk	2.3	2.3	3.1	3.3	3.0	3.3	0.18	2.9[b] ±0.12	***
4 wk	2.5	3.0	3.5	3.5	3.5	3.0	0.19	3.2[b] ±0.12	

P = probability *** p <0.001; †sem = standard error of the mean

Conclusions

This study showed that too frequent defoliation results in tillers not achieving the three leave stage at any time between April and September. In addition there was a suppression of growth evidenced by lower LER. A long regrowth interval results in the production of more than three leaves in the June to August period, which will result in herbage senescence in a standing sward. The three week treatment produced the optimum number of leaves from June to September, with some under production in late spring. Criteria on when to defoliate PRG swards must be based on knowledge of the physiology of the plants and their interaction with the environment.

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Evaluation of the GrazeIn model for predicting individual cow grass dry matter intake and milk production

B.F. O'Neill[1, 2], E. Lewis[1], M. O'Donovan[1], L. Shalloo[1], N. Galvin[1], T.M. Boland[2], F.J. Mulligan[2] and R. Delagarde[3]

[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork;* [2] *College of Agriculture, Food Science & Veterinary Medicine, UCD, Belfield, Dublin 4;* [3]*INRA, UMR1080 INRA-Agrocampus Ouest, Production du Lait, F-35590 Saint-Gilles, France*

Introduction

Grass dry matter intake (GDMI) is the primary driver of production in pasture-based systems and is difficult for farmers to estimate accurately during the grazing season due to the dynamic nature of the factors involved (animal, sward, grazing management). The prediction of GDMI and milk yield would be a useful aid in grazing management and nutritional status decision-making at farm level. It was decided to investigate the prediction of GDMI and milk yield for Irish spring calving dairy cows using the French model GrazeIn (Delagarde *et al.*, 2011). GrazeIn was developed for European grazing systems and uses input variables that are easy for farmers to obtain. GDMI and milk yield are predicted from these input variables. The objective of this study was to investigate the accuracy with which GrazeIn predicted GDMI and milk yield for Irish grazing dairy cows.

Materials and Methods

The variables required to run GrazeIn were extracted from a Moorepark database (O'Neill *et al.*, 2011). They included animal, sward and grazing management variables. The GDMI and milk yield of each individual cow was modelled using GrazeIn. The comparison of predicted (P) (by the model) versus actual (A) (measured) GDMI and milk yield was conducted at the cow level (n=8,787 individual measurements). The database was subdivided for each input variable into three categories to investigate the accuracy of the model for the different categories. The GDMI and milk yield predicted by GrazeIn was regressed on the actual data. The prediction accuracy of GrazeIn was analysed using the mean bias (P-A), mean-squared prediction error (MSPE) and relative prediction error (RPE). A positive or negative mean bias indicated that the model was over- or under–predicting, respectively, compared to A. The RPE was calculated by dividing the square root of the MSPE by the mean A.

Results and Discussion

The RPE for GDMI and milk yield were 15.5% and 16.7% respectively for the total database. When the three categories of each of the input variables were analysed (including age, parity, potential peak milk yield, milk fat, milk protein, bodyweight) there were no differences between them in terms of the prediction accuracy of GrazeIn for GDMI (table 1). Overall the GrazeIn model predicted GDMI with an acceptable level of accuracy (Fuentes-Pila *et al.*, 1996). However for milk yield, the RPE for some categories was higher in comparison to the other categories of the same variable. For example cows in late lactation, characterised as having a high milk fat and protein content, had milk yield predicted by GrazeIn with lower accuracy than their earlier lactation counterparts (lower milk fat and protein content) (Table 1). The lower accuracy in later lactation may be due to a number of factors including the persistency of the theoretical milk curve used by GrazeIn, energy partitioning in late lactation, end of season sward factors such as grass palatability following the build-up of dung pads and the estimation of grass quality in autumn. These issues could lead to an over-estimation of both milk production and energy intake. Thus there may be an opportunity to improve the GDMI prediction by working to improve the milk yield prediction.

Table 1. Prediction accuracy of the GrazeIn model for GDMI and milk yield of Irish dairy cows

Category	Actual A kg d^{-1}	Predicted P kg d^{-1}	Bias P-A kg d^{-1}	MSPE * $(kg\ d^{-1})^2$	RPE ‡ %
Overall GDMI					
0-16 weeks	15.5	15.3	-0.2	5.85	15.6
17-25 weeks	16.4	15.9	-0.5	5.92	14.9
>25 weeks	16.0	15.3	-0.7	6.44	15.9
Overall milk yield					
0-16 weeks	27.0	26.2	-0.8	3.76	13.9
17-25 weeks	21.1	22.3	0.7	3.24	15.4
>25 weeks	15.9	18.2	2.3	3.64	22.9
Milk fat (g kg^{-1}) categories for overall milk yield					
≤37 g kg^{-1}	24.5	25.3	0.8	13.13	14.8
>37-45 g kg^{-1}	21.6	22.3	0.7	11.87	15.9
>45 g kg^{-1}	16.4	17.9	1.5	13.39	22.2
Milk protein (g kg^{-1}) categories for overall milk yield					
≤33 g kg^{-1}	24.7	25.4	0.7	14.15	15.2
>33-36 g kg^{-1}	22.7	23.2	0.5	11.57	15.0
>36 g kg^{-1}	16.6	18.2	1.6	12.40	21.3

*Mean square prediction error ‡Relative prediction error

Conclusions

The GrazeIn model predicted GDMI for the individual cow with an acceptable level of accuracy. GrazeIn predicted milk yield with a high level of error in late lactation indicating that further work is required to improve the milk yield prediction at this time. Modifying the GrazeIn prediction of milk yield in late lactation may also improve the GDMI prediction because of the factors potentially involved.

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Predicting grass dry matter intake of Irish spring calving dairy herds

B.F. O'Neill[1, 2], E. Lewis[1], M. O'Donovan[1], L. Shalloo[1], N. Galvin[1], T.M. Boland[2], F.J. Mulligan[2] and R. Delagarde[3]

[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork;* [2]*College of Agriculture, Food Science & Veterinary Medicine, UCD, Belfield, Dublin 4;* [3]*INRA, UMR1080 INRA-Agrocampus Ouest, Production du Lait, F-35590 Saint-Gilles, France*

Introduction

A large proportion of the feed budget for spring calving dairy cows in Ireland comes from grazed grass. Grazed grass is the cheapest feed available to Irish farmers and maximising grass dry matter intake (GDMI) leads to an increase in profitability (Shalloo *et al*., 2004). In order to maximise performance and profitability the development of accurate, easy-to-use GDMI prediction equations would facilitate increased confidence in dairy cow grazing management at farm level and contribute to optimizing the yield of milk from grazed grass. The objective of this study was to develop equations that would allow farmers, advisors and nutritionists to predict the GDMI of grazing dairy cows.

Materials and Methods

A dataset of 258 herds was used in the development of the GDMI prediction equations. Grass dry matter intake was estimated using the n-alkane technique (Mayes et al., 1986) as modified by Dillon and Stakelum (1989). The GDMI prediction equations were developed on a herd-basis. The dataset was divided into four periods: early spring (5 Mar-10 Apr), late spring (11 Apr-30 Apr), summer (1 May-31 Jul) and autumn (1 Aug-31 Oct). Equations were generated for each of these periods. The significant predictors of GDMI in these periods were elucidated by multiple regression analysis using SAS (2005). Forward step-wise regression analysis was used to develop the multiple regression equations. The first GDMI equation generated contained the variables bodyweight, organic matter digestibility, pre-grazing herbage mass and concentrate consumed. Each equation after the first added a single independent variable. If the significance of the calculated F statistic was $P<0.05$ the variable was retained in the multiple regression equation. Variables were removed from the multiple regression equation if, after the addition of a new variable, the significance of the calculated F statistic became $P>0.05$. The multiple regression equation with the lowest residual standard deviation (rsd) and highest coefficient of correlation (R^2) in each period was chosen.

Results and Discussion

The equations explained between 0.69 and 0.94 of the variation in GDMI and had an rsd of between 0.74 and 1.08 kg/d (table 1). Increased bodyweight was associated with an increase in GDMI in summer and autumn, as was age in spring. Pre-grazing herbage mass had a quadratic effect on GDMI in autumn. Increased post-grazing sward height was associated with an increase in GDMI in spring. Concentrate consumed was associated with a reduction in GDMI by between 0.55 and 0.72 kg/kg of concentrate DM.

Conclusions

The GDMI prediction equations developed in this study can be used by farmers, advisors and nutritionists for dairy herds during the grazing season. Future work could include validating the equations using an independent database.

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	Early spring	Late spring	Summer	Autumn
Herds	39	22	111	86
R^2 (Coefficient of correlation)	0.94	0.80	0.69	0.78
Residual standard deviation (kg)	0.74	0.86	1.08	1.08
Intercept	7.08	6.13	21.74	-13.95
Linear and quadratic coefficients for different animal, grass and supplementation factors				
Age (months)	0.12			
Weight (100 kg)			3.35	3.75
Body condition score at calving			-1.62	
Body condition score during measurement period			1.48	
Week of lactation		0.73		
Days in milk			-0.012	-0.004
Pre grazing herbage mass above 4 cm (t DM/ha)				6.99
(Pre grazing herbage mass above 4 cm)^2 (t DM/ha)^2				-1.75×10^{-3}
Daily herbage allowance above 4 cm (kg DM/cow)				0.26
Fill units (0.10 FU/kg DM)			-1.71	
Neutral Detergent Fibre content (10 g per kg DM)		-0.084		
Dry matter content (10 g/per kg)	-0.17			
Post grazing sward height (cm)	1.52	1.20		
Concentrate consumed (kg DM)	-0.65	-0.55	-0.72	-0.61

Table 1. Equations to predict grass dry matter intake of spring calving dairy herds during different periods of the year

Long term dry matter production of *Lolium perenne* as influenced by management and cultivar.

P. Cashman[1, 2], T.J. Gilliland[3], L. Delaby[4], M. McEvoy[1], M. O'Donovan[1].

[1]*Animal &Grassland Research and Innovation Centre, Teagasc Moorepark, Fermoy, Co. Cork.* [2]*Queens University Belfast, Belfast, UK.* [3]*Agri-food Biosciences Institute, Plant testing station, Crossnacreevy, Belfast, BT5 7QJ, UK.* [4]*INRA, AgroCampus Ouest, UMR 1080, Production du lait, F-35590 Saint-Gilles, France*

Introduction

Long term dry matter (DM) yield is important to ensure sown pastures remain productive long after the initial years of establishment. The establishment of a cultivar with proven DM yield longevity delays the need for the costly reseeding process (Wilkins and Humphreys, 2003) but the effect of management on the cultivar should be taken into consideration (Reed, 1994). The objective of this study was to evaluate the effect of simulated grazing and conservation managements under cutting on the DM yield performance of perennial ryegrass cultivars.

Material and Methods

One hundred and forty four plots (5 × 1.5 m) were sown with twelve cultivars of perennial ryegrass in autumn 2006 in randomised block design. Four diploid cultivars were used with the following heading dates: Alto (15 May), Arrow (22 May), Portrush (14 June) and Tyrella (8 June). Eight tetraploids were used: Bealey (22 May), Dunloy (8 June), Dunluce (31 May), Glencar (6 June), Greengold (31 May), Lismore (28 May), Malone (22 May) and Navan (9 June). Four cutting protocols were imposed on the plots representing simulated grazing (SG); 1 cut silage (1C); 2 cut silage (2C) and 3 cut silage (3C). Each cultivar was replicated three times. The SG consisted of 10 defoliations, beginning on the 20th March and then every three to four weeks until final harvest in late October. The 1C consisted of 7 defoliations beginning on the 1st February, with the 2nd taken 12 weeks later and every 3 to 4 weeks until final harvest in late October. The 2C consisted of 6 defoliations beginning on the 1st April, with 2nd and 3rd cuts taken after 7 and 6 week intervals and the final 3 cuts taken after at intervals of 4, 5, and 6 weeks respectively. The 3C consisted of 5 defoliations with the first taken on 25th May, the 2nd and 3rd taken after 6 week intervals and the final two cuts on 1st Sept and 1st Oct. Plots were harvested with a motor Etesia to 4 cm across 5 full growing seasons, 2007 to 2011, inclusive. All mown herbage from each plot was collected and weighed; 0.1 kg sample was dried for 12h at 80^{o}C to determine dry matter percentage of the sample. Data was analysed using Proc Mixed in SAS (SAS, 2004) with year, block, management, cultivar and their interactions tested for in the model.

Results and Discussions

Year, management and variety (P<0.001) had a significant effect on DM production. There was a significant (P<0.001) interaction between Year × Variety, Year × Management and Management × Variety on DM production. Figure 1 shows the DM production of 12 cultivars for two managements, SG and 3C – the two most extreme managements. Estimated DM yield for SG, 1C, 2C and 3C managements was 60.64 (SE=.28), 67.34 (SE=.24), 73.13 (SE =.44) and 71.43 (SE=.42) t/5 years, respectively. It was evident that each cultivar's performance was unique depending on management protocol applied. Bealey and Tyrella ranked highest in SG dropping to 6th and 12th, respectively under 3C management. Malone and Alto ranked 8th and 11th under SG management rising to 1st and 2nd in 3C. This change in rank of cultivars indicates that cultivar DM yield is strongly influenced by management and cultivar choice must closely relate to the conditions under which it will be grown and utilised.

Conclusions

Management did influence the long term DM production of each cultivar uniquely, causing a large number of cultivars to re-rank between simulated grazing and conservation managements. Clearly each management has an optimum cultivar to maximise DM production, with some cultivars suited to grazing systems while others are suited to intensive silage systems. Choice of cultivar should be based on intended management to maximise long term dry matter production.

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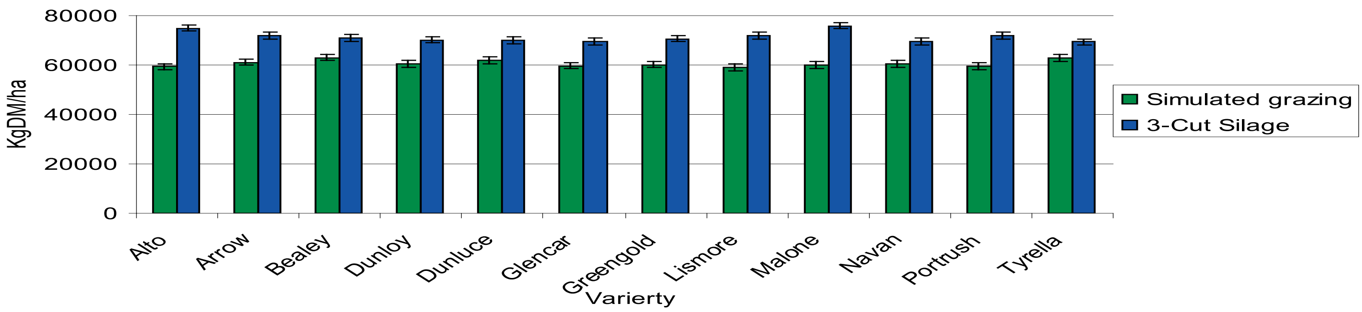

Fig 1: Cumulative DM yield for 2 Managements across 5 years

Effect of post-grazing sward height during the main grazing season on dairy cow performance

E. Ganche[1,2], M. O'Donovan[1], L. Delaby[3], T.M. Boland[2] and E. Kennedy[1]

[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy Co Cork;* [2]*School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4 and* [3]*INRA, UMR Production du Lait, 35590 St Gilles, France*

Introduction

Well managed grazed grass is the cheapest feed available for the dairy cow (Finneran *et al.*, 2010), therefore maximising its proportion in the cow's diet is a major objective of the Irish dairy industry to sustain Ireland's competitiveness within the EU. The anticipated increase in national milk production following 2015 will be associated with an increase in the number and size of dairy farms and improvement in production efficiency, largely based around the utilisation of more grass (Dillon, 2011). Utilising more grass is possible if swards are grazed to low post-grazing sward heights (PGSH). Previous research on PGSH defined severe PGSH as grazing <5cm (O'Donovan, 2000) while more recent work has considered 4 cm as low PGSH (Lee *et al.*, 2008). The objective of this experiment was to establish the effects of PGSH during the main grazing season on dairy cow production performance.

Materials and Methods

Ninety Holstein Friesian dairy cows were balanced on calving date (13 February; s.d. 17.7 d), lactation number (2.1; s.d. 1.05), production variables from the three-week prior to the commencement of the experiment: milk yield (26.2, s.d. 5.37 kg/d), milk fat (40.0, s.d. 0.46 g/kg), milk protein (33.1, s.d. 0.19 g/kg) and milk lactose (47.7, s.d. 0.11 g/kg) concentration, milk solids yield (1.92, s.d. 0.438 kg/d), bodyweight (BW; 460, s.d. 64.3 kg) and body condition score (BCS; 2.87, s.d. 0.171). Cows were then randomly assigned across two PGSH treatments: 3.5 cm (severe, S) or 4.5 cm (moderate, M) from April 25 to November 20, 2011. The difference in PGSH was achieved by maintaining a 2.2 kg DM define /cow difference in daily herbage allowance (DHA). Fresh herbage was allocated daily and pre- and post-grazing sward heights were measured daily by using a folding pasture plate meter.details/ Herbage mass (HM; >3.5 cm) was calculated twice weekly by cutting 2 strips per grazing treatment. Milk yield was recorded daily; milk composition, BW and BCS were measured weekly. Grass dry matter intake (GDMI) was estimated using the *n*-alkane technique (Dillon and Stakelum, 1989) and measured in May and August. Data were analysed using covariate analysis and the PROC MIXED statement of SAS with terms for parity, treatment and the interaction of parity and treatment. Pre-experimental values for what? were used as covariate in the model.

Results and Discussion

Mean DHA was 13.3 and 15.5 kg/cow/day (>3.5cm) and mean PGSH achieved was 3.7 and 4.7 cm for the S and M treatments, respectively (P<0.001). The M cows had greater pre-grazing height (+0.61 cm; P<0.05), and daily area/cow (+11 m^2; P<0.001). Grazing to 3.7 cm improved grass utilisation by +0.13 compared to grazing to 4.7 cm (0.81; P<0.001). The M cows had a greater (P<0.001) milk yield (+1.6 kg/d unnecessary, can be calculated from the table!), milk fat (+54 g/d), milk protein (+68 g/d), milk lactose (+79 g/d) and milk solids (+0.12 kg/d) yields than the S cows (Table 1). Milk protein concentration was also improved (+0.6 g/kg; P<0.01) on the M treatment.. The first GDMI measurement period (May) showed that grazing to a PGSH of 4.7 cm increased GDMI by 1.5 kg DM/cow/d (17.1 kg DM/cow/d; P<0.01). The relatively low level of DHA offered to the S cows mainly contributed to the decline in GDMI which, therefore, resulted in milk and milk solids production losses. No difference in terms of end BCS was observed between treatments, the M animals however were heavier (+12 kg; P<0.01) than their counterparts (499 kg). Grazing pastures to 4.7 cm resulted in increasing ? unclear (P<0.001) cumulative milk production by 311 kg/cow and cumulative milk solids production by 22 kg/cow when compared to grazing to 3.7 cm (3236 kg milk/cow and 255 kg milk solids/cow, respectively).

Table 1. Effect of post-grazing sward height (PGSH) on dairy cow performance from April 25 to November 20

	PGSH[1]		Sig.	
	S	**M**	**SED**	**P-value**
Milk yield, kg/d	17.1	18.8	0.37	0.001
Milk fat, g/kg	43.6	42.6	0.77	0.146
Milk protein, g/kg	35.4	36.0	0.27	0.010
Milk lactose, g/kg	46.2	46.4	0.16	0.424
Milk solids yield, kg/d	1.35	1.47	0.027	0.001
End BW, kg	499	511	5.1	0.008
End BCS	2.70	2.72	0.036	0.573

[1]PGSH: S (3.7 cm), M (4.7cm)

Conclusions

Evidence from the current study indicates that grazing pastures to PGSH which range from 3.5 to 3.9 cm during the main grazing season will increase grass utilisation but this will occur at the expense of animal performance. Grazing to low PGSH during the main grazing season can be an objective to maximise milk production per hectare in very high stocked dairy farms but this practice will be detrimental to milk production per cow.

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Effect of cultivar on sward structural characteristics in a rotational grazing system during the spring and summer period

M. McEvoy[1], M. O'Donovan[1] and L. Delaby[2]
[1]Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork; [2]INRA UMR Production du Lait, St. Gilles, France

Introduction

For several years the focus on perennial ryegrass breeding has been to increase annual DM yield. It is widely accepted that both management and other factors can influence animal performance from grazed swards. These factors include ploidy, heading date, leaf to stem ratio and stage of growth, among others, which have been shown to influence intake and the milk yield of grazing ruminants. The objective of this study was to investigate the phenotypic variation among four perennial ryegrass cultivars for sward structural characteristics considered to be important for intake and production of lactating dairy cows. The milk production data is reported by McEvoy et al. (2012).

Material and Methods

Four cultivars of perennial ryegrass were sown in a split plot design with 4 reps. The cultivars included 2 tetraploids: Bealey (heading date 24th May) and Astonenergy (31st May) and 2 diploids: Spelga (22nd May) and Abermagic (28th May). Cultivars were sown in 2009. From mid March to May 2011 (P1), paddocks were grazed with lactating dairy cows for an eight week period. Cows were offered 16 kg DM cow^{-1} d^{-1}. From May to August (P2), paddocks were grazed for a 12 week period. Cows were offered 17 kg DM cow^{-1} d^{-1}. A similar rotation length was maintained for each cultivar. During weeks 2, 4, 6 and 8 in P1, and weeks 3, 6, 9 and 12 in P2, sward measurements were completed. Within each measurement period the following was completed: pre and post grazed sward height; herbage mass; extended tiller height and sheath heights was measured on 100 tillers in the pre and posts grazed sward; herbage was sampled to ground level for each cultivar and a sub-sample of 50g fresh weight was separated into leaf stem and dead content, before being dried at 80°C overnight. Height was measured daily, with all other measurements occurring twice during each measurement week. Data were analysed using Proc Mixed in SAS. The model included period, season, cultivar and the interaction between season and cultivar.

Results and Discussion

There was no difference in pre or post grazing sward heights between cultivars, which were 9 and 4.3 cm, respectively. Sward results are presented in Table 1. Sward density was lower for Bealey and Astonenergy, than for Spelga and Abermagic. There was no difference in the pre-grazing extended tiller height between cultivars, however the higher pseudostem height of Spelga and Abermagic resulted in these cultivars having proportionately less leaf available in the grazing horizon, compared to Astonenergy. Although not statistically significant, the leaf proportion of Astonenergy was 7% higher than the other three cultivars. Higher leaf proportions have been shown to result in higher intakes from these swards. Milk yield and milk solids production was higher on the Bealey and Astonenergy swards compared to the diploids (McEvoy et al., 2012).

Conclusions

The cultivars used in this study showed significant differences in sward characteristics which have previously been shown to affect intake including sward density, tiller height, pseudostem height and sward composition. In conclusion, differences do occur between cultivars when maintained under similar rotation lengths and managements and this has the potential to influence animal performance.

Acknowledgements

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References

McEvoy, M. O'Donovan, M., Murphy, J.P., and Delaby, L. 2012 *Proc. Ag. Res. Forum p xx*

Table 1. Differences sward structural characteristics between four perennial ryegrass cultivars

	Bealey	Astonenergy	Spelga	Abermagic	SE	P-value Cultivar	Season
Herbage mass (kg DM ha^{-1})	1210^{a}	1183^{a}	1304^{b}	1397c	32.6	0.001	0.001
Area grazed per day (m^2)	166^{a}	148^{b}	139^{b}	121^{c}	6.1	0.001	0.001
Sward Density (kg DM/cm ha)	257^{a}	260^{a}	328^{b}	326^{b}	8.7	0.001	0.001
Tiller height – Pre (cm)	23.1	23.4	21.1	22.3	1.03	NS	0.01
Sheath height – Pre (cm)	8.1^{a}	6.6^{b}	8.0^{a}	8.6^{a}	0.37	0.01	0.001
Free leaf lamina (cm)	15.0^{ab}	16.8^{b}	13.2^{a}	13.7^{a}	0.95	0.05	NS
Tiller height – Post (cm)	7.3^{ab}	7.0^{a}	7.7^{b}	7.0^{b}	0.18	0.05	0.01
Sheath height – Post (cm)	5.9^{a}	5.3^{b}	5.8^{a}	5.6^{ab}	0.15	0.05	0.001
Leaf proportion	0.73	0.80	0.74	0.73	0.031	NS	0.001
Stem proportion	0.20^{ac}	0.13^{b}	0.14^{ab}	0.23^{c}	0.030	0.05	0.001
Dead proportion	0.07^{a}	0.07^{a}	0.12^{b}	0.04^{c}	0.012	0.001	NS

SE=standard error

Effect of post-grazing sward height and autumn closing date on over-winter herbage production

M. Crosse[1,2], E. Ganche1,[2], T. Boland[2], M. O' Donovan[1] and E. Kennedy[1]

[1]Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy Co. Cork; [2]School of Agriculture and Food Science, University College Dublin, Belfield, D4

Introduction

Grass growth is highly seasonal with low growth rates over the winter months (Brereton, 1995). Management practices such as closing date and herbage mass (HM) at closing can have an impact on herbage accumulation from November to February (O'Donovan et al., 2002). The supply of a sufficient quantity of herbage in early spring is essential for spring calving dairy production systems to maximise productivity (Kennedy et al., 2005) and profitability (Shalloo et al., 2004). Carton (1988) has shown that closing date and grazing severity affect herbage availability in spring, however, grazing management practices have changed considerably since this study was carried out. The objective of this study was to investigate the effect of closing date and post-grazing sward height on over-winter grass growth and dry matter (DM) production.

Materials and Methods

This experiment was a randomised block design with a 2 x 3 factorial arrangement of treatments. Two post grazing sward heights (PGSH) and three closing dates (CD) were investigated. Swards were grazed to either 3.5cm (PGSH3.5) or 4.5cm (PGSH4.5) throughout the year. Three grazing blocks (four paddocks) were allocated three different closing dates and all paddocks were grazed to their designated PGSH by lactating dairy cows. Within a block, all 4 paddocks were grazed simultaneously, to achieve mean closing dates of 15 October (CD1), 30 October (CD2) or the 15 November (CD3). The difference in PGSH was achieved by ensuring a 3 kg DM/cow/day difference in daily herbage allowance (DHA). Sward measurements were taken at closing date, 15 December, 15 January and 15 February. Pre and post-grazing herbage mass (HM) were taken using a motor Etesia. HM<3.5 cm was estimated by removing all herbage to ground level within a 0.2 x 0.5 quadrant using a scissors after pre HM cuts. Pre and post-grazing heights were taken pre and post grazing using a rising plate meter. Leaf, stem and dead proportions > and < 3.5cm were taken at each measurement period. All statistical analysis was carried out using PROC GLM in SAS (SAS, 2006), with terms for post-grazing sward height, closing date and their interaction included in the model.

Results and Discussion

Throughout the study (Nov to Feb) there were 68 days where soil temperature at 10cm was below 5^{o}C, which is the threshold for grass growth. This greatly reduced grass growth during the winter months. Pre-grazing DM yield at closing was not significantly different between treatments, however the post-grazing yield tended (P=0.1) to be higher for PGSH4.5. There was no interaction between CD and PGSH for DM yield in February. Both closing date (P<0.001) and PGSH (P<0.01) had a significant effect on DM yield in February (Table 1). Delaying CD by 15 days reduced DM yield by 27% while a month delay in closing date from 15 October reduced DM yield by 50%. Each day CD was delayed after 15 October, DM yield was 12 kg DM/ha lower at opening in February. Grazing swards to 3.5cm compared to 4.5cm reduced the amount of available grass in February by 137 kg DM/ha. There was no effect of CD or PGSH on growth rate from closing to February (0.72 kg DM/day).

Leaf yields (>3.5) in December for all closing dates were 803, 632 and 496 kg DM/ha, for CD1, CD2 and CD3 respectively, however they were 276, 201 and 170 lower at opening in February. Both CD and PGSH had a significant effect on leaf yield (>3.5cm) at opening (15 February) with CD1 (527kg DM/ha) yielding 95kg and 200kg DM/ha more than CD2 and CD3, respectively. Imposing a PGSH of 4.5cm at closing increased (P<0.01) leaf yield >3.5cm (132.7 kg DM/ha) when compared to PGSH3.5. As CD was delayed the proportion of dead material present at opening was reduced (P<0.05; Table 1).

Conclusion

Each day CD was delayed after 15 October, DM yield was 12 kg DM/ha lower in February. This indicates that if there is a high requirement for grass in early spring an early closing date should be imposed. However, an early closing date can result in a higher proportion of dead material in the sward in early spring, suggesting that a balance between DM yield and sward quality needs to be identified.

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Table 1: Effect of closing date and treatment on winter herbage production

	PGSH3.5cm			PGSH4.5cm			Significance			
Closing Date	CD1	CD2	CD3	CD1	CD2	CD3	Sed	CD	PGSH	Inter
Feb DM yld (kg/ha)	668	427	321	787	635	406	35.11	0.0001	0.002	0.370
GR to Feb (kg/day)	1.3	0.0	1.0	2.0	0.0	0.0	0.921	0.364	0.927	0.747
Feb Leaf yld >3.5cm (kg/ha)	437	319	328	616	542	324	31.04	0.002	0.004	0.110
Feb Dead yld >3.5cm (kg/ha)	81	30	24	77	75	24	14.24	0.030	0.380	0.320

CD = closing date, CD1 = 15 October, CD2 = 1 November, CD3 = 15 November, yld = yield, GR =growth rate, PGSH = post grazing sward height, Inter = Interaction, Sed = Standard Error of the Difference

Sward composition dynamics in perennial ryegrass binary mixtures

V. Griffith[1,2], T. J. Gilliland[2,3], M. O'Donovan[1] and M. McEvoy[1].
[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Co. Cork.* [2]*Queens University Belfast, Belfast, UK.* [3]*Agri-food Biosciences Institute, Plant Testing Station, Crossnacreevy, BT5 7QJ, UK.*

Introduction

Perennial ryegrass (*Lolium perenne* L.) cultivars are evaluated as monocultures, however, cultivar mixtures are sown at farm level. This is perceived as giving greater adaptation to diverse farming enterprises. Previous work (Gilliland, 1995) has shown that sward composition changes over time. The factors affecting composition changes are not clearly understood, as individual cultivars in swards cannot be identified botanically. However starch gel electrophoresis can be used to identify the genotype frequency of a mixture and hence estimate the proportions of cultivars within the sward. The swards are examined *in situ* thereby making the results more applicable to farm practice. The aim of the study was to analyse the cultivar proportions in binary mixtures of perennial ryegrass cultivars during the two years after sowing.

Materials and Methods

Plots (1.5m x 5m) were sown in August 2009 in a three replicate, spilt plot design. Three perennial ryegrass cultivars were sown, two diploids AberMagic (AM) (heading date (HD) May 28) and Twystar (TY) (HD June 15) and one tetraploid Greengold (GG) (HD June 2). The sown proportions were AM/TY at 85:15, 70:30, 50:50, 30:70, 15:85; AM/GG and TY/GG at 85:15, 70:30, 50:50. A conservation management was imposed; harvests ran from March to October in 2010 and 2011. The plots were harvested a total of six times each harvest year (two silage harvests) and sampled for cultivar proportion in October of each year. The methodology of the starch gel electrophoresis process was described by Kennedy *et al.* (1985). The genotype frequency of each mixture was compared with those of its constituent cultivars in monoculture to determine the composition. Equations as described by Gilliland and Watson (1987) were used to determine proportions. PROC Mixed in SAS (2003) was used to analysis the proportions, period, cultivar proportion and their interactions were included in the model.

Results and Discussion

There was an interaction between period and treatment (P< 0.001), the interaction was more pronounced in the diploid/tetraploid binary mixtures. The AM/TY mixtures produced stable sward compositions (Table 1), at the end of year 2 only one of the five mixtures had changed from its sown proportions. The results suggest that neither diploid cultivar had a competitive advantage despite an 18 day difference in heading date. Gilliland (1995) found heading date to affect the competitive ability of cultivars in mixture. The failure of heading date to have an effect on the competitive ability of cultivars may be due to earlier spring harvests reducing inter cultivar competition. The GG proportion increased in mixtures with both diploid cultivars. The large increases GG achieved, when included at 15% and 30% of the mixture, were not replicated when GG was included at 50% of the mixture. This suggests that a threshold diploid/tetraploid balance may exist. As the sown proportion of GG increases, there maybe more intra-cultivar plant competition which negates further increases in the proportion of GG. The relatively minor changes from Year 1 to Year 2 suggest that competition between cultivars may be largely completed by the end of Year 1.

Conclusions

Greater stability was observed in the diploid mixtures. Greengold was the most aggressive cultivar when sown with either diploid, leading to the GG contribution increasing as the sward matured.

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Table 1. Sward composition changes in perennial ryegrass binary mixtures during the two years after sowing

	August 2009	October 2010	October 2011
AberMagic/Twystar	85:15	82:18	85:15
	70:30	80:20	72:28
	50:50	61:39	64:36
	30:70[a]	21:79[a]	58:42[b]
	15:85	19:81	26:74
AberMagic/Greengold	85:15[a]	47:53[b]	60:40[b]
	70:30[a]	49:51[b]	54:46[ab]
	50:50	55:45	40:60
Twystar/Greengold	85:15[a]	51:49[b]	50:50[b]
	70:30[a]	46:54[b]	31:69[b]
	50:50	42:58	46:54
		P value	SED
	Period	0.01	1.72
	Treatment	0.001	4.22
	Treatment*Period	0.001	

SED= Standard error of the difference; [abc] values not sharing a common subscript within row differ significantly (P<0.05).

Effects of supplementary concentrates when grazing in autumn on performance of dairy crossbred steers finished at pasture or indoors

A. McNamee, E.G. O'Riordan and M. McGee
Animal and Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co. Meath, Ireland

Introduction

Finishing spring-born steers at two years of age involves an expensive final winter feeding period. As grazed grass is considerably cheaper than grass silage or concentrates, early finishing of cattle off pasture in autumn, before housing becomes necessary, is less costly. However, Aberdeen Angus × Holstein-Friesian (AA×) steers finished off pasture in autumn had light carcasses, of relatively poor conformation that were inadequately, or just about, finished (Keane and Moloney, 2009; 2010). This study aimed to (i) quantify the response to concentrate supplementation on grass intake and steer performance at pasture in autumn and (ii) compare steers finished off pasture in autumn or finished indoors during the second winter.

Materials and Methods

Sixty-six spring-born AA× calves were reared together until July of their second year (approximately 15 months of age) when they were blocked on live weight (370 kg; s.d. 38.2) and assigned to one of three treatments: (i) grazed grass only - (GG0), (ii) GG plus 1.5 kg concentrate (rolled barley) - (GG1.5), and (iii) GG + 3.0 kg concentrate - (GG3.0). They were rotationally grazed on predominantly perennial ryegrass swards. After 112 days, half of the animals in each treatment were slaughtered and the remainder was housed indoors in a slatted floor shed and individually offered, barley-based concentrates *ad libitum* plus ~1 kg/day silage DM until slaughter, 89 days later. To ensure that response to concentrates at pasture was not confounded with differences in herbage allowance or quality, the three grazing groups were allocated herbage of similar pre-grazing height and mass in adjacent sub-paddocks, but these sub-paddocks differed in area, such that, post-grazing herbage height and mass was similar for each treatment. There were three grazing rotations in total and animals typically spent 2 to 3 days in each sub-paddock. Animals were weighed every 3-weeks and post-slaughter, carcass weight, carcass conformation and fat score were recorded. Pre- and post-grazing sward heights (rising plate meter), herbage mass (lawnmower cuts), dry matter (DM) and DM digestibility (DMD) was measured. Data were analysed using the GLM procedure of SAS. The model contained fixed effects for pasture supplementation, finishing strategy and their interaction. Initial weight was included as a covariate.

Results and Discussion

Mean pre-grazing sward height was 10.8 cm and herbage mass was 2,073 kg DM/ha. Mean post-grazing sward heights were 4.71, 4.64 and 4.71 cm and post-grazing herbage yields were 451, 449 and 482 kg DM/ha for GG0, GG1.5, and GG3.0, respectively. Corresponding estimates for daily herbage DMI (herbage disappearance method) were 6.4, 5.8 and 4.3 kg, and respective daily total DMI were 6.4, 7.0 and 6.9 kg. Animal performance did not differ (P>0.05) between the three supplementation groups (Table 1), except for kill-out proportion, which was lower (P<0.05) for G0 than GG1.5 and GG3.0. Animals subsequently finished indoors had higher (P<0.001) carcass weight, carcass fat and conformation score than those finished at pasture. The response to concentrates at pasture for GG1.5 and GG3.0 was 62 g and 43 g live weight per kg DM, respectively. These values are much lower than the 101 g reported by Keane and Drennan (2008) where AA× steers were supplemented at pasture with 3.65 kg concentrates daily for 105 days. This partially reflects the higher DMD (760 vs. 695 g/kg) of herbage offered in this study and the substitution rates obtained. Supplementation for GG1.5 and GG3.0 reduced herbage intake by 0.47 and 0.81 kg DM per kg DM concentrate offered. Indeed, the substitution effect going from GG1.5 to GG3.0 was 1.16.

Conclusions

Response to concentrate supplementation at pasture was poor, partly due to high grass substitution rates. An indoor finishing period after grazing was necessary to produce carcasses of adequate weight, fat cover and quality.

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Table 1: Performance of steers offered supplementary concentrates at pasture and finished at pasture or indoors

	Pasture supplementation[1]					Finishing strategy[1]			
	GG0	GG1.5	GG3.0	s.e.m.	Sig.	Pasture	Indoors	s.e.m.	Sig.
Pasture ADG (kg)	0.80	0.88	0.91	0.037		0.89	-	-	
Indoors ADG (kg)	1.29	1.13	1.18	0.063		-	1.20	-	
Slaughter weight (kg)	517	518	524	4.7		469	570	3.9	***
Carcass weight (kg)	252	257	261	2.8	P=0.09	233	281	2.3	***
Kill-out proportion (g/kg)	487[a]	497[b]	499[b]	3.2	*	496	492	2.6	
Carcass fat (1-15)	6.3	6.8	7.0	0.28		5.5	7.9	0.23	***
Carcass conformation (1-15)	5.4	5.6	5.4	0.20		5.0	5.9	0.17	***

[1] No pasture supplementation × finishing strategy interactions

Effect of a novel cold process seaweed extract on the germination of vegetable seeds and flowering of cyclamen.

T. Lola-Luz[1,2], F. Hennequart.[2], and M. T. Gaffney, [1]
[1]*Horticulture Development Department, Teagasc Kinsealy, Dublin.* [2]*Oilean Glas Teo (OGT), Kilcar, Co. Donegal*

Introduction

Seaweeds have been widely used in horticulture for many years and their beneficial effects are still open to some debate. Reported benefits of seaweed application include improved nutrient availability, seed germination, flowering, increased crop yields and better resistance to stress. Most experiments have been carried out with commercial blends of seaweed extracts enriched with plant nutrients for foliar application to growing crops. The aim of this study was to investigate the effect of the addition of two different concentrations of a pure novel cold process seaweed extract in commercial composts, on both vegetable seed germination and the flowering of ornamental plants. This unique cold extraction process developed by OGT, is vital for the retention of both the micro and macronutrients but also various antioxidants in which *Ascophyllum nodosum* is naturally rich.

Materials and Methods

The experiments were carried out from May-August 2011 (Teagasc, Kinsealy). Seaweed extract was added to the composts at a concentration of 0.5 % or 2 %. The composts used were Jack's Magic (JM), Sure start (SS), and John Innes (JI) (Westland, UK). The experiment with the vegetable seeds (beetroot (Cardeal F1), tomato (Celine F1) and onion (Hybing F1)) was carried out in cell trays (23x23x35mm) and for cyclamen in pots (12x10cm). In each of the composts 400ml of the seaweed extract was added by spraying (Algae Green 200, OGT), control received 400ml of water. For each vegetable, 36 seeds were sown individually in their respective treatments. The experiment was a complete randomised block with 3 replications. Similarly for cyclamens, plugs (conical shaped grown plants) were obtained from Syngenta (Ireland) and 30 plugs were randomly selected and assigned to each treatment. Each plug was placed individually in a 1 L pot. This experiment was a complete randomised block with 30 replications. Data for all experiments were analysed using the Friedman's nonparametric test (Minitab version 14).

Results and Discussion

There was a significant increase ($P<0.05$) in the germination of beetroot seed when seaweed extracts were added to the compost, however, there was no significant rate effect between the seaweed treatments (Figure 1). Germination of tomato seeds in compost amended with seaweed extracts was higher than the untreated controls, although this effect was not statistically significant. There was an average germination of 77% in seaweed treated composts compared to 68% germination in the untreated control. A similar finding was recorded with onion seed germination, where the percentage of seeds germinating was higher in the seaweed treated composts compared to the untreated controls although not statistically significant. Results from the flowering of cyclamen were very promising (Figure 2). There were statistically significant differences between the treatments ($P=0.001$) receiving seaweed extract and the untreated control.

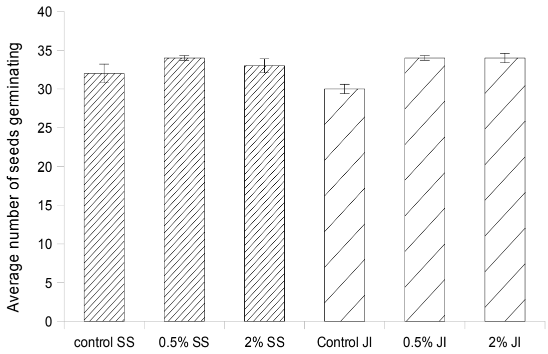

Figure 1. Effect of a novel cold process seaweed extract on beetroot seed germination with the addition of 0.5 and 2 % seaweed extract in two different composts (Friedman, $P>0.05$). Values are the means ($n=36$) with ± standard error of the mean (SEM)

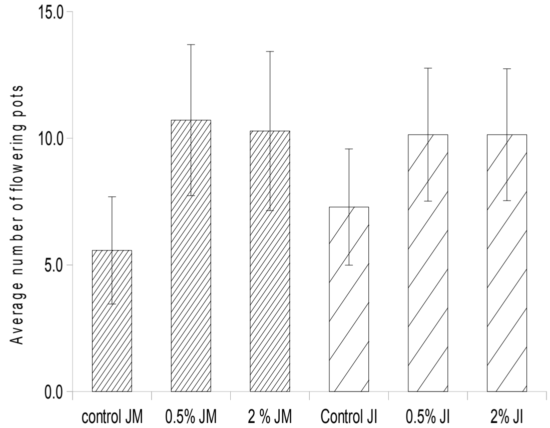

Figure 2: Effect of adding seaweed extract to composts, on the average number of flowers produced by cyclamen after a 39 day period (±SEM, $n=36$).

Conclusions

Overall our results indicate that the seaweed treatment, at both concentrations added to compost, promoted an increase in germination of vegetable seeds and flowering of cyclamen compared to the untreated control. This effect is possibly due to the level of plant like hormones or trace elements in the seaweed extracts. This work indicates the potential to use seaweed extracts to increase the value of horticultural products.

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Development and application of a dosage sensitive assay for resistance to *Globodera pallida* Pa2/3 in potato

E. Dalton[1, 2], D. Griffin[1], T. Gallagher[2], D. Milbourne[1]
[1]*Teagasc, Crops, Environment & Land Use Centre, Oak Park, Carlow*
.[2]*University College Dublin, Belfield, Dublin 4*

Introduction

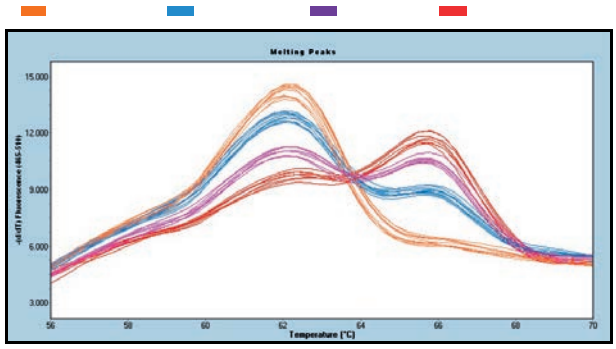
Globodera pallida is a parasitic root cyst nematode which causes severe yield losses to potato crops worldwide. In Europe, the major threat is due to *G. pallida* pathotypes Pa2/3(Evans et al. 2003). Chemical nematicides and crop rotation are relied upon to provide protection. However, the most effective strategy of disease control is to use resistant varieties. A valuable source of resistance to *G. pallida* Pa2/3 derived from *Solanum tuberosum* ssp. *andigena* (accession CPC 2802) is frequently being used in the breeding programme to create highly resistant varieties. In a previous study, a large effect quantitative trait locus (QTL) referred to as $GpaIV^{s}_{adg}$ was mapped to chromosome IV and single nucleotide polymorphisms (SNPs) highly diagnostic for *G. pallida* Pa2/3 resistance were identified. As a result, this allowed development of diagnostic markers for early and rapid selection of resistant material. Assessing dosage has become increasingly important to potato breeders since multiplex parental clones (duplex, triplex, or quadruplex) transmit the resistant allele to the progeny at a greater frequency, and thereby reduce the need for extensive marker and phenotypic screening. Recently, De Koeyer *et al.* (2009) used unlabelled probe genotyping for allele dosage detection in tetraploid potato. This study examined the possibility of using unlabelled probe genotyping to detect various dosages of the diagnostic allele of $GpaIV^{s}_{adg}$ QTL in potato.

Materials and Methods

Leaf material was sampled from progeny of 5 experimental populations segregating for the diagnostic allele of the $GpaIV^{s}_{adg}$ locus and a validation panel consisting of 109 potato varieties and advanced breeding clones used by the Oak Park breeding programme. Genomic DNA was extracted from fresh leaf material using a modified CTAB procedure adopted for 96-well plate. The region surrounding the diagnostic allele for $GpaIV^{s}_{adg}$ locus was amplified using the Contig237 primer set identified by Moloney *et al.* (2009) and sequenced both in forward and reverse directions by Macrogen Inc. (Seoul, Korea). Primers were designed to amplify a small fragment flanking A/T SNP at position 119 from Contig237 primer set. Primer and probe design parameters were as follows: amplicon size between 100 and 250 bp, primer Tm between 58-62˚C, probe Tm >5˚C than primer Tm, and primer size between 20-30 bases. Probes were designed as unlabelled oligonucleotides (20 – 40 bp) to perfectly match the resistant allele and blocked at the 3' end (by addition of a phosphate) to prevent polymerase extension during PCR. Asymmetrical unlabelled probe genotyping PCR followed by melt curve analysis was performed using the Lightcycler 480 Real-time PCR system (Roche Diagnostics). After data acquisition, the region of the probe melt was analysed using the Lightcycler 480 melt genotyping software.

Results and Discussion

In tetraploid potato, a single SNP with the two variant bases (A and T) can have the following five possible genotypes: nulliplex (AAAA), simplex (AAAT), duplex (AATT), triplex (ATTT), and quadruplex (TTTT). This study revealed an unlabelled probe assay, C237dProbe9, which identified four different genotypes for the resistant allele linked to the $GpaIV^{s}_{adg}$ locus. Four melting curve profiles were obtained in the negative derivative melting plots (figure 1). The shape and height of the melting peaks suggested each corresponded to a different allelic dosage state of tetraploid potato. Sanger sequencing confirmed these melt profiles to be nulliplex, simplex, duplex, and triplex for the resistant allele. However, we did not identify any quadruplex genotypes from this study.



4:0 Nulliplex 3:1 Simplex 2:2 Duplex 1:3 Triplex

Figure 1 Unlabelled probe genotyping by melting curve analysis of C237 (119) for $GpaIV^{s}_{adg}$ QTL conferring resistance to *G. pallida* Pa2/3. The unlabelled probe was designed to perfectly match the resistant allele at the $GpaIV^{s}_{adg}$ locus; the peak at 66˚C reflects the presence of the resistant allele. A single mismatch peak is observed at 62˚C, and the relative peak heights at the perfect match (resistant allele) and mismatch (non-resistant alleles) temperature points are used to determine dosage.

Conclusions

Unlabelled probe genotyping can be used to estimate dosage of the diagnostic allele of $GpaIV^{s}_{adg}$ QTL. This is very useful tool for potato breeding programmes that develop *G. pallida* Pa2/3 resistant varieties because it aids multiplex parental development, which increases resistant clones coming through the programme but also the likelihood of developing a resistant variety.

Acknowledgements

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Association of the *CYP51* mutation S524T in Irish *Mycosphaerella graminicola* strains with reduced DMI fungicide sensitivity

S. Kildea, J. Spink & E. O'Sullivan
Crops Environment and Land Use Programme, Oak Park Research Centre, Carlow

Introduction

Due to our geographical location and climatic conditions, Irish wheat crops have the potential to produce some of the highest yields worldwide. These same environmental conditions are conducive to the spread and development of wheat diseases, in particular septoria tritici blotch (STB), caused by the fungal pathogen *Mycosphaerella graminicola* (anamorph *Septoria tritici*). Currently, the majority of commercial winter wheat varieties are unable to adequately resist STB and routine fungicide applications are essential to achieve grain yield and quality. Although more effective fungicides belonging to the succinate dehydrogenase inhibitors (SDHI) group of fungicides have been registered for use in recent years fungicide programmes are still reliant upon the demethylation inhibitors (DMIs) group of fungicides. In addition to disease control the DMIs are also essential partner fungicides in the deployment of SDHI anti-resistance strategies. In this study we report the development of reduced sensitivity to the principal DMI fungicides used for STB control and its association with the mutation S524T in the gene *CYP51* (coding for the triazole target site) of Irish *M. graminicola* strains.

Materials and Methods

Thirty-four monopycnidial *M. graminicola* strains isolated from commercial wheat crops during the 2008 and 2009 were assessed in the study. The strain OPS6 isolated in 2003 was also included as a sensitive control. Sensitivity to the DMI fungicides epoxiconazole, metconazole, prochloraz, prothioconazole and tebuconazole were determined using a microtitre plate assay as described by Kildea (2009).

The complete DNA sequence of CYP51 gene was determined in strains OPS1, OPS4, OPS6 and OPS8. Partial *CYP51* sequences were obtained for the remaining 31 strains.

Results and Discussion

The sequence of the CYP51 in strains OPS1, OPS4, OPS6 and OPS8 were successfully sequenced (Genbank accession numbers GU144807-144810). Both OPS6 and OPS8 had sequences previously detected in the Irish *M. graminicola* population (Kildea, 2009). The CYP51 sequence of strains OPS1 and OPS4 was similar to the most commonly found CYP51 haplotype in Irish populations except with the replacement of threonine for serine at codon 524. The sensitivity profile of these isolates was also different to epoxiconazole and prothioconazole, with both strains showed reduced sensitivity to these chemicals. In the remaining 31 an additional seven *CYP51* haplotypes were identified (Table 1). All but one of the strains with sensitivity profiles similar to those of the strains OPS1 and OPS4 had the mutation S524T.

Conclusions

The emergence of the CYP51 mutation S524T has reduced the sensitivity of Irish *M. graminicola* strains to the principal DMIs used for its control. To date the majority of isolates detected with this mutation remain sensitive to both metconazole and tebuconazole.

Acknowledgements

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Table 1. Affect of *CYP51* alterations on sensitivity of *Mycosphaerella graminicola* to the DMI fungicides

CYP51 Alteration	N	Mean EC50*				
		Epoxiconazole	Metconazole	Prochloraz	Prothioconazole	Tebuconazole
Y461S[OPS6]	1	0.07	0.14	0.05	0.59	0.96
Y461S, V490L	1	0.26	0.45	0.28	2.28	1.88
V136A, Y461S[¥]	4	0.35 (±0.04)	0.20 (±0.10)	0.24 (±0.15)	3.03 (±0.64)	1.65 (±1.49)
V136C, Y461S	6	0.41 (±0.06)	0.32 (±0.03)	0.12 (±0.02)	0.98 (±0.13)	2.01 (±0.24)
I381V, Y461H	2	0.40 (±0.07)	0.33 (±0.08)	0.05 (±0.02)	3.40 (±2.24)	3.50 (±0.71)
S188N, A379G, I381V, Δ459/460 [OPS6]	4	0.66 (±0.13)	0.96 (±0.02)	<0.04*	11.85 (±4.19)	12.46 (±4.25)
V136A, Y461S, S524T [OPS1, OPS4]	13	0.92 (±0.07)	0.30 (±0.26)	0.77 (±0.06)	31.38 (±2.24)	0.53 (±0.06)
V136A, I381V, Y461H, S524T	1	2.21	0.30	0.20	34.74	0.44
D134G, V136G, Y461S	1	1.1	0.14	0.43	0.95	0.14
D134G, V136A, I381V, Y461H	1	0.85	0.19	0.15	33.37	0.65

N=strain number; *measure in mg/l; ± standard errors ; [¥] previously the most common CYP51 haplotype

Using *Populus* Genomic Resources to Assess Variation in Lignin and Cellulose Biosynthesis Genes in Willow (*Salix*)

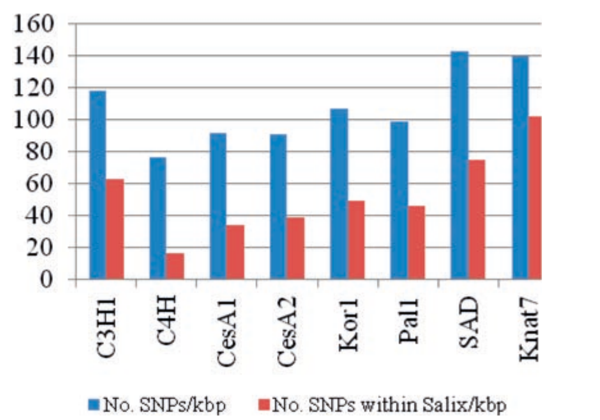
A. Perdereau[1,2,3], G.C. Douglas[2], T.R. Hodkinson[1] and C.T. Kelleher[3]

[1]*Botany Building, School of Natural Sciences, Trinity College Dublin, Dublin 2* [2]*Teagasc, Kinsealy Research Centre, Malahide Road, Dublin 17,* [3]*National Botanic Gardens, Glasnevin, Dublin 9*

Introduction

*Willow (*Salix*) is in Salicaceae, a family that also includes poplar (*Populus*). Wood is a natural and renewable source of energy and, therefore, has a major role as an environmentally cost-effective alternative to burning fossils fuels* between species.

From the initial PCRs, with very little optimisation, we obtained a 44% success rate in terms of amplification of a clear product. This means that we can use about half the resources designed for *Populus* on *Salix*. This is based on a broad approach of trying to amplify from a variety of regions in a large array of species. A more targeted approach based on a limited set of *Salix* species would likely give a much greater success rate.



One of the major components of wood is lignin (25-35%) (Douglas, 1996). Cellulose is a major component of plant cell walls, and is the world's most abundant biopolymer (Taylor, 2008). Specific genes in lignin and cellulose biosynthesis (encoding carbohydrate-active enzymes) have been studied in poplar (Geisler-Lee et al. 2006) but nothing has been published on such candidate genes in *Salix*. Our objectives were to test the utility of *Populus* derived PCR (Polymerase Chain Reaction) primers for amplification and sequencing of orthologous gene regions in *Salix* species. This study examined variation in these genes among *Salix* species.

Materials and Methods

A total of 27 partial genes, involved in lignin and cellulose biosynthesis on 40 samples of willows collected at the National Botanic Gardens, Glasnevin and at the Teagasc Kinsealy Research Centre, Dublin were assessed in this study. These samples include species from the three subgenera of *Salix*, nine commercial clones and six varieties from Irish commercial basket makers. A sample of *Populus tremula* L. was also used as a template. DNA was extracted from dried leaf tissue and PCRs were performed. The desired amplicons were cleaned using a purification kit. Then, an Applied Biosystems 3130xl Genetic Analyzer was used to sequence the samples. Sequences were analyzed for Single Nucleotide Polymorphisms (SNPs) and insertions-deletions (indels). Alignments of the sequences were made against *Populus trichocarpa* model genome. Variation among *Salix* species was assessed by calculating (SNPs/length) x1000 over the consensus sequences obtained from the alignments. The reading frame was determined using DNASP 5.10.

Results and Discussion

From the initial set of 27 primers, 12 amplified loci showed one clear unique band after agarose gel electrophoresis in many of the samples. Out of the 12 loci sequenced, eight yielded clear electropherogram traces. These included genes in the lignin pathway (*C3H1*, *C4H*, *PAL1*, *SAD*), genes for other wood components (*CesA1*, *CesA2* - cellulose synthase genes, *Kor1* - Korrigan) and transcription factor (*Knat7*). A total of approximately 3,458 bp were sequenced per species. From 19 to 28 species have been studied, for a total of 82,550 bp. Between 76 and 143 SNPs/kilo base pairs (kbp) were detected per gene region, between the two studied genera but also within the genus *Salix*. Between 16 and 102 SNPs/kbp per gene region were discovered within *Salix* (Fig 1). An average of 54 SNPs per kbp for commercial clones, 58 for hybrids and 57 for species has been found, these differences are not significant under a t-test at a threshold of 5%. Between 0 and 15 non-synonymous sites were discovered per gene region per species. Ten indels were also identified. Multiple sequence alignments showed variability

Fig. 1. Details of the variation between *Salix* and *Populus* and among *Salix* species

Conclusions

This is one of the first studies to quantify levels of nucleotide polymorphism in a wide range of willows from the three subgenera of the genus *Salix*. The results show that the genus *Salix* harbours significant amounts of genetic variation at these loci (both between the different *Salix* species but also between *Salix* and *Populus*). The study shows that the genomic resources can be transferred directly from *Populus* to *Salix*. Estimates of nucleotide diversity from the targeted genes reveal the variability within genes responsible for wood formation in various individuals and this can aid in selecting species and strains of willow for future breeding programmes.

Acknowledgements

The research is supported by a Walsh Fellowship PhD grant from Teagasc, The Irish Agriculture and Food Development Authority.

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Simulation of beetle defoliation of willow plants (*Salix viminalis*)

P. D. Fanning [1, 2], J-R. Baars [1] and M.T. Gaffney [2]

[1]*School of Biology and Environmental Science, Science Centre (West), University College Dublin, Belfield, Dublin 4, Ireland.*[2]*Horticultural Development Unit, Teagasc Research Centre, Kinsealy, Dublin 17, Ireland.*

Introduction

Willow in Ireland has considerable potential as a renewable energy crop. Leaf eating Chyrsomelid beetles, both Blue (*Phratora vulgatissima*) and Brown (*Galerucella lineola*) are the most serious pests affecting the potential yield. Studies into the degree of susceptibility to pest feeding damage and breeding for resistance in willow provenances are required. Investigations into growth in response to damage have shown that tolerance varies between different provenances of willow (Powers *et al.,* 2005). To assess willow response to varying levels of pest damage, manual defoliation of plants may be used to simulate various levels of damage, in field experiments. This technique has been used previously in potted studies (Powers *et al.,* 2005). However, no studies have shown how well manual defoliation represents the damage to plants that beetle defoliation induces. The aim of this study was to assess how well manual defoliation represents beetle defoliation on four willow provenances ranging in susceptibility to beetle feeding damage. These results will inform the method of defoliation to be used in the field plots.

Materials and Methods

Potted plants were established using rods of four commercial willow provenances. Two 15 cm rods were placed in each pot filled with a peat based media and grown in glasshouses for 153 days. Willow provenances 'Tora', 'Torhild', 'Beagle' and 'Tera Nova' were treated to 2 types of defoliation manual (M) and beetle (B), at 4 levels of defoliation (0, 25, 50 & 75%). Each treatment was replicated 4 times. Adult beetles to be used in these trials were collected from a commercial willow plantation in Donard, Co. Wicklow. Firstly beetle consumption rates were assessed on each provenance to determine the number of beetles required to achieve the different levels of defoliation. Willow provenances were then exposed to beetles, to be fed on in Bugdorms ® mesh cages for a period of one week. Manual defoliations were carried out using the methodology described by Powers *et al.* (2005) to achieve levels similar to beetle damage. Plants were monitored periodically after exposure to assess the rate of recovery, and finally assessed for biomass after 97days, at a 16:8h day: night cycle. Parameters measured include number of leaves, stem height (m), and above and below media level biomass. Data were analysed using t-tests in SAS.

Results and Discussion

Plants exposed to beetles partially defoliated, dropping their damaged leaves at 50% defoliation but suffered complete leaf drop at 75%. Manual defoliation on the other hand did not cause this response. Plants responded by producing new leaves in response to both defoliation types. Therefore when the resulting leaf numbers (Table 1) and biomass were compared there were no differences found between manual and beetle defoliation at each of the levels of defoliation. However, at 50% manual and beetle defoliation of the provenance 'Beagle' there was a significant difference in leaf numbers (P= 0.03), also at 75% defoliation less leaves were produced in response to manual defoliation although not significant (P= 0.08). When effects of leaf numbers on aboveground biomass were compared across the range of defoliation levels (0 to 75%) plants decreased in biomass with increasing levels of defoliation, up to 50%. Plants exposed to either manual or beetle defoliation at 75% seemed to respond by compensating for damage by producing more leaves. As a result the above ground biomass increased at the 75% level of defoliation. The results for each provenance, with the exception of 'Tera Nova', showed this general trend for both methods of defoliation. This indicates that manual defoliation can induce a similar overall plant response that occurs during beetle defoliation.

Table 1. Table showing the mean (±S.E.) no. of leaves post defoliation for both manual (M) and beetle (B) defoliation and t-test comparisons between the different types of defoliation.

%		Tora		Torhild		Beagle	
		M	B	M	B	M	B
0	Mean (±SE)	44.0 (±3)		76.0 (±13)		73.2 (±13)	
25	Mean (±SE)	40.3 (±5)	45.8 (±4)	82.2 (±7)	90.5 (±4)	117.8 (±14)	87.3 (±12)
	t-test(P=)	t=0.8, (0.48)		t=1.4, (0.23)		t=-1.6, (0.18)	
50	Mean (±SE)	83.5 (±11)	105.5 (±20)	45 (±9)	43.8 (±3.6)	77 (±7)	126.6 (±16)
	t-test(P=)	t=0.83, (0.44)		t=-0.12, (0.91)		t=2.75 (0.03)	
75	Mean (±SE)	47 (±6)	58.8 (±20)	81.3 (±11)	119 (±18)	84.62 (±20)	170.3 (±35)
	t-test(P=)	t=0.47, (0.65)		t=1.74, (0.15)		t=2.1, (0.08)	

Conclusions

These results show that the manual removal of leaves, while not causing leaf drop, can induce similar plant responses to that following leaf beetle defoliation. This study supports the use of manual defoliation to achieve different levels of defoliation in field trials, avoiding the difficulties in manipulation beetle populations under field conditions.

Acknowledgements

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New yield Models for Sitka spruce plantations in Ireland

S.Lekwadi[1], A. Nemesova[1] and M. Mac Siúrtáin[1]
[1]*School of Agriculture Food Science and Nutrition, University College Dublin, Belfield, Dublin4.*

Introduction

Sitka spruce is the most important commercially grown tree species, occupying 52.3% of the total area of the managed state and private forests area, in the Republic of Ireland. The understanding and information about the forest dynamics of Sitka spruce is hugely important to foresters, in particular when deciding whether to thin or clarefell a forest and also when deciding the silvicultural treatments options to be adopted to maximize yield. The forest management planning method that is currently used in Ireland depends, partially, if not hugely, on the British Forestry Commission yield tables to predict future stand yields. The objective of this study is to develop (i) reliable yield models for Irish Sitka spruce forest plantations and (ii) an Irish yield table derived from Irish forestry.

Materials and methods

Long term silvicultural experiments were laid out in seven regions of Irish forest by Coillte from the 1960s to cover a wide range of ages and site conditions. The experimental regions are: Galway; Cork; Limerick; Sligo; Wicklow; Mullingar and Kilkenny. The long term experimental units were fixed permanent sample plots (PSPs) and were properly marked and protected. At a regular interval, tree and stand measurements were repeatedly taken and recorded by Coillte from the same randomly assigned PSPs. We extracted main crop and thinning yields for volume (V) in m^3/ha, and age (t) in years and top height in (m) for each region. These were subsequently pooled to constitute 380 national data pairs for modelling.

Yield modelling

Top height-age data was used to initially classify forest stands into site classes I - V in a decreasing order of productivity, using nonlinear quantile regression methodology (Lekwadi, *et al.*, 2011) and chapman-Richard growth function eq.(1)

$$y_t = b_0\left(1 - e^{b_2}t\right)^{b_3} + e_i \qquad (1)$$

The Cumulative volume production (CVP) computed as sum of present volume and the previous thinned volume TV_t eq. (2):

$$CVPt = V_t + TV_{t-1} + V_{t-2} + ...TV_0,\ (m^3ha^{-1}) \qquad (2)$$

The logarithmic transformed model was then fitted using eq. (3)

$$y = e^{(b_0 + b_1t + b_2\ln t) + \varepsilon_i} \qquad (3)$$

where :

y = the computed yields (CVP),

b_i = regression parameter

The predicted site class top heights were transformed into the corresponding yield classes $(\hat{y}_\tau)$ using parameter estimates from eq. (3). The mean annual increment (MAI) was computed as: $MAI_\tau = \frac{\hat{y}_\tau}{t}$ and current annual increment (CAI) as: $CAI_\tau = \frac{\delta y}{\delta t} f(y_\tau)$.

The yield class was defined where the MAI and CAI curves intersect.

Results and Discussion

The MAI and CAI intersect at 29.6, 25.7, 20.8, 16.2, and 11.9 m^3 $ha^{-1}a^{-1}$ at age 30, 32, 33, 38 and 39 years for site class I – V respectively (Fig.1). This indicates that a better site will produce higher yield at a shorter rotation. Figure. 2 shows that the end of juvenile, adolescent, mature and senescent stages occur earlier in site class I. This is useful for forest management decision making of when to thin or clearfell.

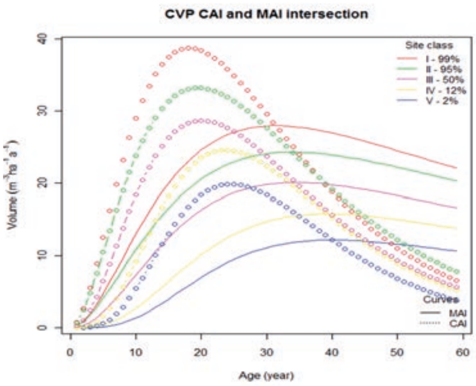

Figure.1 Intersect of MAI and CAI curves for five site classes, with all model parameters significant (P<0.05)

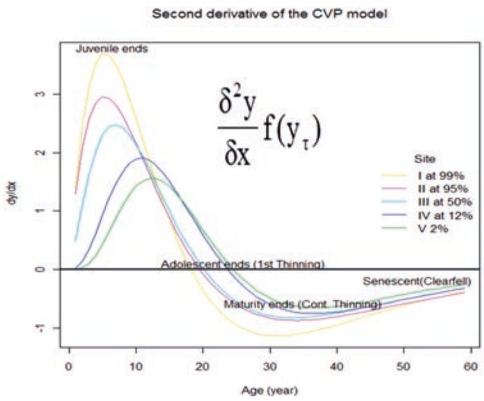

Figure 2. Second derivative of the yield models.

Conclusions

Foresters can now reasonably predict yield at any age and top height across a range of Irish sites. Decisions Wether to thin or clearfell a forest stand can also be made.

Acknowledgement

Conference for Forest Research and Development (COFORD) funded this project

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The use of Model Builder to quantify the geospatial constraints of private sector timber supply within the Republic of Ireland

A. Whelan[1] and M. Mac Siúrtáin[1]
[1]*School of Agriculture and Food Science. University College Dublin, Belfield, Dublin 4.*

Introduction

Forests provide a wide range of habitats for both flora and fauna, helping to increase the levels of biodiversity throughout the county (Forest Service, 2000-1). In order to protect these areas, a number of guidelines have been created by the Forest Service which has set out practical measures based on the principles of Sustainable Forest Management (SFM) (Forest Service, 2000-3). The national objective is to have 17% of the land area under forestry. Through the use of ArcGIS, it will now be possible to accurately quantify areas of forestry that can be considered unproductive (or left for biodiversity) or productive commercial plantations.

Materials and Methods

The most up-to-date georeferenced vector and raster data were made available for the purposes of this research under licence from Ordnance Survey Ireland (OSi) and ESB Ireland. Additionally, the most up-to-date state and private forest coverage were made available under licence by the Forest Service. One of the main tools used for this research was ArcGIS desktop, including a collection of integrated applications: ArcMap, ArcCatalog, ArcToolbox and Model Builder. Obtaining reduction factors within forestry stands can now be achieved through a number of processes within ArcMap (ie buffer, clip, dissolve & erase). This process can now be automated through the use of the Model Builder tool, within ArcGIS. This allows for a more efficient method of applying each buffer and also identifies the reduction factor for each forest polygon. The specifications for the buffer zones created were obtained from the forestry guidelines (Forest Service, 2000), the Forestry Schemes Manual (2004) and the Water Framework Directive (2000). The private forest estate used to test the methodology was Ballycurry Demesne, Ashford, Co Wicklow.

Results and Discussion

Under the forest guidelines, there are a number of areas that require buffers including roads, rivers, dwellings, ESB lines, conservation areas, archaeology sites etc. Therefore, it is essential that any of these sites found within potential or existing forest plantations need to be protected. Through the use of ArcGIS and its tools, it is possible to accurately quantify areas that must be left free (i.e. buffers) from intensive forest management practices. Reduction factors can then be shown for each individual constraint or shown as a combination of constraints. Figure 1 shows the model created within ArcGIS which obtains the reduction factors for each spatial constraint identified in each sub-compartment within Ballycurry. Figure 2 shows the total area within Ballycurry that can be identified as unproductive (or left for biodiversity enhancement) due to the constraints contained within it. A total of 77% is found to be productive compared to 23% unproductive. There is a large area of Natural Heritage Area (NHA) found within Ballycurry, which has resulted in a much larger area being left as unproductive. A general rule if 15% is what is usually left free of intensive forest management in order to encourage biodiversity.

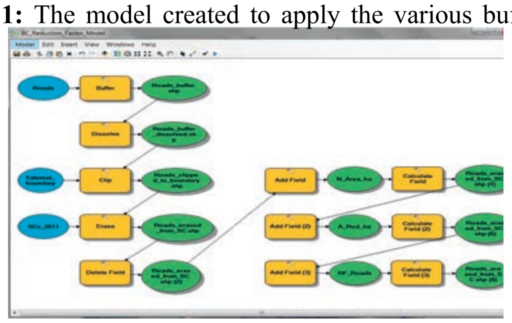

Fig 1: The model created to apply the various buffers within Ballycurry and to identify the reduction factors found within each sub-compartment.

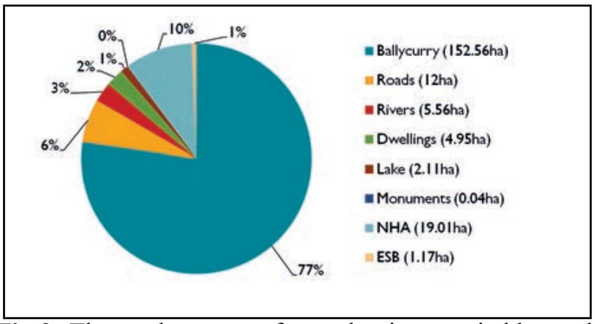

Fig 2: The total amount of area that is occupied by each of the spatial constraints found within Ballycurry.

Conclusion

The development of new enabling technologies including GIS and Remote Sensing have greatly improved the accuracy of geospatial information that can be created, edited and stored. This has allowed the mapping of forest boundaries to be much more accurate and accessible.

Acknowledgements

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GIS Tools for accessing timber and energy forecasts for the Republic of Ireland

A. Nemesova[1], S. Lekwadi[1], H. Phillips[1], J. Redmond [2] and M. Mac Siúrtáin[1]
[1]*School of Agriculture, Food Science and Veterinary Medicine, University College Dublin.* [2]*Forest Service, Department of Agriculture, Fisheries & Food, Johnstown Castle Estate, Co. Wexford*

Introduction

Philips *et al.* (2009) published geospatial forecasts of roundwood production from private sector forests for 2009-2028 in the Republic of Ireland. The objective was to develop a web interface for the provision of national and catchments geospatial forecasts over the internet through easy-to-use tools, using freely downloadable GIS software. GIS tools helps to bridge the gap between those who produce forecasts and forest resource managers and energy users. The target group include forestry companies and professionals, timber processors, energy sector and forestry advisors.

Materials and Methods

The private sector timber supply forecasts are available for the Republic of Ireland, the four provinces, the eight regions, the 26 counties and for 42 towns each with 60 and 80 km catchments, in standard Microsoft Excel® format, stored on a web server and can be accessed by hyperlinked GIS tools. GIS data layers were obtained from Ordnance Survey Ireland and Forest Service sources, and data processing was carried out in ArcGIS 9.3.1. The GIS tools were created by exporting GIS layers, in published map format (*.pmf) and published document format (*.pdf). The GIS tools are made available through an entirely new Excel file interface and this facilitates forestry and energy sector users to use GIS tools to access geospatial forecasts. The new architecture behind the tool is presented (Figure 1).
This GIS tool has been implemented for the timber supply forecast of the private forest estate. Bringing together all of the forecast results into geospatial context.

Results and Discussion

Foresters and the timber processing sector can view state and private forest areas, download private sector forecasts and make decisions on accessibility and harvesting.
The forecasts are available at national, regional, provincial and county levels and provide information on volume by assortments, by species groups, by harvest type and harvest areas. An energy wood assortment is also included. The forecast uses spatial data; therefore it is possible to produce specific catchment area forecasts for 42 county towns and timber processing locations.
The most up-to-date OSi orthophotos are made available through the GIS Tool to forest sector for the first time. The GIS tool allows (Figure 2): state and private forests to be displayed. Bookmarks may be used to zoom to provinces, regions and counties. Data layers may be added or removed; adjustment to transparency of layers (to allow one layer to show through the top layer); zoom, pan, measurement functions; identify and display of information associated with data layer; and access the forecast results database.

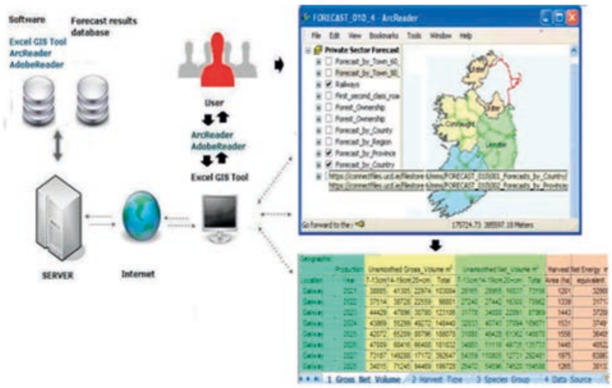

Figure 1. The Excel file interface tool provides a simple unified user interface to access all GIS Tools

The GIS Forecast Tool allows forest sector users to examine a wide range of potential issues including:

- The location of existing sawmills.
- The location of existing private forests timber supply located in specified geographic catchments
- Timber harvesting and transport options.
- The location of potential sources of timber.
- The location of potential timber processing facilities in next 30 years.
- The location of potential spatial restrictions on realizing the forecasts.

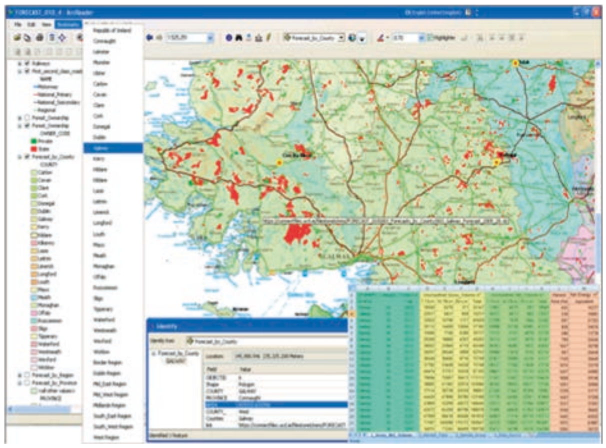

Figure 2. The private sector timber supply forecasts results

Conclusions

The GIS tools make forecasts available at user specified scales through very simple GIS compatible interfaces. Users can very easily view, explore, and print forest maps and predict future growth. Perhaps the main advantage of the GIS Tool is that it introduces forest and energy users to the enormous potential of GIS.

Acknowledgements

The financial support of COFORD is acknowledged.

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Predicting energy balance of Holstein-Friesian cows using mid-infrared spectrometry of milk

S. McParland[1], G. Banos[2], B. McCarthy[1], E. Lewis[1] M.P. Coffey[3], B. O'Neill[1], E. Wall[3], M. O'Donovan[1] and D.P. Berry[1]
[1]Animal & Grassland Research & Innovation Centre, Teagasc, Moorepark, Co. Cork, [2]Aristotle University of Thessaloniki, Greece, [3]Scottish Agricultural College, UK

Introduction
The main hindrance to the inclusion of energy status (ES) in multi-trait genetic evaluations as a predictor of health and fertility is the difficulty and expense of energy intake data collection on large numbers of animals. Recently, the mid-infrared spectrum (MIR) of milk, the method of choice worldwide to routinely predict milk composition, was proposed as an indictor of ES (McParland et al., 2011). The objective of this study was to test the robustness of the equations developed to predict ES across independent populations of indoor-fed and grazing Holstein-Friesian dairy cows.

Materials and Methods
Performance data collected between 1990 and 2011 from two separate research herds were used in this study; data from the Scottish Agricultural College research herd (SAC) and data from the Teagasc Moorepark research herd (MPK). The SAC herd comprised 1,218 cows divided into two dietary treatments, high concentrate and low concentrate. The MPK data set comprised 1,586 animals of differing strains of Holstein-Friesian on a predominantly grazed grass diet with periodic concentrate supplementation. Random regression models were fit, within parity, and within country, to routinely collected dry matter intake (DMI) (SAC only), milk production, body weight (BW) and body condition score (BCS) records to generate daily solutions for each trait and ultimately calculate ES for each day of lactations 1 to 4. Energy status was computed for MPK animals only during periods of lactation where actual DMI was recorded. Energy balance (EB; MJ/d), was computed as a function of milk yield, fat and protein content, DMI, BW and BCS. Energy content (EC; MJ) was computed as a function of BCS and BW predicting body lipid and protein weight.
Morning (MPK(am)) and evening (MPK(pm)) milk samples from MPK animals were analysed weekly using a Foss MIR spectrometer. Morning (SAC(am)), midday (SAC(md)) and evening (SAC(pm)) samples from SAC animals were analysed monthly using the same MIR spectrometer. The Foss MIR spectrum contains 1,060 data points which represent the absorption of infrared light by the milk sample at wavelengths in the 900 cm^{-1} to 5,000 cm^{-1} region. Only spectral data with an actual phenotypic record for all component variables of EB within 7 days of the corresponding milk sample were retained. Spectral data were transformed from transmittance to linear absorbance through a $\log_{10}$ transformation of the reciprocal. In total, 820 MPK(pm) and 844 MPK(am) spectral records from 244 MPK cows with EB data were available together with 2,989 SAC(pm), 2,992 SAC(am) and 2,742 SAC(md) records from 337 SAC cows.
Partial least squares regression was used to predict ES from the MIR linear absorbance data. Predictor variables included a subset of wavelengths from the spectrum of 1,060 correlated wavelengths, together with milk yield. All prediction equations were undertaken using am, md (where available), and pm samples, separately. Accuracy of all equations was tested using both split sample cross-validation and external validation. Two types of analyses were undertaken: 1) prediction equations were calibrated within the SAC data set and externally validated on the MPK data set, and 2) the two research data sets were combined and equations calibrated and validated using the combined data set. When equations were calibrated and externally validated using the combined data set, the data were sorted according to ES and every fourth record removed from the calibration data set for inclusion in the external validation data set. This was done to optimise the robustness of the prediction equation, since samples contained in the calibration data set should represent the variation observed in the phenotype to be predicted.

Results and Discussion
Prediction equations calibrated using data from SAC only, were not useful to predict either EB or EC of MPK animals. External validation accuracies ranged from 0 to a maximum of 0.15 for both sets of equations. The slope between true and predicted EB was close to 0 while the bias was greater than 40 MJ for all equations tested across research data sets. Similarly, the slope and bias between true and predicted values of EC was poor across all equations tested. Prediction equations developed using pooled data from SAC and MPK research data sets were more robust than equations tested across research data set. Combined prediction equations had an accuracy of prediction of EB of 0.69, and had a slope (se) from the regression of true on predicted values of EB of 0.98 (0.03), whilst the mean bias (se) between true and predicted values of EB was 1.12 (0.88) MJ. Very high accuracy of prediction was not expected given the inherent errors in calculation of "true" energy balance. The accuracy of prediction of EC was lower than that of EB, however was more robust when equations were tested across research data set.

Conclusions
Equations have been developed which give accurate predictions of energy balance across lactation using the MIR spectrum of milk. Although equations developed on one production system are not robust to predict energy balance of animals on a different production system, when a combined data set across production systems was used, results were greatly improved.

Acknowledgements
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Effects of winter diet on in-calf heifer weight gain and subsequent milk production performance

E. Kennedy, F. Coughlan, J.P. Murphy and S. Fitzgerald
Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork

Introduction
The cost of rearing replacement heifers contributes significantly to the overall expense of milk production (Heinrichs, 1993), thus it is essential that heifers calve at the correct bodyweight (BW) at 22 to 24 months of age. Many studies have shown a positive relationship between BW at calving and first lactation milk yield (Lin et al.1987). Forage brassicas, such as kale (*Brassica oleracea*), are considerably cheaper as a winter feed than grass silage and concentrates. The objectives of this study were to: i) investigate the effect of winter diet on pre-partum weight gain of nulliparous replacement dairy heifers and ii) to establish the effect of pre-partum feeding treatment on post-partum milk production performance.

Materials and Methods
One hundred Holstein-Friesian replacement dairy heifers were balanced on the basis of age (639 ± 20.5 days), projected calving date (23 February ± 22.0 days), BW (459 ± 43.8kg) and BCS (3.21 ± 0.215; scale 0 to 5) and randomly assigned to one of four feeding treatments. The treatments were: i) indoors offered a silage only diet for the duration of the experiment (SO), ii) indoors offered silage and 2kg concentrate for 46 days followed by a silage only diet – a total of 92 kg fresh weight of concentrate was offered to these animals (SC), iii) outdoors grazing forage kale in conjunction with grass silage bales at an inclusion rate of 30% in the diet (70K) and iv) outdoors grazing a 100% forage kale diet (100K). The over-winter experimental feeding treatments were imposed from 8 November 2010 until calving and the milk production data reported is for the first 29 weeks of lactation.
The SO and SC treatments were all offered the same silage. The 70K animals were offered baled silage. The forage kale was grazed *in situ*. The concentrate fed during the winter period was 0.33 barley, 0.33 citrus pulp and 0.33 distillers grains. The DMD of the silage was 73 (±3.7) %, dry matter (DM) was 29.6 (±3.49) % and crude protein (CP) was 12.0 (±2.63) %. Prior to the commencement of the experiment all animals received one Allsure® bolus to provide iodine, selenium cobalt and copper supplementation. The 100K treatment animals were offered straw for the first week of the study to allow adjustment to the 100% kale diet. It was intended to offer no further fibre source after the first week to the 100K animals, however due to continuous frost 10 bales of silage were offered to 100K group 6 weeks into the experiment for a duration of one-week.
All animals were offered fresh feed daily; the indoor animals were fed using a Griffith Elder electronic feeding system. The outdoor animals were offered a fresh allocation of kale each morning by moving a temporary electric fence. All treatments were grouped individually. During the experimental period all animals were weighed weekly and condition scored every three weeks. Post parturition cows were turned out to grass directly and offered 4 kg DM concentrate for the first 40 days of lactation – all animals received the same concentrate input. Milk yield was recorded daily, while milk composition and BW were measured weekly. Body condition score was measured every three weeks. Data were analysed using PROC MIXED in SAS, terms for treatment, age and block were included in the model. Animal was used as the experimental unit.

Results and Discussion
Following the winter period daily weight gain was similar for the SC and 70K treatments (1.10 kg/heifer/day), weight gain was lower for the SO treatment (0.96 kg/heifer/day), the weight gain of the 100K heifers was significantly (P<0.001) lower than all other treatments (0.78 kg/heifer/day). Figure 1 shows the profile of weight gain during the winter feeding period. At the end of the winter feeding period BCS was greatest (P<0.001) for the SO and SC animals (3.47), significantly lower for the 70K animals (3.25) and lowest (P<0.001) for the 100K animals (3.09).
There was no difference between treatments in cumulative milk yield or milk solids yield for the first 29 weeks of lactation (3656 and 273 kg, respectively). There was no difference between treatments in average lactation fat, protein and lactose concentration (4.10, 3.38 and 4.70%, respectively). Average BW throughout the first 29 weeks of lactation was also similar between treatments (439 kg). Average BCS of animals from the 100K treatment was lower (P<0.001; 2.86) than that of the SC and SO animals (3.00) but was not different to the 70K animals (2.93). There was no difference in average BCS between the SC, SO and 70K treatments (2.98).

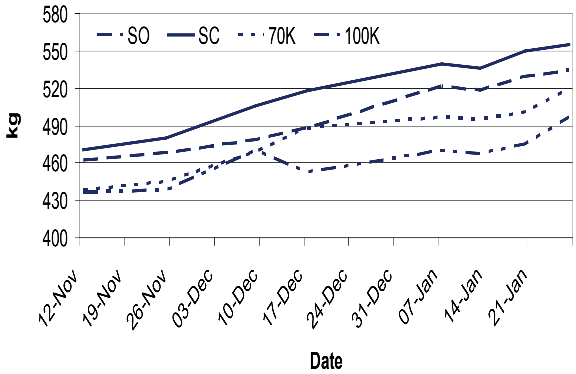

Figure 1. Profile of heifer weight during the winter feeding period

Conclusions
This study has shown that high levels of weight gain were achieved over the winter period by the SC and 70K heifers. Cumulative milk yield and milk solids yield were similar between all treatments. This study suggests that forage crops can be used as a viable alternative to grass silage based feeding treatments over the winter feeding period.

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Effect of white clover inclusion in perennial ryegrass swards on herbage and milk production under frequent tight grazing conditions

D. Enríquez-Hidalgo[1,2], T.J. Gilliland[3], M. O'Donovan[1], C. Elliott[2] and D. Hennessy[1]
[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork,* [2]*Queens University Belfast, Belfast, BT7 1NN, NI,* [3]*Agri-Food and Biosciences Institute, Plant Testing Station, Crossnacreevy, Belfast, BT5 7QJ, NI*

Introduction

White clover inclusion in swards can make an important contribution to the sustainability of ruminant production systems (Peyraud *et al.*, 2009) due to its ability to fix atmospheric nitrogen (N). Mixed swards with high N fertiliser are higly productive but N fertiliser application can reduce sward clover content (Ledgard and Steele, 1992). However, frequent grazing can enhance clover productivity in mixed swards (Black et al., 2009). The objective of this study was to compare the herbage and milk production output from grass only and grass clover swards under frequent tight grazing conditions at a high N input level

Materials and Methods

Two swards, grass only (GR) and grass clover (GC), were sown at the Dairygold Research Farm, Teagasc, Moorepark, Fermoy, Co.Cork in May 2010. The GR swards were a 50:50 mix of Abermagic and Tyrella perennial ryegrass sown at 37 kg/ha. The GC swards contained the same grass mix as above plus a 50:50 mix of Chieftan and Crusader white clover sown at 5 kg/ha. Swards received 240 kg N/ha/year. Thirty cows were randomly allocated to graze each treatment from 17 April to 30 October 2011. Rotational grazing was used and swards were strip-grazed, with fresh herbage offered daily (16 kg herbage dry matter (DM)/cow/d and 1 kg concentrate/cow/d). Pre-grazing herbage mass was measured three times per week using an Etesia mover (Etesia UK. Ltd., Warwick, UK). Pre- and post-grazing sward heights were recorded daily using a Rising Plate Meter (Jenquip, Feilding, New Zealand). Grass and clover components of an herbage sample were separated to estimate sward clover content twice weekly. Milk production was recorded daily and milk composition weekly. Data were analysed using General Linear Models for repeated measures in SAS (SAS, 2005). The statistical model investigated the effect of treatment and time. Covariates used were days in milk and average milk production for the three weeks prior to the start of the experiment.

Results and Discussion

Treatment effect on milk production is shown in Table 1. Cows grazing GC swards produced milk with lower fat and lactose content (P<0.05), but tended to have higher milk yield (P=0.08). Milk solids yield per day and cumulatively did not differ between treatments. The GC swards tended to have higher pre-grazing sward height (9.7 vs. 9.2 cm; sem 0.23; P=0.06). There was no effect of treatment on pre-grazing herbage mass (1720 kg DM/ha; sem 46.3; Fig. 1), post-grazing sward height (4.1 cm; sem 0.06) or total herbage production (12651 kg DM/ha; sem 395.9). Sward clover content on the GC swards increased from 8.8% (DM basis) in April to 19.8% in October, peaking in late August at 22.8% (Fig. 1). Average clover proportion of the GC swards (13%) was low, but was still higher than values observed (3%) in a previous experiment with similar environmental conditions and N application level (Humphreys *et al.*, 2008).

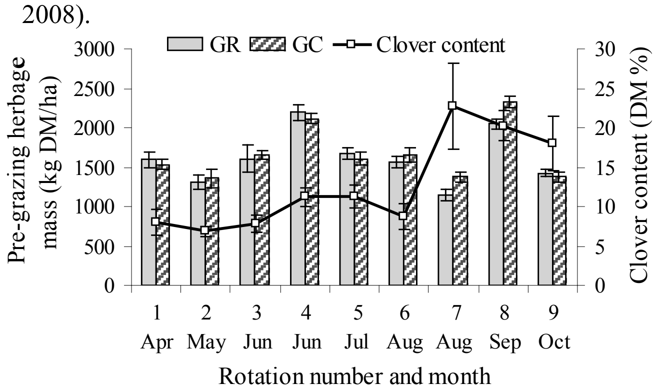

Fig. 1. Pre-grazing herbage mass and sward clover content of the grass clover swards.

Conclusions

Grass clover swards had similar herbage production to grass only swards, in a high N application grazing system. Clover swards supported high milk yields per cow and changed milk fat and lactose composition. Further differences between treatments could be expected if the sward clover content was higher throughout the year.

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Table 1. Effect of grass only and grass clover swards on milk production and composition (17 April to 30 October)

	Grass Only	Grass Clover	SEM	P value Treat	P value Week	P value Treat*Week
Milk yield (kg/day)	19.2	19.5	0.23	0.08	***	NS
Milk solids yield (kg/day)	1.50	1.50	0.003	NS	***	NS
Milk fat (g/kg)	43.7	42.5	0.81	***	***	***
Milk protein (g/kg)	36.3	36.4	0.06	NS	***	NS
Milk lactose (g/kg)	46.1	45.9	0.14	*	***	NS
Cumulative milk yield (kg/cow)	3765	3829	113.4	NS	-	-
Cumulative milk solids (kg/cow)	294.5	293.6	9.09	NS	-	-

*** = P<0.001; *=P<0.05; NS = Non significant

Heat recovery in a milk refrigeration system with variable fan speed control.

M. Murphy[1, 2], J. Upton[1], M.J. O'Mahony[2] and P. French[1]

[1] *Livestock Systems Research Department, Teagasc, Moorepark, Fermoy, Co. Cork,* [2]*Department of Mechanical Engineering, Cork Institute of Technology, Bishopstown, Cork*

Introduction

Milk refrigeration is the largest energy consumer on dairy farms at 37% of total consumption (Upton et al 2010). Direct Expansion (DX) systems are the most popular milk cooling systems employed on Irish dairy farms. A DX milk bulk tank operates on a typical reverse-Rankine vapour compression cycle consisting of four major components; evaporator, compressor, condenser and expansion valve. Liquid refrigerant (404A) evaporates inside the bulk tank evaporator before being lifted to a higher pressure and temperature by the compressor, the super heated gas is then cooled in the condenser by externally mounted variable speed (VS) air fans and returned to liquid form, the expansion valve reduces the pressure before the evaporator in the bulk tank allowing the liquid to once again turn to vapour and thus the cycle is continued. Heat Recovery (HR) is a method of extracting thermal energy from the super heated vapour before it is dissipated into the atmosphere via the air cooled condenser. The recovered energy from the refrigeration cycled can be used to produce hot water for sterilization of milking equipment. The aim of this research is to analyse the effectiveness of a heat recovery unit and its impact on the performance of the refrigeration cycle.

Materials and Methods

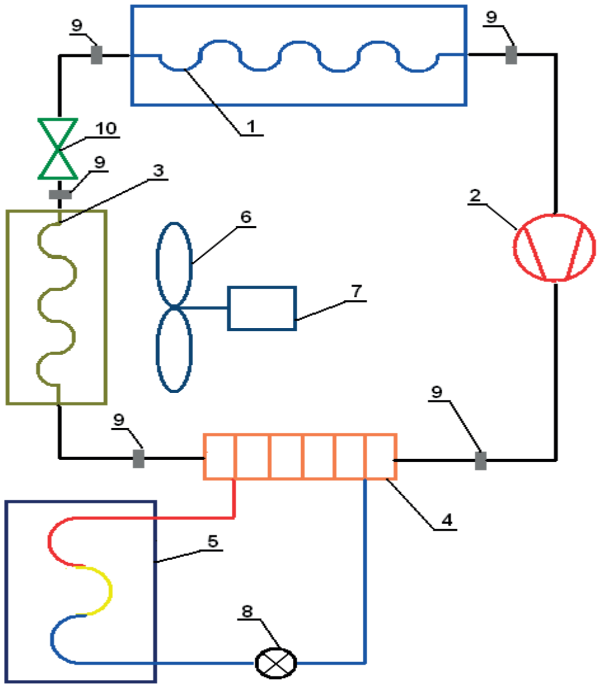

Figure 1: HR test rig: 1-Evaporator, 2-Compressor, 3-Condenser, 4-Heat Exchanger, 5-Water Tank, 6- Air Fan, 7-Variable Speed Control. 8-Water Pump, 9-Pressure-Temperature, Sensor, 10-Expansion Valve.

Two experimental protocols were followed in the testing of the system; the bulk tank was filled with 2000 litres of milk at 35°C and then cooled down to 4°C by the refrigeration system. The heat recovery unit was turned off for protocol 1 and turned on for protocol 2. The experimental test rig consisted of a typical DX bulk tank system with a HR unit. The HR comprised of a smooth plate brazed plate heat exchanger was situated on the refrigeration loop after the compressor. The HR operated on the principle of absorbing thermal energy from the super-heated vapour by pumping water through the HE from a water storage tank and back in a closed loop. Temperature-pressure sensors were placed between each major component of the DX circuit. The condenser was cooled by VS fans. The fan power was dictated by the pressure level in the condenser. To mitigate the disturbing effects of varying ambient temperature; a series of both protocols were run consecutively and the corresponding protocols with the minimum average ambient temperature percentage error were selected.

Results and Discussion

Table 1. Variation between Protocol 1 and Protocol 2.

Protocol	*COP*	*Energy Recovered (kWh)*	*Average Ambient Temperature (°C)*
P1	3.05	0	15.2
P2	3.41	27.6	15.11

The HR unit was capable of increasing the system coefficient of performance (COP) by eliminating the super heat and a portion of the sensible heat from post compressor vapour; this in turn lowered the condensing pressure leading to a reduced work load for the compressor and air fans. The majority of available thermal energy is in the form of sensible heat at low temperatures. This low grade energy is difficult to extract from the system due the small water-vapour temperature differential. While the HR unit did remove some sensible heat from the cycle, the majority of energy came from the super-heated portion. 27.6kWh of thermal energy (34% of thermal energy in the bulk tank) was recovered through the cycle and stored in a water tank. This water can utilised for milking machine and bulk tank wash down purposes.

Conclusions

The HR Unit tested in this study is capable of lowering energy consumption in the refrigeration cycle whilst supplying a substantial amount of thermal energy for water heating. However, the effectiveness of HR relies heavily on the temperature of the milk entering the bulk tank. The introduction of a correctly configured pre-cooling system would greatly reduce the temperature lift in the refrigeration cycle, thus reducing both the impact of the bulk tank HR unit on the system COP and the amount of thermal energy available for recovery.

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Archaeol concentration in total rumen contents of cows offered diets based on ryegrass or white clover

C.A. McCartney[1, 2], I.D. Bull[2] and R.J. Dewhurst[1]
[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Dunsany, Co. Meath;* [2]*School of Chemistry, University of Bristol, Bristol, BS8 1TS, UK*

Introduction

Archaeol is a distinctive membrane lipid in Archaea that has previously been proposed as a potential faecal marker for methanogenesis in cattle (Gill *et al*., 2011). Although the rumen is the main location for methanogens and methanogenesis, there have been no previous studies of archaeol concentration in rumen digesta. This study investigated effects of different diets and time post-feeding on archaeol concentration in rumen digesta. This is important because the rate of colonisation of ingested herbage may be important to understand the diet effects on methane production.

Materials and Methods

Four lactating cows, previously prepared with rumen cannulae, grazed either ryegrass or white clover with 4 kg/d of dairy concentrates in a changeover-design experiment with three 3-week periods. Cows were milked between approximately 7.30 to 8.30am and 3.30 to 4.30pm each day. Rumen contents were obtained by total rumen evacuation on the final 2 d of each period (day 1: 9am; day 2: 3pm). Rumen pH was measured over the 2d prior to the rumen evacuations. Rumen samples were sub-sampled, lyophilised and ground, with 300 mg weighed in triplicate for analysis. Total lipids were extracted from the samples using a modified Bligh-Dyer method. The total lipids were saponified, fractionated into the alcohol fraction, and derivatised prior to analysis by gas chromatography-mass spectrometry (GC-MS). Archaeol was quantified by comparison to an internal standard. Analysis of variance for effects on archaeol, NDF and pH were conducted using REML with 'diet' x 'time' as fixed effects and 'period' + 'cow' as random effects (Genstat, 13th Edition, VSN International).

Results and Discussion

The average coefficient of variation for the archaeol triplicate measurements was 18.6% (SD=1.60). The chemical composition of feeds is provided in Table 1. The lower neutral detergent fibre (NDF) content of white clover herbage was mirrored by lower concentrations in the total rumen contents (Table 2). White clover also led to significantly lower rumen pH at both times, in comparison with ryegrass, and this may relate to the high fermentation rates and reduced levels of rumination and saliva production with white clover (Rutter *et al*., 2002). Concentrations of archaeol in rumen digesta showed a significant diet by time interaction. This effect is probably related to the diurnal grazing patterns and the different rumen conditions associated with ryegrass or white clover diets. Cows tend not to graze at night and have a major grazing bout after morning milking (Rutter *et al*., 2002), so morning samples include a lot of material that has been in the rumen overnight, whilst the afternoon samples include relatively much more recently-ingested herbage. The low concentration of archaeol in the afternoon for cows grazing white clover suggests that Archaea proliferated more slowly with this diet. This may be the consequence of a number of factors, including the lower pH, lower NDF, or higher rumen passage rates (Dewhurst *et al*., 2003). These are all factors that are likely to reduce methane production (Beauchemin *et al*., 2008).

Conclusions

Measurements of archaeol concentrations in the rumen suggest that Archaea were slower to proliferate under the conditions associated with ingestion of white clover, in comparison with ryegrass. This is most likely due to the low rumen pH and NDF concentrations when grazing white clover.

Acknowledgements

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Table 1. Chemical composition of feeds

Component (g/kg dry matter, DM)	Ryegrass	White clover	Concentrates
Organic matter	899	886	914
Neutral detergent fibre	486	231	279
Nitrogen	32.7	49.7	32.0
Water-soluble carbohydrates	101	51.0	89.2

Table 2. Effects of diet and sampling time on rumen pH and the concentrations of NDF and archaeol in rumen digesta

	AM		PM		SED (Diet x Time)	Significance (P value)		
	Ryegrass	White Clover	Ryegrass	White Clover		Diet	Time	Diet x Time
NDF (g/kg DM)	489	402	498	404	14.8	< 0.001	0.551	0.736
Archaeol (mg/kg DM)	5.46	5.82	6.78	3.97	1.039	0.151	0.868	0.040
pH	6.28	5.98	6.07	5.87	0.152	0.036	0.142	0.643

Milking performance of large Irish dairy herds milked in swing-over parlours

J. Jago[1], F. McCoy[2] and P. Edwards[1]
[1]*DairyNZ, Private Bag 3221, Hamilton 3240, New Zealand;* [2]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co Cork.*

Introduction

Reform of the European Union Common Agricultural Policy, to remove milk quotas in 2015 is expected to lead to expansion of dairy herds in Ireland (DAFF, 2010). Larger herd sizes exert pressure on scarce labour resources; therefore more efficient milking systems are required. Farmers need to consider capital investment, labour demand and cow health when designing an efficient milking system. Larger parlours with more units require greater capital outlay but have greater potential throughput. In herringbone parlours, this can result in an increase in the time it takes to milk a batch of cows (row time), unless additional labour is added. Longer row times result in over-milking in parlours not fitted with automatic cup removers and this has been linked with deterioration in teat health (Hillerton et al., 2002). The objective of the study was to quantify the cow throughput and udder health of herds milked in twenty herringbone parlours ranging in size from 14 to 44 units in early and late lactation.

Materials and Methods

The farms involved in this study were participants from a single discussion group, the majority of which were located in the Cork region. Average herd size was 234 (range 76 to 381) cows. Fourteen herds were spring-only calving and four calved cows in both spring and autumn. All farms maintained milking cows in a single herd and were managed so as to maximise pasture grass in the diet. One milking session was observed in September/October 2009 (late lactation) and again in April/May 2010 (early lactation). Total herd milking time (from first cups on to last cups off), number of operators and cows milked were recorded. Labour efficiency measures of cows milked per hour and cows milked per operator per hour were calculated for each herd. Operator work routine time (WRT) was calculated by dividing 3600 by cows milked/operator/h. Milking duration (individual cow cups on to cups off), milk flow duration and over-milking duration (defined as the period when cups are attached but there is no milk flow) were determined for an average of 24 cows (selected by position in row and row number) for each milking session. Teat condition including colour and hyperkeratosis were assessed for 100 teats (25 cows per milking session). Associations between efficiency measures, over-milking duration, hyperkeratosis score and parlour size (linear contrasts) were determined by using REML to fit mixed models including stage (early and late lactation), linear parlour size terms, and interactions of Stage with these as fixed effects and farm as a random effect. The interactions of parlour size and stage were not significant so only the main effects are reported.

Results and Discussion

Parlour size was positively associated with cow throughput ($P<0.001$, Figure 1a) but not cows/operator/hour ($P=0.130$, Figure 2b). Although larger parlours were able to achieve higher throughput they were not more labour efficient than smaller parlours as they required more than one operator. WRT was not associated with parlour size ($P=0.154$). The farms achieving the greatest labour efficiency had WRT of 20-21 s/operator/cow. WRT of less than this required an additional operator, and thus became less labour efficient. When the WRT × units (row time) is greater than individual cow milking time, over-milking will occur. Mean over-milking time was 1.4±0.7 min (range from 0.4 to 2.7 min, early lactation) and 2.3±1.2 min, (range from 0.5 to 4.6 min, late lactation). There was a positive association between parlour size and over-milking duration ($P<0.041$) and hyperkeratosis score ($P=0.049$). Over-milking was positively associated with greater hyperkeratosis in late lactation ($P=0.022$, slope 0.154 $R^2=0.24$).

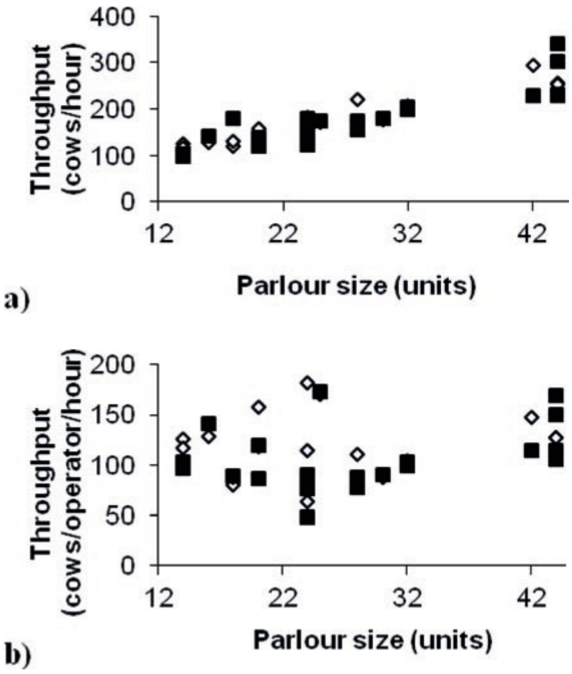

Figure 1. Throughput efficiency (a) and labour efficiency (b) of parlours ranging in size from 14 to 44 units in early (■) and late (◇) lactation.

Conclusions

Larger parlours allow more cows to be milked per hour but are not necessarily more labour efficient. Operators should ensure that row time is matched appropriately to cow milking time. As milking time decreases in late lactation, the WRT may require shortening to prevent over-milking and possible negative impacts on teat end condition and udder health.

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The effect of stocking rate and calving date on grass production, utilisation and nutritive value

B. McCarthy[1], K.M. Pierce[2], L. Delaby[3], A. Brennan[1] and B. Horan[1]
[1]*Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork,* [2]*School of Agriculture, Food Science & Veterinary Medicine, University College Dublin, Belfield, Dublin 4,* [3]*INRA, AgroCampus Ouest, UMR 1080, Production du Lait, F-35590 Saint-Gilles, France.*

Introduction

The Food Harvest 2020 report sets a target for a 50% increase in milk production by the year 2020 (DAFF 2010). This increase will be achieved by maximising milk production from grazed grass (Dillon et al. 2008). Stocking rate (SR), traditionally expressed as cows/hectare (ha), is acknowledged as the main driver of milk production from grass-based systems. There are conflicting reports in the literature regarding the effect of SR on grass production and utilisation (Farina et al., 2011; Macdonald et al., 2008) while little is know of the potential effects of calving date (CD) and interactions between SR and CD. The objective of this study was to investigate the impact of SR and CD on grass production, utilisation and nutritive value.

Materials and Methods

Two groups of dairy cows were established in 2008 and were randomly assigned to one of two mean CD treatments: Early calving (mean calving date: 12th of February) and late calving (mean calving date: 25th of February). Animals within each CD were then randomly allocated to one of three SR treatments, low (2.51 cows/ha), medium (2.92 cows/ha) and high (3.28 cows/ha). A separate farmlet of 18 paddocks was created for each of the 6 treatments. SR treatments were managed independently whereas CD treatments within each SR were managed similarly. Different grazing intensities were imposed on each SR, with target post-grazing residual heights of 4.5-5.0, 4.0-4.5, and 3.5-4.0 for the low, medium and high SR respectively. Concentrate supplementation (per cow) and artificial fertiliser application (per ha) was similar for each SR, however late calving treatments received less concentrate. Pre-grazing herbage mass (HM) and density were measured on each paddock before grazing by cutting and weighing two strips per paddock. Pre and post-grazing sward heights were also measured using a folding pasture platemeter. A subsample was taken from each cut and samples were bulked by week and SR treatment and analysed for chemical composition. Grazing efficiency and total grass production and utilisation were determined using the method of Delaby and Peyraud (1996). Pre-grazing HM, pre and post-grazing sward height, grazing efficiency and the chemical composition of the sward were analysed using mixed models in SAS, with rotation included as a repeated effect. Total production and utilisation was analysed using Mixed models in SAS with block and block*SR included as random effects.

Results and Discussion

Stocking rate had a significant effect on the grazing characteristics as shown in Table 1. Calving date had no effect on any of the grazing characteristics analysed. There was no difference in total grass utilisation between SR treatments although there was a tendency for more grass to be utilised as silage at the low SR. Consequently, insufficient winter feed was produced for the medium and high SR (548 and 492 kg DM/cow) compared with the low SR (885 kg DM/cow). The increased grazing severity of the higher SR treatments resulted in swards of greater nutritive value. The high SR sward had a higher OMD (766 g/kg) and lower ADF and NDF (475 and 279 g/kg) compared with the medium (752, 486 and 284 g/kg) and low SR (748, 481 and 290 g/kg), respectively.

Conclusions

The results of the present study indicate that increasing SR has only a small effect on herbage production but a large impact on grazed herbage utilisation. In the context of the SR used in this study, the results indicate that significant increases in herbage production are required to justify higher SR (the medium and high SR) as insufficient winter feed was produced.

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Table 1: Effect of stocking rate and calving date on grazing characteristics and total production and utilisation

	Stocking rate (SR)				Calving date (CD)			*P*-values	
	Low	Medium	High	s.e.[1]	Early	Late	s.e.[1]	SR	CD
Pre-grazing HM (kg DM/ha)	1349[a]	1243[b]	1252[b]	18.2	1277	1286		<0.001	0.681
Pre-grazing height (cm)	8.4[a]	8.1[b]	8.1[b]	0.07	8.2	8.2		0.002	0.828
Post-grazing height (cm)	4.5[a]	4.0[a]	3.6[c]	0.03	4.0	4.0		<0.001	0.272
Grazing efficiency (%)	82[a]	95[b]	107[c]	0.003	93	96		<0.001	0.493
Feed utilisation									
Grazed (kg DM/ha)	8,989	9,234	9,678	350.9	9,304	9,296	302.0	0.182	0.973
Conserved (kg DM/ha)	2,963	2,134	2,152	385.8	2,411	2,421	320.0	0.086	0.962
Total (kg DM/ha)	11,952	11,368	11,830	248.3	11,716	11,717	219.7	0.072	0.993
Total energy (UFL/ha)	10,281[ab]	9,850[bc]	10,540[a]	206.2	10,221	10,227	182.3	0.013	0.971

[1]s.e. – standard error, [a-c]Means with different superscript within a row are significantly different ($P < 0.05$)

Start up lactation of automatic milking at Moorepark

B. O'Brien, S. Fitzgerald and J. Upton
Livestock Systems Research Department, Teagasc, Moorepark, Fermoy, Co. Cork

Introduction

The use of automatic milking systems (AMS) is becoming increasingly popular. Recent data indicates the presence of AMS on approximately 10,000 commercial farms (De Koning, 2010). The AMS system can perform the tasks of cow identification, teat washing, milking cluster attachment, milking and cluster removal without human intervention. Automatic milking is reliant on voluntary cow traffic i.e. cows present themselves for milking while not being accompanied by a person. This is an extra challenge when cows are at pasture compared to indoors. AMS could be very relevant to dairy farming in Ireland due to labour and land being limiting while simultaneously aiming at expansion of milk production. The objective of this study was to put in place an AMS* at a Moorepark research farm and measure its production characteristics during the start up year.

Materials and Methods

The farm-let with the AMS consisted of a 24 ha milking platform. There were 63 cows in the system with a mean calving date of 15th February (range 1st February-15th March). The dairy featured one Fullwood Merlin 225 AMS unit. Extensive milking and cow information was recorded at each milking (e.g. milk yield, milking time, milk flowrate, somatic cell count (SCC), concentrate level). The grass allocation is critical to optimal cow visits to the AMS unit (it can influence too frequent or infrequent cow visits). The land area was divided into 3 grazing sections of 8 ha each (A, B and C) which are further divided into 1 ha paddocks. The greatest distance between paddock and dairy was 700m which does not deter cows from returning to the AMS for milking. Cows moved between the grazing sections A, B and C at 1:00 am, 11:00 am and 6:30 pm, respectively. Cows were diverted to the AMS for milking as they moved from one section to another. Cows were allocated 5 kg DM in each of the 3 grazing sections (A, B and C) over each 24 h period. Cows grazed to a post-grazing height of 3.5-4.0 cm. All cows received 1 kg concentrate per 24 h during the main grazing period of the lactation.

Results and Discussion

The daily milk yield profile for the start up lactation (to October) is shown in Table 1. Milk protein and fat % ranged from 3.26 and 3.93 in May/ June to 4.20 and 5.04 % in October, respectively. A milk lactose level of 4.47% was recorded in October. Milk SCC was consistently <200x10^3 cells/ml between May and August, and increased to 249x10^3 cells/ml during October. Average milking frequency was 1.8 milkings/cow per day/day, with 113 milkings per day, and 6 milkings per hour between 06:00 and 22:00 (Figure 1). The cows adapted relatively quickly to the AMS (within approx. 4 days). Milk output was influenced by changing cow number as calving occurred and the fact that it was a start-up year when milk yield is expected to be reduced by 10-15% (Wade *et al.*, 2004). Sixty three cows were milked in this study, whereas, up to 112 cows is considered achievable (Jago, *et al.,* 2006) in the longer term.

Table 1. Milk yield profile

Month	Cow no.	milk yield kg/c/d
Mar	42	21.5
Apr	56	21.9
May	60	21.4
Jun	63	23.9
Jul	63	20.9
Aug	63	16.4
Sep	62	14.3
Oct	60	8.5

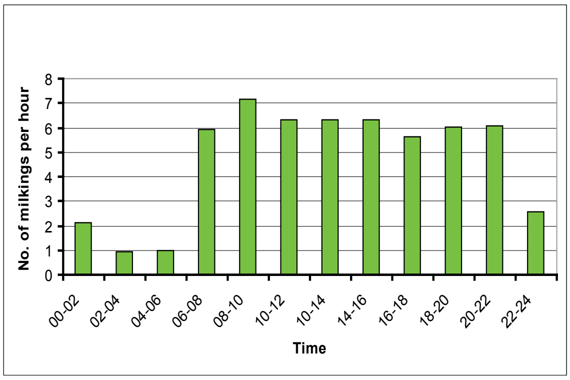

Figure 1. Average distribution of milkings/ 24 h

Conclusions

The aim of the study was achieved in that a herd of 63 cows performed satisfactorily in terms of milk production characteristics and milking frequency during the start up year within an AMS. A number of critical start-up issues were identified, which included (a) a daily data check to ensure milking and health check of all cows, (b) setting aside 0.5 h and 0.25 h at morning and evening time daily for routine maintenance checks, (c) cow selection on udder and teat conformation, (d) replacement of liners at 3-weekly intervals and (f) good backup service

*Merlin AMS supplied by Fullwood Ltd.

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Effect of feed delivery time on the performance of mid/late lactation dairy cows

C.P. Ferris and C.S. Mayne
Agri-Food & Biosciences Institute (AFBI), Largepark, Hillsborough, BT26 6DR

Introduction
Meeting the increased nutrient requirements of high yielding dairy cows remains a key challenge on dairy farms. While many studies have examined nutritional strategies to achieve increased food intakes, for example increasing the nutrient density of the diet, 'non-nutritional' strategies, such as altering feed delivery time, may also have a role to play in achieving higher intakes. While there is evidence that under conditions of heat stress, evening feeding instead of morning feeding can improve feed efficiency and lactation persistency (Aharoni *et al*., 2005), less is known about the effects of time of feed delivery within in a non-heat stressed environment. This may be important, as within a grazing context cows are known to have one of their main grazing bouts during the evening, while on many farms fresh food is offered mid morning, at a time when cows graze relatively little. Thus it has been suggested that synchronising feeding with the time when cows naturally have one of their main 'feeding bouts' may encourage cows to consume more. Indeed, Nikkhah *et al*. (2005) observed that evening fed cows consumed 55% of their total daily intake within 3 hours post feeding, compared to 46% for morning fed cows, while total daily dry matter (DM) intake was 2.0 kg higher with the evening fed cows. Information on milk production was not provided. As this research does not appear to have been replicated elsewhere, a study was conducted to examine the impact of feed delivery time on cow performance under Irish conditions.

Materials and Methods
Twenty-four multiparous Holstein-Friesian dairy cattle (mean lactation number, 3.7: mean live-weight, 637 kg: mean days calved, 210) were used in a two-period (each of five weeks duration) completely balanced change-over design experiment involving two treatments. Treatments examined the effect of either morning (AM feeding) or evening (PM feeding) feed delivery time. Throughout the experiment each treatment group (12 cows/group) was housed in identical, but mirror image pens (16 cubicles). Cows were offered a completed diet (*ad libitum*) containing proportionally 0.55 grass silage (secondary re-growth) and 0.45 concentrate on a DM basis, together with an additional 0.5 kg concentrate (fresh) at each milking. With the AM feeding treatment cows were given access to fresh food at approximately 09.30 h, while with the PM feeding treatment cows were given access to fresh food at approximately 18.00 h. Cows were milked twice daily, being removed for milking at approximately 06.30 h and 14.30 h, with uneaten food from the AM feeding treatment removed when cows were absent for morning milking, while uneaten food with the PM feeding treatment was removed when cows were absent for evening milking. With both treatments, cows were offered fresh food approximately one hour after returning from being milked. Forage offered to cows on each treatment was obtained from adjacent blocks of silage within the silo each day to ensure similar quality. The quantity of fresh food offered, and uneaten food removed was recorded daily, to allow group intakes to be determined. Cow performance data collected during the final week of each experimental period was analysed by ANOVA, taking account of the changeover design nature of the study, with individual cows used as the experimental unit. Group intake data were not analysed statistically, with mean intakes for the two recording weeks presented.

Results and Discussion
Total DM intakes were 20.5 and 20.1 kg/cow/day with the AM and PM feeding treatments, respectively (Table 1). This contrasts with the considerable intake advantage (2.0 kg DM/cow/day) observed with evening fed cows by Nikkhah *et al*. (2005). In addition, feed delivery time had no effect on milk yield, milk composition or fat + protein yield, reflecting the similar intakes observed with both treatments. While it is possible that confined cows may prefer to follow similar feeding patterns as grazing cows, the current experiment was undertaken between early September and early November, at a time of rapidly decreasing day-length.

Table 1 Effect of feed delivery time on dairy cow performance

	Feeding time			
	AM	PM	SEM	Sig
DM intake (kg/day)	20.5	20.1		
Milk yield (kg/day)	25.8	25.4	0.38	NS
Milk fat (g/kg)	46.1	45.1	0.79	NS
Milk protein (g/kg)	37.0	36.5	0.28	NS
Fat + protein yield (kg/day)	2.10	2.05	0.026	NS

Conclusions
Milk production performance was unaffected when fresh food was offered in the evening, rather than in the morning during the autumn period.

Acknowledgements
This study was co-funded by AgriSearch and DARD.

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The effect of roughness of the feeding area surface on the short term intakes of dairy cattle

A.H. Thompson[1] and C.P. Ferris[2],
[1]*Queens University Belfast, Co Antrim.* [2]*Agri-Food and Biosciences Institute, Co Down*

Introduction

In many livestock houses concrete feed passages have become corroded by long term exposure to silage acids, often exposing sharp aggregates within the concrete, and leaving the feeding surface rough. However, there is anecdotal evidence that rough feed passage surfaces may have a negative effect on the intake, behaviour and health of cattle. Indeed, Bickert (1990) suggested that the eating surface must be smooth, clean and free of left over feed and debris in order to encourage high food intakes and minimise the risk of disease. This may be particularly important with high yielding dairy cows where high food intakes are necessary to minimise negative energy balance. To address this issue, an experiment was conducted to examine the effect of roughness of the surface of the feeding area on the short term intake of dairy cattle.

Materials and Methods

Fourteen late lactation Jersey × Holstein crossbred cows (average milk yield, 15.6 kg/day) were used in a two-treatment completely balanced change over design experiment, with cows paired on the basis of milk yield. Cows were offered a mixture of grass silage and maize silage (50:50 dry matter basis), together with 5.0 kg of concentrate in the milking parlour (split between two equal feeds) for a six week period prior to measurements commencing. During this period cows were housed in a pen with a concrete feeding surface with an 'intermediate roughness' and were trained to enter the pen individually and to feed out of a 'wooden frame' placed on the feed passage surface. The frame had internal dimensions of 61 × 61 cm, a depth of 15.5 cm, while the corners of the frame were 'filled in' using wooden triangular blocks to a distance of 15 cm from the corner. The latter was to prevent food being pushed into the corners where it may have been inaccessible. The experiment was conducted in an adjoining pen where the surface of the concrete feeding area was extremely rough, with aggregate exposed. Treatment 'Rough' involved placing the wooden frame over a pre-defined area of the rough surface and allowing cows to feed of that surface. With treatment 'Smooth', cows fed from an identical wooden frame, fitted with a 'Stock Board' base (made of 'smooth' recycled plastic). The experiment was initially conducted using the forage mix described above as the test diet, and then repeated using a pelleted concentrate as the test diet. With each test diet, intakes were measured during two consecutive days. On each measurement day food was removed from the group of cows at 05.30 h (during milking), with cows not having access to food thereafter, until the experiment commenced. On Day 1, one cow from each pair was assigned to the Rough treatment, and the second cow to the Smooth treatment, with treatments reversed on Day 2. Each cow was brought into the pen individually (in the same order each day) and offered 1.5 kg of the forage mix (fresh basis), placed in the centre of the wooden frame. The quantity of food remaining uneaten was recorded after 180 seconds, its DM determined and DM intake calculated. If cows stopped feeding during the observation period the duration of this 'non-feeding' period was recorded. Non-feeding was defined as the cow lifting her muzzle above the top of the wooden frames. This process was repeated approximately one week later, with cows given access to 1.0 kg of pelleted concentrate for 90 seconds. Dry matter intakes per second were subsequently calculated, with data from cows which had a non-feeding period of >30 seconds excluded (n = 7 cows offered the forage mix). Data from each test diet were analysed by ANOVA, taking account of the change over design nature of the experiment.

Results and Discussion

When offered the forage mixture, DM intake was unaffected by roughness of the feeding surface ($P>0.05$). However, when offered the concentrate pellets, intakes were significantly lower for cows feeding from the rough compared to the smooth surface (6.0 and 6.7 g DM/sec, respectively: $P<0.05$). This experiment provided clear evidence that during a short term measurement period cows consumed concentrates at a slower rate from a rough surface than from a smooth surface. That forage intakes were unaffected by the feeding surface may be due to the cows being able to consume the bulky forage while making minimal contact with the surface with their tongues.

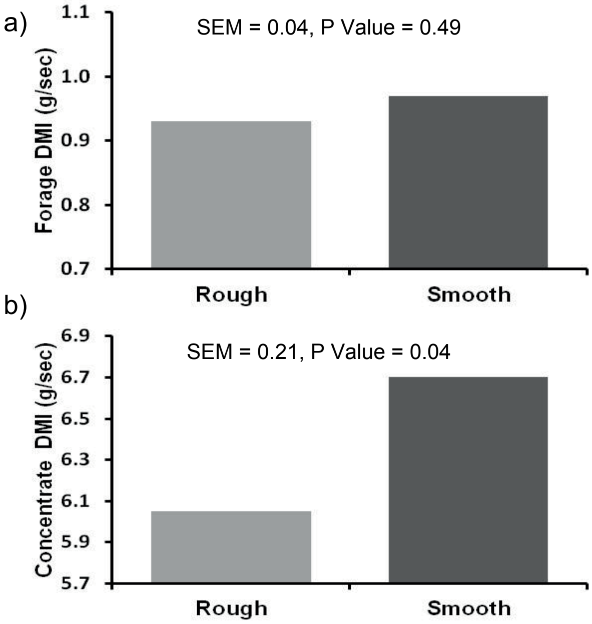

Figure 1. Effect of roughness of the feeding surface on the short term intake of, a) Forage and b) Concentrates

Conclusions

Eating rate of concentrate, but not forage, was reduced with a rough feeding surface.

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The effects of milking machine wash volumes on TCM residues in milk.

Ryan, S[1], Gleeson, D[1], O' Brien, B[1] Jordan, K[2], and Furey, A[2]
[1]Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co Cork, [2] Teagasc Food Research Centre, Moorepark, Fermoy, Co Cork, [3] Cork Institute of Technology, Co. Cork

Introduction

High fat dairy products, such as milk and butter can be contaminated with a residue called trichloromethane (TCM) during processing. TCM target levels of <0.002 mg kg^{-1} in milk have been set by countries importing butter products in order to achieve the required minimum levels in the finished product (<0.03 mg kg^{-1}). TCM results from the use of chlorine detergent/sterilizer solutions as part of the equipment cleaning process. If chlorine comes into contact with milk TCM is formed (Tiefel and Guthy, 1997). An increase in the formation of TCM occurs in recycled detergent solutions when post rinsing is omitted from the milking machine wash procedure (Resch, and Guthy, 2000). Various volumes of rinse water are used on-farm as part of the milking machine cleaning process. A rinse volume of 14 L per milking unit has been recommended for effective cleaning. (O'Brien, 2009). The objective of this study was to investigate the effect of four rinse water volumes (7, 10, 14 and 16.5 L/milking unit) on TCM levels in milk.

Materials and Methods

A circulation cleaning procedure was conducted in a 30-unit milking machine plant. The cleaning stages included (a) an initial pre-wash rinse with cold water at a volume of 14 L per milking unit, (b) a hot (70^{0}C) detergent/sterilizer wash at a water volume of 12 L/milking unit and (c) a post-wash rinse with cold water with different water volumes of 7, 10, 14 and 16.5 L/milking unit. The sterilizer element of the cleaning product contained a working solution of 263 ppm of chlorine. Each rinse water volume was evaluated over a 5-day period (10 milking events). Two milk samples (100 mL per sample) were obtained from the milk line during am and pm milking. The experimental dairy farm milking management procedure involved a milking interval of 17/7 (17 h between evening and morning milking and 7 h between morning and evening milking). Sample one was taken at the start of milking (first milk) as the initial milk was pumped from the receiver jar and the second sample was taken mid-way through milking (mid milk). Milk samples were analysed for TCM using head-space gas chromatography. Statistical analysis included a repeated measures model using ProcMixed in SAS 2009. The model included terms for rinse water volume (L), stage of sampling (first, mid), time (am, pm) and their interactions. Pair-wise comparisons were performed and a Tukey-Kramer adjustment was employed.

Resultsand Discussion

Reducing the rinse water volume from 16.5 to 7 L per milking unit resulted in an increase in TCM concentration of 0.004 mg kg^{-1} in the combined morning and evening milk samples (P<0.001). No statistical difference in milk TCM concentration was observed when 10 L per milking unit was employed compared to the recommended rinse volume of 14 L per milking unit. Reducing the rinse water volume from 16.5 to 14 L per milking unit resulted in an average increase in TCM concentration of 0.002mg kg^{-1} (P<0.05) in the 'first milk' sample but not in the 'mid milk' sample (Table 1). Furthermore, milk TCM concentrations were highest at 'first milk' (0.0097 mg kg^{-1}) with a water rinse volume of 7 L per unit compared to the three other rinse volumes (P<0.05). This effect was observed due to the 'first milk' sample being the first milk to come in contact with the cleaned equipment surface during the milking and TCM in the 'mid milk' sample being diluted by the larger milk volume during the main milking period. When data for am and pm milkings were compared, the average concentrations of TCM were generally higher at the pm milking compared to the am (P<0.01). The shorter interval prior to pm milking means reduced time for drainage of rinse water from the plant and reduced milk yield at that milking. The combined effects of rinse water in the milkline being diluted with a lower milk volume may explain the higher TCM concentrations at pm milking.

Conclusions

Increasing rinse water volume will reduce TCM residue levels in bulk milk. The implementation of the recommended volume of rinse water (14L/milking unit) was highly critical in minimising the accumulation of TCM in milk. A higher rinse water volume of 16 L per milking unit will minimize TCM residues in the 'first milk' and where milk volumes are low.

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Table 1. Effect of varying the rinse water volume of a milking machine wash routine on TCM concentrations in milk

	Trichloromethane concentration obtained, mg kg^{-1}				sed	P-value
Rinse volume	16.5 ^{b}	14 ^{a}	10 ^{a}	7 ^{c}	0.10	***
First Milk	0.0020^{c}	0.0040^{b}	0.0044^{b}	0.0097^{a}	0.12	*
Mid Milk	0.0009 ^{b}	0.0013 ^{ab}	0.0006 ^{b}	0.0017 ^{a}	0.17	*
Am	0.0018 ^{b}	0.0019 ^{b}	0.0015 ^{b}	0.0038 ^{a}	0.10	**
Pm	0.0014 ^{c}	0.0033 ^{b}	0.0036 ^{b}	0.0076 ^{a}	0.10	**

Means with a common superscript are not significantly different; *** <0.001; ** <0.01; * <0.05

Energy consumption of an automatic milking system

J. Upton[1], G. O'Riordan [2], B. O'Brien[1] and S. Fitzgerald[1]

[1] *Livestock Systems Research Dept., Animal & Grassland Research & Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork,* [2]*Dept. of Mechanical Engineering, Cork Institute of Technology, Cork*

Introduction

Recent data shows that there are approximately 10,000 commercial farms worldwide using automatic milking systems (AMS) to milk their cows. This figure is expected to grow rapidly in the coming years (De Koning, 2011). Therefore, the energy consumption of AMSs will become increasingly important. Studies by Bijl *et al,* (2007), and Artmann & Bohlsen, (2000), showed that electricity costs were greater with AMSs compared to conventional milking systems. However these studies did not give detailed component breakdown information. The aim of this study was to document the electricity consumption of a recently installed AMS at Moorepark for the period 1st May to 31st October, 2011.

Materials and Methods

A herd of 63 spring calving cows were milked from pasture using a Merlin AMS*. Data presented here pertains to the period from 1st May to 31st of October. Cows were milked on average 1.8 times per day. Average milk yield over the period was 17 litres per cow per day. The AMS was washed with hot water 3 times per day during weeks 1-6, and twice daily, thereafter. Water heating was provided by electrical water heaters. Milk was pre-cooled using a Packo tubular cooler (model TT2) supplied with well water and subsequently, by a 5,000 litre ice bank tank. The vacuum pump was a vane pump with a 3kW motor. Vacuum level was controlled by a standard regulator from weeks 1-6, while a variable speed drive (VSD) controlled pump with 1.1kW motor was used thereafter. Compressed air was supplied by a 2.2kW compressor. The energy consumption of the AMS was monitored using Sinergy Escot energy monitoring equipment and software. The Escot data-logger can measure power consumption of multiple electrical circuits using clip-on AC current transducers. The logging software records cumulative kilowatt-hour (kWh) readings every 15 minutes. Measurement equipment was calibrated and accurate to ±1% of reading. This equipment allowed for measurement of the following individual components in the dairy: milking robot, vacuum pump, air compressor, milk cooling and water heating.

Results and Discussion

Water heating accounted for 37.1Wh/l (Watt hour per litre) of milk produced. The milk cooling system, air compressor, vacuum pump and robot consumed 14.8Wh/l, 14.7Wh/l, 11Wh/l and 2.9Wh/l, respectively. Miscellaneous items such as lighting and an office consumed 16.4Wh/l. The average total electricity consumed per litre of milk produced between 1st May and 31st October was 97.4Wh/l. When the relevant tariffs are applied the average cost of electricity was 1.25 Euro cent per litre of milk (c/l). The cost of electricity varied from 0.82 to 1.87 c/l as the volume of milk harvested by the AMS varied over the season from the spring-calved herd (Figure 1). Water heating was the largest consumer of electricity in this study at 38% of the total. This requirement is a consistent fixed cost irrespective of the volume of milk produced because wash cycle scheduling is time based. These average costs of 1.25 c/l were high compared to an audit of conventional milking systems (0.43c/l) on 21 commercial dairy farms (May-October 2010) (Upton *et al,*2011). This may be due to (a) reduced milk output from the AMS due to it being the start-up year, when milk yield is expected to be reduced by 10-15% (Wade *et al,* 2004) and/ or (b) under utilization of the AMS. 63 cows were milked in this grazing based study, whereas the possibility to extend capacity to 112 is considered achievable (Jago *et al,* 2006). The change to a VSD vacuum pump in week 6 reduced vacuum pump running costs by 55% (from 0.28 to 0.13 c/l).

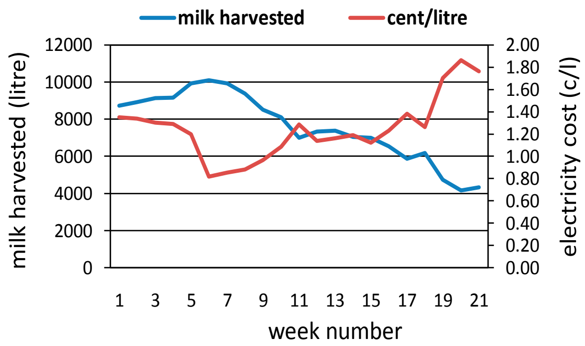

Figure 1; Seasonal variation in electricity costs per litre of milk harvested (c/l) with an AMS system

Conclusions

Average electricity costs of the AMS tested with 63 cows was 1.25 c/l. This is likely to be reduced as cows become familiar with the AMS and optimum herd size/milk output for the AMS is reached. Suitability of a heat recovery system and cold detergent wash cycles will be investigated in 2012 to moderate running costs further.

* Merlin AMS supplied by Fullwood Ltd

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Sulfonylurea herbicide resistance in common chickweed (*Stellaria media L.*) in Irish cereal fields

T O'Donovan[1], J. Kinsella[2] D.Pey[1] and P.D. Forristal[2] [1]*Teagasc, Kildalton College, Piltown,* [2]*Crops Research , Oak Park, Carlow,* [3]*Waterford Institute of Technology.*

Introduction

Common chickweed (*Stellaria media L.)* has been predominately controlled in Irish tillage for the last 25 years by the acetolactate synthase (ALS) inhibiting sulfonylurea herbicides (e.g. metsulfuron). Biotypes of *Stellaria media L. (S. media)* showing resistance to metsulfuron were first reported in 1996 in Ireland (Heap, 2011). The extent of the problem in Ireland was thought to be confined to a small number of fields where metsulfuron had been the sole herbicide used over a number of years. To delay the development of resistance it is recommended to apply herbicides from two or more chemical groups which are active on the target weeds. There has been an increasing number of reports by farmers and advisers of poor control of *S. media* even where two herbicide groups have been applied in combination. This study investigates if ALS resistant *S. media* biotypes have developed in fields where both ALS and non-ALS herbicides have been applied in combination.

Materials and Methods

Samples of mature *S. media* were collected from 20 cereal fields in the major cereal growing regions, where advisors reported unsatisfactory weed control, and where two herbicide chemical groups had been used in combination for a number of years. In addition two *S. media* samples ('susceptible standards') were collected from grassland fields, where ALS inhibiting herbicides had not been applied previously. *S. media* seeds from the sampled fields were sown into potting compost and at cotyledon stage, single plants were transplanted into 10 cm pots. Plants were grown in an un-heated glasshouse to the 4-8 leaf stage, before the application of herbicide treatments on 2nd February 2011. Treatments (representing manufacturers recommended rates) were: (A) metsulfuron-methyl (Lorate, DuPont), at 6 g a.i. ha^{-1}; (B) mecoprop-P (Duplosan KV, Nufarm UK) at 1380 g a.i. ha^{-1} and (C) no herbicide. A total of 10 replicates, with a single plant per pot, of each of the 22 biotypes were allocated to each treatment (660 pots in total). The herbicides were applied using an Oxford precision sprayer delivering 220 l/ha. The individual pots were then randomly assigned to replicate blocks and placed back on the glasshouse bench. Pots were hand watered each day, to avoid wilting. Fresh foliage weights were recorded after 35 days, when all susceptible standards were completely controlled. The weight data was log-transformed and analysed by ANOVA for factorial design (Genstat)

Results and Discussion

Plant weight data for both herbicides is presented in Fig 1. The two susceptible *S. media* standards (biotypes 16 & 17), sprayed with either metsulfuron or mecoprop-p, had a greater than 90% reduction in fresh weight compared to unsprayed controls, indicating satisfactory herbicide performance. However, 14 of the 20 biotypes harvested from the sample cereal fields exhibited reduced sensitivity (<80% control) to metsulfuron. Seven of the biotypes had less than 50% reduction in weight following metsufuron application indicating resistance to this herbicide. While all the populations were sensitive (greater than 80% reduction in fresh weight compared to controls) to mecoprop-P, there were some significant differences in sensitivity between populations to this chemical.

Conclusions

Populations of S. *media* showing both reduced sensitivity and resistance to metsulfuron (and possibly other ALS-herbicides) have developed in fields where ALS and non-ALS herbicides were used in combination. Mecoprop-P remains effective against S. media when used at full rates. Growers need to select appropriate herbicide types and application rates for their weed populations.

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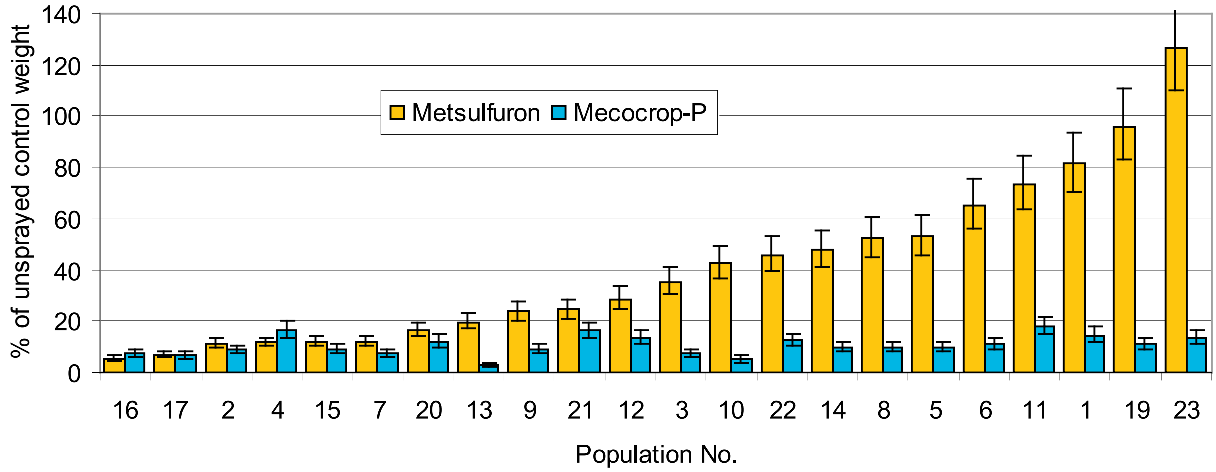

Fig 1: Effect of Metsulfuron and Mecoprop treatment on 22 S. media samples. % of treated sample weight relative to unsprayed control, ranked by metsulfuron sensitivity. (Error bars: 95% confidence intervals).

The effect of straw incorporation and seeding rate on growth and grain yield of minimum-tillage established spring barley over a three year period.

S. Walsh, T. Delaney, W. Corrigan, T. McCabe.
School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4.

Introduction

Residue incorporation in the soil has many benefits, perhaps the most important is to build up organic matter (Holland, 2004), which is a key indicator of soil quality (Schjonning *et al*., 2004). Residues also help to protect the soil from weather erosion and promote microbial activity by providing organic-C (Borresen, 1999). Hackett et al., (2010) outlined how soil organic carbon levels change in response to management practices and increases occur very slowly over time. This study investigated how straw incorporation treatments in a minimum tillage system affected the crop performance and grain yield of spring barley.

Materials and Methods

This field trial study was conducted from 2009 to 2011 on spring barley grown in a minimum tillage cultivation system on a medium-heavy clay soil at UCD Lyons Research farm, Newcastle, Co. Dublin. Four straw incorporation treatment programmes were tested with cumulative incorporation rates of 0, 8, 16 and 24 t/ha according to the schedule in Table 1. For the appropriate treatments 8 t/ha of chopped barley straw was incorporated in late-winter to a depth of 10 cm. The crop was drilled with a Vaderstad disc drill in late-March/early April in each year. The trial had a 4 x 3 factorial design with 4 replications, plots size was 3 x 15m. In both year 2 and 3 three seeding rate treatments (low, medium and high) were tested across the four straw incorporation schedules. In year 1 fungicide strategies were tested across the zero and 8 t/ha straw incorporation treatments but data is only presented here for the mean grain yields for the straw incorporation treatments (Table 1.). The crop was monitored for agronomic performance throughout the season. Visual assessments of the crop were taken over a three week period once the crop had established Pre-harvest yield indicators were taken and grain yield and quality data were collected. Data was subject to analysis of variance in ARM(GDM, 2012).

Results and Discussion

The minimum tillage system was a successful establishment method for spring barley in each of the three years with % crop canopy cover above 81% in all straw treatments. The straw incorporation treatments had an effect on crop canopy cover as the % crop canopy cover was significantly reduced following straw residue incorporation in each season ($P<0.001$). In year 1 and year 2 the grain yield data showed a significantly lower grain yield following straw incorporation in both seasons ($P<0.001$). In year 3 there was no significant yield difference between the four straw incorporation programmes. Over the three years the grain yields were consistently lower where straw residue was applied/incorporated in a growing season and was relatively higher for the no residue or "old" residue treatments. The higher seeding rate treatment significantly increased % canopy cover over the low seeding rate in each year but only significantly increased grain yield in year 3. In this study there was a trend of small increases in soil OM% levels in response to the higher rate straw incorporation treatments but the effects were not significant ($P<0.05$).

Conclusions

After three years of straw residue incorporation on spring barley in this minimum tillage system no grain yield penalty was recorded. However shallow residue incorporation did consistently reduce crop canopy cover , hence higher seed rates may be advisable for spring barley production in a minimum tillage system where straw incorporation is also being practiced.

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Table 1. The effect of straw incorporation rate and seeding rate on % crop canopy cover and grain yield of spring barley over the three years 2009 (Yr 1), 2010 (Yr 2) and 2011 (Yr 3).

Factor A – Straw Incorporation Rate (t/ha)					% Canopy Cover		Grain Yield (t/ha)		
Treatment	Yr 1	Yr 2	Yr 3	3 Yrs	Yr 2	Yr 3	Yr 1	Yr 2	Yr 3
1	0	0	0	0	93.8	86.3	6.67	8.01	7.70
2	0	8	0	8	80.8	84.4	--	7.02	7.74
3	8	0	8	16	93.9	81.6	4.85	8.16	7.52
4	8	8	8	24	84.6	81.4	--	7.51	7.60
Level of significance					***	***	*	***	n.s
L.S.D (P<0.05)					4.6	2.37		0.44	--
Factor B – Seedrate (kgs/ha)									
1	Low - 120 kgs/ha				85.4	77.2	--	7.56	7.48
2	Medium - 180 kgs/ha				87.2	84.0	--	7.58	7.67
3	High - 240 kgs/ha				92.2	89.0	--	7.88	7.77
Level of significance					**	***	--	n.s	**
L.S.D (P<0.05)					4.0	2.05	--	--	0.17

The effect of rotation and input level on winter wheat performance

P D Forristal[1], B.Burke[1], and J. Grant[2]
[1] *Teagasc, CELUP, Crops Research,, Oak Park, Carlow*
[2] *Teagasc, Ashtown, Dublin 15*

Introduction

Crop rotation was an integral part of production systems until relatively recent times (Wibberley 1996). However in Ireland, as only 9.6% of the cropped area is sown to break crops, monoculture or cereal rotations (e.g. oats followed by wheat) are quite common today (Anon 2009). Lack of rotation can increase disease pressure and reduce soil fertility. The use of inputs such as fertiliser and agrochemicals are a significant production cost on farms. Since the introduction of winter cereals and simultaneous development of effective fungicides, Ireland has developed a relatively high-input cereal production system to exploit the high yield potential that the climate brings. The Knockbeg systems trial was established to examine the effects of rotation and input levels on crop production. The aim of the work described here was to determine the effect of rotation type and input level used, on winter wheat grain yield and profit margin.

Material and Methods

The crop systems trial was established at the Knockbeg site (52.864 N, 6.942 W) in south east Ireland in 1996. Winter wheat is grown in two rotations: a five course break-crop rotation including oilseed rape, beans and three cereals (BC); and a three course cereal rotation with winter oats sown prior to wheat (CR). Wheat is also grown as a monoculture (CW). Two levels of input were applied: 'High' where typical commercial rates of all inputs were used and; 'Low' where 80% of the applied N rates and 50% of the rates of fungicide and herbicide products were used compared to the 'High' input treatment. The experiment was laid out as a split-plot structure with a factorial combination of rotation and input as the main plot treatments, which were replicated four times, and crops within rotations laid out as sub-plots (12mx30m). In this paper the performance of winter wheat is considered with yield and profit margin from the period 2004 to 2010 being presented. Net profit margins for each sub-plot were generated using yield data and standard costs for the input levels being used (Anon 2011). Analysis was by SAS Proc Mixed To examine annual variation, best linear unbiased prediction (BLUP) was used with year as a random effect.

Results and Discussion

There was a significant interaction ($P<0.05$) between rotation and input level. The individual input by rotation results are presented for all years in Table 1. Performance varied from year to year. While there was a trend for wheat grown in rotation to yield more than continuous wheat, this was often only significant at the low level of inputs, where the yield drop with continuous wheat was substantial at 1.5t ha^{-1} over all years. There was very little difference in wheat performance between the two rotations. In many of the years, reducing inputs had little impact on the yield of wheat grown in both the BC and CR rotations, but it generally had a significantly negative effect on CW yield. The low input system was significantly more profitable with wheat grown in rotations in 5 of the 7 years. When yield potential was high, input level had no effect on profit margin in the rotation crops. With continuous wheat, the use of low levels of inputs tended to reduce profit margin, although there was year to year variation.

Conclusion

There is a strong interaction between rotation and input level which impacts on crop performance. With wheat grown in a BC rotation inputs can be lowered with no impact on yield, resulting in a significant positive impact on margin. High inputs are beneficial with continuous wheat.

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Table 1: The impact of rotation type and input level on the yield and profit margin of winter wheat.

	Yield (t ha^{-1})						Margin (€ ha^{-1})					
Year	High Inputs			Low Inputs			High Inputs			Low Inputs		
	BC	CR	CW	BC	CR	CW	BC	CR	CW	BC	CR	CW
2004	12.2^{a}	12.9^{a}	11.9^{ab}	11.1^{b}	10.9^{b}	9.4^{c}	832^{a}	945^{a}	790^{a}	813^{a}	788^{a}	544^{b}
2005	9.6^{ab}	10.0^{ab}	9.1^{bc}	10.4^{a}	9.9^{ab}	8.4^{c}	412^{a}	479^{ac}	327^{a}	705^{b}	633^{bc}	392^{a}
2006	10.6^{a}	11.5^{a}	10.5^{a}	10.9^{a}	10.9^{a}	9.4^{b}	574^{a}	716^{ab}	564^{a}	788^{b}	792^{b}	551^{a}
2007	10.0^{ab}	11.1^{a}	9.4^{b}	10.2^{ab}	10.3^{ab}	8.1^{c}	482^{ac}	647^{ab}	382^{ac}	673^{b}	699^{b}	345^{c}
2008	10.5^{a}	11.7^{b}	11.1^{ab}	10.7^{ab}	11.0^{ab}	9.9^{a}	586^{a}	758^{ab}	657^{ab}	770^{b}	804^{b}	614^{ab}
2009	9.7^{a}	10.5^{a}	9.5^{a}	9.7^{a}	9.6^{a}	8.1^{b}	436^{abc}	564^{ab}	403^{bc}	597^{a}	586^{a}	336^{c}
2010	9.9^{a}	9.9^{a}	9.4^{a}	10.2^{a}	9.3^{ab}	8.3^{b}	471^{a}	464^{a}	388^{a}	677^{b}	532^{ab}	367^{a}
All	10.4^{a}	11.1^{b}	10.2^{a}	10.4^{a}	10.3^{a}	8.8^{c}	542^{a}	653^{b}	502^{a}	717^{b}	691^{b}	451^{a}

[*]Means with a common superscript across each treatment row are not significantly different ($P<0.05$).

Simulation of greenhouse gases and organic carbon in an Irish arable land using the ECOSSE Model

M.I. Khalil[1,2], J.U. Smith[3], M. Abdalla[4], P. O'Brien[1], P. Smith[3] and C. Müller[2]

[1]Climate Change Research, Environmental Protection Agency, Wexford, Ireland [2]School of Biology and Environmental Science, University College Dublin, Dublin 4, Ireland. [3]Institute of Biological & Environmental Sciences, University of Aberdeen, Scotland, United Kingdom.[4]School of Botany, Trinity College Dublin, Dublin 2, Ireland

Introduction

Agriculture contributes one-third of global greenhouse gas (GHG) emissions (e.g., N_2O, CO_2 and CH_4) to the atmosphere. Improved understanding and quantification of changes in C and N due to anthropogenic activities associated with agriculture are important to reduce uncertainty in their estimates. Use of a process-based model for more accurate estimation, including reporting and mitigation, of GHGs emitting from agricultural systems is a priority research focus. The notion is that improved modelling of soil processes could greatly enhance the value of national inventories. Our aim is to evaluate simulation of GHG emissions and soil organic carbon (SOC) stock changes under arable farming using a multi-pool dynamic model.

Materials and Methods

The ECOSSE (Estimating Carbon in Organic Soils-Sequestration and Emissions) model has several advantages, including limited meteorological and soil data requirements, compared to other models (Smith et al., 2010). It can simulate the impacts of land-use, management and climate change on C and N emissions and stocks at field and national scales. The model was used to predict GHG emissions and SOC changes in an arable land cropped with spring barley. The crop received different N applications (N_0 = unfertilized control, N_1 = 70-79 kg N ha^{-1} and N_2 = 140-159 kg N ha^{-1}) as calcium ammonium nitrate. The simulated outputs were evaluated statistically (e.g., relative and root mean square errors, correlation coefficient) against measured N_2O fluxes derived from a two-year seasonal study (Abdalla et al., 2009) and for annual CO_2 and CH_4 emissions measured in a nearby field.

Results and Discussion

The modelled responses of N_2O fluxes were mostly consistent with the corresponding measured values (Fig. 1). The bias in the total difference between measured and the corresponding modelled N_2O fluxes was large, due to the impact of a large negative value. In the fertilized fields, significant correlation between modelled and measured N_2O fluxes was observed, with correlation coefficients of 0.54-0.60 and root mean square errors of 18.6-20.8 g N ha^{-1} d^{-1}. The measured seasonal (crop growth period) N_2O losses were 0.41 and 0.50% of the N applied at rates of 70-79 and 140-159 kg ha^{-1}, respectively. The corresponding seasonal simulated N_2O losses, with values for the dates of measurements taken, were 0.69 and 1.11% of the added N. The model estimated 70-123% more N_2O emissions than the measured values, attributing to missed emissions associated with the sporadic timing of mea-surements (2 to 15 days interval). The corresponding simulated annual losses obtained by summing the modelled daily fluxes were 0.49 and 0.62% of applied N, more closely matching the measured values.

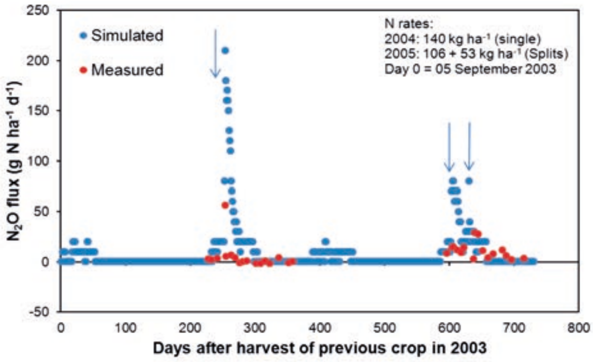

Fig. 1. Measured and simulated N_2O fluxes from spring barley field received the highest N rate (N_2).

Irrespective of N rates, the model estimated on average an annual heterotrophic respiration of 4.0 t CO_2-C ha^{-1} yr^{-1} (Fig. 2). This amount is 42% of the soil respiration measured from a nearby field (9.6 t C ha^{-1} yr^{-1}) and is similar to values reported elsewhere. Regardless of N rates, the simulated CH_4 fluxes were negligible for the arable field, which was identical to a measured one (-0.06 kg C ha^{-1} yr^{-1}). The N application rates had no significant effect but on average a high loss (1.06 t C ha^{-1} yr^{-1}) was predicted, ascribing to an error associated with leftover crop residue-C to enrich total soil C pool.

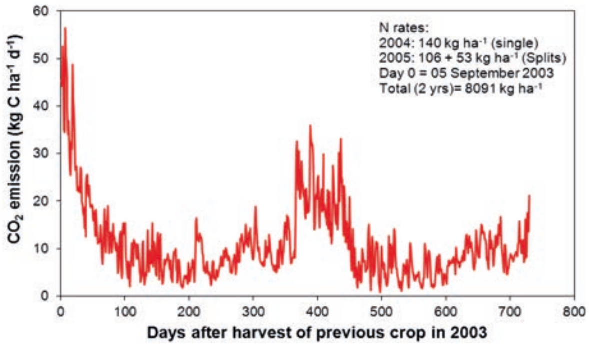

Fig. 2. Simulated soil CO_2 fluxes from the spring barley field received the highest N rate (N_2).

Conclusions

Results suggest that the model can reliably be used to estimate the process-based emissions of GHGs from arable fields. However, further refinement of the model for a reliable estimate of coupled GHG emissions and SOC stock changes in agricultural soils, including analyses to fully determine the uncertainty in their estimates across land-uses and soil types, are required.

Acknowledgements

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Relationship between forage maize yield and early season temperature in a marginal climate

E.J. Meehan and T.J. Gilliland
Agri-Food and Biosciences Institute (AFBI), Crossnacreevy, Belfast BT6 9SH

Introduction

Forage maize (*Zea mays*) varieties have been tested in Northern Ireland since 1996 with the highest mean annual yields occurring in 2010 and the lowest in 2011. The average DM yield (t/ha), starch yield (t/ha) and energy yield (GJ/ha) of the top five varieties was measured annually from 2001 in trials which were sown both in the open (O) and under plastic film (P). This study uses data from the Northern Ireland maize recommended list trials (Gilliland, 2001-2010) (Gilliland and Meehan, 2011) with the objective of understanding the relationship between yield and early season temperatures in plastic mulched and open sown forage maize managements in Ireland.

Materials and Methods

Trials were established and managed in accordance with UK national list testing procedures (www.defra.gov.uk) and seed was sown at 100,000 seeds/ha at a depth of 3 cm and spacing of 13 cm within rows and 75 cm between rows in both open and plastic film systems. Plastic film was a 6 µm photodegradable plastic covering rows 1 & 2 and rows 3 & 4. The yields were based on samples of 100 plants from each of three replications. Mean temperatures were taken from the NI Met Office (www.metoffice.gov.uk). Data from 2001-2011 were analysed for correlation between mean monthly temperatures (May, June, July) and annual maize yields in GenStat (Release 14.1).

Results and Discussion

The DM yield of the top five varieties serves as an overall indicator of maize performance in a given year as the turnover of maize varieties will not allow for meaningful long term controls. Open sown maize data correlated better with a weighted temperature (WT) which is the average of mean monthly temperatures: (May + (2 x June) + July).

Table 1. Correlations between maize yields and temperature measurements (2001-2010)

	Plastic sown maize			Open sown maize			
	DM (t/ha)	Starch (t/ha)	Energy (GJ/ha)	DM (t/ha)	Starch (t/ha)	Energy (GJ/ha)	June temp. (°C)
Starch yield (t/ha)	0.86 **	-	-	0.94 ***	-	-	-
Energy yield (GJ/ha)	0.98 ***	0.89 ***	-	1.00 ***	0.96 ***	-	-
June temp. (°C)	0.70 *	0.66 *	0.65 *	0.68 *	0.68 *	0.71 *	-
WT (°C)	0.62 ns	0.58 ns	0.55 ns	0.79 **	0.79 **	0.79 **	0.78 **
OHU	0.45 ns	0.52 ns	0.36 ns	0.74 *	0.86 **	0.76 *	0.54 ns

Sig. * P< 0.05, ** P< 0.01, *** P<0.001 OHU = Ontario Heat Units

In contrast, the faster developing plastic mulched maize productivity correlated best with the mean June temperature alone. For example, regressions produced in 2010 successfully predicted DM yields in July 2011 for the top five varieties within 0.5 t (DM) /ha of the actual yields achieved in November 2011 (Fig. 1 and Fig. 2). These temperature indicators provided stronger correlations than Ontario Heat Units (OHU) except for open sown maize starch yield (Table 1). In addition, unlike OHU which are only available after harvest, these temperature indicators can be used to provide predictions during a growing season.

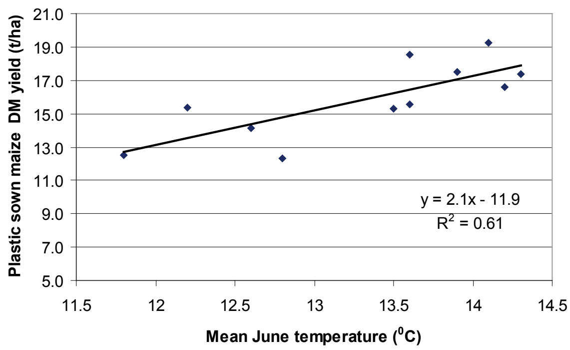

Fig. 1. Correlation between DM yield (P) and June temp.

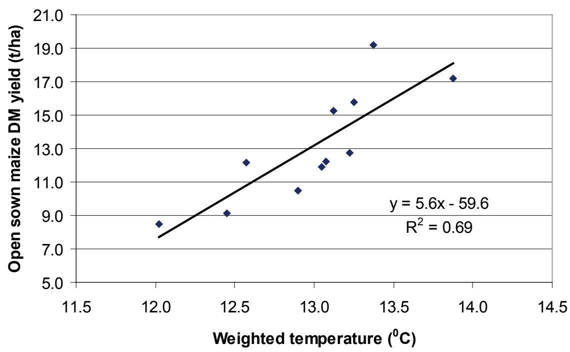

Fig. 2. Correlation between DM yield (O) and WT.

Conclusions

This approach provides a simple method for estimating annual percentage changes in productivity for marginal climates where OHU appear to be less effective. Further study is required to understand the physiological responses underlying this sensitivity to early season temperatures in these conditions and the limits of the predictions. Nonetheless it is possible for growers and advisers to estimate early in the season, the DM, starch and energy yields expected in October/November and aid early budgeting of supplementary feed requirements

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Effect of nitrogen fertilizer application timing on grain yield of winter wheat

A. Efretuei[1], M. Gooding[1], E. White[2], R. Hackett [3] and J. Spink [3]

[1]*School of Agriculture Policy and Development, University of Reading, Reading UK,* [2]*AFBI Crossnacreevy Plant Testing Station Crossnacreevy, Belfast, UK,* [3]*Teagasc Oak Park, Carlow, Ireland.*

Introduction

Maximising grain yield per unit of applied chemical fertilizer nitrogen (N) is a key objective when developing fertilizer application programmes for crops worldwide (Raun, 2002). To achieve high efficiency of use of applied fertilizer N, and avoid losses to the environment, N application should be synchronised as closely as possible with crop demand. A winter wheat crops demand for nitrogen increases with the onset of growth in the spring requiring the addition of fertilizer N, the amount required being influenced by soil N supply (Spiertz and De Vos, 1983). In Ireland the current recommended timing for the initial application of fertilizer N to winter wheat is between late tillering and the onset of stem elongation (GS30). In practice many growers apply N as soon as soils become trafficable in late February/early March, often in advance of significant spring growth, which may be resulting in inefficient use of the applied N. There has been relatively little recent research investigating the effect of the timing of the initial application of N to winter wheat in Ireland. In particular the interaction between timing of the first N application and both plant population density and soil N supply status has received little attention. The primary aim of this study was to determine the appropriate time for the first N application to winter wheat as influenced by plant density and soil N supply.

Materials and Methods

A split-plot design with 4 replications laid out as a randomized complete block design was carried out at Oak Park Carlow on a medium textured soil in 2011. The main plot factor was slurry treatment (with or without slurry). The slurry treatment was introduced to simulate variation in soil N supply. Cattle slurry (22 m^3/ha containing 2.35 kg N/m^3) was applied immediately before ploughing in the autumn. The split-plot treatments included a factorial arrangement of N treatment (5 N timing treatments (Table 1) and an unfertilized control) and seed rate (100 and 400 seeds/m^2). Seed rate was included as a factor to give variation in plant population density. Sub plot size was 24 x 2.15m. The variety Cordiale was used.

Table 1. Fertilizer N application timings.

1st split (and application dates)	2nd split
GS 24 (9th March 2011)	GS 31
GS30 (28th March 2011)	GS 31
GS 31 (11th April 2011)	GS 33
GS 32 (20th April)	GS 39
GS 37 (10th May 2011)	GS 55

A total of 200 kg N/ha, as CAN, was applied to all fertilized treatments with 70 kg N/ha applied in the first application. The remaining 130 kg N/ha was applied to each treatment 15 days after the first application but not before GS 31. Grain yield was determined using a combine harvester and expressed at 85% dry matter. Results were analysed using the linear mixed model analysis in GENSTAT version 13 (VSN international Ltd). The model included slurry (S), N timing, (NT), seed rate (SR) and the interactions S x NT, S x SR, NT x SR, and S x NT x SR Treatment means were separated using Fischer's LSD ($p<0.05$).

Results and Discussion

There were no significant interactions between slurry and N timing, slurry and seed rate or N timing and seed rate on yield. There was no significant effect of slurry on yield. The lack of slurry effect on yield may have been due to the relatively low amount of N applied in the slurry combined with poor recovery of the N in the autumn applied slurry (Jackson and Smith 1997). Both N timing and seed rate had a significant effect on yield ($p<0.001$). The high seed rate gave a significantly higher yield compared to the low seed rate ($p<0.001$). All fertilized treatments significantly out yielded the unfertilised control (Figure 1). Application of the first N at GS 30 gave a significantly higher yield ($p<0.05$) compared to all other N timing treatments. There was no significant difference in grain yield between applying the first N application at GS 24 compared to GS 31. Delaying first N application from GS 31 until GS 32 significantly decreased yield and a further significant decrease was recorded when fertilizer N application was delayed from GS 32 until GS 37.

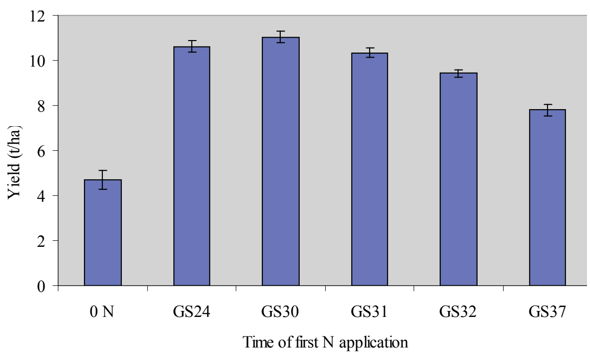

Figure 1. Effect of timing of the first N application on grain yield (t/ha at 85% DM). Bars are SEM.

Conclusions

Application of first fertilizer N at GS 30 gave the highest yield irrespective of plant population density. Earlier or later timings lead to reduced yield. The lack of a slurry effect means that it was not possible to determine the influence of soil N supply on the most appropriate time for first N application.

Acknowledgements

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The effect of crop establishment system on nitrogen use efficiency of spring barley.

J Brennan[1, 2], T McCabe[2], R Hackett[1], P D Forristal[1].
[1] Teagasc CELUP, Crops Research, Oak Park, Carlow;
[2] School of Agriculture, Food Science and Veterinary Medicine, NUI Dublin, Belfield, Dublin 4.

Introduction

Spring barley for malt and feed production is grown on 150,000ha annually accounting for almost 50% of Ireland's arable area (CSO, 2010). Ploughing to 200mm depth followed by a secondary cultivation combined with sowing is the standard establishment system used. While there has been an increased interest in shallow non-inversion minimum tillage (MT) establishment systems for winter sown crops, there has been very little research or practice of MT in spring barley in Ireland. Studies on the effect of establishment system on spring barley in central Norway found significant variations in crop performance with climate and soil type (Riley *et al*., 2005). Any change in soil N availability caused by tillage could have an effect on the overall performance of spring barley due to its short growing season. The aim of this trial was to compare the effects of P and MT establishment systems on grain yield and N uptake patterns of spring barley.

Material and Methods

This continuous spring barley trial commenced in 2006 on an N index 1 soil at Knockbeg Co. Laois. In the 2009 and 2010 growing seasons four cultivation systems were evaluated; Conventional Tillage (P), Min-Till in Autumn (MT-A), Min-Till in Autumn and Spring (MT-A+S) and Min Till Spring (MT-S) in a factorial arrangement of treatments with 5 replications. Sub plots with 5 nitrogen rates were contained within each plot. The fertiliser (CAN 270g N/kg) was applied in 2 splits; 50% at planting and 50% at growth stage (GS) 29. Crop N uptake (N_{upt}) was measured at approx 4 week intervals in each season. Three randomly selected 0.5 m lengths of crop were cut at ground level in each plot, and were dried, weighed, and ground before analysing with a LECO combustion analysis device. Pre-harvest full-crop samples were taken to calculate straw N content.

All plots were harvested, weighed and yielded. Nitrogen use efficiency (NUE) was calculated. Data was subject to analysis of variance for split plots with N rate as the split-plot factor and the factorial arrangement of cultivation system as the main plot factor.

Results and Discussion

There was a significant interaction ($P<0.05$) between cultivation system and N level for some of the parameters. In 2009, the P and MT-A treatments produced significantly higher grain yields at the highest applied N rate. In 2010, the P and MT-S treatments produced significantly higher grain yields at the highest N rate. The results at 135kg N are presented in Table 1. In 2009, the MT-Spring establishment method performed poorly with a significantly lower crop N_{upt} at GS 53 and 90, and reduced grain yield at harvest. The plough-based system had similar crop N_{upt} throughout the season but produced the highest grain yield. The poor performance of the MT-S treatment in 2009 may be attributed to low crop establishment caused by poor percolation and higher than average rainfall.

There was no effect of establishment system on crop N_{upt} at the first two sampling dates in 2010. Although MT-A treatment had the highest crop N_{upt} at GS 73 and the highest straw N_{upt}, these results were not reflected in the grain yield. The MT-S achieved a significantly higher grain yield than the MT-A in 2010. Winter seedbed consolidation caused by higher than average rainfall following autumn cultivation resulted in poor crop establishment conditions and crop performance with the MT-A treatment in 2010.

Grain yields were moderate to low in both years. Crop establishment system had no effect on N use efficiency in both seasons.

Conclusions

The N uptake pattern of spring barley is affected by crop establishment system. These experiments indicate that the performance of MT systems for spring barley establishment is season dependent and the plough-based system is less influenced by seasonal factors than MT based systems in Ireland.

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Table 1: Results of conventional and minimum tillage established spring barley with 135kg N/ha applied.

2009					2010				
	P	MT-A	MT	MT		P	MT	MT	MT
	Spr	Aut	A+S	Spr		Spr	Aut	A+S	Spr
N_{upt} GS 28 (kg/ha)[1]	18.5[b]	16.9[ab]	15.8[ab]	15.2[a]	N_{upt} GS 28 (kg/ha)[1]	8.48[a]	9.07[a]	8.33[a]	8.74[a]
N_{upt} GS 53 (kg/ha)[1]	119.9[b]	115.6[b]	110.1[b]	91.3[a]	N_{upt} GS 47 (kg/ha)[1]	104[a]	94[a]	105[a]	97[a]
N_{upt} GS 83 (kg/ha)[1]	139.3[a]	142.3[a]	138.4[a]	138.6[a]	N_{upt} GS 55 (kg/ha)[1]	139[ab]	139[ab]	156[b]	127[a]
N_{upt} GS 90 (kg/ha)[1]	119.2[b]	132.0[b]	119.9[b]	104.5[a]	N_{upt} GS 73 (kg/ha)[1]	104[a]	125[b]	109[ab]	120[ab]
Grain N_{upt} (kg/ha)	97.8[a]	98.4[a]	92.0[a]	82.8[a]	Grain N_{upt} (kg/ha)	97.9[a]	97.2[a]	96.7[a]	99.1[a]
Straw N_{upt} (kg/ha)	24.89[a]	26.1[a]	26.6[a]	23.1[a]	Straw N_{upt} (kg/ha)	24.5[ab]	28.4[b]	27.0[b]	21.7[a]
N.U.E. %	58.3[a]	56.9[a]	53.1[a]	51.6[a]	N.U.E. %	61.4[a]	58.9[a]	54.4[a]	56.7[a]
Grain Yield (t/ha)	6.16[b]	5.98[b]	5.66[ab]	5.08[a]	Grain Yield (t/ha)	5.85[ab]	5.39[a]	5.59[ab]	5.99[b]

[*]Means with a common superscript are not significantly ($P<0.05$) different.
[1]N_{upt} values at the various crop GS refer to plant N_{upt}

Changes in chemical composition of three maize stover components harvested at sequential maturities and digested by white rot fungi

J.P. Lynch[1,2], P. O' Kiely[1], R. Murphy[3], and E. Doyle[2]
[1]*AGRIC, Teagasc, Grange, Dunsany, Co. Meath* [2]*Microbiology, SBES, Ardmore House, UCD, Belfield, Dublin.*[3]*Alltech, European Bioscience Centre, Sarney, Summerhill Road, Dunboyne, Co. Meath*

Introduction

Maize stover (stem and leaves) is not considered a ruminant feed of high value, and generally supports similar rates of animal performance to what could be achieved with average quality grass silage. The digestion of lignocellulosic agricultural residues with lignin-degrading white-rot fungi (WRF) can result in improvements in feed digestibility. The objective of this study was to determine the effect of digestion with one of two WRF (*Pleurotus ostreatus, Trametes veriscolor*) for four months on the nutritive value of contrasting components of maize stover (leaf blade, upper stem, lower stem) harvested at sequential stages of maturity.

Materials and Methods

For each of three replicate blocks of a split-plot design, three harvest date treatments (7 September, 5 October and 5 November) were randomly allocated to one of three main plots, within which sub-plots were randomly allocated to one of three stover components. On each harvest date either the leaves, upper stem or lower stem were manually separated from all plants present in a plot and precision-chopped. Samples weighing 700 g were allocated to inoculation with one of two fungal additives (*P. ostreatus, T. versicolor*) and one of four digestion durations (1 – 4 months). Prior to inoculation, samples were immersed in 4 litres of room temperature tap water for 20 minutes and autoclaved at 110°C for 1 hour to eliminate epiphytic microflora. Subsequently, for their duration of digestion, samples were stored at *approx*. 20°C in sealed polypropylene bags that had a membrane that facilitated gas exchange and thus, aerobic conditions. Data were analysed using a model that accounted for harvest date (main plot), fungal additive and digestion duration (two x four factorial arrangement of treatments in the sub-plot) for three replicate blocks in a split plot design. All analyses were conducted using the PROC GLM model of the SAS statistical program.

Results and Discussion

Lignin degradation was observed in all sample types digested with *P. ostreatus*, however, the loss of digestible substrate in all samples inoculated with *P. ostreatus* was high and therefore *P. ostreatus*-digested samples had a lower dry matter digestibility than samples prior to inoculation. Similarly, *T. veriscolor*-digested samples underwent a non-selective degradation of hemicellulose and cellulose, although very minor or no lignin degradation occurred in leaf samples. *P. ostreatus*-digested leaf and upper stem samples had a higher ($P<0.001$) DMD and cellulose concentration and lower ($P<0.001$) lignin concentration when digested for longer than two months compared to *T. versicolor* digested samples (Table1). Lower stem digested by *P. ostreatus* also had a higher ($P<0.01$) DMD and cellulose concentration, and a lower ($P<0.01$) hemicellulose concentration than *T. versicolor*-digested samples after two months.

Conclusions

The changes in chemical composition of leaf, upper stem and lower stem digested with *P. ostreatus* or *T. versicolor* were not beneficial to the feed value of the crop, as indicated by chemical composition.

Table 1. Chemical composition of maize leaf, upper stem and lower stem after white-rot fungal digestion

		Leaf				Upper stem				Lower stem			
WRF[1]	Digestion duration	DMD[2]	Hemi.[3]	Cel.[3]	ADL[3]	DMD[2]	Hemi.[3]	Cel.[3]	ADL[3]	DMD[2]	Hemi.[3]	Cel.[3]	ADL[3]
P. ostreatus	1 month	513	215	308	55	342	257	485	66	240	284	493	87
T. versicolor	1 month	512	215	335	62	392	207	489	63	294	283	504	74
P. ostreatus	2 month	558	172	312	48	436	211	495	62	281	233	522	84
T. versicolor	2 month	436	198	286	88	360	208	467	69	264	256	510	79
P. ostreatus	3 month	549	134	317	33	454	202	500	53	358	201	537	75
T. versicolor	3 month	422	150	270	108	366	246	456	69	262	261	497	79
P. ostreatus	4 month	584	103	311	20	471	168	508	46	410	165	544	72
T. versicolor	4 month	361	140	237	139	378	243	454	61	260	265	494	78
SEM	A	14.2	9.1	6.1	6.8	11.6	10.5	6.5	2.5	12.8	6.5	4.4	2.5
	D	10.5	6.6	4.4	4.6	8.2	7.1	4.7	1.8	9.0	4.7	3.4	1.8
	AxD	22.0	14.1	8.5	8.4	16.3	15.0	9.2	3.6	18.0	9.1	6.7	3.4
Sig[4]	H					*	***						
	D		***	***		**			**	**	***	*	
	A	***		***	***	***		***	**	***	***	***	
	H*A	**					*	*				**	
	H*D						*						
	A*D	***		***	***	***	**	*	*	***	***	**	
	H*D*A												
Samples prior to digestion		670	314	354	23	572	313	408	38	524	284	437	50

[1]WRF = white rot fungi, *P.* = *Pleurotus, T.* = *Trametes* [2] g/kg, DMD= dry matter digestibility; [3] g/kg DM, Hemi=hemicellulose (neutral detergent fibre (NDF) – acid detergent fibre (ADF), Cel.= cellulose = ADF – acid detergent lignin (ADL); [4] H= harvest date, A = additive, D= digestion duration; Means are averaged over harvest dates; Interactions between harvest date and other factors were consistent with main effects.

Screening of Irish Fruit and Vegetable Germplasm for Novel Anti-tumour and Pesticidal Compounds

J.M.I. Alqudah [1,2], K. Reilly [2], M.T. Gaffney [2], A.B. Martin-Diana [3] and C. Barry-Ryan [1]

[1]Dublin Institute of Technology, School of Food Science and Environmental Health, Cathal Brugha St, Dublin 1, [2]Teagasc, Horticulture Development Department, Kinsealy, Dublin 17, [3] Instituto Technológico Agrario, Junta de Castilla y León, Consejería de Agricultura y Ganadería, España.

Introduction

Phytochemicals are a rich source of novel therapeutic and insecticidal agents (McLaughlin and Chang, 1999). Considerable research effort has been directed at screening exotic and medicinal plants in the search for novel products. However, plants which have traditional food uses have been little explored. In addition the range, type and level of individual bioactive compounds can vary significantly between different species, different cultivars of the same species and different tissue types of the plant (Reilly, *in press*) Therefore, the objective of this study was to screen a range of fruits and vegetables which can be grown in Ireland for novel bioactive compounds for use in food production and as bio-pesticides.

Materials and Methods

Crude aqueous extracts from 173 samples of fruit and vegetables were screened using brine shrimp bioassay (BSB). Plant material was separated and blended in a juicer (TESCO®) to get sufficient volume of aqueous extract (20 ml). Samples were centrifuged at 7690 g for 10 minutes and the supernatant was stored at - 20 ºC (aqueous extracts). Alternatively plant samples were ground to a fine powder in liquid nitrogen. Five grams of powdered tissue were suspended in 30 ml of aqueous methanol (80% v/v) in a 50 ml tube and mixed using a vortex. Samples were stored at room temperature for 30 minutes and then filtered through Whatman number 1 filter paper. Methanolic extracts were transferred to a rotary evaporator until completely dry. The dried samples were then stored at - 20 ºC (solvent extracts). Brine shrimp bioassays (a rapid bioassay for insecticidal and antitumour compounds) were carried out according to McLaughlin and Chang (1999) for all aqueous extracts. Brine shrimp bioassays using methanolic extracts were carried out for the samples which had shown positive preliminary screening of aqueous extracts in BSB. Data for the BSB were analysed using probit analysis (SAS 9.1) to estimate LC_{50} values and 95% confidence intervals. The potato disc bioassay (PDB) (an anti-tumour bioassay) was carried out according to McLaughlin and Chang (1999) for samples showing positive results from both aqueous and methanolic extracts in BSB. The percent inhibition of crown gall tumours was calculated as outlined below and is considered significant if there is a greater than 20% reduction in galls (McLaughlin and Chang, 1999).

$$\%\,Inhibition = 100 - \frac{Average\ number\ tumours\ of\ sample}{Average\ number\ tumours\ of\ control} \times 100$$

Results and Discussion

Aqueous extracts from beetroot, cranberry, garlic, ginger, red onion and rhubarb showed positive results (LC_{50}<0.02 v/v) and significant inhibition of crown gall tumours (>20% inhibition) in BSB and PDB respectively (Tables 1 and 2). Methanolic extracts were used in BSB from these 6 positive aqueous extracts. Three methanolic extracts (cranberry, ginger and rhubarb) showed positive lethal concentration (LC_{50}<1000 ppm) in BSB. Methanolic extracts of cranberry and rhubarb showed significant inhibition of crown gall tumours in the PDB (>20%).

Table 1. Summary of positive results of the initial screening using brine shrimp bioassay

Plant name	Tissue	Brine shrimp bioassay (LC50)	
		Aqueous (Dilution v/v)	Solvent (ppm)
Beetroot	Root	0.0069 ± 0.0034	>1000
Cranberry	Fruit	0.0039±0.00006	29±28.2
Garlic	Bulb	0.0046±0.0003	>1000
Ginger	Rhizome	0.0088±0.00066	110±14.9
Red onion	Bulb	0.0117±0.0015	>1000
Rhubarb	Petiole	0.0043±0.005	52±83.5

± Standard error for the means of three bioassays (n=3)

Table 2. Inhibition of crown gall tumours in the potato disc bioassay

Plant name	Tissue	Brine shrimp bioassay (LC50)	
		Aqueous (Dilution v/v)	Solvent (ppm)
Beetroot	Root	-25.6 ±12.4	NA
Cranberry	Fruit	-48.3±8.3	- 30 ± 8.5
Garlic	Bulb	-26.7±1.5	NA
Ginger	Rhizome	-53.7±6.3	+15 ± 9.8
Red onion	Bulb	-21.9±3.5	NA
Rhubarb	Petiole	-28.3±11.8	- 41 ± 10.7

*NA: Not applicable

± Standard error for the means of three bioassays (n=3)

Conclusions

The data demonstrate the potential for extraction of antitumour and biopesticidal compounds from 3 traditional Irish fruit and vegetables is comparable to that of 3 fruit and vegetables internationally recognised for beneficial phytochemical production.

Acknowledgments

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Yield and chemical composition of grasses grown under two nitrogen fertiliser inputs and harvested at different stages of maturity

C. King[1,2], J. McEniry[1], M. Richardson[2] and P. O'Kiely[1]
[1]*AGRIC, Teagasc, Grange, Dunsany, Co. Meath,*
[2]*School of Architecture, Landscape & Civil Engineering, UCD, Belfield, Dublin 4.*

Introduction

The main management factors affecting grass yield and chemical composition are species, rate of nitrogen fertiliser application and stage of maturity at harvest. This study investigated the effects of two N fertiliser inputs and five sequential harvest dates in the primary growth on the yield and chemical composition of five common grass species.

Materials and Methods

Perennial ryegrass (PRG; *Lolium perenne* L. var. Gandalf), Italian ryegrass (IRG; *Lolium multiflorum* Lam. var. Prospect), cocksfoot (*Dactylis glomerata* L. var. Pizza), timothy (*Phleum pratense* L. var. Erecta) and tall fescue (*Festuca arundinacea* Schreb. var. Fuego) were grown in field plots (20 m^2) under two inorganic N fertiliser inputs (low=0 kg/ha, high=125 kg/ha) and harvested at five dates (fortnightly from 12 May – 7 July; Harvests 1 to 5) in the primary growth during both 2009 and 2010. At each harvest date, herbage was weighed and a sample taken for chemical analyses. Dry matter (DM) concentration was estimated following drying at 98°C for 16 h. Replicate samples were also dried at 40°C for 48 h before being milled. Dried, milled samples were used for the determination of *in-vitro* dry matter digestibility (DMD), neutral detergent fibre (NDF), acid detergent fibre (ADF), acid detergent lignin (ADL), ash, buffering capacity (BC), crude protein (CP) and water soluble carbohydrates (WSC) as previously described by Purcell *et al*. (2011). Data were analysed as a split-split plot design using the Proc MIXED procedure of SAS, V9.1.2, accounting for year and replicate blocking.

Results and Discussion

On average, there was an increase (P<0.001) in DM yield, NDF, ADF and ADL concentrations with advancing harvest date, reflecting the general decrease in plant leaf to stem ratio and the increasing cell wall content as the plant matured (Table 1). This was accompanied by a decrease (P<0.001) in herbage DMD. On average, the high N fertiliser treatment gave a higher (P<0.05) DM yield (data not shown), but tall fescue was the only species to produce a significantly higher (P<0.001) DM yield. The increase (P<0.001) in herbage BC and decrease (P<0.001) in WSC concentration with the high N treatment may have negative implications for grass ensilability. On average, cocksfoot had the lowest (P<0.001) DM yield, with no difference (P>0.05) observed between the other grass species, and lowest (P<0.001) DMD along with IRG and tall fescue. The higher (P<0.001) WSC concentration and lower (P<0.001) BC of the two ryegrasses likely make them more suitable for ensiling.

Conclusions

With the exception of IRG, each grass had a numerical DM yield response to the high N fertiliser input, but this response was only significant for tall fescue. On average, timothy had a similar DMD to PRG, but this timothy variety was at a less advanced growth stage at each harvest date.

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Table 1 DM yield (t/ha) and chemical composition (g/kg DM, unless stated otherwise) of five grass species at five harvest dates (averaged across year and N fertiliser treatments; only data for Harvests 1, 3 and 5 presented)

Species	Harvest	DM yield	DM (g/kg)	DMD (g/kg)	NDF	ADF	ADL	Ash	CP	WSC	BC (mEq/kg DM)
PRG	1	5.04	195	827	454	238	7.8	84	144	245	522
PRG	3	8.20	207	681	588	342	23.7	72	94	159	391
PRG	5	9.81	296	613	616	372	34.5	66	71	148	272
IRG	1	5.46	211	780	453	240	7.3	82	127	262	426
IRG	3	9.39	252	698	526	314	23.6	67	87	224	331
IRG	5	8.72	295	623	583	363	32.3	79	80	147	277
Tall fescue	1	4.93	198	770	496	262	14.4	80	147	196	485
Tall fescue	3	9.25	223	681	602	364	25.5	79	103	126	407
Tall fescue	5	9.42	280	608	613	366	32.6	80	78	127	336
Cocksfoot	1	4.42	184	771	493	254	14.2	87	156	178	511
Cocksfoot	3	6.77	224	664	599	347	26.4	85	107	113	425
Cocksfoot	5	6.95	252	596	635	365	37.1	95	92	74	363
Timothy	1	4.47	191	821	518	261	11.2	80	154	163	493
Timothy	3	9.37	202	710	651	384	28.4	74	107	80	396
Timothy	5	9.75	309	616	643	389	44.5	66	86	101	304
Standard error of the mean											
Harvest		0.335	5.6	8.1	4.4	3.8	1.27	0.9	2.2	5.2	4.9
Species		0.289	2.6	4.0	4.4	2.0	0.77	0.9	1.7	3.4	3.8
Harvest x Species		0.558	8.0	13.8	7.5	5.8	2.10	2.1	4.3	8.0	9.0
Levels of significance											
Harvest		***	***	***	***	***	***	**	***	***	***
Species		***	***	***	***	***	***	***	***	***	***
Harvest x Species		*	***	*	***	***	*	***	NS	***	***

Comparing the yield and chemical composition of grasses at common phenological growth stages

C. King[a,b], J. McEniry[a], M. Richardson[b] and P. O'Kiely[a]
[a]*AGRIC, Teagasc, Grange, Dunsany, Co. Meath*
[b]*School of Civil, Structural and Environmental Engineering, UCD, Belfield, Dublin 4*

Introduction

Grass species, fertiliser N and growth stage at harvest are the three most important grassland management factors impacting on grass yield, nutritive quality and ensilability. Varieties of temperate grass species can vary widely in their date of heading, which may confound results when comparing different grass species at the same harvest. The objective of this study was to use regression analysis to investigate the effects of two N fertiliser inputs on the yield and chemical composition of five grass species at two common growth stages.

Materials and Methods

Triplicate plots of each of five common grass species [perennial ryegrass (PRG; *Lolium perenne* L. var. Gandalf), Italian ryegrass (IRG; *Lolium multiflorum* var. Prospect), tall fescue (*Festuca arundinacea* var. Fuego), cocksfoot (*Dactylis glomerata* var. Pizza) and timothy (*Phleum pratense* var. Erecta)] were grown in field plots (20 m^2) under two inorganic N fertiliser inputs (low = 0 kg N/ha, high = 125 kg N/ha; applied in mid-March) and harvested at five sequential dates (fortnightly from 12 May – 7 July) in the primary growth in 2009 and 2010. Prior to harvesting, herbage growth stage was determined for 20 randomly sampled plants from each plot, according to Moore *et al*. (1991). At each harvest date, herbage was weighed and a sample taken for chemical analysis. Representative samples were oven dried at 40°C for 48 h before being milled. Dried, milled samples were used to determine *in vitro* dry matter digestibility (DMD), neutral detergent fibre (NDF), water soluble carbohydrates (WSC) and buffering capacity (BC) as previously described by Purcell *et al*. (2011). The DM yield and chemical composition of each of the five grass species was regressed across five harvest dates, for each of two successive years using PROC MIXED in SAS, Version 9.1.2. Predicted yield and chemical composition are presented for two growth stages, 2.7 (stem elongation) and 3.4 (reproductive-floral development) that correspond to two dates (24 May and 17 June, respectively) in the primary growth at which PRG would typically be harvested on Irish farms depending on whether high or moderate digestibility silage was required.

Results and Discussion

Cocksfoot had the lowest (6.24 t DM/ha) and timothy the highest (8.69 t DM/ha) yield while there was little difference between other grass species (Table 1). As expected, herbage harvested at the later growth stage gave higher (8.55 *vs*. 6.70 t DM/ha) yields with the increase in DM yield being mainly attributed to an increase in NDF yield (2.35 to 5.93 t NDF/ha). Overall, fertiliser N increased the DM yield of herbage (7.30 to 7.95 t DM/ha). The most digestible grass species was PRG (738 g/kg), in accord with Wilson and Collins (1980), and with timothy being the lowest (692 g/kg). As expected, herbage digestibility was lower at the later growth stage (679 *vs*. 738 g/kg) corresponding to higher concentrations of fibre components (NDF). Timothy had the highest concentrations of NDF (625 g/kg DM) while IRG had the lowest (522 g/kg DM). The most suitable grass species for ensiling was Italian ryegrass, (particularly when grown without fertiliser N) as it had a higher WSC (221 g/kg DM) and lower BC (372 mEq/kg DM) than the average of the non-ryegrass species (129 g/kg DM and 424 mEq kg^{-1} DM, respectively). Although grass BC was lower for the later growth stage this was accompanied by a lower WSC concentration.

Table 1 Calculated yield (t DM/ha) and chemical composition (g/kg DM; unless indicated in footnotes) at two contrasting growth stages for five grass species grown under two nitrogen fertiliser treatments

N[1]	Species[2]	Growth Stage	Yield	DMD	NDF[3]	WSC	BC
L	PRG	2.7	6.41	768	512	224	463
H	PRG	2.7	7.42	767		178	551
L	PRG	3.4	8.63	709	576	177	398
H	PRG	3.4	8.91	708		150	483
L	IRG	2.7	6.25	727	490	275	359
H	IRG	2.7	7.26	726		229	447
L	IRG	3.4	8.47	669	554	203	299
H	IRG	3.4	8.75	667		176	384
L	TF	2.7	6.23	743	548	186	414
H	TF	2.7	7.24	742		140	502
L	TF	3.4	8.45	684	589	148	356
H	TF	3.4	8.73	683		121	440
L	Cocksfoot	2.7	4.81	734	534	174	441
H	Cocksfoot	2.7	5.82	733		128	529
L	Cocksfoot	3.4	7.03	676	580	126	383
H	Cocksfoot	3.4	7.31	674		98	468
L	Timothy	2.7	7.26	722	602	123	375
H	Timothy	2.7	8.27	721		77	463
L	Timothy	3.4	9.48	663	649	94	316
H	Timothy	3.4	9.76	662		67	400

[1] L = 0 kg N/ha, H = 125 kg N/ha; [2] PRG = Perennial ryegrass, IRG = Italian ryegrass, TF = Tall fescue. For all variables values were averaged over two years for ease of presentation. DMD= dry matter digestibility (g/kg); [3]NDF = neutral detergent fibre, values averaged over effect of fertiliser N which was not significant; WSC = water soluble carbohydrates, BC = buffering capacity (mEq/kg DM)

Conclusions

When grasses were equated to common growth stages, timothy had the highest yield and NDF concentration, which correspond to it having the lowest digestibility. In contrast, PRG had the highest digestibility. The IRG had the highest WSC concentration and lowest BC making it the most suitable for ensiling. Fertiliser N increased herbage yield especially at the early growth stage.

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Effect of closing date on dry matter yield and leaf proportion in perennial ryegrass swards during the early winter period

D. Lawrence[1, 2], M. O'Donovan[1], T.M. Boland[2], and E. Kennedy[1]
[1]Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy Co. Cork; [2]School of Agriculture and Food Science, UCD, Belfield, Dublin 4

Introduction
Herbage growth in Ireland is highly seasonal with peak growth rates in summer and little or no growth in winter (Brereton, 1995). During the winter period, growth of perennial ryegrass (PRG; *Lolium perenne* L.) is characterised by a reduction in leaf extension rate and an increase in leaf senescence rate (Hennessy *et al* 2008). It is common to feed livestock indoors with conserved forage and concentrate for the winter period. One alternative is to accumulate grass so that it can be grazed *in situ* thereby extending the grazing season into the autumn/winter period. The objective of this study was to investigate the effect of closing date on herbage mass (HM), sward morphology, sward chemical composition and PRG population (sward density) throughout the early winter period (October-November).

Materials and Methods
A one year old PRG sward (79% PRG) at Teagasc Moorepark, Fermoy, Co. Cork, which was previously grazed, was divided into 24 (3 x 5 m) plots. The study was a randomised block design with 2 x 4 factorial arrangement of treatments, replicated three times. Two closing dates (CLD: 8 August (E) and 15 September (L), 2011) were defoliated on four harvesting dates (HD: 3 October (HD1), 17 October (HD2), 31 October (HD3) and 14 November (HD4)). In total, the sward received 230 kg fertiliser nitrogen during the year. Plots were harvested with an Etesia rotary blade mower to a stubble height of 4 cm across all treatments. The herbage removed from each plot was weighed and sampled to determine HM. A 100 g sub-sample was dried for 48 h at 40ºC to measure the dry matter (DM) content of the sample and calculate the DM yield/ha. The dried sample was then milled and analysed for dry matter digestibility (DMD) and crude protein using near infra-red spectrometry (NIRS). Prior to harvesting, tillers were sampled by cutting to ground level using a scissors and a 40 g subsample was separated into leaf, stem and dead components above and below a 4 cm stubble height. Also, three 10 cm^2 turves were taken from each plot. The tillers of PRG, weed grass and broad leaf weeds were counted on each sod sample to assess sward density and PRG proportion. Data were analysed using PROC MIXED in SAS 2006, CLD, HD, CLD*HD and replicate were included in the model.

Results and Discussion
There was an interaction between HD and CLD ($P<0.05$). DM yield per ha increased with both closing dates for HD1, HD2 and HD3 however DM yield on the E-CLD plots reached its maximum earlier than the L-CLD plots (Table 1). The E-CLD plots had a significantly higher proportion of PRG tillers in the sward compared to the L-CLD, (0.85 and 0.75, respectively; $P<0.05$). The average number of PRG tillers/m^2 decreased notably ($P<0.01$; Table 1) with later harvesting dates. This suggests that PRG tiller density decreased as HM increased from HD1-HD4. Higher HM can lead to a reduction in light interception and hence shading of tillers causing tiller death. The results also showed an increase in weed grass tillers between E-CLD and L-CLD plots (947 vs. 1949 tillers/m^2, respectively; $P<0.01$). There was an interaction between HD and CLD in terms of leaf proportion in the sward ($P<0.05$; Table 1). There was a decrease in leaf proportion in the >4 cm horizon of the sward, as closing date progressed. There was a slower decline in leaf proportion >4 cm in the L-CLD plots (due to the appreciably higher leaf proportion >4 cm on HD2 and HD3). Considering these results, there was still a larger leaf yield of PRG in the E-CLD over all HD due to the higher DM yields achieved. There was no effect of CLD on sward chemical composition but as HD increased DMD declined ($P< 0.001$).

Conclusions
The earlier closing date resulted in higher overall herbage mass accumulation. As DM yield increased there was a decline in leaf proportion above a 4 cm stubble height and in PRG tiller density. Hence, as grazing date moves later into the season, herbage quality will decrease, in terms of leaf proportion and (DMD). Further investigation is required, but this study shows that swards reach a maximum DM yield during autumn irrespective of rotation length.

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Table 1. The interaction of closing and harvesting dates on DM yield and leaf proportion

CLD	08 Aug				15 Sep					Significance		
HD	3/10	17/10	31/10	14/11	3/10	17/10	31/10	14/11	SED	HD	CLD	INT
DM/ha	1925[a]	2649[c]	2778[c]	2641[c]	889[b]	1632[d]	1960[a]	1977[a]	88.0	<0.001	<0.001	<0.05
Leaf>4	0.82[a]	0.63[b]	0.65[b]	0.55[b]	0.80[a]	0.80[a]	0.78[a]	0.52[bc]	0.05	<0.001	<0.05	<0.05
TLR/m^2	7328	6000	4883	4644	5983	6100	5234	4584	730.4	<0.01	0.581	0.507

CLD=Closing date, HD=Harvesting date, INT=Interaction of HD*CLD, DM/ha= kg, Leaf>4,= Proportion of leaf above a 4 cm high stubble, TLR/m^2=No. PRG tillers/m^2, SED= Standard error of difference

Agronomic studies on the application of increasing rates of compost to grass, clover and grass + clover swards.

S. Walsh, M.B. Lynch and T. McCabe
School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4.

Introduction

The national strategy on biodegradable waste requires the 600,000 tonnes of bio-waste currently produced by Irish households being sent to landfill to be reduced by 330,000 tonnes by 2016. One approach is to produce compost from the bio-waste suitable for land spreading. The application of compost to farmland is potentially an environmentally friendly way and an agronomically beneficial way to utilise organic waste. In addition to being a natural organic fertiliser product compost can also contribute to improved soil fertility and soil quality by increasing soil organic matter (Raviv, 2005). In this field trial study compost applications to grass, grass/clover and clover swards were investigated for effect on yield and CNU.

Materials and Methods

Two trials were conducted in the 2011 season at UCD Lyons Research farm, Newcastle, Co. Dublin. Trial 1 was designed as a 2 x 5 factorial trial, with a plot size of 1.5 x 6.5m in 4 replications. Factor A was sward type (grass or grass +clover). Factor B was compost rate, with application rates of 0, 4, 8, 12 and 16 t/ha. Trial 2 was a 3 x 5 factorial trial with 4 replications and plot size was 7 x 1.5m. Factor A was compost rate of 0, 4, and 8 t/ha and factor B was clover variety. Compost was sourced from an Irish producer and the nutrient content can be seen in table 1. Compost was spread evenly over the plots by hand in early-summer. Three cuts were taken during the season; in mid-summer, early-autumn and late-autumn. A Haldrup plot harvester was used to cut and weigh the plots. Samples were taken to estimate dry matter yield (DMY) and for N content analysis using Leco combustion analysis. Data was subject to analysis of variance in ARM (GDM, 2012).

Table 1. Compost Analysis, grammes per kg.

Parameter	g/kg		g/kg
pH	pH 6.46	Total Potassium	7.75
Dry Matter	621.0	Total Magnesium	4.58
Total Nitrogenn	19.25	Total Sulphur	5.74
Amm. Nitrogen	1.76	Total Copper	0.12
Nitrate Nitrogen	0.06	Total Zinc	0.19
Total Phosphorus	9..95	Total Calcium	26.68

Results and Discussion

In trial 1 the grass+clover sward had significantly higher N%, crop N uptake (CNU) and also increased yields (P<0.001)(Table 2). On each harvest date the DMY increased for higher compost rates with the greatest yield increments recorded on harvest date 1. Figure 1 shows the cumulative yield benefit in response to compost application for the grass and grass+clover swards in 2011. Compost application had no significant effect on DMY or CNU in trial 2 (clover-only), while the clover varieties showed some modest yield differences for harvest dates 1 and 3 (P<0.05).

Table 2. The effect of sward type and compost rate on DM yield on 3 dates and crop N uptake (CNU) in trial 1.

Treatment	Dry Matter Yield			CNU
	Cut 1	Cut 2	Cut 3	Cut 1
Factor A – Grass/Grass+Clover				
Grass	1.54	0.54	1.13	30.7
Grass+Clover	2.78	0.58	1.57	70.5
Level of sig.	***	***	n.s	***
L.S.D (P<0.05)	0.18	0.20	--	6.0
Factor B – Compost Application Rate				
0 t/ha	1.40	0.46	1.12	32.2
4 t/ha	1.80	0.51	1.18	44.0
8 t/ha	2.18	0.55	1.30	54.1
12 t/ha	2.70	0.60	1.44	64.2
16 t/ha	2.73	0.67	1.70	58.5
Level of sig.	***	**	**	***
L.S.D (P<0.05)	0.29	0.10	0.32	9.5

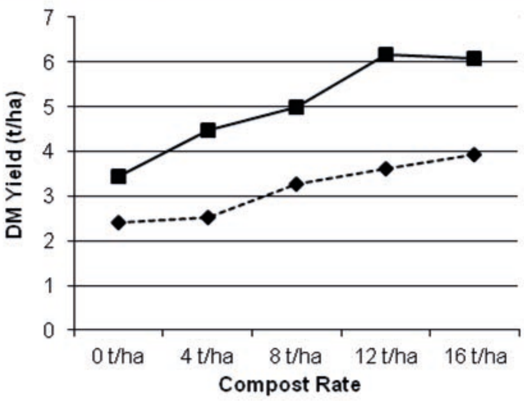

Figure 1. The cumulative yield of the three harvest dates as affected by sward type and compost rate in trial 1.

Table 3. The effect of compost rate and clover variety on DM yield and CNU in trial 2.

Treatment	Dry Matter Yield			
	DM 1	DM 2	DM 3	CNU 1
Factor A – Compost Application Rate				
0 t/ha	3.02	4.55	1.57	165.6
4 t/ha	3.08	4.51	1.56	164.1
8 t/ha	3.02	4.83	1.58	172.5
Level of sig.	n.s	n.s	n.s	n.s
Factor B. Clover Variety				
Crusader	2.84	4.63	1.60	166.8
Chieftain	3.22	4.47	1.42	160.9
Alice	3.00	4.73	1.45	169.8
Aran	3.11	4.81	1.74	171.4
Barblanca	2.92	4.52	1.64	168.1
Level of sig.	*	n.s	*	n.s
L.S.D. (<0.05)	0.25	--	0.20	--

Conclusions

Compost application significantly increased both CNU and DM yield on grass and grass + clover swards. The grass+clover sward showed an excellent yield response to the application of compost. However there was no recorded yield benefit to the use of compost on clover.

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Estimates of carbon sequestration by grassland in Northern Ireland

A.S. Laidlaw[1], P. Christie[2], E.A. Wasson[2] and C.J Watson[2]
[1]*Agri-Food and Biosciences Institute, Crossnacreevy, Belfast BT6 9SH and* [2]*Agri-Food and Biosciences Institute, Newforge Lane, Belfast BT9 5PX*

Introduction

In recently reported carbon budgets of ruminant production in Northern Ireland, carbon sequestration has had to be estimated from the results of studies outside the Province (e.g. Woods *et al.*, 2010) as availability of locally derived data is limited. The estimate of C sequestration is important as it offsets greenhouse gas (GHG) emissions, i.e. the greater the calculated rate of sequestration the smaller is the net balance of emissions. The objective of this study was to analyse the total carbon (C) content in archived soil samples from two long-term grassland experiments carried out in Northern Ireland and to estimate the average rate of change of C content in these soils.

Materials and Methods

The two experiments (Slurry rate trial and N fertilizer grazing trial) were on adjacent sites on a slightly gleyed clay loam soil overlying Silurian shale at Hillsborough, Co Down. The soil is considered typical of a large area of grassland in Northern Ireland. Soils were sampled annually or at longer intervals to 15 cm depth (in 3.5-cm layers). Total C content of soil ball milled to <150 µm was measured on a LECO FP/CNS-200 Analyser. The C content was converted to C mass by multiplying the proportion of C in the soil by an estimate of bulk density in the three layers of 0.99, 1.18 and 1.24 g/cm^3 for layers 0-5, 5-10 and 10-15 cm, respectively. Average C mass per treatment at each sampling date was integrated over the three layers and related to the number of years that the treatments had been applied by linear regression in both experiments.

Slurry rate experiment: The randomised block experiment laid down in 29.75 m^2 plots on a recently established perennial ryegrass sward in 1970 was cut three times each year to simulate a silage cutting regime. Fertiliser or manure, depending on treatment, was applied in spring and after the first two cuts in equal amounts in each year. Soil samples taken from three replicates of treatments that had received no fertiliser or manure, 0F, or slurry applied in three applications to a total of 50 m^3/ha or 200 m^3 /ha annually were analysed for C content.

N fertilizer grazing trial: The 0.2 ha plots were reseeded with perennial ryegrass in 1987 and treatments were imposed annually from 1989. Different annual rates of N fertiliser were applied in six equal applications between March and September and the swards were continuously stocked with 7 to 12 month steers to maintain a sward surface height of 7 cm. Carbon content in soil samples from the plots that received on average 250 kg N/ha annually was determined. Soil sampled for the first 11 years has already been reported (Watson *et al*., 2007). Data from samples taken in years 12 and 17 were added to the data set,.

Results and Discussion

In all three of the treatments under a simulated silage harvesting regime the amount of total C in the top 15 cm of soil increased over the 40-year period that treatments were imposed (Fig. 1). The slope of the regression line is a measure of the average rate at which C accumulated, ranging from 0.46 t C/ha for the unfertilised sward to 1.03 t C/ha for the 200 m^3/ha slurry treatment. So grassland subject to a very low input management is still capable of accumulating almost 0.5 t C/ha in the top 15 cm of soil in the long term. Assuming slurry had on average 5% DM of which 40 % was C, the 200 m^3/ha treatment would receive 4 t C/ha/annum. So most of the C from slurry is readily lost from the top 15 cm of the soil profile. The strong linear association between C accumulation and time over the 40 years is indicative that the soil C content had not reached equilibrium during that period.

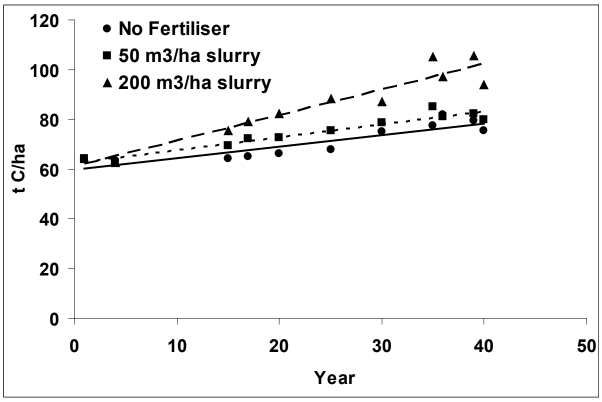

Fig. 1. Total carbon (t C/ha) in top 15 cm soil in swards receiving either no fertilizer or manure or 50 or 200 m^3/ha cattle slurry annually over 40 years. Regression equations are y = 0.46x + 59.9, R^2 = 0.81; y = 0.52x + 62.5, R^2 = 0.93; and y = 1.03x + 61.1, R^2 = 0.91

Regressing total C (t C/ha) from the first 12 years and year 17 of the N fertiliser grazing trial on the corresponding year of the trial, the regression equation was y = 1.28x + 49.1, R^2 = 0.81. As in Fig. 1, the slope of the line is the rate of C accumulated which was similar in both treatments, i.e. 1.28 t C/ha/annum.

Conclusions

These data suggest that the C sequestration rate for well managed swards in Northern Ireland is likely to be, on average, in excess of 0.31 t C/ha as assumed by Woods *et al.* (2010). An intermediate range between 0.48 and 1.28 t C/ha of 700 to 800 kg C/ha would seem to be a more realistic estimate for calculation of carbon budgets of ruminant production in Northern Ireland.

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Identifying profitable beef bulls for use in Irish dairy herds

N. McHugh[1], S. McParland[1], A.R. Cromie[2] and D.P. Berry[1]
[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork and* [2]*Irish Cattle Breeding Federation (ICBF), Bandon, Co. Cork*

Introduction

Considerable transfer of germplasm occurs between Irish dairy and beef herds. In 2010 approximately 40% of dairy cows were bred to beef bulls, with Angus (14%), Hereford (10%) and Limousin (6%) being the most used breeds. When using beef bulls on their herd, dairy farmers wish to produce an easy calved, good quality, live calf that has little effect on the subsequent lactational performance of its dam. To date, however, dairy farmers have no specific tool to facilitate selection of the most profitable beef bull for use in their herd. The aim of this study was to develop a new breeding index for dairy farmers that will aid in the selection of beef bulls.

Materials and Methods

For the development of any breeding goal, knowledge of three key components is required: 1) traits that influence the breeding goal, 2) genetic parameters of traits included in the selection index; and 3) the optimum economic values for each trait. The traits of interest included in the new index were: calving difficulty, calf mortality, gestation length, and calf price. Heritability estimates for these traits have been calculated using Irish data previously (Berry et al., 2011; McHugh et al., 2011). The economic value for calving difficulty was derived from the costs associated with an increase in the incidence of difficult calvings from 6 to 7%. The economic cost includes the costs of increased stockman hours, veterinary interventions, cow mortality, disposal and infertility as well as of loss in milk sales (McHugh et al., 2012). The economic value for calf mortality was calculated as the cost of calf disposal plus the average value of an equivalent live calf. For gestation length the economic value was calculated as the benefit of a one day shorter calving interval. For each of the three traits described above the projected or current prices and costs were used in the calculation of the economic values. As a monetary value is assigned to each calf the economic value for calf price was implicitly assumed in the breeding value of the calf. Calf price was the average price paid for a calf sold between 2 and 42 days of age within the range of €2 to €450 (McHugh et al., 2011). A proportion of resultant female progeny from the mating of a beef bull to a dairy cow are likely to subsequently become replacement females in the beef herd. Therefore, the response to selection on this new index on genetic merit of, in particular, milk yield and fertility in beef animals was of interest. Thus, the correlation between this new index and milk and fertility sub-indices of the existing suckler beef value index (SBV) was quantified by correlating each sire's EBV for both milk and fertility with the EBV calculated for each trait included the new index.

Results and Discussion

The calculated economic weights, along with the relative emphasis on each of the four traits are presented in Table 1. Decreases in calving difficulty, peri-natal mortality and gestation length increase farm profitability and this is reflected in the negative economic weightings for these three traits. Approximately two-thirds of the relative emphasis was placed on calf price, indicating the importance of high calf price to farm profitability as well as the large genetic variation in this trait. However the genetic standard deviation (25.7 kg) was considerably higher for calf price compared the other traits included in the index.

Table 1. Genetic standard deviation (σ_g), economic weighting and relative emphasis (%) for each of the four traits included in the index.

Trait	σ_g	Economic weighting	Relative emphasis
Calving difficulty	2.94	-3.84	27.04
Calf mortality	0.29	-1.78	1.24
Gestation length	1.88	-2.26	10.17
Calf price	25.7	1.00	61.55

Sire predicted transmitting abilities (PTAs) are currently available for calving difficulty, calf perinatal mortality and gestation length and PTAs for calf price will be available from the ICBF in 2012. Therefore the index value of an animal can be calculated simply as the sum of the economic weight times the respective PTA.

The correlation between the new index and the milk and fertility sub-indices of the SBV was moderately positive (r=0.35). This indicates that selection of beef bulls on the new index will result in indirect selection for improved milk and fertility traits in female progeny used as beef herd replacements, both of which are of key economic importance to the suckler herd.

Preliminary analysis of sire breeding values clearly shows that this index favours easier calving sires with shorter gestation lengths. For example, results to date suggest that Aberdeen Angus and Hereford sires will, on average, generate €37 greater profit per calf born to a dairy dam compared to progeny of a Belgian Blue sire.

Conclusions

The formation of this new index will facilitate easy identification of the most profitable beef bulls for use in the dairy herd. It is envisaged that the new index will be launched in 2012.

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Characterisation of the sequence variation in genes of the somatotrophic axis in DNA pools from cattle divergent for carcass weight

M.P. Mullen[1], C.J. Creevey[2], M.S. McCabe[2], D.P. Berry[3], D.A. Magee[4], A.P. Killeen[2], D.J. Howard[1], D.E. MacHugh[4] and S.M. Waters[2].
[1]*Animal and Bioscience Research Department, Teagasc, Athenry, Co. Galway, [2]Grange, Dunsany, Co. Meath, [3]Moorepark, Fermoy, Co. Cork. [4]School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4.*

Introduction
The somatotrophic axis is well established as central to post-natal growth and development in mammals. In domestic livestock the influence of this axis on traits of commercial importance such as body size, carcass weight, milk yield and fertility has been widely published. While there is evidence from our own research (Mullen et al. 2010; 2011) that variation in genes of the somatotrophic axis are associated with production traits in cattle, there is a dearth of information on the effect of causal polymorphisms in genes of this axis and its regulators on animal performance. Sequencing large numbers of complete genomes would prove an invaluable resource for causal polymorphism identification, however this is currently not feasible primarily due to the costs involved. A DNA pooling approach coupled with targeted genome enrichment, prior to high throughput sequencing is a cost effective alternative. The accuracy of allele frequency estimates generated using this approach has recently been demonstrated (Mullen et al. 2012). The aims of this study were: (1) to identify putative coding and regulatory DNA sequence polymorphisms in candidate genes of the somatotrophic axis, and (2) to estimate allele frequency differences at these loci between dairy bulls divergent for genetic merit for carcass weight, using DNA pooling, target enrichment and high-throughput sequencing approaches.

Materials and Methods
DNA from semen samples of 150 Holstein-Friesian (HF) bulls, available through artificial insemination, were divided into two groups divergent for genetic merit for carcass weight while also simultaneously minimising the co-ancestry within each group.
Targeted genes ($n = 83$) included hormones, transcriptional regulators, binding proteins and genes involved in gluconeogenesis and insulin nutrient partitioning-related pathways.
For both sample groups, DNA was pooled using equimolar DNA quantities from each individual animal. The Agilent SureSelect® Target Enrichment System was used to selectively capture whole gene and regulatory DNA sequences for the 83 somatotrophic axis genes, followed by sequencing using the Illumina GAII platform. All DNA sequence data were aligned using the *B. taurus* UMD3.1 reference genome and the BWA aligner software package. DNA sequence polymorphisms were identified using the SAMtools package. A minimum of four non reference allele reads was required to identify polymorphisms across both groups.

Results and Discussion
In total, ~ 10 million reads spanning ~ 2 Megabases (Mb) of sequence data were generated. A total of 4,132 SNPs and 756 indels with on average 53-fold coverage were identified across the 83 genes. Thirty-one percent (n=1288) of SNPs identified were located within putative regulatory regions in the 5' and 3' UTR. Fifty-eight percent (n=2,414) were intronic and the remaining 7% (n=313) were exonic, of which 4% (n=172) were non-synonymous (NS) substitutions. In total, 196 SNPs showed a greater than two-fold allele frequency differential between the low and high carcass weight cattle groups. Table 1 shows four examples of this SNP category.

Table 1. Four SNPs in Holstein-Friesian cattle divergent for carcass weight (CWT). The frequency of the second allele is shown for each SNP.

Entrez Gene ID	Chr.	Location within gene	SNP	High CWT freq	Low CWT freq
GHR	20	Intron	A / G	0.60	0.14
IGF1	5	Intron	A / T	0.44	0.20
GH1	19	Exon (NS)	G / A	0.72	0.35
IGF2R	9	Intron	T / C	0.71	0.21

We previously observed associations between carcass weight and variants in *GHR* and *IGF1* (Waters et al. 2012). Our previous studies encompassed sequence analysis of limited regions of each gene investigated but the polymorphisms presented herein were identified across entire genes and regulatory regions. Therefore it is probable that a subset of these polymorphisms underlie heritable variation in carcass weight.

Conclusions
This study has identified novel variation and allele frequencies of key genes involved in growth and development in cattle. Future work will include genotyping, association analyses as well as *in vitro* testing to identify candidate causal polymorphisms affecting performance in cattle. The ultimate objective will be to validate in independent populations including beef breeds and determine their contribution to genetic variation for carcass weight.

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Genetic variation in pre-miRNAs and mature miRNAs in the genomes of domestic cattle.

M. Braud[1], M Donoghue[1], D. MacHugh[2], D. Morris[3] and C. Spillane[1].
[1]*Genetics and Biotechnology Lab, Plant and AgriBiosciences Centre (PABC), National University of Ireland, Galway, Ireland.* [2]*Animal Genomics Laboratory, Veterinary Science Centre, University College Dublin, Ireland.* [3]*Animal Bioscience Research Department, Animal and Grassland Innovation Centre, Teagasc, Mellows Campus, Athenry, Ireland.*

Introduction
MicroRNA (miRNA) are 19-25 nucleotide small non-coding regulatory RNAs that typically have a repressive effect on expression of genes containing target sites for the miRNA within the transcribed RNA. miRNAs have been identified in many eukaryotes where they play important roles in regulation of gene expression during organismal development. In mammals, only 6-7 nucleotides of the miRNA sequence typically have exact matches with the miRNA binding site on the 3'UTR. This region (nts 1-8) of the mature miRNA is called the seed region. Genetic variation in miRNAs or their target sites in mRNAs can lead to major changes of the regulation of the gene expression. Hence, miRNA could contribute extensively to phenotypic variation in some traits among and within species. A striking example in livestock is where mRNA 3'UTR variation create a new miRNA target which is majorly responsible for the overexpression of the muscular phenotype in Texel sheep (Clop, Marcq et al., 2006). The aim of this study was to investigate the possible impact of miRNA variation on economically important traits in cattle.

Materials and Methods
To identify all cattle miRNAs and single nucleotide polymorphisms (SNPs) within pre-miRNAs and mature miRNAs, we have extracted the data available for cattle on dbSNP and mirbase, respectively. This provides SNPs and pre-miRNA/mature miRNA sequences for cattle (related to the Btau 4.0 annotation release 63). The mirBase file contain 662 pre-miRNA sequences and 676 mature miRNAs (2011-10-27). The dbSNP file contains all the variation, location and modification details on the 2,074,230 SNPs available for Bos taurus genome (2011-06-15). To identify pre-miRNAs containing SNP, a custom-built python script was developed. Using this script, we have indentified nine pre-miRNAs containing SNP polymorphisms in cattle. To visualise and associate the corresponding mature miRNA sequence t_coffee software was used to align and represent the sequences and SNPs (Figure 1).

Results and Discussion
We found that nine miRNA have SNPs in their pre-miRNA sequence. The SNPs are present in four of the mature miRNA sequences and in two seed region of the mature miRNA. The results in Figure 1 show that mir 2313* and mir-29e, both contain SNPs in their seed region. Mir-29e is a predicted miRNA obtained by comparison with other mammalian miRNAs. Mir-2313 has been validated by wet lab experimentation. Mir-2313 and mir-213* have been detected expressed in liver cells (Glazov, Kongsuwan et al., 2009). A blast comparison of pre-miRNA and mature miRNA with all the sequences present in mirbase does not show significant similarity with mir-2313. On the other hand, the same analysis on mir-29e shows a high similarity with miRNA-29b of the mir-29 familly and by aligning these sequences we demonstrate that the seed region is highly conserved. In mammals, the mir-29 family is implicated in muscle development in pigs (McDaneld, Smith et al., 2009), human lung cancer and brain degeneration in human and cattle (Saugstad, 2010).

Conclusions
Genetic variation in miRNAs has major potential in phenotypic modification `and improvement schemes that could lead to improved artificial selection of individuals (Clop, Marcq et al., 2006). Our work provides a basis for the integration of bioinformatic and wet-lab approaches for understanding the contribution of miRNA variation to economically important traits in cattle.

Acknowledgments
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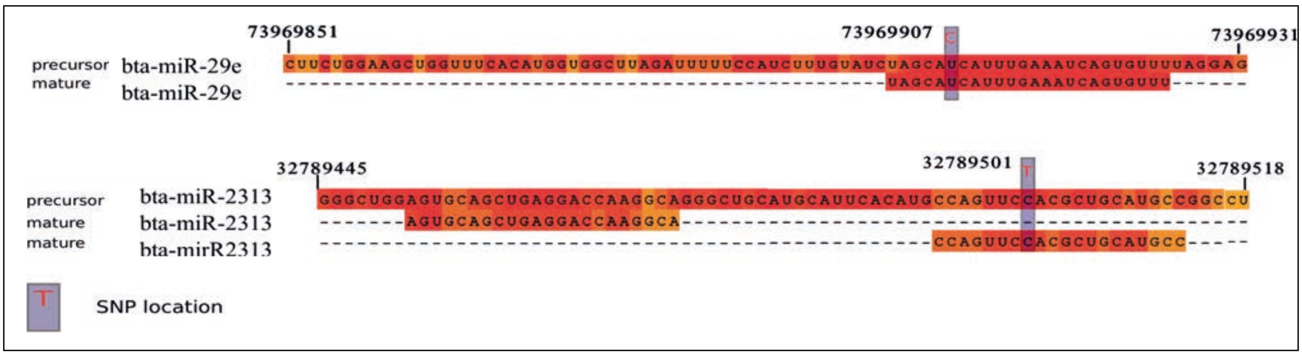

Fig. 1: Variation in cattle miRNA seed region

Multi-breed beef genomic selection

D.P. Berry[1], M.P. Mullen[2], A.R. Cromie[3], P. O'Boyle[2], S.M. Waters[4], and J.F. Kearney[3]

Teagasc Animal & Grassland Research and Innovation Centre, [1]Moorepark, Fermoy, Co. Cork. [2]Athenry, Co. Galway, [4]Grange, Dunsany, Co. Meath, [3]Irish Cattle Breeding Federation. Bandon, Co. Cork.

Introduction

Genomic selection was officially included in the Irish national dairy cattle genetic evaluations in spring 2009, with an increased accuracy of selection anticipated (Berry et al., 2009). Since 2009 approximately 40% of semen sold annually was from genomically selected sires. Retrospective analysis clearly shows an increased accuracy of selection using genomic selection in Irish dairy cattle (Cromie et al., 2011). The objective here was to evaluate the potential of genomic selection to increase the accuracy of selection in Irish beef cattle.

Materials and Methods

Genotypes of 777,962 single nucleotide polymorphisms (SNPs) were available on 2,544 Holstein-Friesian, Charolais, Limousin, Angus, Hereford and Simmental beef bulls. Only animals and SNPs with a genotype call rate >95% were retained. Also, both autosomal SNPs and animals with >2% Mendelian inconsistencies between parent-offspring pairs were discarded. Non-autosomal SNPs, as well as SNPs with a minor allele frequency <2%, poor call clustering, and those deviating from Hardy-Weinberg equilibrium ($P<0.1*10^{-7}$) were discarded. Following all edits 533,463 SNPs from 1,834 beef animals remained, consisting of 587 Limousin, 559 Charolais, 237 Simmental, 236 Angus and 215 Hereford bulls.

The pedigree of each animal was traced back at least four generations, where available. Estimated breeding values (EBV) and associated reliability estimates, for all animals and their parents were obtained for carcass weight, carcass conformation and carcass fat score from the Irish domestic genetic evaluation in August 2011. Estimated breeding values were de-regressed and parental contribution was subtracted from the reliability of each animal. Only bulls with at least 40% reliability (following removal of parental contribution) for the trait under investigation were retained for inclusion in the estimation of SNP effects. A random sample of animals, within breed, was chosen for validating the SNP effects and are referred to as the "validation animals"; the remaining animals, referred to as the "training animals", were used to estimate the SNP effects. An additional group of animals with a reliability of <40% were used to quantify the expected reliability of direct genomic values as well as the weighting on genomics within their genomic breeding value. The genomic relationship matrix was estimated, within breed, by regressing Z'Z on the numerator relationship matrix and scaling the Z'Z matrix with the resulting intercept and regression coefficient from the model; the Z matrix (number of animals by number of SNPs) contained the alleles for each locus as -1 (homozygous), 0 (heterozygous) and +1 (homozygous). Direct genomic values were subsequently estimated as $D\hat{G}V = G*(R+G)^{-1}\tilde{y}$, where G is the genomic relationship matrix among the training animals and G* is the genomic relationships between the validation animals and the reference animals; R is a diagonal matrix containing one divided by the animal's reliability from his daughters less one and $\tilde{y}$ is the deregressed EBV for the trait under investigation.

Results and Discussion

The number of animals in the training population for Charolais, Limousin, Hereford, Angus and Simmental were 371, 393, 124, 151, and 157, respectively. The correlation between the pairwise expected relationships (i.e., from the numerator relationship matrix) and the actual genomic relationships (i.e. from the genomic relationship matrix) varied across breeds from 0.65 to 0.83, most likely suggesting a combination of discrepancies in the recorded pedigree but also the ability of the genomic relationship matrix to capture Mendelian sampling. The mean genomic reliability per breed varied from 17% in the Angus to 27% in the Simmental; the mean weighting on genomics in the genomic breeding values varied from 6% (Angus) to 14% (Simmental). The contribution of genomics to the genomic breeding value of an animal was not only dependent on the size of the training population but also on the relatedness of the young animals to the training population, signifying that genomic selection in the present study at least, was more than likely more accurately tracing relationships rather than quantitative trait loci *per se*. Sufficient validation bulls for Angus, Simmental and Hereford did not exist to generate a meaningful analysis of the accuracy of genomic selection. The correlations between direct genomic values, with a reliability >40%, and traditional estimated breeding values, with a reliability >80%, for the different carcass traits varied from 0.39 to 0.66 in the Charolais and between 0.31 and 0.47 in Limousin. However there were few animals in the comparison.

Conclusions

Genomic information can contribute to the accuracy of selection in beef animals. However, the increase in accuracy in the present study was modest, predominantly due to the relatively small size of the training populations. More genomic information on phenotyped animals is required.

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Genes associated with angularity in dairy cattle are associated with obesity in humans

S. McParland[1], D.P. Berry[1] & A. Coghlan[2]
[1]*Animal & Grassland Research & Innovation Centre, Teagasc, Moorepark, Co. Cork,* [2]*Dept.of Microbiology, University College Cork.*

Introduction

Despite substantial research into the genetic basis for variation in traits of importance to human populations much less research has been undertaken in identifying the functions of bovine genes. Through comparative genome analysis, the research undertaken to understand the functions of human genes can be exploited by cattle breeders. The aim of this study was to identify bovine genes associated with angularity, a genetically similar trait to body condition score (BCS) and to identify novel genes for future obesity studies of mammals.

Materials and Methods

Angularity, a linear type trait classified on dairy animals refers to the "angle and openness of the ribs, combined with flatness of bone". The strong negative genetic correlation between angularity and BCS (Berry et al., 2004) indicates that these traits are genetically similar. Estimated breeding values, and associated reliability, for angularity were provided by the Irish Cattle Breeding Federation (ICBF). Parental contribution to the reliability of each breeding value was removed. Only bulls with an adjusted reliability for any type trait greater than 30% were included in the analysis. Breeding values were de-regressed to be independent of the relationship between animals included in the evaluations, and reverse the shrinkage of breeding values in the mixed model equations.

Holstein-Friesian bulls (n=5,736) were genotyped with the Illumina BovineSNP50 Beadchip (Illumina Inc., San Diego, CA). All genotyped bulls were previously, or are currently available for widespread use through AI in Ireland. A total of 230 single nucleotide polymorphisms (SNPs) were removed due to an observed Mendelian inconsistency rate greater than 0.50%. SNPs with a minor allele frequency <5% (n=7,947), or where greater than 5% of calls were missing (n=1,073) or deviated from Hardy-Weinberg equilibrium (n = 1,755) were removed from the analyses. All SNPs were bi-allelic and were recoded as 0, 1 or 2 according to the number of alleles present at each locus. The final data set comprised 42,996 SNPs from 1,396 bulls with a breeding value for angularity. Single SNP regression analysis was performed in ASReml (Gilmour et al., 2006) using a linear mixed animal model to detect the regions of the genome associated with angularity. Fixed and random effects accounted for in the mixed model were the SNP genotype of the animal and the animal, respectively. A pedigree file, five generations deep, was generated using data obtained from the ICBF national database and contained 6,320 animals. The dependent variable was weighted by its adjusted reliability. The Bonferroni correction was applied.

The Ensembl SNP identifier and gene location of SNPs were obtained using the BioMart interface to the Ensembl database. SNPs located in inter-genic regions were discarded from the analyses. Orthologous genes in *Homo sapiens* were also obtained from BioMart. Due to the strong association between angularity and BCS in cattle, the literature was reviewed and online data bases (eg. OMIM) used to identify a) genes in *Homo sapiens* associated with obesity and bone quality traits and b) biological associations between human orthologs of angularity-associated bovine genes and phenotypic variation in humans.

Results and Discussion

The Bonferroni correction resulted in lowering the statistical significance threshold for the P-value to $P<0.000001$. 262 SNPs within 78 genes across the bovine genome were associated with angularity (Figure 1). SNP rs110342629 (b=-0.99), located on chromosome 19 had the highest probability of association ($P = 3.15 \times 10^{-15}$) with angularity.

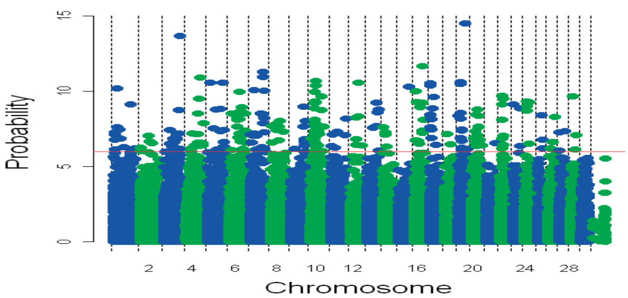

Figure 1. Manhattan plot of the probability ($-\log_{10}$ (p-value)) of SNP associations with angularity

Of the 23 genes most strongly associated with angularity (-log10(p-value)>8.5), orthologs of 8 of the genes are known to be associated with variation in obesity, obesity linked traits and bone quality traits in mammals. Obesity traits associated with mammalian orthologs identified in this study include obesity (*ARID5B, CHCHD3*), fat tissue in mice (*ARID5B*), adipogenesis (*ARID5B*), fatty acid metabolism (*HADH*), insulin resistance (*PDZD2*), diabetes (*CHCHD3, RASPG1*), pancreatic function (*PDIF1*), uric acid (*SLC2A9*) and back fat in pigs (*ANO10*). Bone quality traits associated with mammalian orthologs of bovine genes which in turn were associated with variation in angularity include skeletal dysplasia, bone bowing and reduced bone mineral density (*NF1*) and bone erosion (*SLC2A9*). The SNP with the strongest angularity association in this study was located within *FTSJ3*, a gene homologous to the rRNA methyltransferase *FTSJ* involved in growth rate regulation (Ching et al., 2002).

Conclusions

Orthologs of bovine genes associated with angularity, a genetically similar trait to BCS are associated with obesity linked traits and bone traits of mammals. A potential candidate gene for further obesity work in mammals, *FTSJ3*, was identified.

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Analysis of runs of homozygosity in cattle breeds

D Purfield[1, 2], D.P Berry[2], S McParland[2] and D.G Bradley[1]
[1]*Smurfit Institute of Genetics, Trinity College Dublin.*
[2]*Teagasc Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co.Cork*

Introduction
Runs of homozygosity (ROH) are contiguous lengths of homozygous genotypes that are present in an animal due to parents transmitting identical sister haplotypes to their offspring. The length of an ROH can be an indication of consanguinity as the longer the ROH segment, the more likely recent inbreeding occurred in the pedigree. However, long runs of homozygosity may also persist in outbred animals, believed to be due to the existence of multiple-megabase-scale ancestral haplotypes as a result of the mutation, linkage disequilibrium (LD) and recombination rates at their genomic location (Gibson, *et al.,* 2006). The presence of more ancient relatedness, which is often unaccounted for in an animal's pedigree due to limitations of recording, can also account for shorter ROH lengths (Kirin, *et al.*, 2010). As a result, past and present breeding practices will have played an important role in determining the length of the ROHs for a particular animal. The objective of this study was to quantify the levels of ROH that exist in different breeds of cattle.

Materials and Methods
Genotypes from 891 AI bulls from eight purebred dairy (n=360) and beef cattle breeds (n=420) and one Holstein-Friesian crossbreed (n=111), generated from the Illumina Bovine high-density (HD) panel were used. Only biallelic SNPs on the 29 autosomes were retained and both animals and SNPs with genotype rates <90% were discarded. Also, monomorphic SNPs and SNPs that deviated from the Hardy Weinberg equilibrium (P<0.0001) within breed were discarded. PLINK v1.07 was used to identify ROHs, by taking a sliding window of 5 Mb across the genome, and allowing no more than two missing genotypes and one possible heterozygous genotype per window. A minimum threshold length of 0.5 Mb was set for identification of ROH. The HD genotypes were used for validation of the BovineSNP50 density panel to identify ROH by retaining the 48,734 SNPs (reduced HD panel) common to both the HD and the Illumina BovineSNP50 Beadchip. To establish that this reduced density also predicted the correct ROH length category for ROH, the quantity of ROHs that were correctly assigned to the HD ROH length category was plotted. SNP involvement in a ROH was also calculated by counting the number of times each SNP appeared in a ROH. Measures of homozygosity (F_{ROH}) and the pedigree inbreeding coefficient were calculated and correlated for all animals that had all animals that had a complete generation equivalent value ≥6 (n=230). F_{ROH} was calculated as $F_{ROH} = \sum L_{ROH} / L_{auto}$ where L_{ROH} was calculated as the sum of all ROHs >0.5Mb in length and L_{auto} is the total length of the genome covered by SNPs (i.e., 2.51 GB). The pedigree inbreeding coefficient was calculated according to the Meuwissen and Luo (1992) algorithm.

Results and Discussion
ROHs were common and frequent across all breeds as all animals had at least one ROH present in their genome that was between 1-5 Mb in length. The dairy breeds had a greater incidence of long ROHs (>30 Mb in length) indicative of recent inbreeding, whereas the Angus and Hereford had substantially more of their genome covered in shorter ROHs (1-5 Mb) suggesting a high level of distant ancestral relatedness possibly due to their geographical isolation during breed formation. Analyses of SNP involvement in a ROH revealed that certain areas of the genome were more commonly involved in a ROH than others (Figure 1). In particular a region on chromosome 14 involving the TOX gene, an immune gene, was observed in 87.4% of the HD genotyped population in a ROH. Strong correlations existed between the pedigree-based inbreeding coefficient and F_{ROH} (r=0.75;P<0.0001). A total of 157,600 ROHs were identified using the HD panel, whereas only 19,078 ROHs were identified using the reduced HD panel. The majority of ROH that the reduced panel failed to recognise were between 0.5-1 Mb in length but almost all ROHs in length categories of >5Mb were recognised and assigned to the correct length category >70% of the time, validating the BovineSNP50 array panel for use.

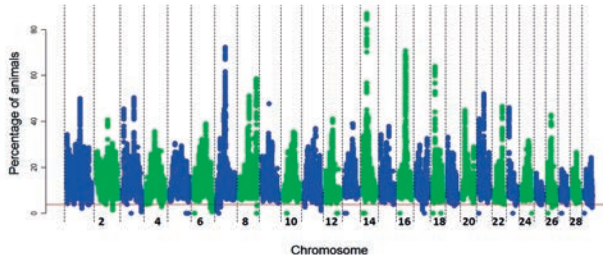

Fig. 1. Incidence of each single nucleotide polymorphism (SNP) in a run of homozygosity (ROH) in the HD panel population.

Conclusions
We show that the extent of a genome under ROH in cattle provides a sufficient predictor of the pedigree inbreeding coefficient, suggesting that in the absence of pedigree data, this method may be used to infer aspects of recent population history.

Acknowledgements
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Genetic parameters for perinatal mortality in Irish dairy cattle

D Purfield[1,2], D.G Bradley[1] , J.F. Kearney[3], and D.P Berry[2],
[1]*Smurfit Institute of Genetics, Trinity College Dublin.* [2]*Teagasc Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co.Cork.* [3]*Irish Cattle Breeding Federation. Bandon, Co. Cork.*

Introduction

Perinatal mortality in cattle is defined as calf mortality shortly before, during or shortly after parturition (Philipsson *et al.,* 1976). Recent studies have highlighted that the prevalence of bovine perinatal mortality is on the increase, with current incidences varying between 2% and 10% internationally. The incidence in Ireland has been previously estimated as 4.29% in Ireland (Mee *et al.,* 2008). Previous heritability estimates for perinatal mortality in Holstein dairy cattle are 4% for the direct genetic effect and 3% for the maternal genetic effect (Steinbock *et al.,* 2003). The heritability of direct and maternal calving difficulty was reported to be slightly higher at 6% and 5%, respectively (Steinbock *et al.,* 2003). The objective of this study was to estimate the heritability of perinatal morality, calving dystocia and also perinatal mortality not associated with calving dystocia in Irish dairy cattle.

Materials and Methods

Date of birth, herd of birth, gender of calf, degree of calving assistance, occurrence of perinatal mortality (recorded as calf dead at birth or within 24hrs), parity and age of dam, as well as breed of dam, calf and sire were available from the Irish Cattle Breeding Federation for the years 2002 to 2011, inclusive. In total data from 3,884,082 birth events were available, of which 2,094,359 had information on the degree of calving assistance at birth. Data for dams of unknown parity and of parities >10 were discarded (n=28,865), as well as births with more than two calves (n=4,854). Dams who calved for the first time less than 608 days of age (n=4,580) as well as dams calving greater than 2 years from the median age within each parity, were discarded (n=95,399). Dam parity was recorded as six classes; 1, 2, 3, 4, 5 and >5. Parity number of the dam in this study was the parity of the cow the day after she had calved. Only data from dairy herds were retained comprising 1,671,296 birth events. Contemporary groups were generated based on grouping animals together for each phenotype (dystocia, perinatal mortality, perinatal mortality without dystocia) within herds that had birth dates in close proximity. Only contemporary groups with at least 5 records were retained. A random selection of contemporary groups comprising 85,776 calves was retained for analysis. These animals originated from 3,523 different herds and from 7,285 and 7,539 unique sires and maternal grand sires, respectively. Factors associated with dystocia and perinatal mortality were determined using univariate repeatability animal-dam models in ASReml (Gilmour et al., 2008). Fixed effects included contemporary group, twins, parity, age within parity, and calf gender. Random effects included were the additive genetic effect, the maternal genetic effect and the permanent environmental effect. Breed was accounted for through the use of founder breed groups in the pedigree.

Results and Discussion

The percentage of data from parities 1, 2, 3, 4, 5, >5 was 26%, 21%, 17%, 13%, 9% and 14%, respectively. The percentage of birth events scored as no assistance/unobserved, slight assistance, severe assistance and veterinary assistance was 72.4%, 22.0%, 3.7% and 1.9%, respectively. The prevalence of perinatal mortality in this dataset was 2.63%, with 42.38% of perinatal mortality occurring in primiparae. The prevalence of twins was 3.59%, of which 58.51% were of the same sex; some level of assistance was reported in 35.2% of twin births. The incidence of dystocia (i.e., calving difficulty score ≥2) was greater in male (31.82%) than female calves (23.20%). The occurrence of perinatal mortality when no dystocia occurred was 0.96%. The prevalence of perinatal mortality when not associated with dystocia was highest (9.42%) when both the sire and dam main breed component was Jersey. The direct heritability for perinatal mortality, dystocia, and perinatal mortality without dystocia was 0.01 (s.e. 0.003), 0.20 (s.e. 0.014) and 0.003 (s.e. 0.002), respectively. Maternal heritability estimates were 0.009 (s.e 0.003), 0.006 (s.e. 0.003 and 0.004 (s.e 0.002). These heritability estimates for dystocia and perinatal mortality are consistent with previous genetic parameter estimates reported in Irish Holstein-Friesians (Hickey et al, 2007; Berry *et al.,* 2011).

Conclusions

The prevalence of perinatal mortality is still quite high in Ireland but the incidence is, nonetheless, low in the absence of dystocia. However, genetic variation clearly exists for traits which influence perinatal mortality suggesting that, if exploited, the incidence could be reduced.

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Breeding for increased flock mean 40-day lamb weight but lower flock variance

N. McHugh[1], and T. Pabiou[2]
[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork and* [2]*Sheep Ireland, Bandon, Co. Cork*

Introduction

Maximising growth rate at an early stage across the entire flock is the primary aim of all sheep producers. However, achieving uniformity of growth can prove difficult as there is anecdotal evidence that some paternal half-sib families exhibit large variation in performance whereas small variation can be observed in other paternal half-sib families. A proportion of the differences in animal performance across different production systems may be described as differences in the residual variance. Genetic models have been designed to account for heterogeneity of variance, or the differences in the residual variance, that allow for breeding values to be calculated based on the residual variance. Knowledge of these breeding values will allow producers to breed animals that are robust across different environments, thus producing more uniform progeny whilst reducing variation in their performance. The objective of this study was to estimate variance components for the genetic effect of mean 40-day weight as well as the genetic effects of the variance in 40-day weight.

Materials and Methods

A total of 20,699 forty day live-weight records taken between the years 2009 and 2011, across 29 commercial flocks were obtained from Sheep Ireland. Only animals aged between 20 and 65 days of age were retained. Animals were discarded if sire, maternal grandsire, or flock of birth were unknown. Animals were also removed if their 40 day weight was not between 8 and 35 kg. Furthermore, animals with 40 day weights greater than ±4 standard deviations from the mean were discarded. Contemporary group was defined as flock by date of weighing. Only records from contemporary groups with at least 4 other records were retained. The fixed effects included in the model used to estimate variance components were contemporary group, gender, age of lamb at weighing (linear and quadratic effect), lambing difficulty, birth and rearing rank of the lamb, month and year of weighing, ewe parity, the main breed fraction of the lamb, ewe, and ram, and ewe age nested within parity. The random effect included in the model was sire. Following all edits a total of 11,099 forty day live-weight records remained.

Variance components for live weight were estimated using a double hierarchical generalised linear model described in detail by Rönnegård et al. (2010) in ASREML (Gilmour et al., 2011). In summary, a linear mixed model was used to calculate estimates for the mean and the variance of the mean with a weighting factor (**W**) equating to the identity matrix for size ***n*** observations. The residual variance for each animal was then used to calculate a weighted gamma generalised linear model for the calculation of the residual variance model. The mean model was rerun to obtain new residual variance estimates which were then in turn used in the residual variance model. These steps were then continually iterated until convergence was deemed to have been reached once the variance components did not change over successive iterations.

Results and Discussion

The genetic (σ^2_a) and phenotypic variance (σ^2_p) of the converged mean and residual variance models are shown in Table 1. The corresponding heritability estimates for the mean and residual variance models were 0.16 (s.e.=0.01) and 0.0001 (s.e.=0.000), respectively. The number of flocks analysed in this study was 29 which may account for the low genetic effect for the residual variance model; increasing the number of flocks analysed in subsequent studies may result in an increase in the genetic effects.

Table 1. Comparison between the genetic (σ^2_a) and phenotypic (σ^2_p) variance calculated using the mean and residual variance models.

Variances	Mean model	Res variance
σ^2_a	2.71	0.001
σ^2_p	13.9	1.02

Similar to previous studies (Rönnegård et al., 2010) the calculated genetic and phenotypic variances for the residual variance model were smaller than the respective estimates for the mean model. However, the calculation of heritability, albeit low (0.0001), for the residual variance indicates that genetic variation exists which can be exploited to help reduce the variation thereby aiding management especially drafting of lambs of similar weight.

The correlation between the estimated breeding values (EBVs) for the mean model and the residual variance for sires with greater than 70 progeny was -0.49 indicating that selection on increasing the mean 40 day live-weight can occur without increasing the corresponding the residual variance. The difference in variation between the EBVs for the mean and residual variance model allow for a genome wide association study (GWAS) to be conducted that could potentially identify recombination hotspots or regions that are associated with epigenetic effects.

Conclusions

Results from this study show that it is possible to change the mean and the variance of traits simultaneously through the genetic heterogeneity of residual variance.

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Genetics of deep phenotypes for fertility

D.P. Berry[1] D. Ryan[2], and S. Coughlan[3]
[1]*Animal & Grassland Research and Innovation Center, Teagasc, Moorepark, Fermoy, Co. Cork.* [2]*Reprodoc Ltd. Fermoy, Co. Cork.* [3]*Irish Cattle Breeding Federation. Bandon, Co. Cork.*

Introduction

Calving interval is the goal trait for fertility in the Irish dairy cattle national breeding objective, the economic breeding index (EBI). However, calving interval is lowly heritable, requires a subsequent calving to occur, requires a long-time horizon to generate an observation, but more importantly is in itself an index of the post-partum interval to oestrus, pregnancy rate, and gestation length. Access to deeper phenotypes (i.e., greater refinement of the trait) for fertility that are less influenced by non-genetic effects (e.g., unrecorded post-partum voluntary waiting period to service), may contribute to greater genetic gain. The objective of this study was to undertake a preliminary quantification of the genetic parameters for a range of deep phenotypes for fertility measured using ultrasound.

Materials and Methods

Information on 60,552 reproductive tract ultrasound scans from 43,124 cows in 531 herds, predominantly from the year 2011 were available. All scans were recorded by one skilled technician (Reprodoc Ltd.). Data included the subjective assessment of the uterus (hereon in known as uterine score; lower scores were more desirable), presence of corpus lutea, gender of calf and approximate day of gestation, where available.

Only Holstein-Friesian cows from a known sire were retained. Phenotypes defined in this study were 1) health status of reproductive tract, 2) presence of ≥1 of corpus lutea, 3) presence of multiple ovulation, and 4) whether the corpus luteum was on the left or right ovary. Reproductive tract status was scored as described by Mee et al. (2008). Contemporary group of herd-year-season of calving was defined for each trait separately and only animals with at least four other contemporaries also with information for the trait under investigation were retained. Lactation yield and subsequent calving interval were also available. Variance components for the fertility traits were estimated using animal linear mixed models in ASREML. Fixed effects included in the models were contemporary group, days post-calving at scan, parity of the cow, and genetic group. Genetic covariances with milk yield and calving interval were estimated using a series of bivariate sire linear mixed models. The impact of selection on the EBI or either of the two main sub-indexes, the milk subindex or the fertility subindex, was estimated by correlating the sire estimated breeding value (EBV) for each of the deep phenotypes with sire genetic merit for the EBI and sub-indexes. No correction for reliability of sire EBV was undertaken.

Results and Discussion

Summary statistics for each of the traits investigated are presented in Table 1. The heritability of the different fertility traits derived in this study was consistent with (inter)national estimates for traditional measures of fertility (Berry et al., 2010). The genetic correlations between traits observed suggest that selection for milk yield alone would be expected to lead to a deterioration in the health status of the reproductive tract post-calving, reduce the probability of a cow cycling, and increase the incidence of multiple ovulation (Table 2). Inferior reproductive tract score was associated with longer calving intervals as was the probability that the cow was not cycling

Table 1. Number of records (N), mean and heritability (h^2; standard error in parenthesis) for each trait

Trait	N	Mean	h^2 (se)
Uterine score (G1,2,3,4)	11390	1.47	0.021 (0.010)
Oestrous cyclicity (Yes/No)	10312	80%	0.057 (0.016)
Multiple ovulation (Yes/No)	848	8%	0.022 (0.062)
Ovary ovulated (Right - Yes/No)	848	56%	0.049 (0.084)
Both ovaries ovulating (Yes/No)	848	7%	0.093 (0.108)

Table 2. Genetic correlations (standard error in parenthesis) between fertility traits and performance

Trait	Milk yield	Calving interval
Uterine score	0.22 (0.21)	0.36 (0.21)
Oestrous cyclicity	-0.45 (0.14)	-0.56 (0.14)
Multiple ovulation	0.66 (0.28)	-0.45 (0.28)

Estimated breeding value for inferior reproductive tract score was associated with lower EBI (r = -0.24), lower fertility subindex (r = -0.28) and greater milk production subindex (r = 0.11). Estimated breeding value for cyclicity was positively correlated with EBI (r = 0.29) and the fertility subindex (r = 0.37) but negatively correlated with the milk subindex (r = -0.17)

Conclusions

Deep phenotypes evaluated in the present study are heritable although heritability estimates are not greater than traditional fertility traits. However, improvements in the statistical model may result in a reduction in residual variance and thus greater heritability. Selection for EBI, and in particular the fertility sub-index, is improving genetic merit for the deep fertility phenotypes investigated in this study.

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Usefulness of health and temperament data from the dairy efficiency program in genetic evaluations

D.P. Berry[1] G. Ramsbottom[2], A.R. Cromie[3] and S. Coughlan[3]

[1]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork.* [2]*Teagasc, Oakpark, Co. Carlow.* [3]*Irish Cattle Breeding Federation. Bandon, Co. Cork.*

Introduction

Accurate genetic evaluations for low heritability traits, such as animal health, require routine access to large quantities of phenotypic data (Berry et al., 2011). An opportunity arose as part of Article 68(1) of Council Regulation (EC) 73/2009 to "… address specific disadvantages affecting farmers …" and encourage efficiency gains through the adoption of best practice. This initiative was exploited to increase the quantity of individual cow information recorded on mastitis, lameness, and temperament, amongst other traits. The objective of this study was to estimate genetic parameters for mastitis, lameness, and temperament recorded in the dairy efficiency program.

Materials and Methods

Data recorded by farmers on 283,300 cows, one lactation record per cow, from 3,492 herds were extracted from the Irish Cattle Breeding Federation database in October 2011. Mastitis and lameness were recorded separately as 0, 1, or ≥2 cases per cow in the current lactation; temperament was recorded as "VG"-very good, "G"-good, "A"-average, "P"-poor, and "VP"-very poor. For the purpose of this study both mastitis and lameness were dichotomised separately as "no case" or "at least 1 case". In total, 299 herds recorded no cases of mastitis, 337 herds recorded no cases of lameness, and 144 herds recorded no variation in cow temperament; of these herds, 30 reported no case of either mastitis or lameness and also reported no variation in cow temperament. Cows from herds that recorded no variation were discarded for the trait under investigation. Contemporary group was defined as herd-year-season of calving and only contemporary groups with at least 5 records were retained. Following edits, 185,335 cows, 187,006 cows and 205,137 cows remained in the analysis of mastitis, lameness, and temperament, respectively. Lactation milk yield and lactation geometric mean somatic cell count data were also available. Somatic cell count was normalised using a logarithm transformation; this variable will be hereon in referred to as somatic cell score (SCS). Genetic and residual variance components for mastitis, lameness, and temperament were estimated using an animal linear mixed model in ASREML (Gilmour et al., 2011). Fixed effects included in the model were contemporary group, parity of cow and pedigree group. Animal was included as a random effect accounting for relationships among animals. Covariance components with milk yield and SCS were estimated using a series of bivariate sire linear mixed models.

Results and Discussion

Mean incidence of mastitis and lameness was 11% and 9%, respectively which is lower than estimated previously using farmer recorded event data in Ireland (Berry et al., 2010). Incidence increased ($P<0.001$) with parity from 6% and 3% for mastitis and lameness, respectively in first parity to 20% and 18%, respectively in parity five and greater. The heritability (in parenthesis) for mastitis and lameness was 0.022 (0.003) and 0.31 (0.003), respectively; the respective genetic standard deviation was 0.44 and 0.47 units. The heritability estimates were lower than previously documented using farmer recorded event data in Ireland (Berry et al., 2010; heritability of 0.05 and 0.04 for mastitis and lameness, respectively) as well as recorded internationally (Mrode and Swanson, 1996; 0.04 for mastitis). The heritability for temperament was 0.14 (0.01); the genetic standard deviation was 0.26 units. The genetic correlation (standard error in parenthesis) between mastitis and lameness was 0.55 (0.060); the respective phenotypic correlation was 0.09 (0.003). The genetic correlation is similar to the 0.48 reported by Pryce et al., (1997) using UK farmer recorded data. The genetic correlations with milk yield and SCS are in Table 1 and are in line with previous analyses of Irish data as well as a review of international studies (Mrode and Swanson, 1996).

Table 1. Genetic correlations (standard errors in parenthesis) between the different traits.

Trait	SCS	Milk yield
Mastitis	0.84 (0.03)	-0.05 (0.06)
Lameness	0.44 (0.05)	-0.12 (0.05)
Temperament	0.01 (0.06)	-0.08 (0.04)

Conclusions

Farmer scored mastitis, lameness, and temperament as part of the Irish dairy efficiency program is heritable and genetic correlations with performance traits are in line with expectations from previous analyses of Irish data as well as other international studies. The participation in recording, as measured by the proportion of herds that reported at least some incidence of mastitis/lameness or variation in cow temperament, was high albeit the incidence of both mastitis and lameness is likely to be biased downwards. These data will be incorporated into a revised genetic evaluation module for health traits.

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Pedigree analysis of Irish sheep populations

S. McParland[1], N. McHugh[1] and T. Pabiou[2]
[1]*Animal & Grassland Research & Innovation Centre, Teagasc, Moorepark, Co. Cork* [2]*Irish Cattle Breeding Federation, Bandon, Co. Cork.*

Introduction

Inbreeding has deleterious effects on many aspects of production, health and fertility in livestock (Mc Parland et al., 2007). The objective of this study was to undertake a pedigree analysis including the quantification of inbreeding levels in the largest sheep populations in Ireland. The sheep populations investigated included the Blackface Mountain (BM), Belclare (BR), Charollais (CL), Galway (GL), Suffolk (SU), Texel (TX) and Vendeen (VN).

Materials and Methods

Ancestry information of all sheep recorded on the Sheep Ireland data base was extracted. The pedigree file comprised 237,695 sheep and was used to compute the number of complete generation equivalents (CGE), inbreeding coefficients, and generation intervals. The number of CGEs with information was computed as:

$$\sum_{i=1}^{n_j} \frac{1}{2^{g_{ij}}}$$

where n_j = number of ancestors of animal *j,* and g_{ij} is the number of generations between individual *j* and its ancestor *i.* Inbreeding coefficients (F) for all animals were calculated using the Meuwissen and Luo (1992) algorithm. Individual pedigree files were constructed for the BM (n=15,090), BR (n=22,596), CL (n=22,744), GL (n=10,411), SU (n=51,488), TX (n=64,055) and VN (n=9,396) populations. Using individual pedigree files the 100 most influential sheep to the gene pool of females born in 2010 for each respective population was determined. Generation intervals for each selection pathway (i.e., sires of males, dams of males, sires of females, and dams of females) were calculated by birth year both across all sheep populations using the full pedigree file as well as for individual populations.

Results and Discussion

Sheep born in 2010 had, on average, between 1.30 (CL) and 4.88 (GL) CGE recorded (Table 1). One CGE is equivalent to one complete generation of ancestry recorded on the Sheep Ireland data base (i.e. both sire and dam known), while 2 CGEs is equivalent to all four grandparents recorded in the database. A minimum of one CGE is required to detect traditional inbreeding in an animal. Twenty four percent of SU born in 2010 had less than one CGE recorded, while 82% of CL and SU had less than two CGE recorded. Similarly, over 62% of BM, TX and VN sheep had less than two CGE recorded. The correlation between CGE and F across the entire pedigree file was 0.23. A positive correlation between these statistics was expected since the more ancestry that is recorded in the data base, the greater the capacity to detect inbreeding.

The average population F of sheep born in 2010 ranged from 0.04 (SU) to 2.00% (GL). However, given the low level of ancestry recorded for CL, SU, TX and VN populations the average F presented in this study may not be truly reflective of inbreeding in those populations. Average F of CL, SU, TX and VN sheep with a minimum of 2 CGEs was 0.80, 0.08, 0.09 and 0.45%, respectively. Genomic information may help elucidate the true degree of inbreeding in these populations as well as correct for any potential pedigree errors. Despite the poor ancestry recording, very high F was recorded for some individual animals. All populations had sheep with an F of at least 25% (i.e father-daughter mating) while one, five and four individual sheep in the CL, SU, and TX populations, respectively, had inbreeding coefficients of 50%. Inbreeding coefficients of this magnitude arise from the mating of both highly inbred and highly related animals.

Table 1. Number of records (No), mean inbreeding percent (F; SD in parenthesis) and mean number of complete generation equivalents (CGE; SD in parenthesis) for sheep born in 2010

Breed	No	F	CGE
Blackface Mountain	206	0.82(2.45)	3.58(0.86)
Belclare	2330	0.82(2.68)	2.70(1.21)
Charollais	1140	0.14(1.27)	1.30(0.67)
Galway	1112	2.00(3.54)	4.88(0.88)
Suffolk	2274	0.04(0.76)	1.82(0.83)
Texel	3413	0.07(0.84)	2.08(0.92)
Vendeen	1144	0.28(1.32)	2.28(0.76)

On average, the generation interval for sire and dam pathways was 3.2 and 4.1 years, respectively when all populations (including those not individually studied here and those of unknown breed fraction) were included. However, the average generation interval varied among individual sheep populations studied. The average generation interval of sires ranged from 1.53 years (BM) to 3.78 years (CL) whilst the average generation interval of dams ranged from 3.31 (BM) to 4.10 (SU). The average generation interval was greater for dams than for sires for all populations studied with the exception of the SU.

The 10 most prominent ancestors to the BM, BR, CL, GL, SU, TX and VN populations cumulatively contributed 50%, 39%, 47%, 42%, 25%, 21% and 38% to the gene pool of females born in each of their respective populations in 2010. The highest contributing ancestor in each of the BM, BR and CL populations contributed over 9% to the gene pool of females born in each of their respective populations in 2010.

Conclusions

The level of inbreeding in sheep varied according to the population studied and ranged between 0.04 and 2.00% for sheep born in 2010. Yet, detection of inbreeding levels are dependent on good ancestry recording which remains poor across most sheep populations investigated in this study with the exception of the GL.

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