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Animal & Grassland
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Moorepark Research Report 2013

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Moorepark Research Report 2013

Teagasc Animal & Grassland Research and Innovation Centre,
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Introduction

The recent weather-induced fodder shortage of spring 3013 reminded us that weather patterns can have a huge impact on dairy farming. Economic analysis indicates that Ireland's competitive advantage in milk production is based on the efficient production and utilisation of pasture. There is nothing dairy farmers can do about the weather, but there are lessons from 2012/2013 that can help minimise the impact of such events in the future. First and foremost, the recent feed shortage has provided a clear reminder that it is necessary to build up and maintain a reserve of winter feed to mitigate against weather-induced reductions in pasture growth. Winter feed stocks were not adequate on many dairy farms when cows were housed last winter, primarily a result of poor weather and low grass growth during the previous summer. Firstly, dairy farmers need to set a realistic target stocking rate for their particular farm; this will vary enormously depending on soil type, location and topography. Secondly, grass production will be maximised on farms where soil fertility status is high, adequate N fertilizer is applied, pastures are predominately ryegrass/white clover and soils are adequately drained. A large proportion of soils are below optimum for pH, P and K (Index 1 and 2) resulting in reduced grass production. Therefore, it is vital that farmers place a much greater emphasis on soil fertility management. Although fertilizer N costs have increased in recent years, it still represents good value for money in well managed grassland farms. Pastures that are predominately ryegrass/white clover will significantly increase both annual and shoulder (spring/autumn) grass production. On heavy soils, current drainage infrastructure needs to be maintained and new drainage infrastructure considered. During waterlogged conditions, poaching by livestock and machinery damage to pasture must be minimised. In the longer term, dairy farms need to grow more grass to prevent a recurrence of the feed shortage that occurred this spring and for the increased stock numbers on expanding farms.

Intensive grassland systems do not necessarily lead to reduced water quality

Ireland's competitive advantage in milk production is based on the efficient production and utilisation of grazed grass and this will become even more important with the abolition of EU milk quotas. Profitable grass-based systems of milk production require higher stocking rates to maximise grass utilisation and therefore derogation to the Nitrate Directive (91/676/EEC) is an essential requirement to achieve this. Ireland was granted a derogation of up to 250 kg nitrogen per ha from livestock manure (equivalent to 2.9 livestock units) on farms with at least 80% grassland provided it did not prejudice the achievements of the water quality objectives of the Nitrate Directive. Groundwater nitrate-N concentrations in excess of 11.3 mg per litre are potentially harmful to the environment. A requirement of the derogation was that a study would be carried out to provide scientific information on nitrate leaching under intensive dairy production system in a vulnerable soil type. The research farm identified for this study was Curtins farm at Moorepark which is representative of the one of the highest risk soils to nitrate leaching in Ireland. Since 2001, 11 borehole wells have been sampled monthly and this data was used to evaluate the influence of local climatic, hydrogeological and agronomic practices on nitrate concentration in groundwater. Over the period 2001 to 2012, best nutrient management practices were introduced which included increased early spring slurry use to replace chemical nitrogen, an overall reduction in chemical nitrogen application, soiled water application was moved to a less vulnerable area of the farm and area allocation for soiled water was increased from 10 to 22 ha and minimum till cultivation reseeding replaced ploughing. Over the study period, groundwater nitrate concentrations decreased from a peak of 16.0 mg L^{-1} in 2002 to a low of 7.3 mg L^{-1} during 2010 and 6.6 mg L^{-1} in 2011. The results of this study indicate that intensive dairy production systems in conjunction with appropriate nutrient management practices are consistent with high water quality standards, even on highly vulnerable free draining soils. Additionally, the results indicate that the adoption of sensible nutrient management practices can quickly improve groundwater quality and lead to the achievement of the water quality targets set by for example the Water Framework Directive. This study is funded under the National Dairy Levy and is a cross-disciplinary collaboration between researchers at Teagasc Moorepark and Johnstown Castle and Karlsruhe Institute of Technology, Germany.

TB testing will interfere with Johnes diagnosis

Johne's disease (JD) is a chronic disease of ruminants caused by *Mycobacterium avium* subspecies *paratuberculosis*, characterised by lengthy incubation period with clinical signs usually evident from 3-5 years of age. In sub-clinical stages, there are no obvious signs of infection though reduced milk yield and sub-optimal reproductive efficiency have been reported. Clinical disease results in chronic diarrhoea and progressive severe weight loss leading to fatality. The potential association between JD and Crohn's disease in humans make this disease an important issue for the Irish dairy industry. At present, Irish levels of JD compare favourably with other milk producing/exporting nations, with the potential to yield a competitive advantage for Irish milk and milk products in global markets. As part of the Food Harvest 2020 roadmap, Teagasc in 2012 set up a pilot JD disease control programme with 20 dairy farmers (involving regular testing of individual milk/blood samples). At present, diagnosis relies on testing individual animal for blood, milk or faeces for either evidence of exposure or JD itself, with bulk milk analysis proving to be less than optimal. Research results has highlighted that testing for bovine TB may interfere with blood and milk analysis, and testing for exposure to JD should be delayed until at least 80 days post-TB test. On a single farm where monthly blood and milk sampling was, and continues to be conducted, preliminary results show no significant different in the proportion of ELISA positives between blood and milk samples, although milk testing consistently yielded a lower proportion of positive results (approx 9% blood vs. 7% milk). On this farm, animals yielding positive milk results have always yielded a positive blood result, though not vice versa. Is it essential that Ireland continues to build JD diagnostic capabilities and a database of 'low-risk' animals. In 2013 AHI established a voluntary national programme which will greatly assist this process.

Developing Profitable Milk Production Systems for the BMW Region

The Ballyhaise College dairy project was initiated in 2005 to investigate the profit potential of dairy production systems within the BMW region. The main issues identified as hampering profitability on dairy farms were lower growth and utilisation of grazed grass on wetter soils, farm fragmentation and poor herd fertility. Profit monitor data indicate that average farm output in the region is 900 kg of milk solids (MS; fat plus protein) per hectare with average concentrate input of 890 kg per cow. The MS production per hectare at Ballyhaise increased from 950 kg in 2005 to 1,250 kg in 2012. This increase was achieved primarily because of improved grazing management and better herd fertility. The herd empty rate decreased (36% to 7%) while six week calving rate increased (56% to 83%) during the period from 2005 to 2012. Today, the overall herd EBI is €175. In each of the last 2 seasons, surplus dairy stock have been sold, capturing the financial benefit of a healthier and more robust high EBI herd. Grass production increased steadily from 12 tons DM/ha in 2008 to 15.2 tons in 2011. Poor weather during 2012 reduced grass growth to 11 tons DM per hectare, and grass growth during the first quarter of 2013 was 20% behind normal. Concentrate feed inputs increased by 36% in 2012 to 850 kg per cow. Combined with higher prices, total concentrate feed costs were €240/cow in 2012 compared with €130/cow in 2011. In addition, €140/cow was spent on winter forage during autumn 2012. The higher profits demonstrated at Ballyhaise demonstrates the potential for long term profitable milk production in the BMW region. This model remains the only viable low risk expansion model available to Irish family farms into the future.

Is there a role for sexed semen?

With the milk quota era ending in 2015, dairy farmers will be able to expand for the first time in a generation. For many years, sexed semen has been capable of increasing the likelihood of a heifer calf from 50% to 90%. To date, however, the uptake of sexed semen has been low for a number of reasons. First, published data indicates that conception rates with frozen sexed semen are ~75% of conception rates with conventional semen; this reduction in fertility is unacceptable in pasture based systems. Second, the sexed semen available was mostly imported sires, and typically had poor EBI values. Third, sexed semen is at least twice the price of conventional semen. In spring 2013, a large sexed semen trial involving over 15,000 inseminations on almost 400 dairy farms was carried out in conjunction with ICBF, Dovea Genetics, Munster AI, NCBC and Progessive Genetics, with financial support from meat processors and the Agricultural Trust. Preliminary results indicate that frozen sexed semen achieved conception rates that were 85 to 87% of those achieved with conventional semen. This is a substantial improvement over previous performance, and makes sexed semen a viable product for use on Irish dairy farms. Sexed semen has the potential to alter the profile of both the dairy and the beef industries in Ireland. By breeding more heifer calves, dairy farmers can expand more quickly. The flip side of this is that there will also be a reduction in the number of low value male dairy calves. After generating enough pregnancies with sexed semen for replacement heifers, easy-calving short gestation beef AI sires can be used to increase the value of beef output from the dairy herd.

Land drainage project on the Heavy Soils Programme

Approximately 30% of milk produced in Ireland originates from farms where the soils can be classified as heavy. Heavy soils add complexities to the production system that are aggravated by inclement weather conditions like those experienced in 2012 and spring 2013. A Heavy Soils programme was initiated in 2009 to investigate the challenges facing farmers on heavy soils. Farms in Macroom, Kishkeam, Castleisland, Listowel, Athea, Rossmore and Doonbeg were selected, representing a range of challenging soil types. All are participants in the Heavy Soils Programme, and can be followed on: http://www.teagasc.ie/heavysoils/ Two significant factors were identified as limiting grass production and utilisation on these farms were (1) low level of soil fertility (P, K and pH) and (2) poor drainage infrastructure on these poorly naturally draining soil types. Average grass production in 2011 on the seven farms was 11.6 tonnes of grass dry matter per Ha. This was reduced to 7.8 tonnes per ha in 2012, highlighting the huge effect the wet summer of 2012 had on pasture growth on these farms. The continuing downward trend in soil fertility nationally is also evident on the farms in the Heavy Soils programme, with recent soil analysis indicating suboptimal soil fertility results. The soil results for 2013 (2010 results in brackets) were pH 5.73 (5.54), P 4.16 mg/L (5.54 mg/L) and K 84.04 mg/L (116 mg/L). To establish and maintain good ryegrass swards, soil fertility has to be maintained at optimal levels (pH 6.2; P 5.1 – 8 mg/L; K 101 – 150 mg/L). A programme has been put in place in each farm to increase soils fertility to recommended levels. On each of the seven participating farms 2 Ha of land was identified to be drained. Soil type ranged from peat to carboniferous shale to red sandstone till. After site investigation, the most appropriate drainage solution was selected. Deep drains (1.7 m), shallow drains (0.9 m), mole drains and gravel mole drains were installed and ripping was carried out where necessary on the farms during the summer of 2013 when weather conditions were ideal. Measurements of milk and grass production combined with metrological and drainage flow rates are on-going and will be used to evaluate the effectiveness of the drainage work.

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ANIMAL RESEARCH PROGRAMME

Genetic Improvement of Animals

Simulation of optimal herd-dynamics for dairy herds using a Markov-chain model to study the economic impact of replacement decisions

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Introduction

Misinformed voluntary culling of dairy cows can erode farm profits if animals of inferior performance are not culled. Similarly, when replacement costs are high relative to cull cow values, excessive culling can be costly (Lehenbauer and Oltjen, 1998). The objective of this study was to quantify the impact of alternative culling strategies on herd profit.

Materials and Methods

A Markov chain model was developed using starting states, transition probabilities, and economic parameters. A three-dimensional array (calving group × production level × parity) was populated with the proportion of animals in each starting state determined from data from Irish commercial dairy herds stored in the Irish Cattle Breeding Federation (ICBF) database between the years 2010 and 2013. Data from 2,025,330 spring calving cows were available and 10 calving groups were defined, 14 days in length, between 15st January and 4th June. Production values were calculated from 6,652,385 cow records as the sum of individual animal predicted transmitting ability, heterosis and recombination loss, and permanent environmental effects for milk, fat and protein each weighted by their respective economic value. Cow-lactations were categorised into twenty classes based on production values. A number of matrices of transition probabilities were used to determine the proportion of cows (P) at time t that have a calving group in the current parity c^i which is c^* as well as having a milk production group in the current parity m^i which is m^* (Figure 1). Matrix X was a calving group transition matrix giving the probability of a cow in calving group c from the previous lactation (i-1) being in production level c* in the current lactation i. Matrix W was a production level transition matrix giving the probability of a cow in production level m from the previous lactation (i-1) being in production level m* in the current lactation i. Matrix I was a vector of involuntary culling probabilities of cows not being involuntarily culled corresponding to each parity, and V was a voluntary culling transition matrix in calving group c, production level m, and parity i. Elements of V were choice variables where a value of 0 denoted cull and 1 denoted retain. In order to maintain a constant herd size, the number of first calving heifers at a given time point s_t, entering the herd in calving group c and milk production level m was determined from the national database. The algorithm (Figure 1) ran until the transition from one year to the next reached a steady state. Steady state was assumed when the proportion of cows in each calving group, production level, and parity did not change more than 0.001 between successive iterations. Economic parameters from the Moorepark Dairy Systems Model MDSM (Shalloo *et al.,* 2004) were applied to calving date groups, production levels, parities and cull cow salvage value. Six culling strategies were investigated: culling solely on 1) calving date, 2) production level, combinations of 3) calving date × production level, 4) calving date × parity, 5) production level × parity, and finally culling on all dimensions 6) calving date × production × parity.

$$\begin{aligned} P^t_{c^{i-1}=c^i, m^{i-1}=m^i, i} &= \sum_{c=1}^{10}\sum_{m=1}^{20} P^{t-1}_{c^{i-1}\ \ ,m^{i-1}\ \ ,i-1} * W_{m^{i-1}, m^i=m^*} * X_{c^{i-1}, c^i=c^*} * I_i * V_{c^{i-1}, m^{i-1}, i}\,, \quad for \quad i>1 \\ &= H_{c,m} * (1-s_t), \quad for \quad i=1 \qquad where \quad s_t = \sum_{c=1}^{10}\sum_{m=1}^{20}\sum_{i=2}^{5} P^t_{c,m,i} \end{aligned}$$

Figure 1: Equation to determine proportion of cows at time t, per calving group (c), production level (m) and parity (i)

Result and Discussion

Average expected net return per cow from the alternative culling strategies are presented in Figure 2. Profitability was maximized when cows were culled based on a combination of calving date, milk production level and parity. Culling on a production and parity was the least profitable culling strategy due to retaining cows that underperform.

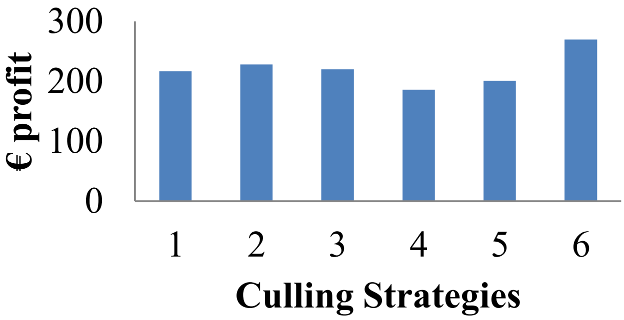

Figure 2. Average net return per cow for culling strategies (1) calving date (2) production (3) calving date × production (4) production × parity (5) calving date × parity (6) calving date × production × parity

Conclusions

Adopting a multi-dimensional culling regime within a cow culling index, taking cognisance of non-additive genetic and permanent environmental effects, as well as age and seasonal effects improves net return.

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RMIS Project Number 6027

Description and evaluation of the Herd Dynamic Milk (HDM) Model on different herbage allowance, concentrate supplementation and milk yield potential

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Introduction

Modelling of biological systems is complicated due to the interaction of numerous variables, which is particularly the case in grass-based dairy systems. However, a well developed and calibrated model can be used to simulate the impact of different management (e.g. feeding levels) on cow milk production and subsequent fertility performance. While there are considerable amounts of these models available in the literature, most of them have been parameterised and optimised for the conditions where they were developed. The objective of this study was to develop a model that was able to accurately simulate animal performance under various grazing conditions.

Materials and methods

The Herd Dynamic Milk (HDM) model is a dynamic stochastic and agent-based model developed using the programming language C++. Animals in the model are described individually from birth to death. The HDM model is able to take into account the impact of the genotype of the animal, diet, and management decisions on milk production and body condition score. This model is also able to model both indoor and grazing systems. The main daily outputs of the HDM model are dry matter feed intake, milk yield, body condition score (BCS) for every animal for every day of the year. The intake of the animal is calculated using the French model for nutrition (Faverdin *et al.*, 2011) and the GrazIn (Delagarde *et al.*, 2011) intake model for cows at grazing. The daily milk production is calculated depending on the energy intake, the milk potential and BCS change of the cow. The sensitivity of the model was evaluated by testing the responses to various scenarios and by comparing the model outputs in terms of milk production and BCS with data available from the literature. Variation around the milk yield potential (30, 40 and 50 kg of milk per cow per day at peak), the daily herbage allowance (14, 18 and 22 kg of DM per cow per day) measured to 4cm and the concentrate allocation (0 or 4kg of concentrate per cow per day) were simulated resulting in 18 different scenarios. The simulations were carried out for a full 12 month period (starting on the first of January) allowing the observation of the whole lactation and it was assumed that the cows were at grazing for the whole period. Grass quality was held constant throughout the simulation and was based on published experiments.

Results and Discussion

The output of the model resulted in an average milk yield through the lactation of 6,012kg, 7,246kg and 8,391kg for the cows with 30, 40 and 50kg of potential milk respectively. Body condition score nadir was 3.29, 2.77 and 2.25 for the 30, 40 and 50kg milk groups respectively. The impact of the genetic potential for milk production was shown in the model through an average increase of 0.44kg of milk per day per cow per increase of 1 kg of potential milk production and a decrease of 0.03 units of BCS at nadir. Over the entire lactation the 50 kg of milk group produced 1,147 kg and 2,375 kg more milk than the 40 and 30kg groups, respectively. A herbage allowance increase of 1kg per cow per day resulted in an average increase of 0.20kg of standard milk per cow per day and an increase of the BCS nadir of 0.01 points. The response to an increase of herbage allowance ranged from 0.13 to 0.28 kg for the 30 kg and 50kg potential group of cows. The impact of the increase of 1kg of herbage allowance is higher at 14 herbage allowance (0.25kg per cow per day) while at 18 the response was 0.16kg per cow per day. Herbage allowance did not have a big impact on BCS loss irrespective of the genetic profile of the cows and whether they were offered supplementary feed or not (overall variation from 0.02 to 0.04 units at nadir due to herbage allowance).

On average the impact of 1kg of concentre resulted in an increase of 0.8kg of standard milk per day per cow and an increase of the nadir BCS of 0.05 units. Once again the response to the addition of concentrate increases with the milk potential (from 0.58 for the 30kg genetic group to 0.94 for the 50kg genetic groups). The impact of the concentrate supplementation decreases with an increase in herbage allowance as shown by McEvoy *et al.* (2008). The impact of offering 4 kg of concentrate results in a higher increase of the nadir for the 30kg potential cow (increase of 0.21 unit) than the 50kg cow (increase of 0.16 unit). All model outputs were in the range of published experiments (McEvoy *et al.*, 2008; McCarthy *et al.*, 2007).

Conclusion

The model is able to respond in a realistic way when subjected to various scenarios. The model outputs are in the range of outputs from the literature.

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RMIS Project Number 6159

Mid-infrared spectroscopy to predict important milk quality traits in Irish cows

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Introduction

Despite its potential importance for adding value to the Irish food industry, milk product quality traits are not adequately accounted for in Irish national dairy breeding objectives. Mid–infrared spectroscopy (MIRS) is a technique used to measure milk fat and protein in the Irish national dairy cow herd and has recently has been used to predict more detailed milk composition (De Marchi *et al.,* 2009). The aim of this study was to test the ability of MIRS to predict milk protein composition and colour. Using MIRS to predict milk quality could aid selective breeding since it facilitates the collection of milk quality phenotypes quickly and at a low cost.

Materials and Methods

Between August and October 2013, 152 individual cow milk samples were collected from four breeds of cattle (Holstein Friesian, Jersey, Norwegian Red and Holstein-Jersey crossbreds) across five research farms in the south of Ireland. Spectral data were recorded for all milk samples using the Foss MilkoScan FT6000 (Foss Electronic A/S, Hillerød, DK). Within 24 hours of sample collection, milk samples were assessed for detailed protein composition using the Agilent 1200 reversed phase HPLC parashell column at 214 nm. Simultaneously, colour traits were measured using a Chroma Meter CR400 (K.M.S Europe, Edisonbaan 14-F, NE) and milk colour was expressed according to the CIE-Lab colour space by reporting lightness (L*), redness (a*), and yellowness (b*) values (CIE, 1978). All data were quality assessed and 2 and 7 outliers were removed from the colour and protein analyses, respectively. Principal components analysis was carried out on MIRS data to identify spectral outliers which were subsequently removed from the data set (n = 6). Equations were developed to predict each dependant variable separately through partial least squares regression using regions of the mid-infrared spectrum as predictor variables (Unscrambler ver. 9.6, Camo A/S, Oslo, Norway). Cross validation was performed to test the goodness of fit of each prediction equation.

Results and Discussion

Milk samples were collected from first to ninth parity cows that were 104-361 days in milk. Mean gold standard values together with the general fitting statistics for all MIRS prediction models are summarized in Table 1. Results are consistent with those reported by Bonfatti *et al.* (2011) who used a large MIRS data set to predict the milk protein fractions of Simmental cows. Accuracy of prediction of protein composition ranged from $R^2_C = 0.44$ for total whey protein to $R^2_C = 0.17$ for α_{S2}-casein; total proteins can be predicted with greater accuracy than their components since they are present in larger amounts in the milk (Bonfatti *et al.* 2011). Accuracy of prediction of colour traits ranged from $R^2_C = 0.51$ for b* index to $R^2_c = 0.07$ for a* index. The ratio of α_{s1}-casein, β-casein, K-casein, and α_{s2}-casein fractions across all milk samples was 3:3:1:0.8. The prediction accuracy obtained for α_{s1}-casein, β-casein, K-casein, and α_{s2}-casein are comparable to those described by De Marchi *et al.* (2009) whose prediction models had a range in R^2_C of between 0.33 and 0.50 for casein components. The residual prediction deviation (RPD) of prediction models ranged from 3.07 (α-lactoalbumin) to 0.97 (β-casein). An RPD value greater than 3 indicates an accurate prediction equation.

Table 1: Mean values and fitting statistics[1] of models to predict milk protein composition and milk colour.

Trait	Mean	SD	RMSE$_C$	R^2_C
k-casein[2]	6.21	1.46	1.14	0.42
á$_{S1}$- casein[2]	14.52	3.17	2.64	0.39
á$_{S2}$-casein[2]	3.47	0.97	0.92	0.17
â-casein[2]	12.76	2.35	2.29	0.23
Total whey [2]	7.42	2.73	2.03	0.44
â-lactoglobulin[2]	6.08	2.32	1.81	0.39
á-lactoalbumin[2]	1.32	0.98	0.28	0.4
Lightness (L*)	81.28	1.68	1.33	0.25
Redness (a*)	-3.99	0.77	0.47	0.07
Yellowness (b*)	8.59	2.54	1.71	0.51

[1] SD= Standard Deviation; RMSE$_C$ = Root mean square error of calibration; R^2_C = Coefficient of determination of calibration; [2] µg/µL

Conclusions

These initial results indicate that MIRS may be effective to predict both milk protein composition and colour. Improved accuracies could be obtained by increasing the size of the calibration data set.

Acknowledgments

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RMIS Project Number 6161

Relationship among milk coagulation properties and milk protein composition in Irish and Italian dairy cow milk

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Introduction

Milk coagulation properties (MCP) are associated with cheese making efficiency and yield (De Marchi *et al*., 2009) and include parameters such as rennet coagulation time (RCT, min), curd-firming time (k_{20}, min) and curd firmness after 30 minutes from rennet addition (a_{30}, mm). The objective of this study was to investigate the characteristics of MCP in Irish and Italian dairy cows and their relationships with milk chemical and protein composition.

Materials and Methods

Between September 2013 and November 2013, 270 late lactation milk samples were collected from 5 Irish research farms. Breeds comprised of Holstein-Friesian (HF), Jersey (JE), and their respective crosses. In November 2013, 73 milk samples of Italian Holstein-Friesian cows, from 2 different dairy farms in Veneto Region (North of Italy) were also collected. MCP in both countries were quantified using a Formagraph within 5 days of sample collection. Statistical analysis (ANOVA, proc GLM) was carried out with the software SAS (SAS Institute Inc., Cary, NC, USA) and aimed to investigated the breed effect (JE vs. HF) within country for the Irish cows and within HF breeds across country (Irish vs. Italy) to compare country effect.

Results and Discussion

Descriptive statistics are in Table 1. Compared to Italian milk, Irish samples had shorter ($P<0.05$) RCT and superior ($P<0.05$) a_{30} values (Figure 1); the mean days in milk for the Irish and Italian samples was 232 and 252, respectively and the respective mean parity number was 2.20 and 2.77. JE cows had the best ($P<0.05$) MCP with average values of 10.95 min and 48.54 mm for RCT and a_{30}, respectively (Figure 1). Phenotypic correlations between MCP parameters and other milk constituents are in Table 2. Correlations between MCP and other milk traits were generally similar between countries. MCP traits were strongly correlated with each other, especially RCT and a_{30}. Strong positive correlations existed between RCT and pH corroborating results from Finnish Ayrshire cows (Ikonen *et al*., 2004). Moreover, favorable correlations existed between MCP and k-casein.

Conclusions

This is a preliminary characterization of milk coagulation traits of Jersey and Holstein Irish breeds. JE breed evidenced better MCP compared to HF, moreover Irish HF seems to be better than the Italian one. Results should be confirmed investigating more milk samples.

Table 1. Number of records (N), mean and standard deviation (SD) of MCP in Irish (IE) and Italian (IT) samples.

Variable	N	Mean	SD
IE RCT, min	252	15.63	8.59
IE k_{20}, min	246	3.77	2.33
IE a_{30}, mm	239	41.32	15.66
IE a_{60}, mm	241	38.83	14.90
IT RCT, min	45	21.85	8.62
IT k_{20}, min	26	7.43	2.40
IT a_{30}, mm	40	20.94	9.57

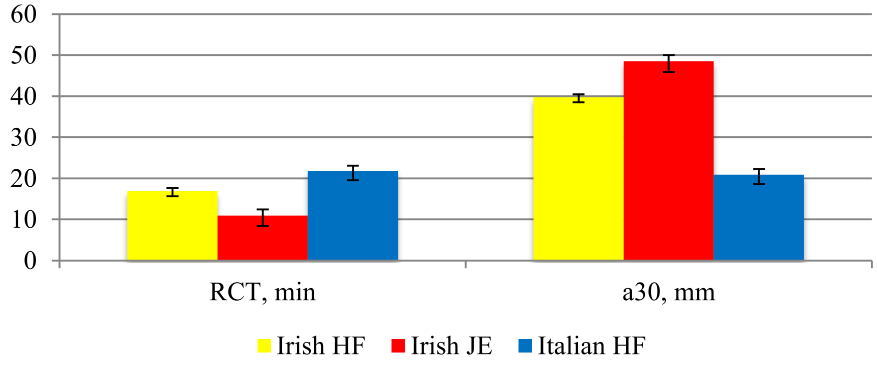

Fig. 1. Mean (± 1 standard error) RCT and a30 for different breeds and countries.
Significance of difference from zero * = $P>0.05$; ** =$P<0.05$; *** = $P<0.01$

Table 2. Correlations between MCP and other milk quality traits in the Irish (IE) and Italian (IT) datasets.

	RCT	k_{20}	Fat	Urea	Casein	Protein	k casein	α_{s1} casein	pH
IE RCT			-0.30^{***}	-0.07^{*}	-0.13^{**}	-0.16^{**}	-0.12^{*}	-0.20^{**}	0.42^{***}
IE k_{20}	0.78^{***}		-0.35^{***}	-0.09^{*}	-0.43^{***}	-0.07^{*}	-0.31^{***}	-0.31^{***}	0.32^{***}
IE a_{30}	-0.55^{***}	-0.74^{**}	0.15^{**}	0.02^{*}	0.30^{***}	-0.44^{***}	0.36^{***}	0.30^{***}	-0.18^{**}
IT RCT			-0.20^{*}	0.23^{*}	-0.07^{*}	-0.32^{**}	-0.31^{**}	-0.07^{*}	0.54^{***}
IT k_{20}	0.40^{**}		-0.15^{*}	0.15^{*}	-0.31^{**}	0.31^{**}	-0.29^{*}	-0.18^{*}	-0.06^{*}
IT a_{30}	-0.81^{***}	-0.63^{***}	0.07^{*}	0.01^{*}	0.15^{*}	0.15^{*}	0.30^{*}	0.20^{*}	-0.09^{*}

Acknowledgements

Funding from BreedQuality (11/SF/311).

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RMIS Project Number 6161

Retrospective analysis of the accuracy of genomic selection in Irish dairy cattle

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Introduction

Genomic selection involves the use of individual animal genomic information in an attempt to more accurately predict its genetic merit. Genomic selection for dairy bulls was launched in Ireland in 2009 and is now routinely used as a method to select young dairy bulls for breeding programmes. The objective of this study was to determine, through retrospective analysis of data since its implementation in Ireland, if genomic selection is more accurate than traditional pedigree analysis at predicting genetic merit.

Materials and Methods

The original parental average (PA), direct genomic values (DGVs; estimated entirely from genomic information) and genomically enhanced predicted transmitting ability (GPTAs; blend of parental average and DGV) for milk, fat and protein yield of bulls genomically tested between 2009 and 2011, inclusive, were obtained from the Irish Cattle Breeding Federation database. The daughter-based milk production predicted transmitting abilities (PTA) of each bull from the August 2013 genetic evaluation were also available. Fertility traits were not included in the present study because the genetic evaluation model changed in 2010. Only bulls with a minimum of 50 Irish daughters included in the August 2013 national genetic evaluation were considered in this analysis; no genomic information is included in the PTA of these bulls. In total, 33, 38 and 64 bulls genomically evaluated in 2009, 2010 and 2011, were available.

The original PA, DGV and GPTA were compared to the August 2013 daughter-based PTA both within and across years. Statistics used for comparison included the correlation between measures, the mean difference (i.e., bias) and variation in the difference (root mean square error) between predicted and daughter-based PTA, and the linear regression coefficient of daughter-based PTA on each original genetic merit estimate separately.

Results and Discussion

Bulls genomically selected in 2009, 2010 and 2011 had, on average, 600, 233, and 254 daughters contributing to their daughter-based PTA in August 2013, respectively. Mean reliability of the daughter-based PTAs was 93% and varied from 86% to 99%. PA, DGV and GPTA all overestimated milk and protein yield (Table 1). The GPTA, on average, overestimated milk PTA by 54 kg, however individual bull bias (for the bulls selected in 2011 alone) ranged from -251 kg to +334 kg (Figure 1). Predictions based on PA had a greater mean bias but also greater variation in the bias which would have resulted in greater fluctuations in bulls if selection had been based on traditional PA. The bias and variation in the bias was always least for the DGV which uses only genomic information.

Table 1. Mean (standard deviation in parenthesis) prediction bias between daughter-based PTA and DGV, PA, and GPTA

	Milk (kg)	Fat (kg)	Protein (kg)
DGV	36(135)	-0.56(4.69)	0.62(3.65)
PA	67(135)	1.74(5.55)	2.37(4.40)
GPTA	54(127)	1.82(4.76)	2.16(3.69)

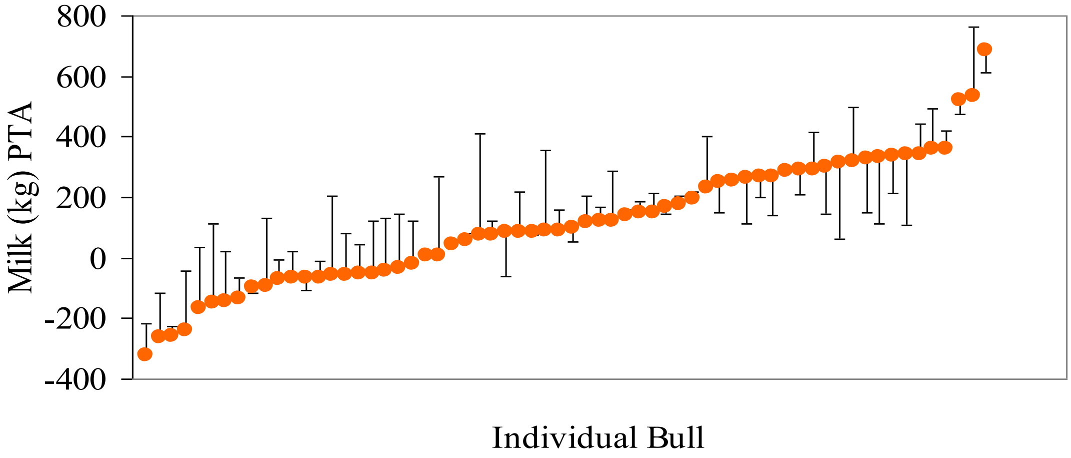

Fig. 1. Variation between the daughter-based PTA (●) and the GPTA (error bars) for milk of the 64 bulls genomically evaluated in 2011.

The slope (standard error in parenthesis) of the linear regression of daughter-based PTA for milk yield on PA, DGV and GPTA was 0.83 (0.07), 0.86 (0.07), and 0.82 (0.06); the corresponding values for protein yield were 0.62 (0.07), 0.80 (0.07) and 0.74 (0.06), respectively and were 0.63 (0.09), 0.84 (0.08) and 0.76 (0.08) for fat yield, respectively. A value of unity is expected. The GPTA was most strongly correlated with the daughter-based PTA while the PA was least correlated with the daughter-based PTA (Table 2).

Table 2. Correlation between daughter-based PTA and PA, DGV and GPTA predictions for milk, fat and protein

	PA	DGV	GPTA
Milk	0.72	0.72	0.77
Fat	0.51	0.65	0.66
Protein	0.59	0.70	0.72

Conclusion

Genomic evaluations, for milk production traits at least, are more accurate at predicting genetic merit than the traditional genetic evaluations based on PA as evidenced by less mean and variation in bias, linear regression slopes closer to unity and stronger correlations. The correlation analysis suggests up to 29% improvement in prediction accuracy with the GPTAs compared to the PA. The bias in genomic evaluations should be addressed.

RMIS Project Number 6164

Genetics of ewe mature weight

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Introduction

Ewe mature live-weight is a key indicator of the productivity potential in sheep flocks; this has been reflected in the inclusion of ewe mature weight as a goal trait in the national genetic evaluations (Byrne *et al.*, 2010). To date the use of actual ewe mature weights in the evaluations has been limited due to lack of phenotypes. Ultrasound scan information on lamb eye muscle area and fat depth, as well as lamb weight, are currently used as predictor traits for ewe mature weight, but the genetic associations between ewe mature weight and lamb ultrasound information have not been quantified. The aim of this study was to estimate phenotypic and genetic parameters for ewe mature weight and to quantify the genetic associations between ultrasound data and ewe mature weight.

Material and Methods

Data on 40,195 ewe mature weights from 10,479 ewes across 42 flocks over a 4 year period (2008 to 2012) were obtained from the Sheep Ireland database. Mature ewes were defined as ewes that had lambed at least once and were greater than 24 months and less than 8 years of age when weighed (Byrne et al., 2010). Ewe parity was categorised as 1, 2, 3, 4, or ≥5. Only ewes weighing between 35 and 100 kg were retained. Furthermore, ewe weights greater than ±4 s.d. from the mean estimated within the breed group of that animal were set to missing. Animals were discarded if sire or flock of weighing (n=6,820) were unknown. Only ewes with ≥50% of their breed composition known were retained. Animals were classified into 5 main breed categories based on their dominant breed composition; terminal (n= 907), maternal (n=859), dual purpose (n=63), hill (n=612), or other breeds (n=1,478). Ewes were grouped according to the time span between their last lambing date and the date of weighing: less than 60 days; 61 to 120 days; 121 to 180 days; 181 to 210 days, and greater than 210 days post-lambing. Litter size (single to quadruplet), number of lambs reared (single to triplet) and the lambing difficulty (1 = no lambing assistance /unobserved, 2 = slight assistance, 3 = severe assistance and 4 = veterinary assistance) of the last lambing relative to date at weighing was also available.

Muscle and fat depth ultrasonic scan data on 18,931 lambs across 331 flocks between the years 2008 and 2012 inclusive were available from the Sheep Ireland database. Ultrasound scan records were retained on animals aged between 85 and 170 days of age at date of measurement and with muscle depth scores between 18 and 40 mm and fat depth scores between 0 and 4 mm. Only lambs weighing between 25 and 65 kg at scanning were retained. Contemporary group was defined separately for ewe mature weight and ultrasound data as flock-date of weighing (ewe weight) or scanning (ultrasound records). Following all edits 20,331 ewe mature weights from 37 flocks and 12,194 ultrasound records from 293 flocks remained.

Variance components for ewe mature live weight were estimated using a repeatability animal model (i.e., animal permanent environmental effects was included in the model) in ASReml (Gilmour *et al.*, 2012). Fixed effects considered for inclusion in the model were: contemporary group, breed category, ewe parity, days since last lambing, litter size recorded at last lambing, number of lambs reared in last lambing event, average lambing ease score for last lambing, month and year of weighing, and heterosis and recombination loss. A series of bivariate analyses were undertaken using a sire model to estimate genetic correlations between ewe mature weight and ultrasound scan data.

Results and Discussion

The average ewe mature weight across all animals was 60.3 kg (s.d. = 14.3). Relative to the terminal type ewes, hill, dual purpose and maternal ewes were on average 5.8 kg (s.e. = 1.2), 4.0 kg (s.e. = 8.5), and 0.8 kg (s.e. = 1.1) lighter (P<0.001). Heaviest ewe weight were recorded in parity four and declined thereafter (P<0.001). Ewes that were weighed within 60 days post-lambing were on average 3.8 kg (s.e. = 1.2) lighter than ewes that were ≥ 210 days post-lambing.

The genetic coefficient of variation for ewe mature weight was 4.3%. The heritability for ewe mature weight was 0.37 ± 0.03, which is consistent with previously reported ewe mature weight heritabilities (Safari *et al.*, 2005). The repeatability of ewe weight was 0.65 ± 0.01. The heritability for the ultrasound scan data ranged from 0.15 (0.02) for ultrasound fat score to 0.38 (0.02) ultrasound muscle depth.

The phenotypic correlations between ewe mature weight and the ultrasound data ranged from 0.01 (ultrasound fat score) to 0.33 (scan weight) and in all cases were lower than the corresponding genetic correlations.

A weak positive genetic correlation was recorded between ewe weight and ultrasound fat depth (0.03 ± 0.23). The genetic correlation between ewe weight and ultrasound muscle was moderate (0.26 ± 0.19) suggesting that lambs with larger muscle depth tend to reach greater ewe mature weights. The genetic correlation between ewe mature weight and ultrasound weight was strong (0.69; s.e. = 0.11), indicating that lamb weights taken from 65 days onwards are good predictors of a ewes final mature weight.

Conclusions

Significant genetic variation existed for ewe mature weight. Ultrasound scan measurement especially muscle depth and scan weight are good predictors of genetic merit for ewe mature weight. Therefore a combination of ewe mature weight and ultrasound scan data should be incorporated into the national genetic evaluations to increase the accuracy of selection for ewe weight.

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RMIS Project Number 6195

Economic appraisal of April born early maturing dairy cross steers slaughtered at 21 and 26 months of age

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Introduction

Keane *et al.* (2009) found that a 23-month production system was suitable for early maturing dairy cross steers. The profitability of that system, most likely, stemmed from a short finishing period with low concentrate input. Animals in that system were February born whereas beef crossbreds born to dairy cows are typically March and April born. Since steer production is expected to remain the predominant system for male cattle in Ireland, alternative production systems must be established that optimise performance from pasture for these later spring-born animals. Hence, the aim of this study was to complete an economic appraisal of April-born early maturing dairy crossbred steers slaughtered in 21 month (21MO) and 26 month (26MO) production systems.

Materials and Methods

Performance data were available from 32 April born early maturing dairy crossbred steers from a 2 production system (21 and 26 months of age) × 2 breed group (Aberdeen Angus × Holstein-Friesian and Hereford × Holstein-Friesian) factorial experiment. This study was conducted at the Johnstown Castle Research Centre and animal performance details have been described by Prendiville et al. (2014). For the first grazing season (15 May to 1 December 2011), animals were at pasture and supplemented with 1.5 kg of concentrate dry matter (DM) per head. Steers were housed for 74 days and were turned out to pasture for the second season on 13 February 2012. Animals grazed as a single group throughout the second season. At housing, steers in the 21MO were finished on grass silage *ad-libitum* with 6 kg of concentrate DM. Animals in the 26MO were stored through the second winter on an *ad-libitum* grass silage diet and returned to pasture for a third grazing season in February and grazed until April without supplementation. Thereafter, they were supplemented with 2.5 kg of concentrate DM daily at pasture for 60 days pre-slaughter. 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 and thus, net margin represents the return to land and labour. Animal mortality was 5% from arrival to slaughter with 3% of this occurring at the calf rearing stage. Production systems were evaluated per head and per hectare (ha) with stocking rate set at 210 kg organic nitrogen (N) per ha. Sensitivity analyses were carried out on concentrate price and beef price by varying these prices by +/-€10/t fresh and +/-10 c/kg to the baseline scenario, respectively.

Results and Discussion

Due to the difference in carcass weight, output value per head was greatest for steers in the 26MO system (Table 1). The 26MO system also benefited from a higher beef price as a result of a more favourable sale date. Despite the increased variable costs associated with production, gross and net margin per head was considerably greater for steers in the 26MO system on a per head basis. Although the number of animal units per ha was lower for the 26MO system, gross and net margins per hectare remained greater when compared to the 21MO system. Results also indicated that fluctuations in concentrate price had a modest impact on the profitability of dairy calf to beef systems. In contrast, variations in beef price have the potential to significantly alter the profitability of the systems.

Conclusions

Results from this study indicate that systems of production that finish April born early maturing steers off pasture during the third grazing season are more profitable than the 21MO production system.

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Table 1: Economic appraisal[1] of April born early maturing steers slaughtered at 21 (21MO) and 26 (26MO) months of age

	21MO		26MO	
Animal units per hectare[2]	3.3		2.3	
Beef price[3] (€/kg)	4.02		4.23	
Profitability (€)	Per head	Per hectare	Per head	Per hectare
Output value	809	2546	1060	2425
Variable costs	513	1613	566	1295
Gross margin	297	933	494	1130
Fixed costs	267	839	267	610
Net margin	30	94	227	520
Sensitivity:				
Concentrate price (+/- €10/t)	6.78	21	4.56	10
Beef price (+/- 10c/kg)	26.97	85	31.50	72

[1] Beef price, €4.15/kg carcass; concentrate price, €260/t; calf price, €259/head. [2] An animal unit represents a calf through to slaughter. [2] Actual price received depends on date of sale (i.e. seasonality effects) and carcass grading assuming a base price of €4.50/kg carcass.

RMIS Project Number 6164

Risk factors associated with lambing traits

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Introduction

Lamb survival and lambing ease are major contributors to overall sheep productivity and profitability (Morris *et al.,* 2000). Considerable labour input is still required at lambing to ensure high levels of lamb survival. Lamb mortality and lambing ease have been reported as being influenced by a range of factors including ewe maternal traits and lamb viability as well as lambing management and environmental factors (Morris *et al.,* 2000). The objective of this study was to establish the risk factors associated with lamb mortality and lambing ease score in the Irish sheep purebred and commercial population.

Material and Methods

A total of 90,443 lambing events from 28,952 ewes in 564 flocks (33 crossbred and 531 purebred flocks) in Ireland were available from the years 2008 to 2012, inclusive. The two traits considered in the present study were lambing ease score and lamb mortality. Lambing ease score is recorded by producers on a scale from 1 to 4 (1 = no lambing assistance /unobserved, 2 = slight assistance, 3 = severe assistance and 4 = veterinary assistance). Lamb mortality is recorded by producers as whether a lamb was alive (mortality=0) or dead (mortality=1) within 24 hours of birth; lamb mortality was not recorded in commercial flocks. Lamb events were discarded if flock of birth or date of birth were unknown. Only lambs with ≥50% of their breed composition known were retained.

Only records from parity one to eight ewes were retained and ewe parity was categorized as 1, 2, 3, 4 or ≥5. Age of the ewe at first lambing was categorised as: 1) lambing between 8 and 18 months of age (i.e. ewe lambs), or 2) lambing between ≥18 and 28 months of age (i.e. hogget). Litter size was defined as the number of lambs born (alive or dead) per lambing event. Only litter sizes between 1 (singles) and 4 (quadruplet) were retained for analysis. Only lambs with a recorded weight at birth between 2 and 8 kg were retained for analysis. For lamb survival, only purebred flocks that recorded between 1 and 25% lamb mortality annually were retained for analysis. Contemporary group for the lambing ease and lamb mortality was defined as flock-year-week of lambing separately for each trait. Following all edits 36,593 lambing difficulty records from 21,906 lambing events remained from 248 purebred and 16 crossbred flocks and 23,950 lamb mortality records from 14,454 lambing events in 172 purebred flocks remained. Risk factors associated with lambing ease score were determined in crossbred and purebred flocks combined using linear mixed models in PROC HPMIXED (SAS, 2012). Risk factors associated with the logit of the probability of lamb mortality was modelled using generalised estimating equations in ASReml (Gilmour *et al.,* 2012). In all models both ewe and the contemporary group of flock-year-week of birth were included as random effects. Risk factors considered for both traits included: month and year of lambing, gender, ewe parity, age at first lambing, lamb breed composition, litter size and birth weight. For lamb survival, lambing ease score was also included as a risk factor. Potential risk factors were considered separately in a series of univariate analyses and in a multiple regression model.

Results and Discussion

The mean prevalence of perinatal mortality was 8.26%. The average lambing ease score recorded for crossbred and purebred lambs was 1.33 (SD = 0.69) and 1.48 (SD = 0.75), respectively.

Lambing ease score. In the univariate analysis male lambs experienced more ($P<0.001$) difficult lambings compared to females and the association persisted ($P<0.001$) in the multiple regression. No difference in mean lambing difficulty existed for lambs weighing between 2 and 5 kg at birth but a notable increase in lambing difficulty occurred in lambs weighing >5 kg at birth ($P<0.001$); the association remained in the multiple regression. Greater lambing ease scores were recorded for terminal bred lambs (1.56 ± 0.01; $P<0.001$) compared to maternal lambs (1.41 ± 0.02) in the univariate analysis; these differences persisted in the multiple regression model. Greater lambing difficulty was recorded for first parity ewes (1.54 ± 0.01; $P<0.01$) compared to 5th ewes (1.51 ± 0.02).

Lamb mortality. Factors associated with lamb mortality were year and month of birth, gender, birth weight, litter size, lambing ease score, breed of the lamb, and ewe parity. Greater predicted probabilities for lamb mortality ($P<0.001$) were recorded for light lambs (i.e., 2 to 3 kg) and very heavy lambs (i.e., >7.5 kg). Relative to twin born lambs, the odds of a single, triplet and quadruplet born lamb dying at birth were 1.05 (95% CI = 0.93 to 1.19; $P<0.001$), 1.73 (95% CI = 2.58 to 4.87; $P<0.001$) and 3.72 (95% CI = 1.40 to 1.93; $P<0.001$), respectively and the association remained ($P<0.001$) in the multiple regression model. Lambs that experienced more difficult lambings had a greater probability of dying ($P<0.001$). Greater predicted probabilities of lamb mortality were recorded in the univariate model for Vendeen, Easy Care, Llyen and Galway lambs compared to Texel, Suffolk and Blackface Mountain lambs; however breed type was not significance in the multiple regression model. Ewes that lambed for the first time as ewe lambs had greater predicted probabilities ($P<0.05$) of having a dead lamb (0.10) compared to ewes that lambed as hoggets (0.07). First and fifth parity ewes had a greater probability of lamb mortality occurring at birth compared to other parities.

Conclusions

A large number of phenotypic factors were associated with lambing ease score and lamb survival. Many of these factors can be managed by producers to improve lambing ease score and reduce lamb mortality.

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RMIS Project Number 6195

Determination of the effect of breed variation on the Complement System response of bovine milk

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Introduction

Complement system proteins form part of the innate immune response and their potential migration into human milk during secretion has focused attention on their contribution to neonate defense (Cole *et al.*, 1982). In one reported study, a sequestration assay using a complement-sensitive bacterial strain demonstrated antimicrobial activity, thus confirming the presence of complement proteins in human milk and their potential role *in vivo* in protecting breast-fed young infants (Ogundele, 1998). The use of a Complement-sensitive strain of pathogenic *E. coli* O111 provides not alone in vitro evidence of an antimicrobial effect but also overcomes the complexity of Complement's multiple pathways, cascades and activation steps. Much attention focusses on the comparability between human and bovine milks, particularly since the latter provides the base for infant milk formula manufacture. By the 1970s most components of the complement system were identified in human and bovine milk. (Reiter and Brock, 1975; Nakajima *et al.*, 1977). It has been seen that there is approximately 70% homology between particular proteins in the cascade in the mammalian milks (Farrell Jr *et al.*, 2004). However, there is little scientific evidence of the biological comparability between human and bovine milk Complement systems. Hence, the approach to this study from a dairy cow breed perspective recognised on-going improvements in genetics, lactational performance and animal health (Beecher *et al.*, 2010), and provided a backdrop to the study of milks from a range of commercially-farmed dairy cow breeds (purebred and crossed) for the presence of Complement System activity.

Material and Methods

Based on statistical power calculations, 17 dairy cows from each of 6 breeds were selected for milk sampling: Norwegian Reds, Holsteins, Jerseys, Friesians, Norwegian Red crossbreed and Holstein-Friesian crossbreed. The animals were selected based on overall good health status and confirmed low somatic cell counts (SCC) (<200,000). The samples were collected from 3 different, primarily grass-fed, herds located at Teagasc research stations in the south of Ireland during May - July. Milk samples were aseptically collected on three consecutive mornings and immediately subjected to a bactericidal sequestration assay i.e. the anti-bacterial effect of a complement-sensitive strain of Escherichia coli NCTC 8007, serotype 0111 K58(B4) H2 incubated in the milks quantifies (colony forming units) the amount of bacteria sequestered by Complement. The remaining milk samples were frozen at -20^{0}C for further testing. The SCC of the milk samples was quantified on the day of sampling and all samples were screened for the presence of pathogens using Aesculin Blood agar (ABA) plates, Luria Broth agar and Baird Parker agar. C5a ELISA kit (BlueGene, Shanghai, China) assay was used to detect the convergent C5a Complement protein in the milks.

Results and Discussion

The results of both the bactericidal sequestration assay and the C5a ELISA assay showed that the milks of the Norwegian Red pure and crossbred dairy cows were significantly different ($p<0.05$) from the other 4 breeds (Fig. 1). Milks from this breed were particularly effective in reducing the number of colony forming units of the Complement sensitive *E. coli* O111 strain employed by the sequestration assay. This is further confirmed by ELISA detection of the Complement fragment C5a, a pro-inflammatory polypeptide produced during the activation of the Complement cascade. Again, levels of C5a were higher in the milks of the Norwegian Red breeds

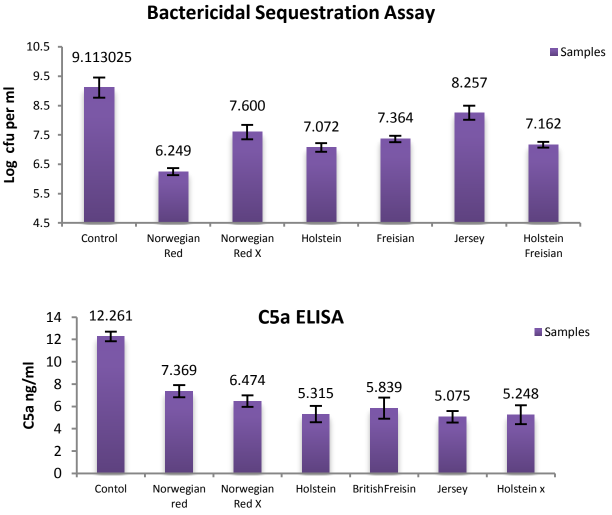

Fig. 1. Bactericidal sequestration assay and C5a ELISA indicate increased Complement system activity in the milks of Norwegian Red dairy cow breeds ($p<0.05$).

Conclusions

Breed of cow has a profound effect on the Complement levels in milk as indicated by the bactericidal sequestration assay and ELISA testing. Milks from the Norwegian Red breed stand out in terms of their strong Complement activity, and this genetic trait appears to be well manifested also at the cross-breed level. This enhanced antimicrobial activity due to Complement would appear to align with previous findings (Begley *et al.,* 2009) regarding the superior udder health status of the NR breed.

Acknowledgements

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RMIS Project Number 6407

Physiology of Reproduction, Growth & Lactation

The effect of genetic merit for fertility traits on the transcriptome of the bovine endometrium on day 13 of the oestrous cycle

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Introduction

In cattle, elevating circulating concentrations of progesterone have been shown to advance temporal changes in the endometrial transcriptome and to promote conceptus elongation (Forde *et al*, 2009). Cummins *et al.* (2012) reported greater circulating P4 concentrations during the oestrous cycle in cows with good genetic merit for fertility (Fert+) compared with cows with poor genetic merit for fertility (Fert-). The objective of this study was to use RNA-seq to (1) compare the endometrial transcriptome in Fert+ and Fert- cows on day 13 of the oestrous cycle and (2) to determine the concordance between the differentially expressed (DE) genes and the frequency of SNP associated with calving interval.

Materials and Methods

At ~60 d postpartum, 14 cows (8 Fert+, 6 Fert-) were enrolled in an ovulation synchronisation protocol. On day 13 of the oestrous cycle, endometrial biopsies were collected and snap frozen in liquid nitrogen. RNA was extracted from tissues using TRI Reagent (Sigma). RNA cleanup was performed using the RNAeasy kit (Qiagen) to remove RNA < 200 bp and genomic DNA. The transcriptome was analysed by RNA-seq. PolyA mRNA were selected, fragmented and cDNA libraries were created for each sample, following the instructions of the TruSeq RNA Sample Prep kit v2 (Illumina). cDNA was amplified by 11 cycles of PCR. Libraries were sequenced on the HiSeq 2000 platform (Illumina) to generate 40 million 100 bp paired-end reads.

Raw reads were aligned to the bovine reference genome (UMD 3.1) using Tophat. A table with counts of each gene was generated for each library. Differential expression analysis of the count data was analysed using the Bioconductor software package edgeR with the R statistical programming language.

Genes with <1 count per million in only 6 endometrium samples (the lowest level of replication) were removed from the dataset. A negative binomial distribution was assumed. Data were analysed using the GLM approach with genotype, parity and sample date included as fixed effects. Library size was normalised by the Trimmed Mean of M-values. The biological coefficient of variation was calculated from genewise dispersion estimates. Differentially expressed genes were identified by computing likelihood ratio tests. To control for multiple testing, P-values were adjusted using the Benjamini and Hochberg method.

Two fertility GWAS experiments had previously been performed: RobustMilk (50k SNP; Berry *et al*, 2012) and 10,000 Holstein project (800 k SNP; Kemper *et al*, personal communication) to determine the association of SNP with calving interval. The number of SNP, significant ($P<0.001$) and total, located 500kb either side of the centre of DE genes was determined. A false discovery rate (FDR; 0.1%) was applied to determine how many SNP were expected to be significant by chance (Pryce *et al.* 2011). Differentially expressed genes with more significant SNP than expected by chance implied they were true positive findings.

Results

On average, 90% of reads mapped uniquely to the reference genome. At a FDR of 5%, 9 endometrial genes were DE between Fert+ and Fert- cows. The concordance of RNA-seq and

GWAS was higher than expected by chance for six and two genes using the results of the 10,000 Holstein and RobustMilk projects, respectively (Table 1).

Table 1. Endometrial genes DE between Fert+ and Fert- cows on day 13 of the oestrous cycle

		Number of significant SNP		More significant SNP than chance	
Gene ID	Log FC	RobustMilk	10,000 Holsteins	RobustMilk	10,000 Holstein Project
Uncharacterized	-1.92	0	13	No	Yes
LOC509034	-1.76	0	2	No	No
GPC3	1.60	0	12	No	Yes
PRKAG3	1.63	1	1	Yes	Yes
SPP1	1.76	1	0	Yes	No
SAA3	1.80	0	2	No	Yes
LOC782922	2.01	0	5	No	Yes
KCNE3	2.30	0	1	No	No
LOC528412	3.09	0	22	No	Yes

DE genes: FDR P-value < 0.05; FC: fold change (positive values indicate up-regulation in Fert- cows)

Conclusions

The application of next-generation sequencing identified DE genes in key reproductive tissues. The GWAS results confirmed that RNAseq is a powerful method to identify DE genes.

Acknowledgements

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RMIS Project Number 6075

Population genetic gain achievable through the use of multiple ovulation embryo transfer

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Introduction

Breeding programmes globally seek to maximise population genetic gain through widespread dispersion of elite genetics. Traditionally, elite germplasm was identified at birth and potentially elite bulls were progeny tested (PT) to add confidence to predicted breeding values before widespread distribution. A benefit of using genomic selection (GS) in breeding programmes is more accurate prediction of breeding values at birth compared to parent average. Widespread use of young genomically tested bulls thereby reduces the generation interval dramatically and reduces the requirement for progeny testing. In multiple ovulation embryo transfer (MOET) schemes, high merit embryos are implanted into surrogate females facilitating an increase in the number of offspring produced from genetically elite females. The aim of this study was to quantify the genetic gain achievable through the use of 1) traditional PT, 2) current GS or 3) MOET in an Irish breeding programme.

Materials and Methods

The genetic gain achievable from alternative breeding schemes was modelled using the methodology described by Pryce *et al.* (2010). The assumptions in the schemes were modified to reflect the Irish national dairy herd. The breeding schemes evaluated were 1) traditional PT where 100 bulls were selected using parent average Economic Breeding Index (EBI) and were progeny tested. Based on progeny results, the best 30 bulls were selected for widespread use; 2) GS where 1,000 bull calves were genotyped and the 30 bulls with the highest genomic EBI were selected for widespread use; this scheme mimics the current approach operated by the majority of Irish breeding companies; and 3) MOET where 600, 800 or 1,000 heifers were selected from the population and were genotyped. Between 60 and 410 of the genotyped heifers (in increments of 50 heifers) were selected for embryo flushing on the basis of their genomic EBI. All resulting male calves were genotyped and the 30 bulls with the highest genomic EBI were selected for widespread use.

Across all schemes, a sex ratio of 50% males was assumed and the 30 bulls selected for widespread use were the progeny of 10 sires selected from the population. The PT scheme assumed a calving rate to first service of 60% and a replacement rate of elite females of 31.25%. Assumptions for MOET were that four embryos were harvested per flush with 50% of embryos resulting in viable pregnancies; one flush was undertaken per selected breeding female.

Genetic gain was quantified using the response to selection equation of Rendel and Robertson (1950); the results are presented in units of the EBI with an assumed standard deviation of €62. The reliability of genomic selection (for EBI) was assumed to be 0.55 for both GS and MOET schemes and was 0.9 and 0.3 for bulls and cows, respectively, for the PT scheme. Average generation intervals for male and female pathways for each scheme were 6.5 and 4.1 (PT), 3.0 and 3.5 (GS) and 3 and 2 (MOET), years, respectively.

Results and Discussion

The annual response to selection in EBI was €12.0 and €22.2 for the PT and GS schemes, respectively. The €12 response in the PT scheme is greater than the €8 observed in the Irish PT scheme operated until recently, indicating that current selection practices are sub-optimal. The better selection response of the GS scheme is due to the greater selection intensity and reduced generation interval of bulls made possible by the relatively inexpensive genotyping of large numbers of potentially elite bull calves. As the number of genotyped heifers selected from the population increased from 600 to 1,000 in the MOET scheme, the overall response to selection increased (Figure 1). However, as bull selection intensity increased, the selection intensity of their dams decreased. Therefore, the overall response to selection was curvi-linear reflecting the potential genetic gain lost through the bull dam pathway when their sons were selected very intensively. Incorporating MOET into a breeding programme with 600 females genotyped offered only a slight advantage over GS in terms of response to selection (a maximum of €0.70 annual genetic gain above GS when 110 females were flushed). This was because a small population does not result in sufficient intensity of selection on either the bull or cow lines. Populations with greater than 600 genotyped females required a maximum bull selection intensity of 30% (i.e. minimum of 100 heifers flushed) to achieve genetic gain above what is available through GS (Figure 1).

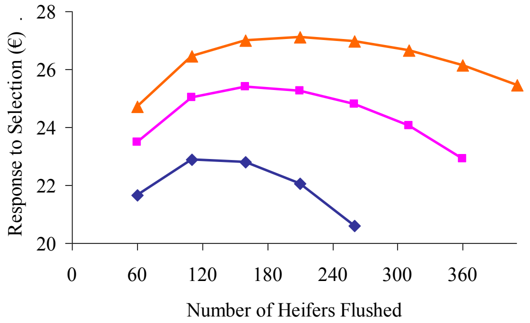

Figure 1. Response to selection from MOET where bull dams were selected from 600 (-●-), 800 (-■-) and 1,000 (-▲-) heifers and between 60 and 410 heifers were flushed to produce 30 selected bull calves

Conclusion

Embryo transfer offers advantages to population genetic gain where bull dams are selected from a sufficiently large population of genotyped animals and bull sires are selected with selection intensity lower than 30%.

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RMIS Project Number 6195

Survey of temporal variation in pasture mineral concentrations and total dietary mineral intake in pasture-based dairy herds

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Introduction

Grazed grass is the predominant feed in Irish dairy production systems. Subclinical mineral deficiencies are common, and can manifest in poor reproductive performance and suboptimal animal health (NRC, 2001). The objectives of this study were to: (i) benchmark the seasonal variation in forage mineral concentrations across a range of different soil types; and (ii) determine the mineral nutritive value of these swards for lactating dairy cows.

Materials and Methods

Forty four spring calving dairy farms were selected based on region and soil type and enrolled in the study in March 2013. Each farm was visited once in March, May and August 2013. Samples of the grass being grazed and all other dietary feeds being consumed (silage, concentrate and other miscellaneous feedstuffs) were collected. The percentage of each feedstuff in the diet was recorded. Total feed intake was estimated to be 16.9 kg DM/day during March (early lactation) and 18 kg DM/day in May and August (O'Neill et al., 2013). Each farmer collected grass samples cut to a stubble height of 4cmfrom paddocks grazed during the week before each visit. These grass samples were placed in a plastic bag and stored at -20 ºC. The daily grass samples were then mixed to form one composite sample representative of the grass grazed in the week before the visit. The composite grass samples and other feedstuffs from each farm were analysed for mineral concentrations using inductively coupled mass spectrometry (ICP-MS). Total dietary intake of each mineral was estimated based on the quantity of each feedstuff allocated. The mean, range and standard deviations for each mineral were calculated at each time point.

Results and Discussion

Pasture mineral results are summarised in Table 1. Across all farms, a pasture-only diet would have provided 85%, 73%, 52%, 50% and 38%of the requirements of an average lactating cow (NRC, 2001) for P, Cu, I, Zn and Se, respectively. When total dietary mineral intakes were estimated, on average, the diet provided 95%, 160%, 107% and 58% of the lactating cow requirements for P, Cu, Zn and Se, respectively (Table 2).No herds were iodine deficient during March, but 4.5% and 56.8% were deficient in May and August, respectively. When concentrate supplements were fed (March, May), iodine was generally over-supplied in the total diet, with average estimated intakes exceeding 400% of requirements. The greatest estimated iodine intake identified was over 1800% of lactating cow requirements (9.03 mg/kg DM).

Table1. Mineral concentrations (± standard deviation) in grass samples collected on 44 dairy farms during March, May and August 2013 (values in parentheses represent the range in mineral concentration).

Mineral	March (mg/kg)	May (mg/kg)	August (mg/kg)	Requirements (mg/kg)
Phosphorus	**3368 ±550** (2157-4456)	**3391 ±651** (1482-5213)	**3531 ±1266** (1811-6040)	4000
Magnesium	**1732 ±315** (1113-2566)	**1706 ±351** (490-2546)	**2028 ±603** (1230-3450)	1100
Calcium	**5330 ±993** (3356-7373)	**5668 ±1090** (3283-8580)	**6137 ±1669** (2695-12505)	6000
Iodine	**0.24 ±0.15** (0.04-0.63)	**0.26 ±0.42** (0.042-2.71)	**0.26 ±0.20** (0.04-0.97)	0.5
Copper	**10.09 ±3.14** (6.03-19.9)	**11.97 ±2.61** (6.59-19.48)	**10.62 ±4.91** (1.58-19.6)	15.7
Selenium	**0.21 ±0.18** (0.01-0.67)	**0.05 ±0.03** (0.01-0.13)	**0.08 ±0.04** (0.01-0.18)	0.3
Zinc	**27.4 ±5.6** (15.8-39.1)	**31.5 ±5.6** (20.1-43.7)	**36.6 ±11.6** (22.5-62.9)	63

Table 2. Estimated total dietary mineral intake per cow (± standard deviation) on 44 dairy farms during March, May and August 2013 (values in parentheses represent the range in mineral concentration).

Mineral	March (mg/kg)	May (mg/kg)	August (mg/kg)	Requirements(mg/kg)
Phosphorus	**3866 ±469** (2759-5286)	**3816 ±660** (2307-5445)	**3670 ±1172** (2163-6065)	4000
Magnesium	**4228 ±1174** (2327-8211)	**3527 ±1126** (1866-6690)	**2800 ±848** (1358-4477)	1100
Calcium	**7753 ±1345** (5180-11406)	**7876 ±1900** (5100-13324)	**6633 ±1506** (4599-12279)	6000
Iodine	**2.82 ±1.63** (0.76-7.92)	**2.35 ±1.7**(0.04-9.03)	**0.78 ±1.01** (0.08-4.15)	0.5
Copper	**29.82 ±8.50** (13.7-58.0)	**27.70 ±12.04** (11.18-63.81)	**16.70± 7.59** (2.75-33.46)	15.7
Selenium	**0.19 ±0.08** (0.07-0.43)	**0.22 ±0.12** (0.02-0.54)	**0.11 ±0.05** (0.03-0.306)	0.3
Zinc	**83.8 ±29.6** (44.6-183.2)	**68.22 ±28.97** (34.46-154.8)	**50.85 ±21.07** (26.49-116.7)	63

Conclusions

The results indicate that grass grown on Irish dairy farms does not contain adequate P, Cu, I, Zn and Se to meet cow requirements when fed as the sole feed. This has implications for animal health and fertility performance. The results also indicate that some minerals are supplemented in excessive quantities, especially iodine, with potential negative effects for milk entering the human food chain. Regular forage mineral analysis is recommended to ensure that appropriate supplemental minerals are fed.

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RMIS Project Number 6387

Preliminary results from a field trial to evaluate sexed semen in dairy cows and heifers

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Introduction

With conventional semen (fresh or frozen), the likelihood of a heifer or a bull calf is roughly equal at 50 %. Sexed semen (90 % X-sorted) will alter this ratio to 90 % heifer calves and 10 % bull calves. Relative to the number of sperm required for each AI straw, sperm sorting is slow. As a result, the number of sperm per sexed semen AI straw is lower than conventional AI straws (2 million sperm vs. 20 million sperm). Due to a combination of the lower dose and sperm damage, the fertility of sexed semen is reduced compared with conventional semen (75 to 80% of conventional semen). The objective of this trial was to evaluate the fertility performance of both fresh and frozen sexed semen in Irish dairy cows and heifers.

Materials and Methods

In spring 2013, a temporary sexed semen laboratory was established at Moorepark to facilitate a large field trial. In total, 394 herds were recruited onto the trial. Ejaculates were collected at bull studs operated by NCBC (Mallow and Enfield) and Dovea Genetics (Thurles) and transported to the sexed semen laboratory at 18 ºC. Semen was sorted using fluorescence-activated cell sorting as previously described (Garner et al., 2013). Four semen treatments were evaluated: fresh conventional (3 × 106 sperm/straw); frozen sexed (2 × 106 sperm/straw); and two fresh sexed semen treatments (1 × 106 sperm/straw and 2 × 106 sperm/straw). All insemination were conducted by qualified AI technicians on both heifers and lactating cows. In total, 15,304 inseminations were recorded (9153 on cows and 6151 on heifers).

At 55 to 80 days post AI, 3943 pregnancy exams were conducted (2160 on cows, 1783 on heifers) and BCS was recorded. Foetal gender was determined on 708 pregnancies. This preliminary dataset was used in the current analysis. A generalized linear mixed (PROC GLIMMIX) for a binary distribution was used to evaluate treatment effects. The model contained fixed effects of herd, treatment, parity, bull, treatment by bull interaction, days in milk and BCS. Cow within herd was included as a random effect.

Results and Discussion

The conception rate results are reported in Table 1. It is important to note that the field trial took place in the midst of a prolonged fodder crisis. It is likely that suboptimal nutrition reduced the conception rates achieved for all treatments, and this effect was most noticeable for the heifers. Previous reports in the literature, primarily with heifers, indicated that frozen sexed semen would achieve conception rates of 75 to 80% of conventional semen. The preliminary results presented here indicate that the fertility performance of frozen sexed semen relative to conventional semen has markedly improved. The performance of the fresh sexed semen, however, was poor. Of note, frozen sexed semen was the best sexed semen treatment in lactating cows. The relative performance of frozen sexed semen compared with conventional was approximately similar in both cows and heifers (85% and 87%, respectively). The use of frozen sexed semen (rather than fresh) relieves the logistical pressures of transporting the semen from the bull stud to the sorting laboratory, and from the sorting laboratory to the farm in a short time period throughout the breeding season. The use of frozen sexed semen will also provide greater opportunity for DIY AI farmers to utilise the technology. Large variation between herds was observed; herd mean conception rate for all trial straws ranged from less than 10% to over 70%. Conception rates increased with improving BCS (cows and heifers; $P < 0.001$) and greater days in milk (cows; $P < 0.001$) at insemination. The scanning results indicate that the expected 90% gender bias was achieved in the sexed semen treatments.

Table 1. The effect of sexing semen on conception rate to first service, performance relative to conventional semen and percentage of heifer foetuses

	Conventional	Sexed Fresh 1m	Sexed Fresh 2m	Sexed Frozen 2m	P-value
Cow conception rate (%)	49	32	37	42	< 0.001
% of conventional	-	64	76	85	-
% heifer foetuses	54	88	94	92	-
Heifer conception rate (%)	53	39	46	46	< 0.001
% of conventional	-	75	87	87	-
% heifer foetuses	56	93	87	90	-

Conclusions

The results for the frozen semen has beneficial implications for the future use of sexed semen in Ireland. Further research is necessary to improve the performance of fresh sexed semen (1 × 106 sperm per straw or less).

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Acknowledgements

The field trial was a collaboration between Teagasc, ICBF, Sexing Technologies, Dovea Genetics, Munster AI, Progessive Genetics and NCBC. Financial support from ABP, Dawn Meats, Kepak, Slaney, Agricultural Trust and DAFM is gratefully acknowledged.

RMIS Project Number 6448

Effect of weaning weight on subsequent weight gain in replacement dairy heifers

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Introduction

Replacement dairy heifers should enter the milking herd at 22 to 24 months of age (Tozer and Heinrichs, 2001). A recent Irish study has shown that the most profitable replacement heifer rearing systems are those where heifers attain a target bodyweight (BW) which is 60% of mature herd BW at mating start date (MSD; Archbold *et al.*, 2012). As ADG during the pre-weaning period affects BW post-weaning (Jasper and Weary, 2002) this may have repercussions on the attainment of target weight at MSD. The objective of this study was to investigate the effect of three different weaning weight categories on days to weaning and weight gain during the pre- and post-weaning period.

Materials and Methods

Forty-eight replacement dairy heifer calves were enrolled on an experiment at Teagasc Moorepark Research Farm, Co. Cork from 19 January to 26 October, 2013. Calves were blocked on the basis of date of birth (DOB; 9 Feb ± 10.9 days), birth BW (35 ± 5.6 kg) and breed (39 Holstein-Friesian (HF) and 9 Jersey x HF; JEX). They were randomly assigned to one of three feeding treatments: i) weaning at 60 kg (W60); ii) weaning at 80 kg (W80) and iii) weaning at 100 kg (W100). Weaning weights for JEX animals were 10% less than the HF to allow for breed differences in mature BW. Thus, animals were weaned at approx. 11, 15 and 18% of the BW of mature cows within the herd. All calves were removed from their dam within one hour of birth and fed 8.5% of birth BW in colostrum in one feed. Transition milk was offered for the subsequent three days. Milk replacer was group fed, at a daily rate of 6 litres/calf, was offered twice daily for the first four weeks and once daily thereafter. All calves were offered fresh water, *ad libitum* concentrate and hay throughout the milk feeding period. Calves were turned out to pasture from 5 weeks of age. Weaning was gradual over a one-week period. Following weaning, all calves were offered *ad-libitum* grass outdoors; concentrate input was equal across treatments. Calves were weighed weekly pre-weaning and every three weeks post-weaning. As all calves were weighed on a fixed calendar date variation existed in the actual age of calves at each weighing event. Therefore, BW closest to 40, 65 and 190 days of age is reported. Data were analysed using mixed models in SAS; animal was included as a repeated measure. The model included treatment, breed, age and birth weight.

Table 1. Effects of imposing different weaning weights on days to weaning and average daily gain (ADG)

	W60	W80	W100	SE	Sig
Days to weaning	59	83	95	2.9	0.001
ADG birth to wean (kg/d)	0.55	0.56	0.70	0.024	0.001
Weight at 190 days	156	162	171	4.0	0.039
ADG birth to 190 days (kg/d)	0.64	0.67	0.71	0.018	0.037
ADG weaning to 190 days (kg/d)	0.70	0.75	0.72	0.027	0.411

SE= Standard error; Sig = significance

Results and Discussion

As all calves were fed similar quantities of milk and concentrate, there was no difference in calf weight at 37 (47.5 kg) and 64 days of age (67.0 kg). Consequently, ADG was similar for all treatments from birth to 37 days (0.41 kg) and from 37 to 64 days (0.71 kg). Weaning weight ($P<0.001$) of the W60 calves was 62 kg while it was 80 kg and 99 kg for the W80 and W100 treatments, respectively. The number of days to weaning was least ($P<0.001$; Table 1) for W60, greatest for W100, with W80 calves being intermediate. At 190 days, the W100 calves were 15 kg heavier ($P<0.05$) than the W60 calves and they tended to be heavier than the W80 calves ($P=0.09$). There was no difference ($P>0.05$) between the W60 and W80 calves indicating that the advantage to weaning calves at a heavier weight only arises when they are weaned at approximately 18% of their mature BW rather than <15% mature BW. The W100 calves had a greater ($P<0.05$) ADG from birth to 190 days than the W60 calves and also tended ($P=0.09$) to be greater than W80. Interestingly, there was no difference in ADG from weaning to 190 days of age between treatments, indicating that no compensatory growth occurred and that differences in BW at 190 days were due to differences in weaning BW rather than differences in post-weaning BW gain which may lead to differences at MSD, this however requires investigation.

Conclusion

In this study BW gains were similar between treatments post-weaning. Thus, differences in BW at weaning were maintained up to at least 190 days of age indicating that heifers should be weaned at approximately 18% of mature BW.

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RMIS Project Number 6448

The effect of storage temperature and sperm concentration on liquid stored bull sperm

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Introduction

Currently in Ireland, liquid bull sperm contains approximately 5 x 10^6 sperm per insemination dose, is stored at unregulated ambient temperature and is inseminated within 2.5 days of collection due to concerns of declining fertility. We have recently shown that lower sperm concentrations reduce oxidative stress in liquid stored bull sperm (Murphy *et al*., 2013) and this coupled with storage of sperm at 5°C, which has been shown to reduce metabolic activity, may be a viable way to extend the fertile lifespan of liquid stored bull sperm. The objective of this study was to evaluate the best storage temperature for liquid stored bull sperm stored in a range of sperm concentrations.

Materials and Methods

Semen was collected from Holstein Friesian, Norwegian Red, Limousin and Aberdeen Angus bulls at a commercial AI centre (5 collections with 3 bulls per collection; collection = replicate). Sperm concentration was assessed and the ejaculate was diluted in a 5% egg yolk Caprogen diluent to a final concentration of 10 (T_{10}), 5 (T_5), 1 (T_1) and 0.5 ($T_{0.5}$) x 10^6 sperm per 0.25 mL straw. Semen from each bull was kept separate and each bull was represented in each treatment. For experiment 1, post packaging, straws were split into two groups and stored at either 15°C or 5°C and assessed *in vitro* on Days 0, 1, 3 and 5 post-collection (Day 0 = day of collection). On each assessment day, sperm from each sperm concentration and temperature group were evaluated for total motility (Phase-contrast microscope; 400X), viability, acrosomal status, osmotic resistance (ORT; T_{10} only due to logistical constraints) and DNA fragmentation using fluorescent probes (Life Technologies, USA) and flow cytometry (Guava EasyCyte 6HT; Merck Millipore). For experiment 2, sperm was collected from 6 bulls (Holstein Freisian, Aberdeen Angus and Hereford), diluted to the same concentrations as experiment 1, packaged, as above, and stored at either 15°C, 5°C or fluctuated between 15 and 5°C (Flux) so as to mimic fluctuation from day to night time temperatures. For Flux, straws were stored in a waterproof container and submerged in water, and incubated at either 15°C during the day or at 5°C at night, to allow a gradual temperature fluctuation. Sperm were assessed *in vitro* on Days 0, 1, 3 and 5 for total motility, viability and ORT. Flow cytometry plots were gated and 10,000 events were analysed. Data were examined for normality, tested for homogeneity of variance and analysed using the repeated measures procedure in the Statistical Package for the Social Sciences (SPSS; version 20.0), with the exception of ORT which was analysed using the univariate procedure. The model included the main effects of day, sperm concentration, temperature, replicate and their interactions.

Results and Discussion

In experiment 1, total motility declined with duration of storage irrespective of temperature ($P<0.01$). Storage at 15°C had higher motility post Day 1 in comparison with 5°C ($P<0.001$). There was no effect of sperm concentration on motility at 15°C, however, at 5°C, $T_{0.5}$ had lower motility than both T_{10} and T_5 ($P<0.05$). There was no effect of day, sperm concentration or temperature on viability, acrosomal status or DNA fragmentation. The ORT of sperm declined with duration of storage and this decline was greater at 15°C than at 5°C ($P<0.001$).

In experiment 2, total motility declined with duration of storage irrespective of temperature ($P<0.01$), with the 15°C and Flux treatments maintaining a greater motility post Day 3 ($P<0.01$; Fig. 1). For Flux, T_{10} and T_5 maintained a greater motility than $T_{0.5}$ ($P<0.01$). There was no effect of sperm concentration or temperature on viability. The ORT of sperm declined with duration of storage, as in experiment 1, however the Flux storage treatment maintained a greater ORT post Day 3 in comparison with the 15°C treatment ($P<0.001$)

Conclusions

When stored at 15°C the motility of liquid stored bull sperm was retained for longer compared to storage at 5°C. Despite this, sperm stored at 15°C had reduced membrane function as is evident by reduced osmotic resistance. However, storing sperm under controlled conditions, fluctuating between 15°C and 5°C, was not detrimental to either motility or osmotic resistance, compared to storage at 15°C or 5°C, respectively.

Acknowledgments

We gratefully acknowledge support from the Irish Research Council and the Department of Agriculture, Food and the Marine under the Research Stimulus Fund (Project 11/S/116). Semen was donated by Dovea Genetics, Co. Tipperary.

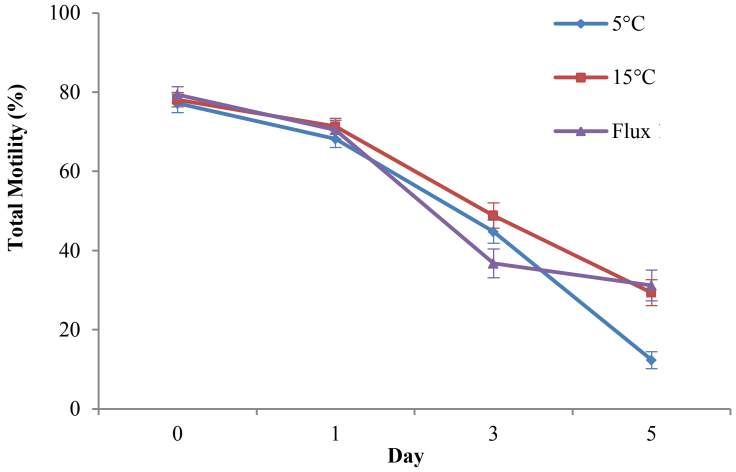

Fig. 1: Experiment 2; the percentage of progressively motile sperm (mean of all sperm concentrations) at 15°C, 5°C, and Flux. Vertical bars represent ± s.e.m.

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RMIS Project Number 6450

Impact of administration of inactivated BVD vaccines on bulk milk p80 (NS3) ELISA readings

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Introduction

Control of Bovine Viral Diarrhoea (BVD) is based on removal of persistently infected (PI) animals, biosecurity and vaccination (Moennig *et al*., 2005). Bulk milk (BM) antibody ELISA is routinely used to both determine herd status prior to introduction of BVD control measures and for surveillance purposes post-control programme implementation (Houe *et al*., 2006). Use of BVD vaccines has the potential to interfere with interpretation of BM results through generation of vaccine antibodies undistinguishable from natural infection. Vaccination, however, is often the predominant BVD control measure in high seroprevalence countries such as Ireland (Moennig et al., 2005) thereby restricting the usefulness of BM analysis as a surveillance tool. The aim of this study therefore was to investigate the impact of three inactivated BVD vaccines on BM analysis to assess the potential of these vaccines to allow differentiation between infected and vaccinated (DIVA) herds in a high BVD seroprevalence region such as Ireland.

Material and methods

A total of 312 commercial dairy farmers volunteered to partake and submitted four bulk milk samples over the 2009 lactation period (March, June, August, November). Each farm was also visited to blood sample a minimum of five unvaccinated homeborn weanlings by coccygeal venepuncture. Bulk milk and serum samples were analysed using a p80 blocking ELISA (Institut Pourquier). Milk samples from March and August were also tested using an indirect total antibody ELISA (IDEXX). Herds were classified as vaccinated (V) or unvaccinated (UV) and the brand of vaccine used was recorded for each vaccinated herd. Herds having at least one weanling greater than 270 days of age and serologically positive for BVD were classified as 'having evidence of recent infection' (RI). Those recording no positive weanlings were classified as 'not recently infected' (NRI). Normality of each dataset was assessed by Shapiro-Wilk normality test in Stata (Version 12). Differences between V and UV herds of varying infection status (RI and NRI) were examined using non-parametric Wilcoxon rank-sum analysis.

Results and discussion

Of those herds that vaccinated (n=187), 25%, 20%, and 44% administered Pregsure (Zoetis), Bovilis BVD (MSD), and Bovidec (Novartis), respectively. The most common time of year to vaccinate for BVD was between January and April when 149 herds vaccinated. At least one seropositive weanling over 270 days of age was identified in 33% of the study herds indicating a high level of RI.. . Quarterly median p80 % inhibition values for vaccinated NRI herds and unvaccinated RI herds across vaccine brand over time are outlined in Figure 1. This highlights that under field conditions using BM samples in a high seroprevalence region, Bovilis BVD displays characteristics of a DIVA vaccine when used in conjunction with the p80 blocking ELISA used in this study.

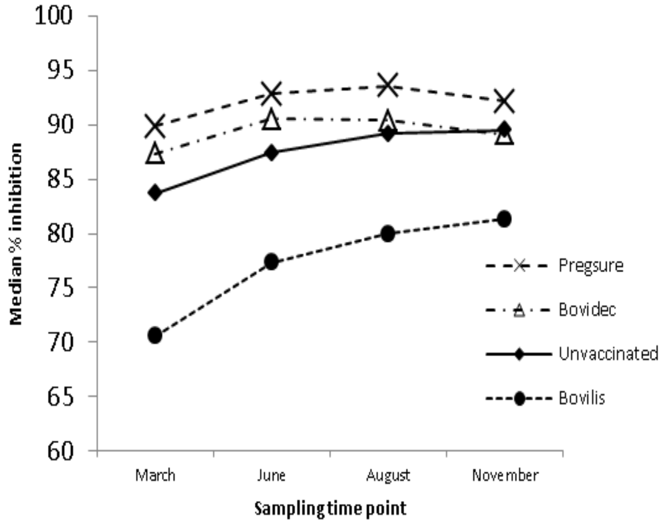

Fig. 1. Quarterly median P80 ELISA % inhibition values across NRI V and RI UV herds.

Additionally, use of Bovilis in NRI herds did not result in significantly higher % inhibition readings compared to UV NRI herds, and total antibody readings highlight that Bovilis induced an immune response at least comparable to Bovidec. Corresponding Wilcoxon rank-sum *z* and *P* values are outlined in Table 1.

Table 1. Wilcoxon rank sum *z* and *P* values for V NRI *vs.* UV RI herds (March and August results displayed)

Vaccine	Pourquier p80		IDEXX	
Date	*z*	*P*	z	P
Bovidec	Bovidec *vs.* UV		Bovidec *vs.* UV	
Mar	-0.44	0.659	-0.92	0.359
Aug	-0.24	0.814	0.48	0.633
Bovilis	Bovilis *vs.* UV		Bovilis *vs.* UV	
Mar	2.38	0.019	0.16	0.873
Aug	2.99	0.003	1.52	0.129
Pregsure	Pregsure *vs.* UV		Pregsure *vs.* UV	
Mar	-2.11	0.035	-3.776	<0.001
Aug	-2.67	0.008	-3.957	<0.001

These results indicate that minimal, if any, additional antibodies to p80 antigen were induced from administration of Bovilis BVD. NRI V herds which administered Bovilis did, however, record median readings ≥55% inhibition (positive cut-off) as the study was carried out in a high seroprevalence region with high levels of historical infection.

Conclusion

Bovilis BVD displays characteristics of a DIVA vaccine. In high seroprevalence regions, however, it is more accurate to state that its administration allows unambiguous interpretation of BM results.

Acknowledgements

This study is an output from Dairy Levy funding.

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RMIS Project Number 5900

Association between exposure to *Salmonella*, *Neospora caninum* and *Leptospira interrogans* serovar *hardjo* with performance in Irish dairy herds

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Introduction

An investigation of bulk milk samples in Irish dairy herds in 2009 documented a prevalence of antibodies to *Salmonella*, *N. caninum* and *L. hardjo* of 49%, 19%, and 86%, respectively (O' Doherty *et al*., 2013). The objective of this study was to quantify the association between bulk milk antibody status of these pathogens and performance parameters in 312 Irish dairy herds.

Material and Methods

Herds were classified as negative for exposure to each respective pathogen if the herd recorded a negative reading for exposure to bulk milk antibodies at all four sampling time points in 2009 (O' Doherty *et al*., 2013). Information on herd vaccination status for *Salmonella* and *L. hardjo* was also available. Data on milk production, reproductive performance, and mortality rates for 312 dairy herds were sourced from the Irish Cattle Breeding Federation (ICBF) database. Milk production and duration of calving season were calculated separately for primiparous and multiparous cows. Three categories of mortality were defined which included: 1) neonatal mortality, 2) young-calf mortality, and 3) adult cow mortality. The associations between both bulk milk antibody status or vaccination status for *Salmonella*, *N. caninum*, and *L. hardjo* and herd level 305–day milk yield, milk fat yield, milk protein yield, and somatic cell score (SCS; natural logarithm of somatic cell count), reproductive performance, and mortality were quantified using linear fixed effects models (SAS, 2009). Models were controlled for herd size, average herd parity, proportion of Holstein-Friesian animals, median calving date in 2009, and herd average EBI value.

Results and discussion

Exposure to *Salmonella* was associated with reduced milk yield and milk solids yield in cows (Table 1). As 49% of unvaccinated study herds recorded positive bulk milk *Salmonella* readings, it is unlikely that all represent new infections in 2009. The reduction in milk yield and milk solids yield highlighted in this study, therefore, are likely to reflect losses associated with endemic *Salmonella* infection. Wray and Sojka (1977) highlighted that the clinical manifestations of *Salmonella* infections are particularly evident in calves less than two months of age. The greater prevalence of mortality amongst calves (<12 months old) in *Salmonella* positive herds in the present study supports this finding (Table 1). Vaccination against *Salmonella* was associated with a reduction in SCS in multiparous cows (P=0.04) and greater neonatal mortality (P=0.02). As the majority of study herds vaccinated against *Salmonella* in the autumn [greatest period of risk for *Salmonella* associated abortion (Wray and Sojka, 1977)], it is possible that the timing of cow vaccination is not optimal to provide adequate passive immunity to calves born in the spring. Exposure to *N. caninum* was associated with a six day longer calving interval (P=0.004) and in primiparous cows an 11-day longer calving season (P=0.008) compared to cows in non-exposed herds; this association is most likely a result of the clinical manifestations of infection such as early foetal loss or mid-term abortion. An unexpected finding in the present study was the association between exposure to *N. caninum* and a greater rate of mortality amongst animals more than 12 months of age (P=0.04). Previous studies have not detected such an association (Chi *et al.,* 2002) and current knowledge of the pathogenesis of *N. caninum* infection does not present an obvious means by which such an association might occur. It is possible, however, that complications due to abortion (e.g. metritis) may increase the risk of mortality in this group. A 16% lower 42-day calving rate in 2009 (P=0.01) and an 8% lower 42-day calving rate in 2010 (P=0.05) in multiparous cows was evident in herds positive for exposure to *L. hardjo* compared to test-negative *L. hardjo* herds. *L. hardjo* antibody-positive herds also had a 9% greater rate of carryover cows (P=0.03). Vaccination against *L. hardjo* was associated with reduced SCS in cows irrespective of parity

P<0.05) and an increased 42-day calving rate. Additionally, herds that vaccinated against *L. hardjo* had a reduced proportion of non-pregnant cows (P=0.005) and more calves per cow per year (P=0.05).

Table 1: Associations between production parameters and *Salmonella* status in unvaccinated herds

Variable	status		P-value
	Neg	Pos	
Multi[1] milk yield (kg)	6219	5826	0.002
Multi fat yield (kg)	258	241	0.0006
Multi protein yield (kg)	226	211	0.0008
Primi[2] milk yield (kg)	4762	4505	0.02
Primi fat yield (kg)	215	203	0.02
Primi protein yield (kg)	182	172	0.01
Calf mortality (%)	1.69	3.22	0.0006

[1] Multi=multiparous, [2] Primi=primiparous

Conclusions

Exposure to *Salmonella*, *N. caninum*, and *L. hardjo* was associated with varying degrees of compromised performance in Irish dairy herds. The improved herd performance associated with vaccination against both *Salmonella* and *L. hardjo* would suggest that Irish dairy farmers, having such a reliance on compact spring-calving, should consider vaccinating for these pathogens if not already doing so.

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RMIS Project Number 5900

National prevalence of exposure to BVDv and BoHV-1 in Irish dairy herds

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Introduction

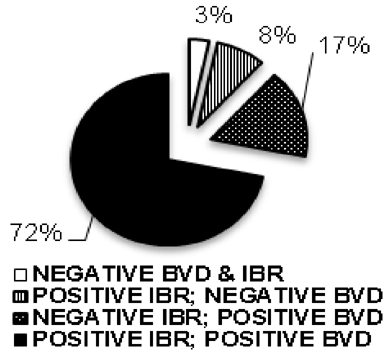
Bovine Viral Diarrhoea (BVD), caused by BVD virus (BVDv), and Infectious Bovine Rhinotracheitis (IBR), caused by Bovine Herpesvirus 1 (BoHV-1), are highly contagious viral diseases of cattle (Moennig *et al*., 2005). To determine the necessity for an eradication programme, and to measure its on-going success, it is useful to conduct prevalence studies to obtain baseline data. The advent of bulk milk (BM) testing for pathogen-specific antibodies yields a practical, inexpensive, and efficient means of generating herd-level prevalence data. The primary objective of this study was to use BM analysis of Irish dairy herds to generate national prevalence data for exposure to both BVD and BoHV-1. A secondary objective was to examine seasonal variations in BM antibody levels for these viruses.

Material and methods

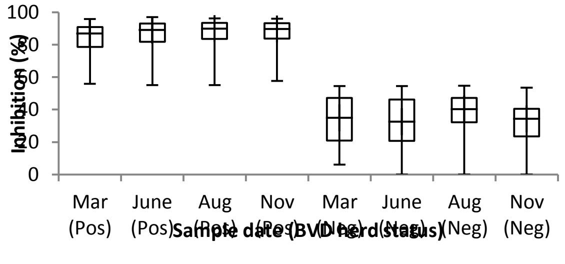
Stratified proportional sampling based on herd size and geographical location was used to randomly select herds from the Irish Cattle Breeding Federation database. A total of 312 geographically representative herds (O'Doherty et al., 2013) were recruited to the study, yielding a sufficient sample size to achieve a 95% confidence level and precision of 5% with an expected national prevalence of 70%. Participating farmers submitted four BM samples over the 2009 lactation (March, June, August, November). BVDp80 (Pourquier), IBR lysate (Pourquier), and IBRgE (IDEXX) ELISA kits were used to analyse samples. Herds were classified as 'positive' or 'negative' at each of the four sampling time points using manufacturer recommended cut-offs. Herds were also categorised by combined BVD and IBR BM status. To investigate associations between season and BM data, box plots were constructed and each dataset examined using Generalised Estimating Equations (GEE). Both univariable and multivariable analysis of BM results [constructed as both categorical ('positive' *vs*. 'negative') and continuous (BM raw data) variables] and sampling time point was completed. Herd was included as a repeated measure. For categorical variable analysis, a binomial distribution was assumed and a logit link function used. For continuous variable analysis, a Gaussian distribution and an identity link function was used.

Results and discussion

The apparent prevalence (Ap) of BM antibody positive herds for BVDv and BoHV-1 was approximately 88% and 78%, respectively. The proportion of herds recording concurrent exposure to BVDv and BoHV-1 (IBR) is outlined in Fig. 1. Multivariable analysis of exposure to BVDv and BoHV-1 as continuous variables highlighted a general increase in ELISA readings as the year progressed (Fig 2 a and b) most likely due to a decrease in milk yield in Spring-calving herds as cows move into late lactation. Changes in BVD herd status were statistically significant over time but on examination of raw data, the majority of increases in BVD %inhibition were not biologically significant being just higher than the positive cut-off value. In the case of 4 farms, however, increased readings indicative of BVDv introduction were recorded.



(a)



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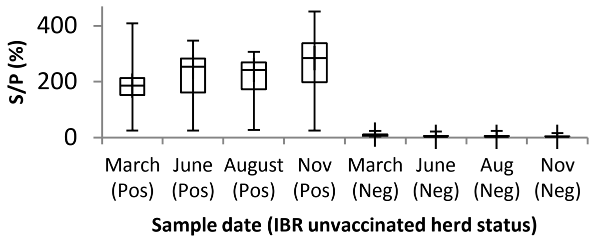

Fig. 2. Box plots outlining seasonal trends in BM ELISA readings across positive (Pos) and negative (Neg) (a) BVD, and (b) IBR-unvaccinated herds.

Conclusion

The results of this study highlight high levels of exposure to BVDv and BoHV-1in Irish dairy herds. Although BM analysis is a useful tool for determining BVDv and BoHV-1 herd status, multiple tests over a lactation in Irish seropositive herds would appear superfluous, given the lack of seasonality highlighted.

Acknowledgements

This study is an output from Dairy Levy funding.

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RMIS Project Number 5900

Production losses associated with the presence of BVD seropositive weanlings in Irish dairy herds.

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Introduction

Bovine Viral Diarrhoea (BVD) is a highly contagious viral disease of cattle. Ireland initiated a voluntary BVD eradication scheme in 2012 which lead to introduction of a compulsory scheme in 2013. The scheme is co-ordinated by Animal Health Ireland (AHI) and is based on ear-notch testing of all new-born calves for BVD virus (BVDV). Analysis of bulk milk (BM) has, and is, being routinely used in Ireland to monitor BVD herd status. As BM BVD antibody detection may reflect historical rather than current herd viral status (Lindberg and Alenius, 1999), it is useful to test unvaccinated homeborn youngstock (weanlings) for antibodies against BVDVi.e. a SPOT test (Mars and Van Maanen, 2005). As these individuals have only joined the herd within the previous year, positive antibody readings in this group, once maternal antibodies have dissipated, can be indicative of current or recent viral circulation (Lindberg and Alenius, 1999). Such viral circulation can result from a contemporaneously born persistently infected (PI) individual. Recently, AHI published a study outlining the overall cost of BVD to Irish herds (Stott *et al.*, 2012). The aim of this study was to assess associations between antibody status of dairy replacement heifer weanlings (SPOT test) and production losses at individual herd level.

Materials and methods

In all, 312 commercial dairy farmers volunteered to partake in a study in 2009. Farms were visited to blood sample a minimum of five unvaccinated homeborn weanlings by coccygeal venepuncture. Serum samples were analysed using a p80 blocking ELISA (Institut Pourquier). Herds were classified as vaccinated (V) or unvaccinated (UV) based on questionnaire data. Those herds recording at least one BVDV seropositive weanling greater than 270 days of age were classified as 'having evidence of recent infection' (RI). Those recording no positive weanlings were classified as ‘not recently infected’ (NRI). Production parameters examined related to milk production, fertility, and mortality. All performance data were sourced from the ICBF database. Variables were checked for normality and transformed as necessary. Associations between herd classifications and production parameters across both V and UV study herds were quantified using linear regression models in Stata (Version 12) with a post-estimation contrast of margins analysis completed subsequently. Variables were considered significant at $P< 0.05$. Models were controlled for herd size, average parity, proportion of Holstein-Friesian animals, median calving date, and average EBI value in 2009. An additional four bio-containment related variables were included as indicators of good farm management.

Results and discussion

A total of 2171 weanling serum samples were analysed across vaccinated and unvaccinated herds. Of 113 UV herds, 39 recorded at least one seropositive weanling over 270 days of age. Significant differences in predictive margins across V and UV RI and NRI herds are outlined in Table 1. This highlights that the main losses associated with the presence of a BVD seropositive weanling relate to poorer fertility and increased calf mortality.

Table 1. Significant associations between SPOT testing and production parameters (RI vs. NRI herds)

Parameter Contrast examined	**Contrast of margins**	***P* value**
Fertility parameters		
Cows not calved (%)		
UV RI *vs.* UV NRI	2.08 %	0.027
Calves/cow/year		
V RI *vs.* UV NRI	-0.03	0.034
UV RI *vs.* UV NRI	-0.03	0.035
V NRI *vs.* UV RI	0.03	0.058
Calving interval 2009 (days)		
UV RI *vs.* UV NRI	6.24 days	0.052
V RI *vs.* UV NRI	6.63 days	0.047
Recycled cows (%)		
V RI *vs.* UV NRI	2.93 %	0.042
UV RI *vs.* UV NRI	3.53 %	0.011
V RI *vs.* V NRI	3.53 %	0.011
Calving to conception (2008)		
V RI *vs.* UV RI	-1.21 days	0.051
V NRI *vs.* UV RI	-6.18 days	0.002
V RI *vs.* UV NRI	3.76 days	0.059
UV RI vs. UV NRI	4.97 days	0.10
Mortality parameters		
Calf mortality as % of		
Calves born in 2009	1.04 %	0.004

It is interesting to note that losses are similar across infected herds regardless of vaccination status when compared with unvaccinated herds not containing seropositive weanlings. An exception to this is calving to conception interval in 2008, where vaccination would seem to reduce the impact of viral circulation. Examination of the preceeding year is useful as virus circulation at this time can result in production of PI individuals which subsequently result in positive SPOT tests. These results highlight the necesscity of preventing virus circulation on farm and the importance of the removal of persistently infected animals from herds. A detailed economic analysis incorporating the results of this study will be reqiured to calculate the total losses accrued in dairy herds due to BVDv circulation.

Conclusion

A number of important associations have been documented which highlight on-farm production losses that can result from recent BVDV circulation.

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RMIS Project Number 5900

Effect of feeding different volumes of colostrum on serum IgG concentration of dairy calves

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Introduction

Transfer of sufficient immunoglobulin G (IgG) to the new born calf via colostrum is vital to provide adequate immunological protection and resistance to disease (McGuirk and Collins, 2004). Adequate transfer of immunity has occurred if calf serum IgG is ≥10 g/l at 24 hours of age (Weaver *et al.,* 2000). However, two-thirds of tests carried out in Irish Regional Veterinary Laboratories indicated inadequate transfer of passive immunity (All-island Animal Disease Surveillance Report, 2011). Inadequate colostrum feeding practices may be an important contributing factor to the mortality rate of dairy calves in Ireland (6.5% calves die in the first 12 months of life, excluding stillbirths: AIM Statistics Report, 2012). Previous colostrum feeding recommendations suggested a certain quantity (i.e., 3l) of colostrum (Chigerwe *et al.,* 2008) but since there is considerable variation in calf size and breed in Ireland, one recommendation may not be suitable for all. The present study aimed to determine whether there is a particular volume of colostrum, fed as a percentage of calf birth bodyweight (BW) that would ensure optimum transfer of immunity to the calf.

Materials and Methods

The experiment was carried out at the Teagasc Animal & Grassland Research and Innovation Centre Research Farm, Fermoy, Co. Cork, from 27 January to 9 April 2011. Ninety-nine dairy calves were stratified based on breed, gender, and BW at birth and randomly assigned to one of three experimental treatment groups: fed either i) 7% (7C), ii) 8.5% (8.5C) or iii) 10% (10C) of their BW in colostrum within two hours of birth. The colostrum fed was pooled colostrum obtained at the first milking post-calving from the freshly calved cows. Concentration of IgG in the serum of calves was measured at 0, 24, 48, 72 and 642 hours of age by an ELISA method (Bovine IgG ELISA Kit Cat. No. 8010, Alpha Diagnostic International, San Antonio, TX, USA*)*. A fixed effects model in PROC GLM (SAS, 2009) was used to establish whether serum IgG at 0 hr differed between experimental groups prior to feeding of colostrum. The independent variable was colostral treatment of calf. Mixed models in PROC MIXED (SAS, 2009) were used to determine the effect of colostral treatment on serum IgG concentration at different ages. The model included colostral treatment group of calf and the repeated measure of calf age when serum was sampled (24h, 48h, 72h, 642h).

Results and Discussion

Mean IgG concentration of colostrum fed to calves was 111 g/l. The concentration of IgG measured in the serum of calves following administration of colostrum was generally high (mean serum IgG at 24 hours of age was 33.7 g/l across treatments). Concentration of IgG in serum of calves was negligible at 0 hr of age (i.e., 1 g/l), reached a maximum at 24 hours and declined subsequently. Calves fed colostrum at 8.5% of BW had a greater ($P<0.05$) mean serum IgG than calves fed 7% or 10% of BW at 24, 48 and 72 hours of age (Fig. 1). At 642 hours of age, serum IgG of calves fed 8.5% of BW (24.3 g/L) and calves fed 10% of BW (21.7 g/L) did not differ, although the serum IgG of calves fed 8.5% of BW was still greater ($P<0.05$) than that of calves fed 7% of BW (20.8 g/L). There was no difference between calves fed 7% of BW and those fed 10% of BW at any age. Early intake of high quality colostrum is the likely reason for the high serum IgG concentration of calves in the present study. A reduction in the rate of abomasal emptying caused by mechanical distension of the abomasum leading to reduced absorption of IgG may explain the lower serum IgG of calves fed 10% compared to those fed 8.5%.

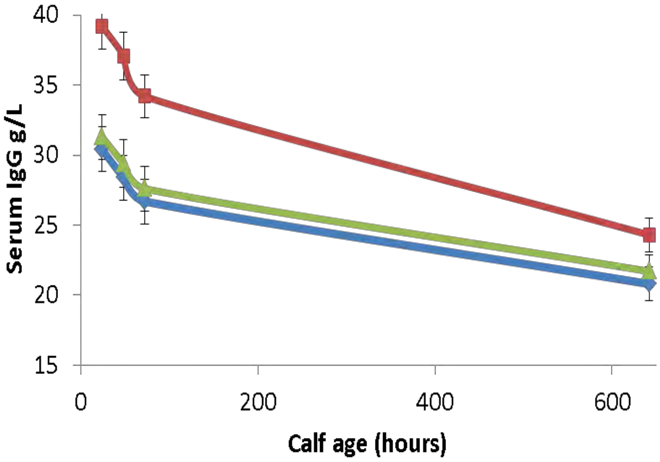

Fig. 1. Mean (± SE) serum IgG concentration (g/l) at 24, 48, 72 and 672 hours of age for calves fed colostrum at 7% of BW (blue), 8.5% of BW (red) and 10% of BW (green) within 2 hours of birth.

Conclusion

Calves fed colostrum at 8.5% of BW within two hours of birth achieved greater concentration of IgG in serum in the first three days of life than calves fed 7% or 10% of birth BW in colostrum.

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RMIS Project Number 6009

A survey of calving and colostrum management practices on Irish dairy farms

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Introduction

Calving management practices such as pen type used (group or individual pens), hygiene, and removal of the calf from the cow after birth, can all influence the risk of disease, thus they are important factors governing calf health (Gulliksen *et al.*, 2009). As calves are born without immunity they completely depend upon absorption of antibodies from colostrum (i.e. passive transfer) to combat disease due to the nutrients and antibodies it contains (Godden, 2008). To avoid failure of passive transfer (FPT), three litres of good quality colostrum must be fed to the average dairy calf within two hours of birth (Chigerwe *et al.*, 2008). Of serum samples submitted to Irish regional veterinary laboratories, 63% displayed FPT (DAFM & AFBI, 2012) indicating that colostrum management may be a significant contributing factor to calf morbidity and mortality on Irish dairy farms. The hypothesis of the present study was that current calving and colostrum management practices on Irish dairy farms are not optimal, thereby compromising calf health.

Materials and Methods

The study population was selected from the Irish Cattle Breeding Federation (ICBF) HerdPlus members (n=320). Selection was random and was based on herd size and geographical location. Questions were predominantly close-ended, and were structured to obtain concise and accurate information, while also ensuring ease-of-use. The survey consisted of four sections: 1) cow management, 2) calving management, 3) colostrum management and 4) calf management (sections 2 & 3 are described in the current abstract). Questions included type of calving pens used and hygiene practices, time of calf removal from cow after birth, colostrum collection, storage, and feeding practices such as volume fed and timing of first feed. Surveys were distributed via mail between 11 July and 15 August 2013. A univariable chi-square analysis was performed using the PROC FREQ statement in SAS, (SAS, v9.3) using two independent variables: (i) 'quota' (Qcat), and (ii) enterprise. Quota categories were divided into three groups, stratified according to the quota of each individual farm. Quota category 1 (Qcat 1) included producers with quota to supply ≤380,000L; Qcat 2 included milk producers with a quota to supply >380,000L and <600,000L); and Qcat 3 included milk producers with a quota to supply ≥600,000L. Enterprise was divided into specialist dairy farms (SD) or dairy farms with an additional enterprise (DO).

Results and Discussion

The survey response rate was 85% (*n*=271). Qcat 3 were more likely to use group calving pens than Qcat 1 (60% vs. 37%; P<0.05) with Qcat1 more likely to use individual pens (47% Qcat1 vs. 24% Qcat3; P<0.05). Cleaning of calving pens was infrequent across the entire study population (42% cleaned pens no more than once a month). This may result in newly born calves being exposed to an increased pathogen load (Gulliksen *et al.*, 2009). In addition, 81% of respondents did not remove calves from the calving pen within two hours of birth which can increase calf morbidity (Gulliksen *et al.*, 2009). In terms of colostrum collection, Qcat 3 (43%) were more likely to collect colostrum at the first herd milking post-calving rather than Qcat 1 (32%) and 2 (33%), the majority of which collected colostrum within two hours of calving (P<0.05). A similar finding was found on SD farms (43% collected colostrum at first milking) compared to DO farms (26% collected colostrum at first milking; P<0.01). This is sub-optimal in terms of calf health as increased time between calving and colostrum collection leads to a decrease in colostrum quality i.e. lower immunoglobulin content (Godden, 2008). A higher percentage of Qcat 1 allowed calves to consume colostrum from their own dam (79%) compared to Qcat 2 (56%) and 3 (44%), and also allowed calves suckle their dam (48% Qcat 1 vs. 40% Qcat 2 and 32% Qcat 3). Consequently calves received colostrum earlier in Qcat 1 (45% within 1 hour) compared to Qcat 3 (35% within 1 hour; P<0.05). Of farms not feeding calves colostrum from their own dam, a larger number of Qcat 3 used a pooled colostrum (first milking) supply for the calf's first feed (32%) compared to both Qcat 1 and 2 (13% and 25%, respectively), which can lead to a lowering of colostrum quality due to the potential dilution effect of higher quality colostrum when mixed with lower quality colostrum (Godden, 2008). Of those that reported the volume of the first feed, 51% of Qcat 3, 40% of Qcat 2, and 37% of Qcat 1 offered 2 to 3 litres. This is below the recommended volume suggested by Chigerwe *et al.* (2008). As an alternative to fresh colostrum, transition milk was used by 15% of all respondents for the first feed. This milk does not contain sufficient immunoglobulins to ensure adequate passive transfer in the neonatal calf (Godden, 2008). The most common method of colostrum storage among the entire study population was freezing (46%). This was most frequently used for long term storage (44% for 1 to 6 months). Room temperature storage alone was used by 15% of respondents and the majority of these farms stored it under these conditions for ≥48 hours (67%), which could result in undesirable proliferation of bacteria (Cummins *et al*., 2014).

Conclusion

This study indicates that calving and colostrum management practices on many Irish farms are suboptimal.

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RMIS Project Number 6009

Effect of storage temperature on the bacterial growth and pH of dairy cow colostrum

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Introduction

On Irish dairy farms colostrum is frequently stored at ambient temperature in calf houses, rather than being refrigerated. This can increase proliferation of bacteria and result in a reduction in the pH of colostrum (Stewart *et al*., 2005). A higher bacterial load in the neonatal calf gut has reportedly been related to lower rates of passive transfer (James *et al.,* 1981). A low pH (<4.7) has also previously been shown to reduce passive transfer (Foley *et al*., 1978). There have been limited investigations into the area of bovine colostrum storage and previous work examined colostrum stored at high temperatures (23°C; Stewart *et al*., 2005). However, ambient air temperature in Ireland during the spring rarely exceeds 13°C (Walsh, 2012). The objective of this study was to investigate the effect of storage at differing temperatures on changes in bacterial growth and pH in colostrum from Holstein-Friesian cows in Ireland.

Materials and Methods

Between 5 and 12 March 2013, colostrum from six Holstein-Friesian cows (≥3rd lactation) was collected to investigate three storage temperatures: 4°C (T1), 13°C (T2) and 20°C (T3) in separate temperature-controlled units. All cows were milked within nine hours of calving. Immediately after collection, samples were weighed and separated into 100ml aliquots, all of which were replicated (each aliquot in duplicate). Aliquots were collected and frozen at 0, 6, 12, 24, 36, 48, 60 and 72 hours of storage. Subsequently, aliquots were defrosted at 4°C to obtain total bacterial count (TBC) using serial dilution. Dilution rates varied according to length and temperature of storage, ranging from 1:10,000 (lowest expected count) to 1:10,000,000 (highest expected count). Diluted 1ml samples were incubated on 3M Petrifilm aerobic count plates at 32°C for 48 hours and total counts were recorded using a 3M Petrifilm Plate Reader. Duplicate TBC results were prepared and an average of the two was calculated. Simultaneously, samples were measured for pH status using an

OHM Delta 2105.2 datalogger (www.lennox.ie). Calibration was carried out before each test period and the probe was cleaned weekly using the product guidelines. An average of two readings was obtained for each aliquot. Data was tested for normality using PROC UNIVARIATE in SAS (v9.3).This data was right-skewed, thus a log transformation was performed. Analysis of variance on the transformed data was carried out using a mixed model (PROC MIXED statement in SAS, v9.3). The model included treatment, time and the interactions between them.

Results and Discussion

The TBC of samples stored in T3 was greater ($P<0.001$) than both T1 and T2 when stored for ≥12 hours (Figure 1). From 24 hours of storage, though significantly lower than T3, the TBC of T2 was significantly higher than T1 ($P<0.001$). This supports the findings of Stewart *et al.* (2005) while additionally indicating that colostrum stored at the lower temperature of 13°C also experiences significantly higher proliferation of bacteria than refrigerated colostrum. In the current study, pH was also significantly affected by storage temperature (Figure 2), again supporting work previously carried out by Stewart *et al.* (2005) where, in line with high bacterial growth, colostrum also suffered significant pH reductions when stored at higher temperatures. After 24 hours of storage, pH was significantly lower in T3 colostrum compared to T2 and T1 ($P<0.001$) while T2 was significantly lower than T1 when stored for ≥60 hours ($P<0.01$). The low pH (>5.0) observed in this study was however higher than previous research (<5.0; Foley *et al.*, 1978; Stewart *et al.,* 2005). This may be due to variation in storage duration and temperature between the current study and previous studies.

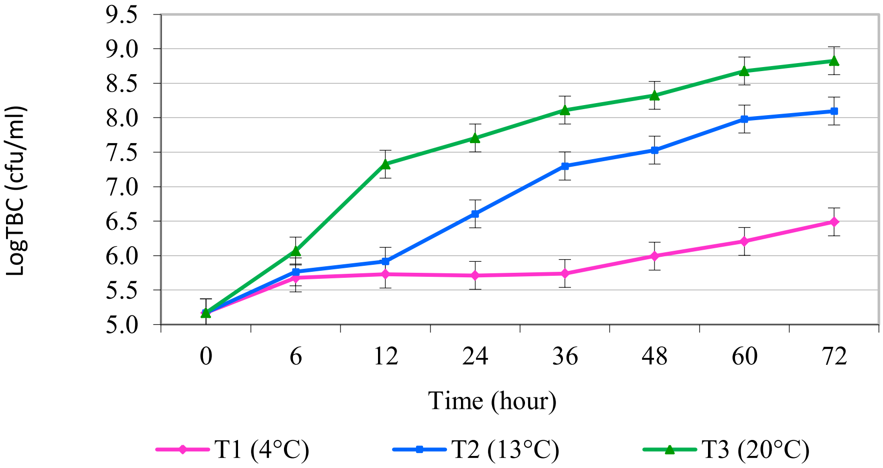

Fig. 1. Comparison of TBC in colostrum stored at 3 separate temperatures with SE ($P<0.001$)

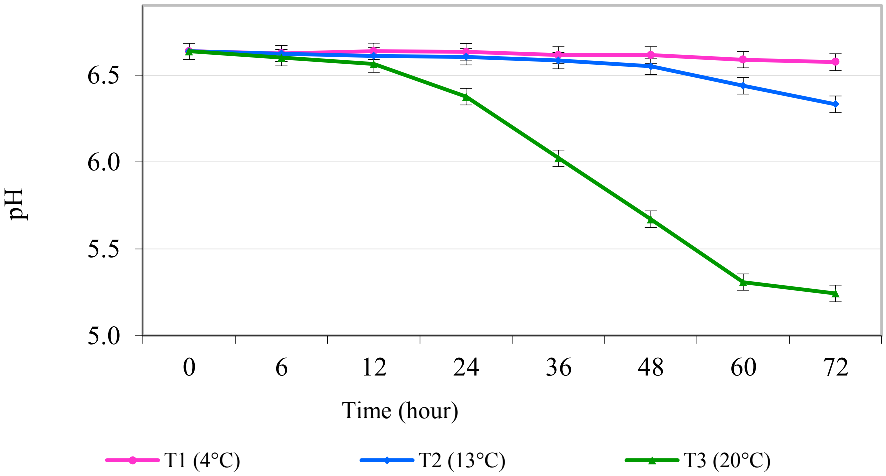

Fig. 2. Comparison of pH in colostrum stored at 3 separate temperatures with SE ($P<0.001$)

Conclusions

This study concludes that storage of colostrum collected from Holstein-Friesian dairy cows in Ireland, at differing temperatures has an effect on both bacterial growth and pH. Storage at temperatures above 13°C increase bacterial proliferation and reduces pH compared to storage at 4°C. This suggests that colostrum should be refrigerated at 4°C to minimise bacterial growth and maintain pH.

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RMIS Project Number 6009

Nematode control in suckler beef calves using targeted selective anthelmintic treatments

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Introduction

Anthelmintics are central to the control of gastrointestinal tract (GIT) nematode infections in cattle. As anthelmintic resistance in cattle has been reported worldwide (Sutherland and Leathwick, 2011), there is a need to explore novel approaches to GIT nematode control so as to reduce the use of anthelmintics and thus delay the selection of resistant nematode alleles. An example of such an approach is the use of targeted selective anthelmintic treatment (TST) where only the individual animal is treated. The objective of this study was to determine if anthelmintic usage could be reduced using a TST approach without affecting calf performance.

Materials and Methods

Sixty-nine Charolais (CH) and nineteen Blonde d'Aquitaine (BA) sired spring-born suckler beef calves with an initial mean age (s.d.) and liveweight (s.d.) of 159 (22.4) days and 221 (42.4) kg, respectively, were used in this study. All calves were vaccinated at pasture against dictyocaulosis (hoose pneumonia) (Bovilis Huskvac, Intervet Ireland Limited) at eight weeks old and all calves received a booster dose four weeks later. Beginning on May 29 2013, calves were weighed, blood and faecal sampled over two days every three weeks until housing (November 5) to determine parasite burden. Faecal egg count (FEC) and plasma pepsinogen concentrations (PP) were determined using the methods of Urquhart *et al.* (1996) and Ross *et al.* (1967) , respectively. Samples collected on July 31 (Time 0) were used as baseline covariates (FEC and PP). On August 9, calves were randomised by age, weight, sex, dam breed and sire breed to one of two treatments; 1), Standard treatment (control) (n = 44) and 2), TST (n = 44). Each treatment group was replicated once. All calves in the control treatment groups were treated subcutaneously with levamisole at a dosage rate of 1.0 ml per 10 kg bodyweight (Levacide Injection 75mg/ml, Norbrook Laboratories Limited) on August 9 and on September 20. Individual calves in the TST groups were only treated at pasture with the same product at the same dosage rate if a pre-determined threshold was reached (PP $\geq$ 2.0 units of tyrosine/L and FEC $\geq$ 200 eggs per gram of faeces (epg)). Data were analysed using repeated measures mixed models ANOVA (PROC MIXED) (SAS (9.3)). Data are presented as LSmeans ± s.e.m. Calf was the experimental unit. The model included fixed effects of treatment, sampling time, gender, dam breed and sire breed. Calf was included as a random effect.

Results and Discussion

No calves in the TST groups were treated for GIT nematodes during the study period as they did not reach pre-determined treatments thresholds. Calf daily live weight gain for control and TST groups was 0.90 (±0.04) and 0.92 (±0.03) kg, respectively (P=0.68). There was a treatment × time interaction for FEC (P<0.0001) whereby FEC increased from baseline in control calves at time 2 (P<0.05) and time 4 (P<0.05) whereas FEC increased (P<0.05) in TST calves at time 2 and 3 (Table 1). FEC was greater (P< 0.0002) in males (138 (9.7)) than females (96 (10.6)). There was no treatment × time interaction (P>0.05) but there was an effect of time for PP concentrations (P<0.0001) (Table 1). Clinical signs of dictyocaulosis were not evident in calves during the study.

Table 1. FEC and PP concentrations in control and TST suckler beef calves

		Date				*P*-values		
	Treatment (TRT)	21-22 Aug (Time 1).	12-13 Sept (Time 2).	2-3 Oct. (Time 3)	24 Oct. (Time 4)	TRT	Time	TRT × Time
FEC (epg)	Control	$11^{a,x}$ (11.1)	$99^{b,x}$ (30.0)	$20^{a,x}$ (21.2)	$79^{b,x}$ (25.5)	P<0.0001	P<0.0001	P<0.0001
	TST	$78^{a,y}$ (10.5)	$252^{b,x}$ (28.3)	$245^{b,y}$ (20.2)	$149^{a,x}$ (24.0)			
PP (U/L)	Control	$0.2^{a,x}$ (0.04)	$0.7^{b,x}$ (0.04)	$0.5^{b,x}$ (0.05)	$0.6^{b,x}$ (0.06)	NS	P<0.0001	NS
	TST	$0.3^{a,x}$ (0.03)	$0.6^{b,x}$ (0.04)	$0.6^{b,x}$ (0.05)	$0.5^{b,x}$ (0.06)			

Values are expressed as Lsmeans (± s.e.m.). ^{a,b,} means within row not having a common superscript differ (P<0.05) from Time 1. NS; not significant. ^{x,y,} means within columns and within measured parameter not having a common superscript differ (P< 0.05)

Conclusions

GIT nematode infections in suckler beef calves at pasture can potentially be controlled with fewer anthelmintic treatments without a significant effect on performance if calves have been vaccinated to prevent dictyocaulosis from occurring.

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RMIS Project Number 6134

A survey of Irish farming practices with emphasis on Johne's disease transmission risk areas

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Introduction

Johne's disease (JD) is caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP) (Manning and Collins, 2001) Concern has been raised regarding the production losses associated with MAP infection on farm and also a potential link between JD and Crohn's disease in humans has been postulated (Manning and Collins, 2001). To minimise potential economic losses and underpin the quality of Irish dairy produce, therefore, Ireland is currently embarking on a pilot programme for the control of JD. Animal Health Ireland's (AHI) pilot programme employs an on-farm risk assessment and management plan (RAMP) encompassing investigation of calving, youngstock management, and biosecurity. Periparturient cow-calf management and exposure to faeces of infected animals constitute major risk factors for JD (Manning and Collins, 2001). The purpose of this survey was to provide baseline data prior to RAMP implementation to inform future evaluation of the success of the programme.

Material and Methods

A survey questionnaire was formulated which focused on MAP transmission risks. This 17-question survey was sent to 312 randomly selected dairy farmers from the ICBF database. A total of 306 farmers responded yielding a 98% response rate. Surveymonkey, an on-line tool, was used to manually enter survey responses and download summary datasets. Microsoft excel was used to collate the data and to fix variables for directionality. Statistical analysis was carried out using Stata (Version 12). Survey questions (dependent variables) consisted of three response options i.e. No (N), Sometimes (S), or Yes (Y). For analysis these non-binary variables were dichotomised. Two separate analyses were performed using N versus S plus Y, and, N plus S versus Y. Four independent variables were examined. These included region (dairy dense, not dairy dense), herd size (small: 31-65, medium: 66-99, large: >99 cows), calving season (Spring-calving: ≥85% of herd calved January to March, not Spring-calving), and enterprise (dairy livestock only, mixed livestock). Pearson's chi-squared analysis was performed to identify univariable associations between independent and dependent variables. Independent variables recording $P \leq 0.15$ were included in a multivariable logistic regression analysis using a manual backwards elimination with a forward step. Variables were considered significant at the 5% level.

Results and Discussion

The space designated as the calving area (CA), irrespective of design, was used frequently for more than one calving at any time by over 97% of those surveyed. Over 42% overcrowded the maternity pen, with greater than five cows in the CA at any one time. Larger herds were more likely to overcrowd the CA (Table 1). Approximately 34% of those surveyed stated that they never clean the CA between calving's. Large herds and Spring-calving herds were almost half as likely to clean the CA at least sometimes, than smaller or non-Spring-calving herds, respectively. Almost 75% of those surveyed fed replacement heifer calves pooled colostrum, large herds 3.55 times more likely to do so. Milk from sick or mastitic cows was used to feed 40% of replacement heifer calves, with larger herds in the regions of Ireland densely populated with dairy farms, more likely to do so.

Table 1. Significant associations between independent and dependant variables

Dependent Variable *(Y+S vs. N)* Independent Variable	OR	*P*
Crowded CA		
>99 *vs*. 31-65 cows	3.78	0.001
Clean pen between calving's		
>99 *vs*. 31-65 cows	0.47	0.022
Non-Spring *vs*. Spring	2.41	0.046
Calves fed pooled colostrum		
>99 cows *vs*. 31-65 cows	3.55	0.001

OR: Odds ratio, *P: P* value

Larger herds, presumably with the aim of reducing workload, and improving resource efficiency (housing, colostrum, waste milk), are increasing their risk of JD transmission by employing more risky management practices. Similar reasoning most likely underpins the decreased likelihood of Spring-calving herds to clean the CA, as compact calving may overload housing facilities during the busy calving period. The proportions of farmers applying additional JD-risk associated management practices are included in Figure1.

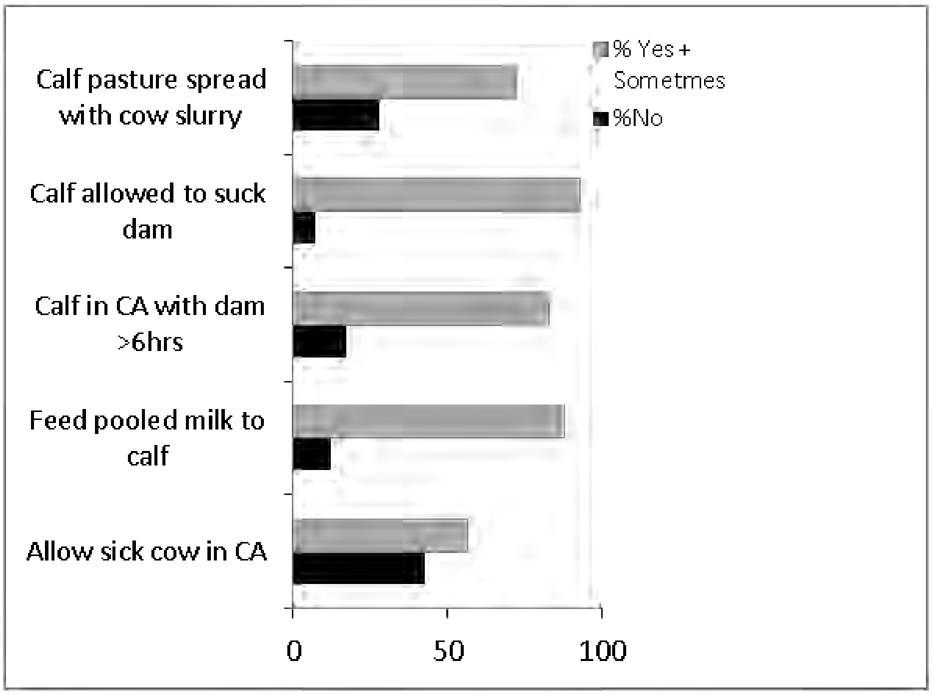

Fig. 1. Proportion (%) of study farmers employing JD-relevant management practices.

Conclusion

Many management practices negatively associated with risk of MAP transmission were commonly applied on Irish dairy farms in 2009. Improved management practices will be necessary to limit JD transmission

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RMIS Project Number 6325

Preliminary results examining the impact of the single intradermal comparative test for bovine tuberculosis on Johne's disease ELISA diagnostics

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Introduction

In 1962, Ireland established an eradication programme for bovine tuberculosis (bTB) due to: public health risks; trading requirements; and production losses associated with *Mycobacterium bovis.* The standard ante mortem test used in Ireland for bTB is the single intradermal cervical comparative tuberculin test (SICCT) which involves parenteral administration of avian and bovine purified protein derivative (PPD). Approximately 9 million SICCTs are performed in Ireland on an annual basis with all herds tested once annually as a statutory requirement. Herds contiguous to, or epidemiologically linked to, infected herds undergo additional testing (Good, 2006). Another pathogenic member of the genus Mycobacterium is *Mycobacterium avium* subspecies *paratuberculosis* (MAP) which causes chronic granulomatous enteritis of ruminants known as Johne's disease (JD). Currently the gold standard test for MAP diagnosis is faecal culture. Due to its low sensitivity and MAP's slow growth in culture, ELISA of individual milk and blood samples is often used as a screening assay to determine MAP herd status. Sensitivity (Se) and specificity (Sp) of ELISA results are highly variable, with the potential for both false positives and false negatives hindering accurate MAP diagnosis (Nielson and Toft, 2008). Additionally MAP ELISA Se and Sp can be impacted by SICCT (Varges et al., 2009). The aim of this study was to examine the impact of SICCT on the prevalence of ELISA positive results in an Irish dairy herd.

Materials and methods

This study was conducted on a 140-cow spring calving dairy herd consisting of 54% Holstein-Friesian and 46% Jersey cross cows. Blood and milk samples were collected between 6 and 13 days prior to administration of the routine SICCT annual herd test which was conducted by the farm's private veterinary practitioner. Samples were collected at varying time points post-SICCT i.e. milk samples collected day 6 post SICCT, blood samples collected day 14 post SICCT. Subsequently, matched bi-monthly blood and milk samples were collected for a period of four months and monthly samples collected for a further 5 months. Samples from all cows were tested using ID Screen Paratuberculosis Indirect Screening Test (ID Vet). Faecal samples were collected on a weekly basis from consistently ELISA positive cows from 90 days post-SICCT for PCR and faecal culture analysis (CIT). Data was collated in Excel (MS office 2010) and statistical analysis performed using SAS 9.3. A repeated measures linear mixed model (PROC MIXED) was applied to highlight statistical differences in within-herd prevalence of positive cows pre- and post-SICCT.

Results and Discussion

Prior to the SICCT, 6% of the herd tested positive on milk ELISA, with 8% of blood samples testing positive. Following administration of PPD, a significant increase in the prevalence of ELISA positives recorded, 38% of the herd yielding positive results on both blood and milk samples ($P<0.02$). Statistical analysis of pre- and post-SICCT MAP ELISA readings highlighted a significant difference ($P<0.03$) in milk samples until day 43 post-SICCT test ($P=0.29$) and in blood samples until day 71 ($P=0.79$). If the 'new' positives detected post-SICCT are deemed false positives due to generation of cross-reacting antibodies by administration of PPD, milk would appear a more suitable sample for JD ELISA testing within two months of SICCT. Analysis of blood samples, however, although maintaining a lengthier non-specific response post-SICCT, did yield a higher rate of MAP antibody positive individuals over the duration of the trial. This difference in prevalence between blood and milk positives only reached statistical significance, however, until day 70 post-SICCT. Whether the increased prevalence of blood positives relates to increased assay sensitivity or decreased specificity is unknown and highlights the necessity for further investigation in this area.

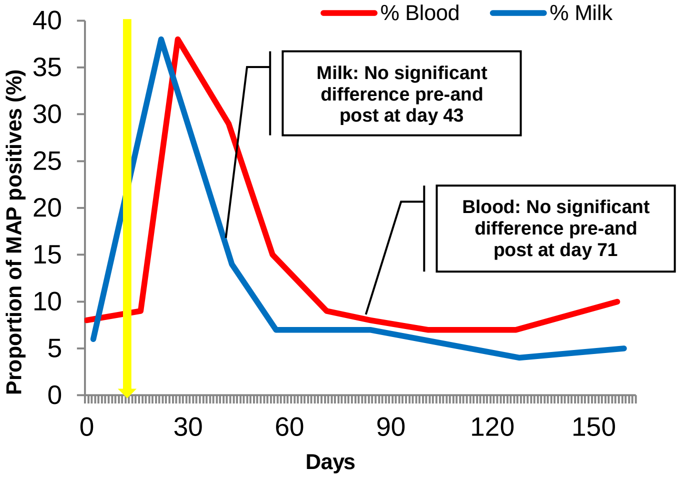

Fig 1. Prevalence of ELISA positives over time pre-and post-SICCT using blood and milk samples.

It should be noted that although this study has highlighted that administration of the SICCT results in a greater rate of MAP ELISA positives, it relates to a single dairy farm and a single ELISA kit. This research is continuing in order to extend the period of investigation into a second year, add further study herds to the investigation, and use additional commercially available ELISA kits. Finally, no faecal culture positives were detected over the 9 months of this study, although six cows did record positive PCR results, each of which recorded multiple positive ELISA readings outside the period of SICCT influence.

Conclusions

Based on the results of this study, testing of herds for JD in the 80-days post SICCT will result in an increased prevalence of JD ELISA positives.

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RMIS Project Number 6325

Direct water use of Irish dairy farms

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Introduction

70% of global fresh water use is attributed to the agricultural sector. Quantifying the volumes of water used in the production of agricultural products is an important metric of the sustainability of food production. From an Irish perspective the main concerns are the cost of supplying water on farms, microbial or other contaminants of water and the negative impact of poor water management on the environment. A water-footprint is a quantitative indicator of freshwater use referring to the total volume of water (both direct and indirect) consumed over the lifecycle of a product as defined by the Water Footprint (Hoekstra *et al.*, 2011). In the case of milk production, indirect water use includes evapotranspiration of growing grass and crops and water used in producing energy, fertilizers and concentrates. Direct water use is the water used on site to facilitate the production process such as drinking water for livestock, washing the milking machine, bulk tank and milking parlour and milk pre-cooling. The objective of this study was to quantify the direct water use of milk production from cradle-to-farm-gate from 25 farms in Ireland as a first step to completing a water footprint of milk production.

Material and Methods

Water meters were installed on 25 Irish commercial dairy farms in 2012. Farms were selected from a database of advisory clients within Teagasc. Selection criteria included availability of farm data and an ability and willingness of the farmer to collect and maintain accurate data. Data were collected from May 2012 to April 2013. Up to 8 water meters were installed on each farm to record total direct water use including water used in the milking parlour and water consumed by livestock. Domestic water use was measured where necessary and subtracted from total water supply to give water supply to farm only. Water meter data (m^3) were recorded on a monthly basis. The water meter data were categorised from the supply into parlour and other uses. Parlour includes the water heater, plate cooler and wash-down readings. 'Other' consists of livestock drinking water and miscellaneous water use on the farm. Milk production data was sourced from the Irish Cattle Breeding Federation (ICBF) records.

Results and Discussion

Average herd size was 104 dairy cows, which ranged from 45 to 194. Herd size was calculated as the average number of cows milked from June to October, which represents the average number of cows milked over the peak milk production period. Average milk production per farm was 519,324 litres (range 275,409 to 875,267L). Higher than national average milk production (316,000L) and herd size (66) is indicative of future industrial farm sizes, a result of farm expansion in preparation for quota abolition in 2015. The average volume of water used for the production of milk per farm was 3,121,242 L, which ranged from 1,115,000L – 7,041,310L. The average total volume of water consumed per litre of milk produced was 6.40 L.

Table 1. Direct water use on 25 commercial dairy farms between May 2012 and April 2013.

Process	Total Water Use (L)[a]	Specific Water Use (L/L)[b] (Range)
Supply	3,121,242	6.40 (1.16 – 12.01)
Livestock & miscellaneous[c]	2,090,783	4.38 (1.18 - 9.51)
Parlour	1,030,459	2.02 (0.2 - 4.59)
	Within Parlour[d]	
Plate Cooler	918,469	1.69 (0.0 - 4.36)
Water Heater	91,045	0.17 (0.0 - 0.42)
Wash-down	685,103	1.28 (0.2 - 3.02)

[a] Litre; [b] Litres of Water / Litres of Milk; [c] consumed by livestock and other miscellaneous use; [d] $\sum$ parlour processes $\neq$ parlour, due to the reuse of water within the parlour network.

Consumption by livestock and other miscellaneous use accounted for two thirds of water use on farms (Table 1 The second largest use of water was the plate cooler (1.69 L/L). The recommended optimum ratio of water:milk in the plate cooler from an energy consumption perspective is 2:1 (Upton *et al.*, 2011). Finding efficient recycling strategies for this plate cooler water will be key to reducing the direct water footprint of dairy farms while maintaining energy efficiency. Our result of 6.40 L/L is similar to the direct water use figure of 5.40 L/L in the study of De Beor *et al.* (2013) which examined water use on a single farm. This figure was not directly measured on-farm and was calculated from assumptions regarding the water requirements for livestock drinking and cleaning services on a Dutch dairy farm.

Conclusions

The direct water use of milk production from our sample farms was quantified as 6.40 litres of water per litre of milk. The results of this study can be used as a benchmark of sustainability for milk production in Ireland.

Acknowledgements

The authors acknowledge the support of the Carbery Greener Dairy Farms project.

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RMIS Project number 6190

A comparison of different milking frequencies in an automated milking system integrated with grazing

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Introduction

In 2001 automatic milking (AM) technology was incorporated with a commercial pasture-based system (Greenall *et al*., 2004). A study by Garcia and Fulkerson (2005) revealed a reduced milking frequency and milk yield and increased milking interval with AM in a pasture system compared to an indoor system. A recent study by Lyons *et al*. (2013) observed that operating a three-way grazing system, where the herd has access to three different grazing sections over 24 hours, increased milking frequency and milk production and reduced milking intervals compared to a two-way grazing system. Three-way grazing therefore allows better flexibility to manage milking intervals and thus increase the utilisation of the AMS unit. The aim of this study was to assess the effects of different milking frequencies on milk production characteristics and cow traffic in a three-way system in late lactation.

Material and methods

The farm-let with the AMS consisted of a 24 ha milking platform. The land area was divided into 3 grazing sections (A, B and C) of 8 ha each and these sections were further divided into 1 ha paddocks. Cows moved voluntarily between the grazing sections A, B and C. Cows had access to new pasture in A from 12:30am, B from 09:30am and C from 16:30pm. The dairy featured one Fullwood Merlin 225 AMS unit. There were 70 primiparous and multiparous cows of various breeds on the system. Cows were randomised into two groups of 35 cows based on lactation, breed, the average milk yield and milking frequency from the previous 21 days milking results and days in lactation. Settings on the AMS were manipulated to allow one group of cows to milk 2 times per day (Group 1) and the other group to milk 3 times per day (Group 2). There was an adjustment period of 10 days (August 21st to 31st 2013) prior to the data collection period (September 1st to 20th 2013). During the trial period 11kg DM grass, 4kg concentrate and 5kg DM silage were fed per cow per day. A non-parametric statistical model (Mann-Whitney test) was used to determine significance between groups using Graphpad Prism software.

Results and discussion

The milk quality for the herd was characterised by an average fat percentage of 5.12% (range: 4.81 – 5.44%), protein of 4.14% (range: 4.02 – 4.27%), lactose of 4.51% (range: 4.41 – 4.56%) and somatic cell count (SCC) of 130×10^3 (range: $85 - 199 \times 10^3$). The trial targeted a milking frequency of 2 and 3 times a day. However as the system relies on cows voluntarily presenting themselves for milking without being fetched from the paddock, a milking frequency (MF) of 1.4 and 1.9 was achieved. Although these milking frequencies were significantly different between the groups the milk yield (MY) per day was not significantly different between groups (Table 1).

Both groups were allocated the same amount of concentrate at the AMS (FA), cows with the higher milking frequency consumed significantly higher amounts of feed (AFI) (0.4 kg/day). Cow traffic analysis revealed that cows voluntarily returned (R) to the AMS yard the same number of times regardless of milking frequency. The return time (RT), from when a cow left the AMS yard until return, and the wait time (WT) in the milking yard were not different between groups. Although the milking interval (MI) was significantly longer per visit for cows with the lower milking frequency (2hours 37min), milk yield and cow traffic performance indicators were unchanged (Table 1).

Table 1: Average milking frequency (MF), milk yield (MY), feed allowance (FA), actual feed intake (AFI), number of returns (R) per cow per day and the average return time (RT) [hh:mm] wait time (WT) [hh:mm] and milking interval (MI) [hh:mm] per cow per visit for each group.

	Group 1		Group 2		
	Aver-age	**SEM**	**Aver-age**	**SEM**	***P*-value**
MF/Day	1.4	0.03	1.9	0.04	<0.001
MY/Day (kg)	13.4	0.61	13.73	0.76	0.946
FA/Day (kg)	3.33	0	3.33	0	>0.999
AFI/Day (kg)	2.31	0.05	2.71	0.04	<0.001
R/Day	2.8	0.08	3	0.11	0.196
RT/visit	06:07	00:09	05:45	00:10	0.139
WT/visit	01:24	00:10	01:16	00:10	0.613
MI/visit	14:29	00:39	11:52	00:25	<0.001

Conclusions

In the latter end of lactation it is possible to reduce the milking frequency of cows on an automated milking system without compromising milking characteristics of the herd, reducing milk production or affecting voluntary cow traffic performance.

Acknowledgements

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RMIS Project Number 6237

Dairy cow performance within a total-grazing, partial-confinement or total-confinement system

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Introduction

While traditional dairy grazing systems involve ‘24-hour’ (i.e. total) grazing, the adoption of partial or total confinement systems has become increasingly common in Northern Ireland. The reasons for this change are many, and include an inability to consistently meet the higher nutrient requirements, and thus to maximise milk yields, of high-yielding cows offered grazed-grass based diets due to the inconsistent quality of grass throughout the grazing season; grazing platforms that are no longer sufficiently large to meet the grazing requirements of larger herds; fragmented land blocks that make access to grazing difficult; and difficult weather conditions and consequential sward damage and poor grass growth. Although many studies have compared milk production, cow liveweight (LW), and cow body condition score (BCS) data from experiments in which cows were managed in either low concentrate-input grazing systems or high concentrate-input confinement systems (e.g. Vance *et al.*, 2012), few studies have compared cow performance within total-grazing, partial-confinement or total-confinement systems at a common concentrate allocation. Thus, the objectives of the current study were to compare the performance of dairy cows managed on either a total-grazing, partial-confinement, or total-confinement system, where all cows were offered a similar concentrate allocation.

Materials and Methods

Sixty-six Holstein-Friesian dairy cows (42 multiparous, 24 primiparous; mean day-of-lactation at the start of the experiment of 152 (s.d. 72.3) days) were allocated to one of three treatment groups (14 multiparous and 8 primiparous cows per treatment). The treatments comprised three management systems, namely a TG (Total-Grazing: cows grazed for the entire day throughout the experimental period), a PC (Partial-Confinement; cows grazed between morning and afternoon milking, and were confined between afternoon milking and the morning milking of the following day), and a TC (Total-Confinement: cows were confined for the entire day throughout the experimental period) system. The experiment commenced on May 4 and finished on September 30. The TG and PC treatment groups grazed separately, but in adjacent ‘paddocks’, within a ‘flexible’ rotational grazing system in which cows were given access to fresh herbage daily. With each of TG and PC, cows were managed so as to achieve a target residual (i.e. post-grazing) sward height of 4.5 cm following grazing each day. To achieve this, target herbage allowances for TG and PC throughout the experiment averaged 9.5 and 3.6 kg of dry matter (DM)/cow/day, respectively. Across these two treatments, mean neutral detergent fibre (NDF), crude protein (CP), and water soluble carbohydrate concentrations of the herbage offered were 433 (s.d. 29.9), 260 (30.0), and 128 (31.9) g/kg DM, respectively. Cows on the TC treatment were offered grass silage (mean NDF and CP concentrations of 494 (s.d. 29.2) and 161 (20.6) g/kg DM, respectively; mean daily silage DM intake for PC and TC treatments were 9.3 (s.d. 1.45) and 12.0 (1.98) kg DM/cow/day, respectively) *ad libitum* (1.10 of the previous day’s intake). All cows were offered 8.0 kg of concentrate (either a ‘grazing’ (for TG) or ‘indoor’ (TC) concentrate, or 4 kg/cow/day of both (PC)) per day in-parlour, split between two equal feeds (morning and afternoon milking). All cows were milked twice daily throughout the experiment, with milk yields being recorded at each milking. Milk samples were taken at two consecutive milkings each week, and analysed for fat and protein concentrations. Cow LW were recorded twice daily using an automated weighbridge. Cows’ BCS were estimated every 14 days according to Edmondson *et al.* (1989). Data were analysed (GenStat) as a single-factorial design using analysis-of-variance. Appropriate pre-experimental co-variates were included in the model when analysing dependant variables.

Results

Despite the grass silage being of generally lower quality than the grazed herbage, management system had no effect ($P>0.05$) on total or daily milk yield, milk protein concentration, or final cow BCS. Cows in PC and TC produced milk with a greater ($P<0.05$) fat concentration than those in TG. Cows in the TC system had greater ($P<0.05$) daily fat-plus-protein yields than those in TG. Final cow LW were greater ($P<0.05$) for cows in the TC or PC systems than for those in TG (Table 1).

Table 1. Effect of management system on cow performance throughout the grazing season

	TG	PC	TC	SEM	Sig.
Total milk (kg/cow: 149 d)	3399	3310	3395	71.8	NS
Milk (kg/cow/d)	26.8	26.4	27.1	0.60	NS
Milk fat + protein (kg/cow/d)	1.94^{b}	2.06^{ab}	2.11^{a}	0.041	*
Milk fat (g/kg)	38.0^{b}	43.2^{a}	42.7^{a}	0.81	***
Milk protein (g/kg)	34.7	34.4	34.9	0.42	NS
Final cow LW (kg)	585^{b}	621^{a}	625^{a}	9.6	**
Final cow BCS	2.4	2.6	2.6	0.06	NS

SEM, standard error of the mean. Sig., significance. NS, not significant. *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$.

Conclusions

Management system had no effect on milk yield, milk protein concentration, or final BCS for cows offered similar concentrate allocations. However, cows managed in the TG system produced milk with a lower fat concentration and had lower milk fat plus protein yields, as well as lower final LW, than cows managed in TC.

Acknowledgements

Department of Agricultural and Rural Development

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RMIS Project Number 6337

Life cycle assessment of energy use on Irish dairy farms

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Introduction

Energy consumption in milk production is important because it impacts directly on profitability and environmental footprint. In order to reduce energy consumption we must first understand how, and where it is consumed. The aim of this study was to measure baseline data on the total energy inputs of Irish dairy farms.

Materials and Methods

To calculate these energy inputs data on farm production, direct farm energy inputs (i.e., fuel and electricity) and indirect inputs (i.e. fertilizers, purchased feed and chemicals) were collected from 22 commercial dairy farms for 12 months (2011). The energy use of each input was calculated using energy coefficients. The energy coefficients for chemical fertilizers, herbicides, and ingredients of purchased concentrates were based on the international Life Cycle Assessment (LCA) database Ecoinvent (2010), and used to convert all inputs to the common unit of energy, the mega-joule (MJ). Mean herd size was 118 cows (range 47-290) and mean stocking rate was 2.27 LU/ha (range 1.68-3.45). The farms in this study represent the larger than average modern dairy farm, with a higher stocking density per ha. However, milk output and hence herd size will increase in future if farmers respond to the potential for expansion in milk production identified in the *Food Harvest 2020* report. Results of this study and hence the conclusions drawn are relevant for larger and more intensive dairy farms.

Life cycle assessment and data collection

In order to identify hot spots of energy use it was necessary to perform a LCA of energy use according to ISO (2006). Results were quantified in MJ per kg of milk solids (MS). Over the calendar year of 2011 all data necessary to compile the life cycle assessment were recorded using a combination of manual recording and wireless data transfer. Each farmer completed monthly questionnaires. Data collected included; quantity and type of fertilizer used, quantity of diesel consumed, area of land worked by contractors, concentrate feed used, forage/manure/slurry imported or exported from the farm, quantity and type of farm chemicals used and a stock take of all animals. In addition to these data, milk production data were obtained from the milk processors. Electricity consumption was recorded using a wireless monitoring system. Domestic use was excluded from the measurements. The system boundary of the LCA was defined as being from cradle-to-farm-gate, which implies that energy use is quantified for all processes involved up to the moment that milk leaves the farm gate, including production and transport of concentrates, roughage, seeds, herbicides and chemical fertilizer. Such a cradle-to-farm gate LCA, therefore, resembles quantification of the direct (i.e. energy use on-farm) and indirect energy use (i.e. energy needed to produce farm inputs) of milk production (De Boer 2003). Besides milk, the production system also yields meat from culled cows and calves. In such a multiple-output situation, the energy use of the system has to be allocated to these various outputs. Economic allocation was used, implying that the energy use was allocated to the various outputs based on their relative economic value (i.e. 88.3 % to milk).

Results

Total energy use averaged 31.73 MJ/kg MS, ranging from 15.28 to 49.00 with a SD of 7.72 MJ/kg MS, (Table 1). About 57% of this energy use was accounted for by the application of chemical fertilizers. Other energy consuming processes included production and transport of purchased concentrate feed (21%), electricity (12%) and liquid fuels such as diesel, petrol and kerosene (8%). Other items such as seeds and herbicides represented 2% of total energy use.

Table 1. Total energy consumption values (mean with SD in parentheses, min and max) per energy input category, expressed in MJ/kg of milk solids (MS).

	Energy Consumption (MJ/kg MS)		
Category	Min	Mean (SD)	Max
Fertilizer	10.54	17.96 (6.25)	30.71
Concentrates	2.17	6.55 (2.57)	11.87
Electricity	2.25	3.91 (1.06)	6.75
Fuel	0.04	2.54 (1.32)	6.18
Other	0.00	0.77 (1.11)	5.08
Total	15.28	31.73 (7.72)	49.00

Conclusion

On average, a total of 31.73 MJ was required to produce one kg of milk solids, of which 20% was direct and 80% was indirect energy use. Electricity accounted for 60% of the direct energy use and appeared centred around milk harvesting operations.

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Acknowledgements

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RMIS Project Number 6495

ANIMAL NUTRITION AND PRODUCT QUALITY

Effect of concentrate feeding level and allocation pattern on milk production of autumn calving cows

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Introduction

Winter milk production in Ireland is characterised by feeding early to mid-lactation cows indoors with conserved forages and concentrate. When concentrate is offered at higher rates, with *ad libitum* forage, increased milk yield is achieved (Ferris *et al.,* 2002). Offering concentrate based on individual cow milk production has been shown to increase milk solids output compared to flat rate feeding (García *et al.,* 2007). The objective of this study was to investigate the effects of offering concentrate based on a cow's early lactation milk yield, or at a flat rate regardless of milk yield, at both a high and low level of concentrate supplementation.

Materials and Methods

The 11-week study began on 22 October 2012. Forty eight (12 primiparous and 36 multiparous) autumn-calving Holstein-Friesian cows were blocked according to parity (2.3 s.d. 1.18) calving date (13 September s.d. 13 d); milk yield (22.7 s.d. 3.37 kg), fat (44.8 s.d. 6.23 g/kg), protein (33.6 s.d. 2.60 g/kg) lactose concentrations, (45.5 s.d. 1.66 g/kg), body condition score (BCS; 2.94 s.d. 0.197) and body weight (BW; 518 s.d. 62.0 kg) during the third and fourth week of lactation. The study used a randomised block design with a 2 × 2 factorial arrangement of treatments. Cows were offered one of two concentrate levels, high (7.0 kg DM (Hi)) or low (4.0 kg DM (Lo)), at a flat rate (F) or feed to yield (Y). Within each treatment cows were sub-grouped as high, medium and low milk yield based on the milk yields during weeks three and four of lactation. On the HiV treatment cows received 8.7, 7.0 or 5.3 kg DM of concentrate/cow per day in the high, medium and low subgroups respectively. On the LoV treatment cows received 5.7, 4.0 or 2.3 kg DM of concentrate/cow per day in the high, medium and low subgroups respectively. Flat rate treatments were offered 7.0 kg DM (HiF) or 4.0 kg DM (LoF) of concentrate/cow per day. All cows remained on a fixed level of concentrate for the duration of the experiment. The concentrate allocation included a 0.18 crude protein dairy nut, which was offered in the parlour using automatic feed dispensers (Dairymaster Causeway, Co. Kerry, Ireland); soya bean meal and molasses were included in the TMR. Both groups were offered a TMR *ad libitum;* the individual intake of which was recorded using an electronic feed intake measurement system (MealMaster, Griffith Elder, Suffolk, England). The Hi group TMR consisted of (DM basis) maize silage (0.44), grass silage (0.42), soya (0.12) and molasses (0.02). The Lo group TMR consisted of maize silage (0.45), grass silage (0.40), soya (0.14) and molasses (0.02). Milk yield was recorded daily and milk composition was recorded weekly. Data were analysed as repeated measures using the MIXED procedure of SAS, with treatment, time and treatment by time interactions included in the model; block was included as the random variable.

Results and Discussion

There was no concentrate feeding level by allocation pattern interaction for any of the variables measured. Cows on the Hi diet had higher DM intake (DMI) and energy intake than those on the Lo diet (Table 1). The milk yield response of cows on the Hi treatment to increased concentrate above the Lo treatment was +0.6 kg milk per kg of concentrate DM offered. Ferris *et al.* (2002) found a similar response when using similar quality grass silage as the basal feed. The increase in milk solids on the Hi treatment was largely due to the increase in milk yield, as concentrate feeding level had no effect on the concentration of milk fat or protein. Concentrate allocation pattern had no effect on DMI or energy intake and as a result there was no effect of concentrate allocation pattern on milk yield or milk solids yield.

Table 2. Daily intake and milk production of cows offered high and low concentrate at a flat rate or fed to yield

	Feeding Level		Allocation Pattern			Significance	
	High	Low	Flat	F.T.Y	S.E.	Level	Pattern
Total intake (kg DM/cow/d)	19.0	17.9	18.4	18.5	0.23	<0.01	N.S.
Energy intake (UFL/cow/d)	17.4	16.3	16.8	16.7	0.21	<0.01	N.S.
Milk yield (kg/cow/d)	25.3	23.5	24.8	24.1	0.36	<0.001	N.S
Milk fat (g/kg)	43.3	43.5	44.0	42.9	0.57	N.S.	N.S.
Milk protein (g/kg)	33.6	33.6	33.8	33.5	0.36	N.S.	N.S.
Milk solids (kg/cow/d)	1.93	1.85	1.95	1.88	0.037	<0.05	N.S.

High= High concentrate, Low= Low concentrate, Flat=Flat rate, F.T.Y= Feed to yield; S.E. = Standard Error; N.S. not significant; UFL= energy value described in Jarrige (1989)

Conclusion

Allocating concentrate based on the milk production of cows in early lactation gave no significant production benefit over a simple flat rate allocation pattern. There was a significant increase in milk yield when the proportion of concentrate in the diet was increased from 190 g/kg to 420 g/kg DM.

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RMIS Project Number 5798

GRASSLAND RESEARCH PROGRAMME

Grass Breeding Including Establishment & Renovation

Using the grass economic index to quantify the economic performance of perennial ryegrass cultivars

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Introduction

The key traits of importance in an Irish seasonal grass-based production system have been identified as spring, mid-season and autumn dry matter (DM) yield, 1st and 2nd cut silage DM yield, grass quality from April to July inclusive and grass cultivar persistency (McEvoy *et al*., 2011). These authors introduced the concept of applying monetary values to a set of traits that have been identified as the most economically important within grass based production systems in order to determine the total economic merit of a cultivar. The objective of this study was to apply economic values to individual cultivar data to quantify the total economic merit of cultivars when all traits are included.

Material and Methods

In 2010, the Department of Agriculture, Food and the Marine sowed 63 cultivars (Cv) (33 diploids and 30 tetraploids) in their Value for Cultivation and Use trials. Cultivars were sown in experimental plots at 5 locations throughout Ireland: Backweston, Co. Kildare; Raphoe, Co. Donegal; Fermoy, Co. Cork; Athenry, Co. Galway and Kildalton, Co. Kilkenny. The experiment was a randomized complete block design with three replicates of each cultivar at each site. Plots were harvested in 2011 and 2012. A simulated grazing management (defoliations taken every 3 – 4 weeks from mid-March to mid-October) was implemented at the Raphoe, Athenry, Fermoy and Backweston sites. A 2-cut silage management was implemented at the Kildalton site. A total of 310 kg N/ha was applied per year, P, K and S levels were applied to meet growing requirements. Plots were harvested with a Haldrup mower to 4.5 cm. Harvested material was weighed, a 300 g sample was dried at 80ºC in an oven for 16 hours to determine DM content. Dried samples from the Backweston site were analysed for DM digestibility (DMD) using near infra-red spectrometry. Ground score (GS) was visually estimated in December 2011 and 2012 on a scale of 0-9 (0=no perennial ryegrass, 9=100% perennial ryegrass). Seasonal production was defined as spring (herbage harvest prior to Apr. 10), mid-season (herbage harvested from Apr. 11 to Aug. 10) and autumn (herbage harvested from Aug. 11 to year end). Data from the 1st and 2nd silage harvest within the 2-cut silage management were used to determine cultivar silage performance. The difference in GS between the two years was used to determine GS change (GSΔ) and this was used to quantify cultivar persistency. The economic values for each trait were reported by McEvoy *et al*. (2011). To investigate the effect of a change in Cv performance within each trait, base values (BV) were necessary to quantify the economic merit of each Cv for each trait. The DM production BV was calculated using the average DM production level on commercial grassland farms in Ireland (9.1 t DM/ha; Shalloo, 2009). The BV for quality (g/kg DMD) for each month was: April (849.6), May (848.6), June (814.4) and July (810.2), BV for 1st and 2nd cut silage DM yield was 3,785 and 3,692 kg DM/ha, calculated from the mean performance of the 63 cultivars. Economic values were applied to the difference between the BV and individual cultivar performance within each trait. The total economic merit of each cultivar was then calculated. Statistical analyses were conducted using SAS (SAS institute Inc, Cary, NC, USA). Information on the seasonal DM yield was obtained from an analysis of variance on the combined data (4 sites and 2 harvest years) using the model: $Y_{ijk} = \mu$

$+ Y_i + S_j + C_k + P_l + e_{ijkl}$ Where, μ = mean; Y_i = year effect (i= 1 to 2); S_j = site effect (j= 1 to 4); C_k = cultivar effect (k= 1 to 63); P_l = plot effect (l= plot) and e_{ijkl} = residual error term.

Results and Discussion

There was a significant effect of Cv ($P<0.001$) on spring, mid-season and autumn DM yield. Spring DM yield was highest for Cv118 (1875 kg DM/ha) and lowest for Cv215 (1165 kg DM/ha). Mid-season DM yield was highest for Cv225 (7863 kg DM/ha) and lowest for Cv222 (6408 kg DM/ha). Autumn DM yield was highest for Cv108 (2666 kg DM/ha) and lowest for Cv204 (1878 kg DM/ha). The GSΔ ranged from -0.1 to -1.43 from Year 1 to Year 2. The mean DMD (g/kg DM) of the cultivars was: 850±9.6 (April), 849±11.1 (May), 814±11.8 (June) and 810±16.4 (July). Table 1 shows a range of cultivars within the total merit index. Cv111 had the highest total economic merit of €228/ha compared to Cv201 (-€12/ha) which was lowest.

Table 1. Total economic merit and sub-indices value (€ per ha/year) of 10 cultivars

Cultivar[1]	Sub-indices (€ per ha/yr)				€ per ha/yr
	Yield	Quality	Silage	Pers[2]	Total
111 (T)	167	46	15	0	228
108 (D)	212	21	-6	-45	182
129 (T)	172	19	0	-29	162
226 (T)	111	33	0	0	144
130 (T)	145	-23	0	0	123
232 (D)	141	-17	0	-17	107
218 (D)	135	-49	-9	0	77
213 (D)	68	-7	-13	0	49
230 (D)	51	-26	0	0	25
201 (D)	71	-14	-24	-45	-12

[1] ploidy is indicated in parenthesis (T= tetraploid; D=Diploid); [2] Persistency

Conclusions

The use of the grass economic index enables the identification of cultivars which provide the greatest economic contribution to a ruminant grazing system, while the sub-indices demonstrate for which traits a cultivar is over or under performing.

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RMIS Project Number 6196

Genotype × management interactions in perennial ryegrass pastures

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Introduction

Perennial ryegrass (PRG) is the most important grass species in Ireland accounting for 95% of seed sales (Culleton *et al.,* 1992). In Ireland, PRG cultivars are currently evaluated in monoculture swards under a cutting protocol with high levels of nitrogen (N) fertiliser (350 kg N/ha/yr; DAFM Rec List (2010)). However, on farm PRG swards are grazed directly and often sown in a mixture with white clover (WC) under reduced N inputs. As PRG and WC interact in a mixed sward (Camlin, 1981) there is a risk that current evaluation protocols are not capturing sward interactions.

The aim of this experiment is to evaluate PRG cultivar performance when sown with and without WC at two different nitrogen application levels.

Materials and Methods

An experiment was established in June 2012 at the Animal and Grassland Research and Innovation Centre, Moorepark, Co. Cork. The experiment was a randomised block design with a 2 x 2 factorial arrangement of treatments with 5 replicates. Plots were 18 × 3 m. Eight PRG cultivars (4 diploids and 4 tetraploids) were sown as grass only (-C) or grass + WC (+C). Two fertiliser N rates were applied: 100 (low) and 250 (high) kg N/ha. Sowing rates were 37 kg/ha for the tetraploid cultivars and 34 kg/ha for the diploid cultivars while the medium leaf WC, Crusader was included in the (+C) plots at 3 kg/ha. Treatments were high nitrogen sown without clover (HN-C), high nitrogen sown with clover (HN+C), low nitrogen sown without clover (LN-C), and low nitrogen sown with clover (LN+C). Rotation length was adjusted depending on the N application level (HN - 21 days; LN - 30 days). Plots were grazed by dairy cattle to a target post grazing residual of 4 cm. Dry matter yield (DMY) was estimated in each plot by cutting a strip (5 × 1.2 m approx.) with an Etesia mower. Harvested herbage was weighted and a subsample of 100g was used to determine dry matter (DM) content. There were nine grazing rotations on the HN plots and seven grazing rotations on the LN plots from February 25th to November 15th 2013. Seasonal yields composed of spring (Feb-Apr), mid-season (May-July) and autumn (Aug-Nov). Data were analysed using PROC MIXED in SAS (2011) with block, treatment, cultivar and their interactions tested for in the model.

Results and Discussion

There was no interaction between cultivar and treatment, indicating that the relative performance of the eight cultivars tested was the same across treatments. Treatment had a significant effect on DMY (P<0.001; Table 1) with lower annual herbage production recorded from the LN-C management (7306 kg DM/ha) compared to the other three managements (9204 kg DM/ha). While the relative performance of the cultivars tested remained similar the results demonstrated that the absolute DMY values changed between the managements. In comparison to the LN-C management, there was a response of 14 kg DM per additional kg N applied, which is similar to responses recorded by O'Donovan *et al*. (2004) at the same site. Cultivar also had a significant effect (P<0.001) on annual DMY ranging from 9489 kg DM/ha to 7628 kg DM/ha. Diploid cultivars recorded a higher DMY (+1379 kg DM/ha; P<0.001) compared to the tetraploid cultivars (8040 kg DM/ha).

Treatment	HN-C	HN+C	LN-C	LN+C	SE	Cultivar	Management
Total (kg DM/ha)	9417^{a}	9111^{a}	7306^{b}	9085^{a}	237	0.001	0.001
Spring (kg DM/ha)	1301^{a}	1100^{b}	1312^{a}	1258^{a}	57	0.001	0.01
Mid-season (kg DM/ha)	4717^{a}	4701^{a}	3906^{b}	4702^{a}	157	0.001	0.001
Autumn (kg DM/ha)	3398^{a}	3311^{ac}	2088^{b}	3126^{bc}	110	0.001	0.001

HN-C = high nitrogen no clover; HN+C = high nitrogen with clover; LN-C= low nitrogen no clover; LN+C = low nitrogen with clover; $^{a-c}$ Means within a row with different superscripts differ (P <0.01); SE = standard error.

Conclusion

The results from this study suggest that for the PRG cultivars examined differences in DM production performance exist across cultivars but are not significant across contrasting management regimes. The range in DMY between cultivars again highlights the importance of selecting the correct cultivars on farm. While these results are from one year's full production, more solid conclusions can be drawn from further year's results.

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RMIS Project Number 6262

Grass Growth, Sward Dynamics & Utilisation under Grazing

Milk production performance of lactating dairy cows grazing four different perennial ryegrass cultivars

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Introduction

Perennial ryegrass cultivars are selected for commercial use based on DM yield, digestibility and tiller density evaluated under mechanical defoliation. Previous studies showed that cultivars differing in heading date and ploidy had a significant effect on performance of grazing dairy cows (Gowen *et al.,* 2003, Wims *et al.,* 2013). In contrast, Tas *et al.* (2006) found no difference in animal performance when grazing different cultivars. Identification of optimum cultivars is essential to allow selection of appropriate cultivars for use on farm. The objective of this study was to evaluate the milk yield and milk solids of lactating dairy cows when grazing different monocultures of perennial ryegrass cultivars.

Materials and Methods

Two diploid (D) and two tetraploid (T) perennial ryegrass cultivars were sown as monocultures. The cultivars and there heading date were AstonEnergy (T; 30 May), Delphin (T; 31 May), Glenroyal (D; 03 June) and Tyrella (D; 03 June). Four primiparious and eight multiparious cows were assigned to each cultivar on the 15 April and remained grazing a single cultivar until the 15 July when the experiment ended. Cows were blocked based on parity (2.90), days in milk (44.4 d), milk yield (26.8 kg/d), fat (47.4 g/kg), protein (32.0 g/kg) lactose (46.2 g/kg), body weight (480 kg) and body condition score (3.2; based on a scale of 1 to 5, 1=emaciated, 5=extremely fat) prior to the experiment commencing. Cows were allocated an area of pasture to ensure cows achieved a stubble height of 4 cm in 24−36 hrs. They were then offered fresh grass. Pre-grazing herbage mass (>4 cm) was calculated by cutting two strips (1.2 m × 10 m) with a motor Agria (Etesia UK Ltd, Warwick, UK) twice per week from each cultivar. Ten compressed grass heights were recorded before and after harvesting each strip using a rising plate metre with a steel plate (diameter 355 mm, 3.5 kg/m^2; Jenquip, Fielding, New Zealand). All mown herbage was collected and weighed. A 0.1 kg subsample was dried at 90^oC for 16 hours for DM determination. Pre-grazing sward height was measured during the experimental period by measuring 50 heights per treatment. Fifty post-grazing sward heights were also measured directly after grazing. Milking took place at 0700 and 1600h daily. Individual milk yields (kg) were recorded at each milking (Dairymaster, Causeway, Co. Kerry, Ireland). Milk fat, protein and lactose concentration from a consecutive AM and PM milking were taken weekly. Statistical analysis was conducted for all animal variables using Proc MIXED in SAS 9.3, with cultivar, week and a pre−exp. covariate included in the model as fixed effect and cows included as a random effect.

Results and discussions

The same pre-grazing herbage mass, pre-grazing sward height and post-grazing sward heights was achieved for all four cultivars in this experiment (Table 1). This experiment was successful in creating swards of four cultivars that were consistent, minimising the effect of management and allowing unbiased investigation of the effect of cultivar on animal performance. Animal performance is shown in Table 1. Although only tending toward significance (P=0.09) the AstonEnergy sward resulted in higher milk yield than the lowest producing cultivar, Glenroyal (+1.9 kg/cow/d). It is possible that the short duration of this study could have caused the failure of biological difference to indicate statistical significance. There was no difference (P>0.05) in the proportions of milk fat, milk protein or milk solids between the four cultivars. In contrast, Wims *et* *al.* (2013) found that cows grazing the diploid cultivar Abermagic had a significantly lower milk yield and milk solids output when compared to other cultivars.

Table 1. Effect of perennial ryegrass cultivars on milk production, pre- and post-grazing sward height and pre-grazing herbage mass

	AstonEnergy	Delphin	Glenroyal	Tyrella	SED	P-Value
Milk yield (kg/cow/d)	24.3	23.3	22.4	23.1	0.75	0.09
Milk fat (g/kg)	43.2	43.1	46.2	43.9	0.18	ns
Milk protein (g/kg)	33.9	33.3	34.7	33.2	0.06	ns
Milk solids (kg/cow/d)	1.84	1.78	1.79	1.76	0.06	ns
Pre-grazing sward height (cm)	8.8	9.0	9.0	8.6	0.61	ns
Post-grazing sward height (cm)	3.9	4.1	4.1	4.2	0.26	ns
Herbage mass (kg DM/ha)	1230	1231	1332	1226	155	ns

Conclusions

The hypothesis that cultivars could influence animal performance was not supported by the finding in this experiment, but a trend for higher milk yield was observed, especially between AstonEnergy and Glenroyal. Future studies should be conducted for a longer period than the current study to capture the complete effect of the cultivar on the production of the grazing animal across a full grazing season.

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RMIS Project Number 6091

Potential of fertilised grass clover swards to produce adequate herbage to support dairy cow milk production in high stocking rate grass based systems

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Introduction

White clover (WC; *Trifolium repens L.*) can play a role in grass-based milk production systems by reducing the nitrogen (N) fertiliser input and evening out the annual herbage production curve (Frame and Newbould, 1986). Milk production benefits of WC over perennial ryegrass (PRG) swards have been observed, particularly in the second part of the year (July onwards) (Riberio Filho *et al.,* 2003). High N fertiliser application rates can reduce sward WC content since PRG utilises N more efficiently than WC and therefore PRG grows faster than WC in a mixed sward (Ledgard and Steele, 1992.). The objective of this study was to compare herbage and milk production from a PRG only sward receiving 250 kg N/ha and PRG/WC swards receiving either 150 or 250 kg N/ha in an intensive grazing system.

Materials and Methods

A farm systems experiment was established at Teagasc, AGRIC, Moorepark, Fermoy, Co. Cork, in February 2013. Forty two spring calving Holstein-Friesian dairy cows (33 multiparous and 9 premiparous) were blocked based on calving date, pre-experimental milk yield and parity and randomly allocated to one of three treatments (n=14); PRG only sward receiving 250 kg N/ha/yr (Gr250), PRG/WC sward receiving 250 kg N/ha/yr (Cl250), PRG/WC sward receiving 150 kg N/ha/yr (Cl150), from 17 Feb to 17 Nov 2013. As this was a farm systems experiment, fertiliser rates apply across the whole farm. Treatments were stocked at a whole farm stocking rate of 2.74 LU/ha. Fertiliser N application was the same across treatments until May, after which N application to Cl150 was reduced. Herbage was allocated daily to achieve a target post-grazing sward height of 4 cm. Pre-grazing herbage mass (>4 cm; HM) was determined twice weekly using an Etesia mower. Pre- and post-grazing sward height was measured daily using a rising plate meter. Sward WC content was estimated twice weekly as described by Egan *et al.* (2013). Data were analysed using a mixed model in SAS with terms for treatment, time (week or rotation) and the associated interaction. Fixed terms were treatment and week or rotation, and random terms were cow and paddock.

Results and Discussion

There was a treatment-by-week interaction (P<0.01) on daily milk, milk solids (MS) yield and fat content. All treatments were similar until experimental week 12 (May) after which Cl250 had higher milk production compared to the other two treatments until week 16. Milk production was similar from week 16 to week 19 for all treatments. From week 20 (June) to the end of the experiment, milk production was greater on Cl250 than on the other treatments; and from week 24 (July) milk production was higher on Cl150 than GR250 and was similar to Cl250; similar to Riberio Filho *et al*. (2003) and Egan *et al*. (2013). Milk fat content was similar on all treatments at the beginning of the experiment. Cl150 had higher daily milk fat content compared to the other treatments from week 20 (June) to week 35 (October). Treatment had no effect (P>0.05) on daily milk protein content. Pre-grazing HM was not significantly different between treatments (Table 1). There was a treatment-by-week interaction (P<0.01) on sward WC content, which was similar on both WC treatments until July. From July to the end of the experiment WC content was higher on Cl150 than Cl250. The increase in Cl150 WC content coincided with the reduction in N fertiliser application to Cl150. Ledgard and Steele (1992) found a similar effect of reduced N fertiliser application on sward WC content. Rotation had an effect on sward WC content (P<0.01) which increased from 0.05 g/kg in February to a peak of 0.43 and 0.33 g/kg in Cl150 and Cl250, respectively, in August.

Table 1. Effect of fertiliser rate on grass only and grass clover swards on milk production and herbage production.

	Cl150	Cl250	Gr250	S.E.^{1}	TRT	TRT * Week
Milk yield (kg/cow/d)	21.10	21.81	20.56	0.28	<0.001	<0.001
Milk solids (kg/cow/d)	1.70	1.71	1.61	0.02	<0.001	<0.001
Milk fat (g/kg)	4.60	4.41	4.39	0.42	<0.05	<0.01
Milk protein (g/kg)	3.59	3.59	3.58	0.04	NS	NS
Cumulative milk yield (kg/cow)	5908	6107	5757	78.40	<0.001	-
Cumulative milk solids (kg/cow)	476	479	451	5.60	<0.001	-
Pre-grazing herbage mass (kg DM/ha)	1400	1370	1575	90.54	NS	0.07
Clover content (DM %)	24.4	21.2	-	1.95	NS	<0.01

Conclusions

There was a positive effect of WC on milk production regardless of N fertiliser application rate especially in the second half of lactation. Herbage production was not different between treatments. Reducing N fertiliser application in summer increased sward WC content.

Acknowledgements

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S.E.^{1} = Standard Error

RMIS Project Number 6120

The effect of ploidy, clover content and cultivar on herbage dry matter production over the grazing season

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Introduction

The Food Harvest 2020 report sets a target of a 50% increase in milk production by the year 2020 (DAFM, 2011). This increase in milk production will be achieved by maximising the use of grazed grass in seasonal calving grass-based production systems. Recent research has indicated that tetraploid cultivars may have higher growth rates than diploid cultivars (McEvoy *et al.*, 2012). Enriquez-Hidalgo *et al.* (2013) reported that grass clover swards had greater cumulative herbage dry matter (DM) production than grass only swards. Therefore, the objective of this study was to investigate the impact of grass ploidy, cultivar and clover content on cumulative herbage DM production during the grazing season.

Materials and Methods

A farm system experiment to investigate the impact of grass ploidy and clover content on milk production, herbage DM production and herbage nutritive value was established in Clonakilty Agricultural College in 2012. The experimental design was a randomized complete block design with a factorial arrangement of treatments, i.e. two grass ploidies (tetraploid and diploid) x two clover treatments (clover and non-clover), resulting in four treatments (tetraploid only, diploid only, tetraploid + clover and diploid + clover swards). There were 30 cows per treatment group and all treatments were stocked at 2.75 cows/ha and received 250 kg N per hectare. Twenty blocks of four paddocks each were created, thereby creating a separate farmlet of twenty paddocks for each treatment. Four tetraploid (Aston Energy, Kintyre, Twymax and Dunluce) and four diploid (Tyrella, Aberchoice, Drumbo and Glenveagh) cultivars were sown as monocultures with and without clover. Tetraploid cultivars were sown at 37 kg per hectare (ha) (plus 5 kg of clover (2.5 kg Chieftain and 2.5 kg Crusader) in clover paddocks) and diploid cultivars were sown at 30 kg per ha (plus 5 kg of clover (2.5 kg Chieftain and 2.5 kg Crusader) in clover paddocks). However, due to the inclement weather during 2012, only 15 of the 20 blocks were reseeded. Blocks 1 to 10 were reseeded in May and blocks 11 to 15 were reseeded in July and August. The remainder of the experimental area was reseeded in May 2013. Therefore only data from the blocks that were reseeded in 2012 were analysed. Weekly farm walks to measure grass growth were performed and the data entered onto

PastureBase Ireland. Cumulative herbage DM production (kg DM/ha) from grazing, silage and total DM production, for the year, were then calculated within PastureBase, exported to MS-Excel and analysed using PROC MIXED in SAS. Terms included in the model were ploidy, clover content and ploidy*clover content, with block included as a random effect. The performance of the individual cultivars was also analysed with terms for cultivar and clover content, with ploidy nested within cultivar included as a random effect.

Results and Discussion

Ploidy had no effect on grazing, silage or total herbage DM production (10,247, 4,432 and 14,678 kg DM/ha versus 10,252, 4,349 and 14,601 kg DM/ha for tetraploid and diploid treatments respectively). Clover content did not significantly affect grazing DM production (10,148 vs. 10,350 kg DM/ha for non-clover and clover swards, respectively) but had an effect ($P < 0.05$) for silage and total DM production (4,177 and 14,325 kg DM/ha vs. 4604 and 14,954 kg DM/ha for non-clover and clover swards, respectively). There was no interaction between cultivar and clover content. The performance of the individual grass cultivars is presented in Figure 1. Cultivar did not have a significant effect for grazing or silage DM production, however it did have an effect ($P = 0.015$) on total DM production. There was no interaction between cultivar and clover content.

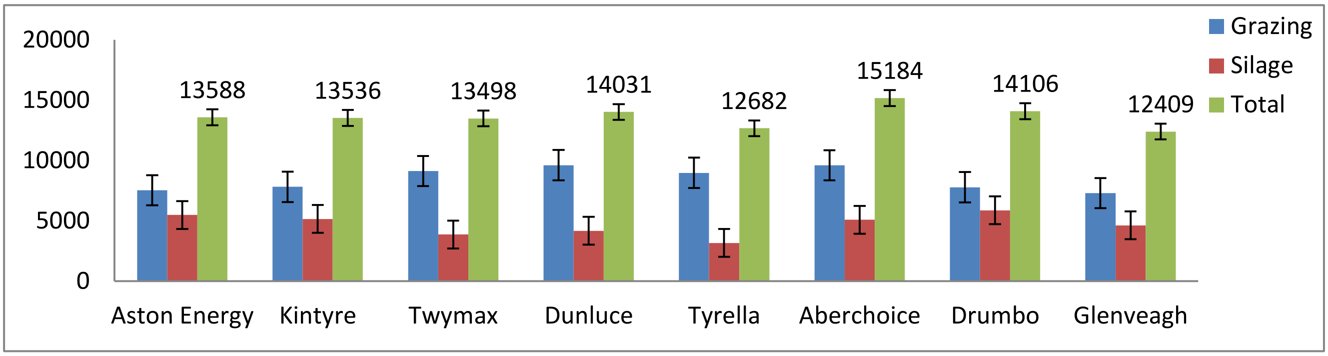

Fig. 1. The effect of grass cultivar on grazing, silage and total dry matter production (kg DM/ha) in

Conclusion

Although ploidy had no effect on herbage DM production, clover swards had a greater total herbage DM production than non-clover swards. Cultivar had an effect on herbage DM production. However, this is only year one of the experiment so further work is required.

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RMIS Project Number 6310

Modelling soil nitrogen and water in a dairy cow grazed pasture

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Introduction

Water availability and nitrogen (N) nutrition are two key factors affecting grass growth. In grass based systems, increasing grass growth leads to increased grass utilisation, and therefore increased productivity. In this study, models of soil organic and mineral N, as well as soil moisture, within grazed pastures were developed.

Materials and Methods

The model is composed of six linked sub-models, fertilisation, vegetation, organic N pool, mineral N pool, soil water and atmospheric N (Figure 1), which describe the daily fluxes of water and N.The fertilisation sub-model includes chemical N fertiliser,slurry applications and N returned to the pasture in faeces and urine by grazing animals. The vegetation sub-model incorporates plant N uptake forgrowth, and N returned to the organic N pool through abscission, and calculates evapotranspiration. The organic N pool sub-model takes into account mineralisation which transfers N from the organic pool to the mineral pool using equations from Mary *et al.* (1999). The mineral N pool sub-model includes immobilization which transfers N from the mineral N pool to the organic N pool. The water sub-model includes precipitation and evapotranspiration to calculate drainage and evaluate the water stock of the soil and nitrate leaching. The structure of the soil (porosity, wilting point, water holding capacity (WHC), saturation level and conductivity) depends on soil composition described by Rawls *et al.* (1982). The atmospheric sub-model incorporates N deposition, nitrous oxide and dinitrogen emissions from slurry, and ammonia volatilization from fertilizer and urinary N.

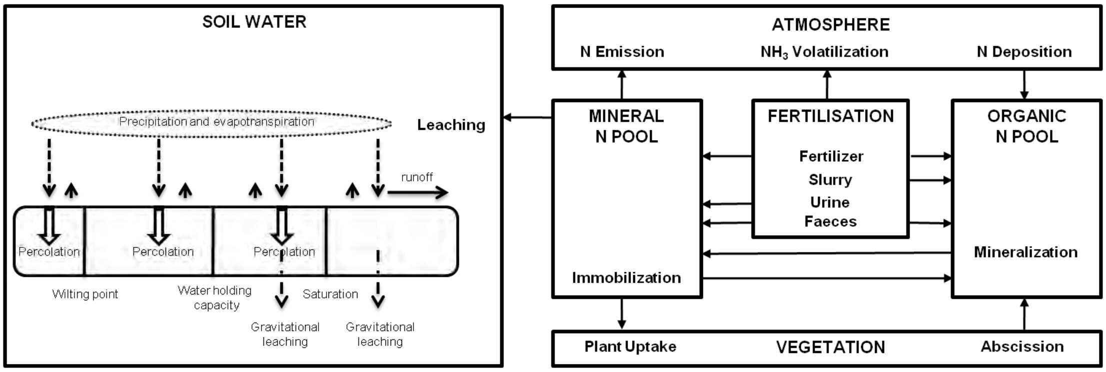

Fig. 1. Schematic representation of the modeldescribing the flows of water, organic and inorganic N in grazed grassland

Results and Discussion

The model was validated by comparing the magnitude of the various flows in the model against experimental data using mean percentage of prediction error. In the example used here the soil N dynamic and water reserve were predicted on a paddock grazed on 6 occasions in 2001, receiving fertiliser N and slurry at Moorepark, Co. Cork.

Figure 2 shows that by the end of the year organic N increased by around 100 kg N/ha while mineral N cycled back to the initial level. Both N pools spiked when a fertilisation event occurred. Mineral N gradually declined after a fertilisation event due to uptake by grass and N losses. Figure 3 shows that the water reserve of the soil increases over WHC in autumn and winter, and declines below WHC during summer when evapotranspiration is higher than precipitation.

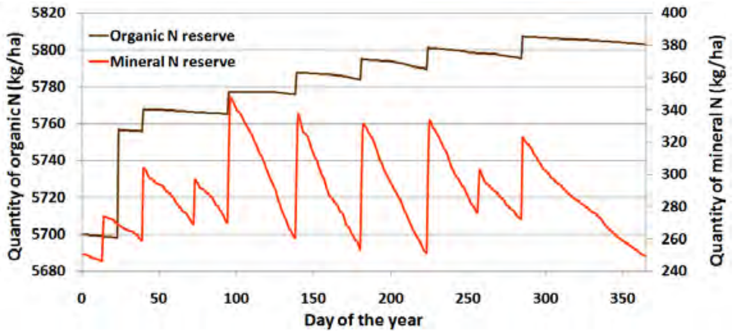

Fig. 2. Daily mineral and organic N reserves (kg N/ha) predicted for a grazed paddock in 2001.

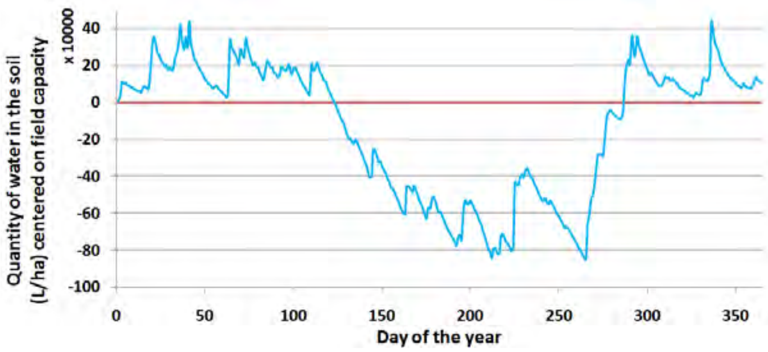

Fig. 3. Daily water reserve (L/ha in the top 1 m of soil) centred on water holding capacity predicted for 2001.

Conclusion

The model describes daily soil water and N flows. Fertilisation events increase organic and inorganic N reserves. As grass growth occurs, the quantity of N in the mineral N pool declines. The model can be used as a prediction tool to assess water and N availability, and N losses in a grazed paddock.

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RMIS Project Number 6334

Grass Feed & Value

Effect of a period of confinement in tie-stalls on lying behaviour of different breeds of dairy cows

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Introduction

Cows in experimental grazing herds are often confined in tie-stalls (TS) to take detailed metabolic and physiological measurements. However, the change from pasture to an environment in which movement is severely restricted could have a negative effect on cow welfare. Confinement could inhibit lying behaviour, reducing cow comfort and potentially increasing the risk of lameness. Difficulties in adjusting to confinement are also likely to be dependent on the size of the cow relative to the stall; larger cows may take longer to adapt due to a higher space requirement for standing and lying transitions. This study aimed to establish how transfer from pasture to TS affects lying behaviour and locomotory ability of different breeds of dairy cows.

Materials and Methods

The study was carried out between July and October 2010 at Moorepark Research Centre as part of a project investigating grass digestibility and the effect of stocking rate (SR; high or low) in 3 dairy breeds (Jersey (J), Holstein-Friesian (HF), J×HF (F1); n = 16 cows/breed). The study was carried out in 4 replicates balanced for breed and SR (n=12 cows/rep). Cows (187±26.5 days in milk (DIM)) were transferred from pasture to TS (d0) and fed freshly cut ryegrass according to their SR at pasture and breed (J: high = 14, low = 17 kg dry matter (DM)/day; HF and F1: high = 16, low = 20 kg DM/day). TS consisted of 12 stalls (1.91×1.17cm) with solid rubber walls (1.35 cm high) and a rubber floor. The back of the stall was open. Cows returned to pasture on d12. Lying behaviour was recorded for 24h on d-2, d-1, d3, d10, d11, d13 and d14 using dataloggers (Tinytag Plus, Re-Ed volt, Gemini Dataloggers (UK) Ltd., Chichester, UK), attached to the right hind leg. Lying behaviour of cows in 3 replicates was also video-recorded during the first 15h in the TS. Five aspects of locomotion were scored from 1 to 5 (1 = normal; 5 = anomalous) on d-3, d12 and d16. Data were analysed using the PROC MIXED statement of SAS. Breed, SR, day, replicate and interactions were inserted into the model as fixed effects and day as a repeated measure.

Results and Discussion

Cows spent less time lying/24h on d3 than on any other day ($P<0.001$; Fig. 1A). By d10 the total daily lying time was similar to d-2 and d11, but still shorter than on d-1 ($P<0.01$), d13 ($P<0.001$) and d14 ($P<0.01$), and was lower on d11 than on d13 ($P<0.01$). Breed tended to have an effect on lying time (HF = 10:02 ± 00:12 (hh:mm); J = 09:28 ± 00:12; F1 = 09:42 ± 00:12; $P=0.1$). High SR cows spent more time lying than low (09:59 ± 00:10 v's 09:29 ± 00:10; $P<0.05$) probably because they had less to eat. There was no effect of breed or SR on the duration or number of lying bouts. However, lying bouts were shorter on d3 than on d-2, d-1, d11, d13 and d14 ($P<0.01$), and tended to be shorter than on d10 ($P=0.07$). Lying bout duration was shorter during housing than at pasture (Fig. 1B). Cows had more lying bouts per day while they were in the TS than at pasture (Fig. 1C). In fact, the number of lying bouts continued to increase while cows were in the stalls, whereas once they returned to pasture, the number of bouts per day halved from just over 14 to approximately 7 per day. A high frequency of posture changing combined with short bouts of lying is indicative of discomfort while lying in dairy cows (Drissler et al., 2005). During the first 15h in TS there were no effects of breed or SR on lying behaviour. However lying time (01:30 ± 00:19 hh:mm), no. lying bouts (3.1 ± 0.4), no. lying attempts (15.1 ± 2.2) and no. attempts/lying bout (5.6 ± 1.3) during these 15h were outside the normal ranges for dairy cows (Jensen et al., 2005). Locomotion scores of J cows (9.2 ± 0.2) were higher (worse) than HF cows (7.9 ± 0.2; $P<0.01$), and tended to be higher than F1 cows (8.5 ± 0.2; P=0.1). Locomotion scores were lower on d-3 (7.6 ± 0.2) than on d12 (9.2 ± 0.2; P<0.001) and d16 (8.7 ± 0.2; P<0.001). Locomotion score on d12 tended to be higher than d16 (P=0.06).

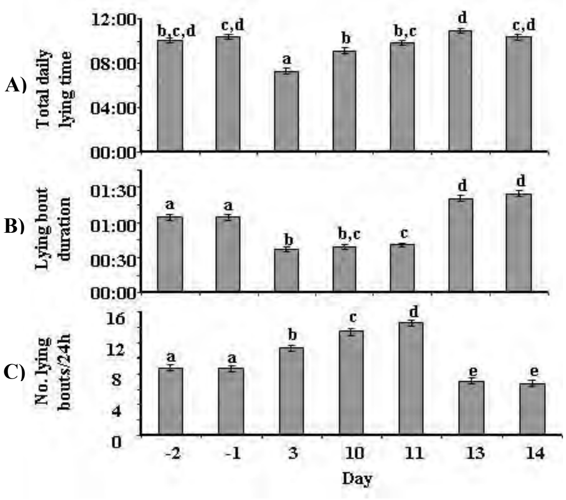

Fig. 1. A) total daily lying time, B) lying bout duration and C) no. lying bouts across the experimental period.

Conclusions

Lying behaviour was disrupted during the 15h after transfer to TS, irrespective of breed and continued to reflect discomfort (short but frequent lying bouts) throughout the period in TS. Furthermore, 12d confinement in TS caused deterioration of locomotory ability which persisted for at least 4 days following return to pasture. However, this was not affected by SR or breed. Further work could investigate whether these behavioural changes are reflected in physiological responses and how quickly locomotion scores return to pre TS level.

Acknowledgements

Thanks to M. Lucas for help with the video recordings.

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RMIS Project Number 6194

Effect of perennial ryegrass cultivar on *in vivo* dry matter intake and dry matter digestibility

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Introduction

Grazed grass is the dominant feedstuff in Irish milk production systems. Perennial ryegrass is the most commonly used grass species, as it has high growth potential and high nutrient value at a relatively low cost (Tas *et al.*, 2005). However, variations in nutritional traits exist between perennial ryegrass cultivars. Tetraploid cultivars have been shown to have higher *in vitro* organic matter digestibility (OMD) in comparison to diploid cultivars (Wims *et al.*, 2013). There is a need to quantify any differences between cultivars *in vivo*, to be confident that *in vitro* differences reflect differences using animals. The objective of this experiment was to determine the effect of four perennial ryegrass cultivars on dry matter intake (DMI) and dry matter digestibility (DMD) in sheep.

Materials and Methods

The experiment was run as a 4×2 incomplete Latin square design. Twelve Texel wethers were blocked by BW and used to determine the DMI and *in vivo* DMD of four perennial ryegrass cultivars: Astonenergy (tetraploid, heading date 31st May) (AS), Delphin (tetraploid, heading date 1st June) (DE), Tyrella (diploid, heading date 3rd June) (TY) and Glenroyal (diploid, heading date 3rd June) (GR). Each period was 11d consisting of 5d adaptation and 6d measurement (MP). The experiment was repeated twice: time stage 1 (TS1) was from 13th May to 7th June 2013 and TS2 was from 19th August to 13th September 2013. The sheep were housed in individual stalls that allowed for total collection of urine and faeces. Fresh herbage was cut once daily using a motor Etesia (Etesia UK Ltd., Warwick, UK). Sheep were fed at 110% of *ad libitum* intake, split into a.m. and p.m. feeds. On day 8 of each period a 40 g sample of each cultivar was separated into leaf, pseudostem, true stem and dead proportions above a 4 cm stubble. Herbage mass was measured using a Gardena hand shears (Accu 60, Gardena International GmbH, Ulm, Germany) and a 0.25 m^2 quadrant on days 1, 4, 7 and 10 within each period. During the MP, a representative sample of the grass offered and faeces voided was collected from each sheep daily. Daily faeces samples (0.20 of total) were dried before being bulked to obtain the DMD for the MP. Data were analysed using PROC MIXED in SAS (2002). Treatment, period within TS, TS and the interaction between TS and treatment were included as fixed effects. Sheep was included as the random effect.

Results and Discussion

There was no significant difference between cultivars in DMI (AS: 1.51±0.063 kg, DE: 1.56±0.064 kg, TY: 1.53±0.063 kg, GR: 1.48±0.064 kg). The DMI for TS1 was 1.53±0.069 kg and for TS2 was 1.50±0.065 kg ($P=0.78$). For DMD, there was a significant treatment × TS interaction ($P<0.01$). In TS1 TY had a significantly higher DMD than DE ($P<0.05$). The other two cultivars were intermediate ($P>0.05$). In TS2 all four cultivars had similar DMD to each other ($P>0.05$). The difference in DMD between cultivars could be due to differences in chemical composition (Wims et al., 2013) or to differences in sward structure (Beecher et al., 2013), which can be particularly evident during the reproductive phase. The reproductive phase coincided with TS1. The DMD of AS, GR and TY decreased significantly from TS1 to TS2. The DMD of DE did not significantly decrease from TS1 to TS2. The decrease in DMD in TS2 compared to TS1 can be attributed to the high soil moisture deficit which occurred in July and September 2013. This resulted in an increase in the dead proportion in the sward, which is the most indigestible morphological fraction in perennial ryegrass (Beecher et al., 2013). The dead proportion was higher in TS2 compared to TS1 ($P<0.001$) for each cultivar (TS1: AS 0.093, DE 0.081, GR 0.092, TY 0.087; TS2: AS 0.159, DE 0.149, GR 0.219, TY 0.191, s.e.m 0.0011).

Conclusion

Cultivars had similar DMI across both TS. There was an effect of cultivar on DMD during TS1 as DE differed from TY. There was a significant drop in DMD from TS1 to TS2. Further investigation is required into the seasonal and environmental effects on perennial ryegrass cultivars DMD.

Acknowledgements

The authors gratefully acknowledge the contributions of Andy McGrath and Mick Feeney.

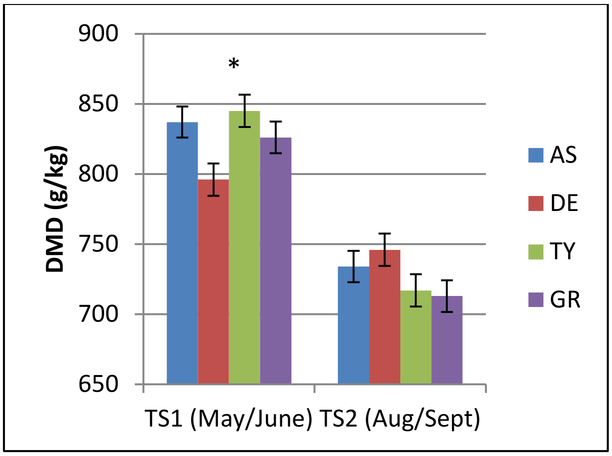

Fig 1. Effect of cultivar and time of year (TS) on dry matter digestibility (DMD) of perennial ryegrass

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RMIS Project Number 6194

Prediction of residual feed intake in lactating dairy cows using mid-infrared spectroscopy of milk

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Introduction

Interest is increasing in the use of feed intake, or residual feed intake (RFI) in dairy cow breeding programmes. McParland *et al.* (2012) previously documented the ability of the mid-infrared (MIR) spectrum of milk to predict feed intake and energy balance. Because RFI can be mathematically similar to energy balance (the only difference is a correction for body reserves through change in body weight and sometimes body condition), we hypothesised that milk MIR could also be a useful predictor of RFI.

Materials and Methods

Performance data collected between 2008 and 2012 from grazing dairy cows at the Teagasc Animal and Grassland Research & Innovation Centre, Moorepark were available. Splines were fit, within parity, to body weight (BW) and body condition score (BCS) records to generate daily estimates and daily change for both traits. Dry matter intake (DMI) was estimated using the n-alkane tracer technique periodically throughout lactation. Energy intake (EEI, MJ/d) was computed as a function of organic matter intake and its digestible crude protein and metabolisable energy content (Banos and Coffey, 2010). Energy balance (EB; MJ/d), was computed as the difference between EEI and energy output (i.e., milk production and maintenance). RFI was calculated as the residual from a multiple linear regression equation of EEI on milk yield, fat yield, protein yield, BW, BCS, change in BW and BCS and the interaction between BW and BCS.

Evening milk samples from all animals were analysed weekly using a Foss FT6000 MIR spectrometer and the resulting spectrum in the 900 cm^{-1} to 5,000 cm^{-1} wavelength region was stored. Only spectral data with a phenotypic record for all component variables of predicted traits within 7 days of the corresponding milk sample were retained. In total, 1,338 spectral records from 535 lactations on 378 first to fifth parity cows were available. Partial least squares regression was used to predict RFI, EEI, EB and BCS change from the MIR spectrum. Accuracy of all equations was tested using both split sample cross-validation and external validation. When equations were externally validated, the data were sorted according to the trait analysed and every eighth 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. All records from all cow-lactations in the original validation dataset were retained for external validation. Accuracy of prediction was determined as the correlation (r) between true and predicted values.

Results and Discussion

The milk samples analysed were evenly distributed across lactation. Mean DMI across the dataset was 15.7 (SD=3.1) MJ. Mean values of true EB, EEI, BCS change, and RFI in the calibration dataset are presented in Table 1 together with the fit statistics from both cross validation and external validation models. The accuracy of predicting EB in this study was similar to the accuracy obtained by McParland *et al.,* (2012) where they predicted EB using a subset of this data set.

Overall the prediction equations were moderately accurate; the slope between true and predicted values of EB, EEI and RFI was not different from one, the mean bias for all predictions was small and correlations between true and predicted values ranged from 0.59 (RFI) to 0.73 (BCS change). However given the potential for error, statistical or otherwise, in the calculation of these “gold standard” traits, extremely high accuracies of prediction will be difficult to attain. BCS change had the greatest accuracy of prediction from the MIR. This is not surprising given that mobilisation of BCS releases different fatty acids into the milk, and the MIR is an accurate predictor of individual milk fats (Soyeurt *et al., 2011*). The correlation between true EB and RFI across the data set was 0.85 (i.e., superior RFI is associated with greater negative energy balance). The corresponding correlation for predicted values was 0.70.

Table 1. Mean gold standard values and fit statistics * of cross-and external-validation prediction equations

	Cross Validation							*External Validation*	
Trait	Mean (SD)	No. Recs	RMSE	R	No. Recs	Bias	RMSE	Slope (SE)	R
EB (MJ/d)	52.52 (35.25)	929	24.81	0.66	409	1.44	24.24	0.95(0.05)	0.68
EEI (MJ/d)	184.99 (37.78)	949	28.4	0.65	389	2.93	26.77	1.04(0.06)	0.66
BCS change	-0.0009(0.0026)	938	0.0017	0.78	400	0.0001	0.0018	0.91(0.04)	0.73
RFI (MJ/d)	-0.05(29.97)	925	23.68	0.58	413	-0.16	22.86	0.90(0.06)	0.59

*RMSE=root mean square error; r= correlation between true and predicted value

Conclusion

The MIR spectrum of milk offers a viable method of predicting feed intake and RFI in dairy cows. Since the MIR spectrum is generated routinely through milk recording, capturing this data for inclusion in the national breeding programme can be achieved through national milk recording.

Acknowledgements

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RMIS Project Number 6407

Examination of drying protocols for perennial ryegrass samples in preparation for chemical analysis

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Introduction

Grass samples are dried in preparation for chemical analysis. Variations in drying protocols exist, i.e. different combinations of temperature and time duration, without a definitive assessment of the appropriateness or consistency of the results obtained. The objective of the study was to determine if differing drying protocols gave diverging results when drying grass samples in preparation for chemical analysis.

Materials and Methods

On three different dates perennial ryegrass samples were taken randomly from throughout one paddock with a pre-grazing herbage mass (above a 4 cm stubble) of >1000 kg dry matter (DM) ha^{-1}. Three drying protocols were investigated: oven drying at 40°C for 48 hours, 60°C for 48 hours and 95°C for 15 hours. There were four replicates per drying protocol per date. Three forced convection ovens were used (two Carbolite ovens (Carbolite Limited, Parsons Lane, UK) and one Binder FED 720 oven (Binder Inc. NY, USA)). Grass samples (~100 g) were weighed onto porous foil trays. The times were extended beyond what was normally used in the drying protocols to determine if any change in DM occurred after 48 hours for drying at 40°C and 60°C and after 15 hours for the 95°C protocol. At 0, 3, 7, 10, 13, 15, 24, 27, 31, 34, 48, 51, 55, 58, 72, 75, 79 and 82 hours the samples were removed from the oven and the weight recorded. A separate dataset of 12 samples were dried using both the 40°C and 60°C protocols. Those samples were analysed for ash, crude protein (CP; Leco FP-528; Leco Corporation, MI, USA), neutral detergent fibre (NDF), acid detergent fibre (ADF; ANKOM Technology, NY, USA) and organic matter digestibility (OMD; Morgan *et al*., 1989). Samples dried at 95°C were not chemically analysed as thermo-chemical degradation, destroying or modifying some plant constituents such as amino acids, can occur when samples are dried at above 80°C (Johnson, 1978). The DM data were analysed using PROC MIXED in SAS (2002). Date, drying temperature and time were included in the model. Time was included as the repeated measure and subsample within drying temperature as the random variable. The separate dataset of 12 samples was analysed using PROC GLM with drying temperature as the fixed effect. For both datasets the Tukey-Kramer multiple range test was used for mean separation (P<0.05).

Results and Discussion

The samples were removed from the 40°C oven after 82 hours, from the 60°C oven after 75 hours and from the 95°C oven after 24 hours. The final DM concentration did not differ between treatments ($P>0.05$), demonstrating that all protocols were acceptable for determining DM concentration (95°C for 15 hours: 153.8 ± 6.8 g/kg; 60°C for 48 hours: 155.2 ± 7.0 g/kg; 40°C for 48 hours: 159.4 ± 8.0 g/kg). There were no differences in ash or CP concentration of the samples dried using the 40°C and 60°C protocols (Table 1). This was expected as it is the nitrogen degradability rather than concentration that is affected by drying temperature (Deinum and Maassen, 1994). However, in the present study the OMD, NDF and ADF concentrations differed between the grass samples dried at 40°C and 60°C (Table 1). The results showed that NDF was lower and ADF higher in samples dried at 40°C compared to 60°C, indicating that there may have been a loss of hemicellulose thus reducing NDF when samples were dried at 40°C. This loss in hemicellulose may have contributed to the lower OMD of the samples dried at 40°C. Additionally the OMD analysis method of Morgan *et al.* (1989) was established using samples dried at 60°C and so that drying temperature may be more suitable for that particular method. Unpublished data investigating different *in vitro* methods to predict *in vivo* OMD showed that the correlation between the *in vitro* and *in vivo* data was better with samples dried using the 60°C drying protocol than with samples dried using the 40°C protocol (Beecher *et al*., unpublished)

Table 1. Chemical composition of grass samples dried at 40°C for 48 hours and 60°C for 48 hours

	40 °C	60°C	SEM	*P*-value
Ash (g/kg DM)	91.4	85.0	4.50	ns
Crude protein (g/kg DM)	220.5	215.9	3.29	ns
OMD (g/kg DM)	752.6	820.4	4.79	***
NDF (g/kg DM)	424.6	451.4	18.98	**
ADF (g/kg DM)	239.2	229.5	6.91	*

Conclusion

The results indicate that the three drying protocols (40°C for 48 hours, 60°C for 48 hours and 95°C for 15 hours) adequately dried grass samples to a similar final weight. Differences in OMD and fibre concentrations in grass samples dried using the 40°C and 60°C protocols suggest that future work should investigate which method is more accurate by conducting further chemical analysis such as for WSC and lignin concentration.

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RMIS Project Number 6194

In vivo dry matter digestibility and dry matter intake of perennial ryegrass differing in pre-grazing herbage mass

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Introduction

Ruminant production systems in Ireland are primarily grass-based (O'Donovan et al., 2011). It is important to measure key variables that effect output in grazing systems, such as grass dry matter intake (DMI) and dry matter digestibility (DMD). Grass DMI is maximized by optimising sward management tools such as pre-grazing herbage mass (PGHM). Increasing PGHM has been shown to reduce DMI and DMD (Wims et al., 2010). However, it is important to quantify this. The objective of this study was to determine the effect of PGHM on the *in vivo* DMD and DMI of perennial ryegrass in sheep.

Materials and Method

Twelve Texel wethers used to determine the DMI and *in vivo* DMD of three treatments, namely grass at different PGHM (1000 kg DM/ha-LM, 2500 kg DM/ha-MM, 4000 kg DM/ha-HM), using a 3×3 Latin square (LS) design which was repeated three times (Apr-Jun, Jun-Aug, Sept-Oct 2013). The sheep were housed in individual stalls for the total collection of urine and faeces, and were blocked on body weight at the start of each LS. Each LS had three periods of 11 days: 5 days adaptation and 6 days measurement (MP). Fresh grass was cut daily using a motor Etesia (Etesia UK Ltd., Warwick, UK). Sheep were fed *ad libitum* (110% of DMI) and grass DMI was recorded daily. On day 8 of each period a 40 g sample of each PGHM was separated into leaf, pseudostem, true stem and dead proportions above 4 cm stubble. Pre-grazing herbage mass was measured using a Gardena hand shears (Accu 60, Gardena Int. GmbH, Ulm, Germany) and a 0.25 m^2 quadrant four times during each period. During the MP, a representative sample of the grass offered and faeces voided by each sheep was collected daily. Daily grass and faeces samples were dried and then bulked to give one sample of each per PGHM per MP. Data were analysed using PROC MIXED in SAS (2002). Treatment, period within LS, LS and the interaction between LS and treatment were included as fixed effects. Sheep was included as the random effect.

Results and Discussion

There was a treatment × LS interaction for each variable in Table 1 (P<0.001). In LS 1, there was no difference in DMI between treatments but there was a tendency for LM to be higher than HM (P=0.06) and LM had a higher DMD than HM (P<0.001). The LM sward had a significantly higher leaf proportion than the HM sward, which likely contributed in part to the differences in DMD and DMI. This is because leaf is the most digestible morphological fraction in the sward (Beecher *et al.*, 2013). In LS2 the DMD values for each treatment were lower than in LS1 (P<0.001). During LS2, grass was in a reproductive growth stage, which has a lower DMD due to an increase in the true stem and dead material proportion and a decrease in the leaf proportion when compared to vegetative grass (Beecher *et al.*, 2013). Also DMD was lowered by a high soil moisture deficit in July, as perennial ryegrass becomes less digestible in times of high evapotranspiration (Deinum, 1966). This was confirmed by the lower leaf proportions found in LS2 compared to LS1 for each treatment. In LS2 and LS3 all three treatments were different to each other in relation to DMI and DMD (P<0.001). This is related to a decrease in leaf proportion in higher compared to lower PGHM swards. In LS2 there was a significant difference between the three treatments in leaf proportion. In LS3 although the leaf proportion of MM and HM swards was not significantly different, there was a significant difference between them in terms of the combined true stem and dead material fractions (LM: 0.135^a, MM: 0.168^a, HM 0.484^b, s.e.m 0.0215, P<0.01). True stem and dead material are the most indigestible morphological fractions in the sward (Beecher *et al.*, 2013).

Table 1. The effect of PGHM on grass dry matter intake, dry matter digestibility and sward leaf proportion (>4 cm) in Apr-Jun, Jun-Aug, Sept-Oct

	PGHM kg DM/ha	Leaf prop.	DMI kg DM	DMD g/kg
LS1 (Apr-Jun)				
HM	4002^{c}	0.489^{d}	1.45^{cd}	772^{b}
MM	2718^{b}	0.559^{e}	1.57^{cb}	792^{ab}
LM	1289^{a}	0.625^{f}	1.59^{cb}	805^{a}
LS2 (Jun-Aug)				
HM	5401^{d}	0.242^{a}	1.33^{de}	663^{e}
MM	2697^{b}	0.425^{c}	1.64^{b}	701^{dg}
LM	1131^{a}	0.546^{e}	1.79^{a}	728^{c}
LS3 (Sep-Oct)				
HM	4493^{c}	0.345^{b}	1.28^{e}	631^{f}
MM	2283^{b}	0.688^{fg}	1.49^{c}	693^{de}
LM	1305^{a}	0.731^{fg}	1.68^{ab}	725^{cg}
S.E.M	156.9	0.0160	0.492	7.5
LS	***	***	**	***
TRT	***	***	***	***
LS×TRT	***	***	***	***

Conclusions

There was an effect of PGHM on *in vivo* DMD and DMI mediated through changes in sward structure. Future work should explore in more detail the accompanying changes in chemical composition and seasonal changes in sward nutritive value.

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RMIS Project Number 6194

The effect of stocking rate on nitrate leaching from a free draining dairy farm system in Ireland

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Introduction

Efficient nitrogen (N) management is critical to the sustainable intensification of Irish dairy farming and the achievement of Food Harvest 2020 targets post EU milk quota abolition. Principle among the environmental impacts, N leaching from the soil profile to groundwater is the main N loss pathway within grass-based milk production systems (Treacy *et al*., 2008). Although stocking rate (SR; cows/ha) governs milk productivity per ha at grazing (McCarthy *et al.,* 2011), and increased grassland SR is expected post quota abolition, previous studies have indicated that where increased SR's is achieved based on increased chemical fertiliser N application and increased off-farm supplementary feed importation, N loss to groundwater is increased (Treacy *et al.,* 2008). The objective of this study was to evaluate the effect of three whole-farm SR on nitrate (NO_3^-) loss from a free draining soil type using modern grazing and nutrient management practices over three full grazing seasons.

Material and Methods

The experiment was conducted over three years (from January 2011 to December 2013) on a permanent grassland site at Curtin's Research Farm, Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork. In each year, 138 spring calving dairy cows were randomly assigned to one of three SR treatments, Low (2.51 cows/ha), Medium (2.92 cows/ha) and High (3.28 cows/ha). Each SR group had its own individual farmlet. Concentrate and chemical N fertilizer use were held constant across SR (1,150 kg concentrate DM/ha and 209 kg N/ha, respectively). Slurry produced by the animals while indoors was spread back on each farmlet over the first four months of the year at a rate consistent with the overall SR of each farmlet. Sixteen ceramic cups were installed to a depth of 1 m within 3 grazing paddocks (representing 18% of each farmlet) to measure total N (TN) loss. Sampling occurred biweekly during the drainage period (September to April) and once per month during the summer (May to August). Samples were analysed for TN content using standard methods. Total N loss (kg ha^{-1}) was determined annually by multiplying the average TN concentrations (mg L^{-1}) with effective drainage (Schulte et al., 2005; mm). Data were analysed using PROC Mixed in SAS (SAS, 2002). Paddock was included as a random effect while year and SR were included as fixed effects.

Results and Discussion

Average annual rainfall and effective drainage during the three year study period was similar to the 10 year average (966 and 478 mm, respectively). Effective drainage was highest in 2012 (502mm), lowest in 2011 (315mm) and intermediate in 2013 (400mm). There was no significant effect of SR on total annual TN loss during the study (135 kg N/ha) nor was there any interaction between SR and year (Table 1). The lack of difference in TN losses between SR highlights the possibility for sustainable expansion through increased grazed grass utilisation on Irish dairy farms post EU milk quota abolition. The temporal changes in N loss observed within this study suggest that such evaluations should only be considered over a minimum of 3 years.

Table 1. Effect of stocking rate[1] (SR) on total nitrogen (TN) loss (kg N/ha) over three grazing seasons (2011 – 2013).

	SR				Significance†		
TN loss (kg/ha/yr)	Low	Medium	High	SEM[2]	SR[1]	Y	SR*Y
Average	127.8	136.6	141.2	15.10	NS	NS	NS
2011	*129.2*	*136.8*	*142.2*				
2012	*144.1*	*152.9*	*119.9*				
2013	*110.1*	*120.0*	*161.5*				

†Significance: NS = not significant ; [2]SEM = Standard error of the mean

Conclusions

The results of this study indicate that TN loss to 1 m is not increased where higher overall farm SR are achieved through increased grazed grass utilisation and without added chemical N fertilizer or additional external feed supplementation.

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RMIS Project Number 5891

The effect of mole drainage on the hydrology of a clay-loam soil in the south of Ireland

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Introduction

Where soils are impermeable to depths of >2.5 m, the cost of a conventional drainage system to control the watertable is generally prohibitive because of the very close drain spacing needed (Rodgers *et al.*, 2003). Under such circumstances a more viable option is to use drainage methods that incorporate soil disruption techniques. These include mole and gravel mole drainage. The success of mole drainage can be highly variable. The stability and long term effectiveness of mole drains depends upon the soil texture, stability of the soil aggregates to wetting and soil moisture status at the time of installation (Mulqueen, 1985). Traditionally mole drainage has been successful in the north and north east of Ireland, where the soils have high clay content and rainfall is lower (Galvin, 1969). Both are conducive to the creation of a stable mole channel. The objective of this study was to compare the effectiveness of mole and gravel mole drainage in removing excess water and controlling the watertable position from a soil with 35-45% clay content in the south of Ireland.

Material and Methods

The site was poorly drained grassland (6.5 ha), with slope of 1.4% and perched watertable consistently < 1m below ground level (BGL). An open drain was excavated to 2 m BGL at the base of the site to act as a collector drain for the drainage treatments. The experimental area was hydrologically isolated by a 1m deep ditch. Inside this area four blocks (60 m wide x 100 m long) were established. These were further sub-divided into four plots (15 m x 100 m). The experiment was laid out in a randomized complete block design with four replicates. The four treatments were: (A) no intervention, (B) mole drainage installed in January 2011, (C) mole drainage installed in July 2011 and (D) gravel mole drainage installed in July 2011. Mole drainage was installed at a depth of 0.55 m and spacing of 1.2 m (€291/ha), while gravel mole drainage was installed at a depth of 0.40 m and spacing of 1.2 m (€2816/ha). Rainfall (tipping bucket) and runoff and drain flow from each isolated plot (collection tanks and v-notch weirs) were measured continuously while groundwater recharge was estimated by subtraction. Watertable depth was measured weekly. The response of treatments to rainfall was analysed for 12 events from June 2012 to March 2013. Data were analysed using ANOVA with treatment as a fixed effect.

Results and Discussion

Across replicates the watertable depth was consistently shallower in treatment A (Table 1). The change in watertable depth during events was more pronounced in treatment A, rising 11.6 cm on average, relative to 9.8, 7.9 and 9.0 cm in treatments B, C and D, respectively. Flow from the drainage treatments was seen to reduce with time. During Event 1 (02/06/12) all drains performed well with high ratios of drain flow to effective drainage, as defined by Schulte et al. (2005), (Fig. 1a). From event 5 there was an increase in total runoff relative to drain flow. In event 6 (14/08/12) ratios of runoff to effective drainage in treatments B, C and D were 50, 41 and 41%, respectively (s.e. 5.9 %, NS), while the ratio of drain flow to effective drainage in the treatments was 4, 11 and 40% respectively, with treatment D outperforming both B and C (s.e. 6.5%, $P<0.05$). At event 10 (27/12/12) ratios of runoff to effective drainage remained high, while drain performance in all treatments was poor (Fig. 1b).

Table 1. Mean pre and post event watertable depth (cm) below ground level for treatments A (undrained control), B (mole drainage installed in January 2011), C (mole drainage installed in July 2011) and D (gravel mole drainage installed in July 2011)

Treatment	A	B	C	D	SEM	Sig.
Pre-event	65^{a}	80^{b}	80^{ab}	87^{b}	3.8	*
Post-event	52^{a}	71^{b}	72^{b}	78^{b}	4.1	*

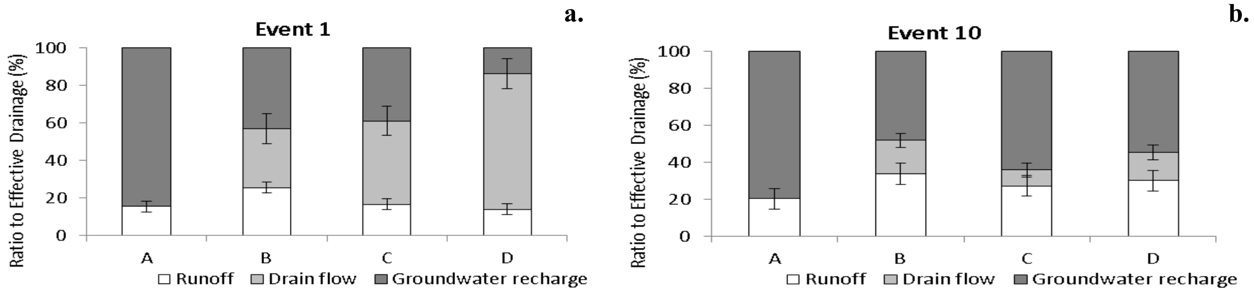

Fig. 1. Ratio of runoff, drain flow and groundwater recharge to effective drainage (a) event 1, and (b) event 10 for treatments A (undrained control), B (Mole drains installed in Jan. 2011), C (mole drains installed in July 2011) and D (gravel mole drains installed in July 2011). Error bars show the treatment s.e.m.

Conclusion

Mole and gravel mole drainage effectively lowered the water table relative to the control during the experiment. The effectiveness of all drainage treatments deteriorated within the time frame of the experiment. This is attributed to rapid deterioration of soil macropores formed during moling in persistent wet weather.

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RMIS Project Number 6012

Farmers in a Deregulated Dairy Regime: insights from Ireland's New Entrants Scheme

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Introduction

While Irish milk production has remained relatively stagnant since 1985, milk production in other countries, for example New Zealand, where deregulation has already taken place has increased by 62% between 1983 and 2003. Dairy quota abolition post-2015 represents an economic but also socio-cultural disruption for existing and new entrant farmers, arguably requiring adaptation to more market-driven production strategies. The focus of this paper is the interplay between quota abolition and farm-level decision-making in the pre-abolition period. Drawing from a broader multi-disciplinary research project, this paper identifies the key policy and market related factors influencing the current decisions and future plans of participating dairy farmers in Ireland's New Entrants Scheme (NES 2009-2013).

Theory & Methodology

A qualitative approach to empirical analysis is required to explore farmer behaviour in-depth. The interviewing methodology used in this analysis (n=8) is based on the Biographic-Narrative-Interpretative-Method (BNIM), providing a systematic approach for examining the complexity of human biography as a representation of lived experiences, individual as well as communal cultural values, and social relationships that are key to the research question under study (Wengraf, 2001). A thematic approach, led by grounded theory, is used for the analysis of the transcribed narrative data.

Results and Discussion

The group of new entrants (Nes) has differentiated characteristics in the context of the farming population generally - they are a particularly 'motivated' group that has a young age profile. However, dairy farms are identified as the most profitable farm enterprises in Ireland representing the youngest cohort (NFS, 2012) of farmers and the NEs provided in this context a valuable case-study prior to quota abolition to gain insights to the key factors that influence farm-level decision-making processes and attitudes post-2015. Of particular interest to the policy-making field is identifying the primary motivational factors influencing the farmers' actions and rationale.

The NEs, all of whom originated in the conventional farming sector, consistently gave evidence of actively anticipating future directions of policy and market related forces, evaluating and speculating on the various possible directions, and discussing these possibilities with a wide range of actors. In the advent of a deregulated dairy production regime, dairy farmers are carefully deliberating their responses at farm level, drawing from formal policy and market related information, their own personal speculations, and conventional wisdom shared with other members of the farming community. The NEs, to some extent comparing with the stereotypical characteristics of entrepreneurs set forth in the literature, demonstrated significant profit-maximising drive and risk-taking but also attached strong importance to family and socio cultural land values and maintained flexibility in their various income-generating activities with a view to enhancing farm family resilience. Their entrepreneurial behaviour was tempered by an unwillingness to seriously jeopardise family farm ownership or the welfare of farmily farm members. The NES's impact as a scheme that seeks to promote productive and efficient, 'specialised' and 'commercialised' dairy farming (DAFM, 2012) was constrained by the scheme's imposition of an upper earning limit of approximately €14,000 per annum on participating new dairy farms. This was a contributing factor in a scenario where many of the NEs remained involved in pluriactive income generating activities as well as their subsidiary drystock enterprises. The mainstream economics literature suggests that maintaining such other income sources constrains the future scale and profitability of dairy businesses, and this may be perceived as being at odds with the objectives of the NES as a policy instrument to encourage specialised, commecial dairy farming. However, the narratives of the NEs evidenced that even with unlimited quota and no upper limits on earnings, they may not cease or downscale non-dairy farming activities in the future. Decisions relating to such will be determined by a range of socio-cultural as well as economic values relating to family farm resilience. In this sense the NES's limitation on quota is unlikely to have been the primary cause of NEs' pluriactivity.

Conclusions

The NEs are influenced not only by motivations to increase productivity and scale but by a tenacious approach to farm economic sustainability and resilience that is informed by past experiences of farming and seeks to preserve and promote socio-cultural farming values. The NES has been successful in encouraging younger people to enter the dairy industry as farmers with autonomy in family farm settings. The NEs' narratives indicate the likelihood that farmers will not necessarily convert to full-time, specialised dairy farming post-2015.

Acknowledgements

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RMIS Project Number 6090

An actor-oriented approach to understanding dairy farming in a liberalised regime: a case study of Ireland's New Entrant Scheme

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Introduction

Critical research questions arising in the context of quota deregulation are how farmers will react to the myriad of challenges coming forth from changed policy circumstances and, relatedly, what influences will ultimately determine their strategies at farm level? As part of a broader multi-disciplinary research project, this paper focuses specifically on key actor-oriented dynamics determining the decisions of farmers (NEs) participating in the New Entrants Scheme (NES) in this critical period of dairy production transformation.

Theory and Methodology

A qualitative approach to empirical analysis is required to explore farmer behaviour in-depth, and this study involved eight case-studies. The interviewing methodology used in this analysis is based on the Biographic-Narrative-Interpretative-Method (BNIM), providing a systematic approach for examining the complexity of human biography as a representation of lived experiences, individual as well as communal cultural values, and social relationships (Wengraf, 2001). A grounded theory approach was used in the analysis, a means of identifying primary and sub-themes.

Results and Discussion

Led by Long's (1992) actor-oriented approach, we examined the complex social interfaces where NEs interacted with *'experts'; family members*; and *peers.* The following is a summarised version of key findings arising from the analysis.

NEs did not tend to or expect to have trustful relationships with industry experts affiliated to institutions that could withhold or regulate their access to financial services or benefits. In their relationships with advisers, NEs had expectations of mutual respect with relatively equal power relations and that the information provided should be customised to their individualised goals. Contextual analysis showed that NEs' propensity to critique advisors was largely attributable to NEs' relatively high expectations of advisors in contrast to NEs' relatively lower expectations from other industry experts. The NEs were averse to instructive or prescriptive forms of agricultural advice, preferring more participatory forms of extension. The influence of family members on the NEs' decisions was significant in relation to the nature of the (economic, social and cultural) goals associated with their new dairy enterprises'. The main objective of the NEs in developing new dairy enterprises was to maintain the resilience of the family farm for succession purposes. Family members were highly involved in the decision to establish a new dairy enterprise. The NEs depended significantly on the assistance of family farm members, as without their support and labour/other inputs the establishment of their new dairy enterprises would not have been possible. Family members' mentoring and advice was also cited as a highly valued resource in the NEs' establishment of new dairy businesses, underpinned often by NEs' high regard for the farming abilities of the family members whom they had witnessed farming for many years.

As regards peer-to-peer influence between NEs and fellow farmers, it was strongly oriented to the translation of ideas and information into practical options for the enhancement of the farm. The NEs would discuss with their peers information derived from scientific/professional sources and in so doing translated the information to have practical relevance. Similar to the basis for the credibility of family members' advice, the advice of fellow farmers was valued because of its grounding in practical experience and trial and error on-farm. The importance of local 'role models' arose frequently in the NEs narratives. The perceived value of discussion groups among NEs was firmly linked to peer-to-peer interactions and learning from the experiences of other farmers. It was also clear from the biographical nature of the NEs' narratives that they were beginning to 'outgrow' their discussion groups and often their peer-to-peer learning networks. This process of 'outgrowing' was linked to the strengthening positions of NEs as 'role models', giving rise to altered forms of social interfaces and extension opportunities (Macken-Walsh *et al.*, 2012).

Conclusions

A contrast was evident between the actors who influenced major strategic decision-making affecting the operation of the farm in the long term, and decision-making relating to management techniques that were less transformative. The views of family members were fundamental to the New Entrants' decisions to embark on new enterprises, while peer-to-peer learning interfaces were highly influential on habitual production and management techniques.

Acknowledgements
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RMIS Project Number 6090

Auditing the carbon footprint of milk from commercial Irish grass-based dairy farms

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Introduction

As awareness grows of the potential adverse affects of climate change, the demand for products that generate low greenhouse gas (GHG) emissions or carbon footprint is expected to increase (Roy *et al.*, 2009). Although, several studies have estimated carbon footprint of milk (Yan *et al.*, 2011), they have usually been limited to a low number of farms (< 30) and rarely verified to international standards e.g. British Standards Institute publicly available specification 2050 (PAS 2050). The goal of this study was to conduct an audit of carbon footprint (CF) of milk from over 100 grass-based farms by verifying data collection and analysis according to PAS 2050 standards using an accredited third party (Carbon Trust). An additional aim was to assess relationships between farm measures and CF of milk.

Materials and Method

Annual farm audits were conducted in 2010 and 2011 using on-farm surveys, milk processor records and national livestock databases for 171 grass-based Irish dairy farms. The farms were located in the northeast, east, southeast, south and southwest of the country. The farms assessed were therefore a subset of the countries farms and not representative of the CF of Irish milk. Information was successfully obtained electronically from 124 farms and fed into a cradle to farm-gate LCA model (O'Brien *et al.*, 2011). The model estimated all sources of GHG associated with dairy production until milk leaves the farm, including off-farm sources such as fertilizer production. However, the model was adapted based on the advice of the Carbon Trust to include GHG sources such as refrigerant loss from milk cooling. On and off-farm GHG emissions were converted to CO_2 equivalents (CO_2-eq) using conversion factors of 1 for CO_2, 25 for methane and 298 for nitrous oxide (IPCC, 2007), and summed to compute dairy farms annual GHG emissions. The CF of milk was estimated by firstly allocating GHG emissions between farm outputs. Where possible, allocation was avoided, but this was only achieved for exported crops by constraining the model to quantify emissions from crops grown for dairy cattle. When allocation was required, GHG emissions were allocated between milk, meat and manure based on their economic value. Annual GHG emissions attributed to milk were expressed per kg of fat and protein corrected milk (FPCM) to quantify the CF of milk. The Carbon Trust tested the LCA model for non-conformities with PAS 2050. PAS 2050 certification was achieved when non-conformities were fixed or where the affect of all unresolved non-conformities on CF of milk was < ± 5%. PROC Reg of SAS was used to evaluate relationships between farm measures and CF of milk.

Results and Discussion

The combined effect of LCA model non-conformities with PAS 2050 on CF of milk was < 1%. Thus, PAS 2050 accreditation was granted. The mean certified CF of milk from grass-based farms was 1.11 kg of CO_2-eq/kg of FPCM, but varied from 0.87-1.72 kg of CO_2-eq/kg of FPCM (Fig 1).

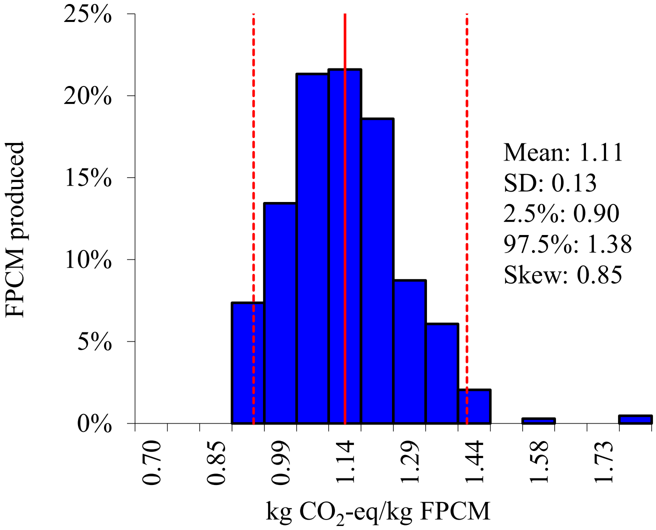

Fig. 1. Histogram of CF of fat and protein corrected milk (FPCM) for 124 dairy farms in CO_2 equivalent (CO_2-eq). The middle vertical solid line indicates the mean value and the dotted vertical lines to the left and right of the mean indicate the interval between the lower 2.5% and upper 97.5% of values

Stepwise multiple regression (Table 1) showed that CF of milk could be reasonably explained using N efficiency (N exports/N imports), milk yield/cow, replacement rate (RR) and grazing days (R^2 = 0.75). Management changes can be applied to improve these traits. Thus, grass-based farmers that increase productivity can significantly reduce CF of milk.

Table 3 Multiple regression coefficients and standard errors (SE) for CF of milk

Parameter	Coefficient	SE	P value
Intercept	2.19	0.08	< 0.05
N efficiency, %	-0.98	0.10	< 0.05
Grazing days	-2.16×10^{-3}	2.71×10^{-4}	< 0.05
Milk, kg/cow	-7.76×10^{-5}	9.87×10^{-6}	
RR[a], %	3.37×10^{-3}	9.43×10^{-4}	< 0.05

[a] RR = Replacement rate

Conclusion

Differences between dairy farms CF of milk were explained by variation in measures of farm performance. Thus, this implies that improving farm efficiency can mitigate CF of milk.

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RMIS Project Number 6241

An evaluation of the effect of greenhouse gas accounting methods on a marginal abatement cost curve for Irish agricultural greenhouse gas emissions

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Introduction

Marginal abatement cost curve (MACC) analysis is a tool used to assess opportunities to reduce agricultural greenhouse gas (GHG) emissions relative to some baseline scenario e.g. "business as usual" scenario and their associated costs or benefits. Generally, MACC analysis follows the Intergovernmental Panel on Climate Change (IPCC) methodology to estimate the abatement potential of mitigation measures. There is however an alternative to the IPCC method, known as life cycle analysis (LCA), which is the preferred method to assess the GHG intensity of food (kg of GHG/unit of food). The aim of this study was to compare the effect of using the IPCC and LCA methods when completing a MACC analysis of Irish agricultural GHG emissions.

Materials and Method

For this study, the 'Food Harvest 2020' scenario as outlined by Donnellan and Hanrahan (2012) was adopted as the reference scenario in the MACC analysis. Mitigation measures were then selected, following a scoping and screening exercise. The criteria used to screen measures were: 1) mitigation measures must be applicable to typical Irish farming systems, 2) scientific data, from completed research, must be available on the relative cost/benefit of each mitigation measure as well as their relative abatement potential, 3) for each measure, activity data (e.g. national livestock population) must be available to assess the total national abatement potential and associated cost/benefit. The result of the screening phase was a list of 10 mitigation measures suitable for Irish agriculture (O'Brien et al., 2013). The national abatement potential of mitigation measures was estimated separately using the IPCC and LCA methods. The IPCC method was employed to assess the effect mitigation measures have on national and sectoral GHG emissions. The sources of GHG attributed to the agricultural sector using the IPCC method are enteric fermentation, manure management and agricultural soils. The LCA method was applied to quantify GHG emissions from all on and off-farm sources associated with agriculture up to the farm gate. Thus, the approach included upstream emissions from the manufacture of inputs e.g. fertiliser even if they occur outside national boundaries. For this analysis, downstream emissions from the processing and distribution of agricultural produce were not included. The abatement potential of mitigation measures was only constrained by the biophysical environment. The rate of adoption of mitigation measures by farmers was not constrained, because it depends on multiple factors in addition to the economic cost/benefit of a mitigation measure, which are difficult to quantify. Most of the mitigation measures assessed, when applied in combination can interact. Thus, the abatement potential of a group of mitigation measures may not be additive. Where possible, interactions between measures were accounted for.

Results and Discussion

Table 1 shows that the total abatement potential that can be accredited to Irish agriculture using the IPCC method amounts to about 1.1 Mt of CO_2 equivalents per annum by 2020, compared to the

Food Harvest 2020 reference scenario. Almost all of this abatement potential can be achieved without financial cost by adopting measures that improve efficiency. The LCA results show that the total abatement potential was approximately 3.4 Mt of CO_2eq, 73% of which could be achieved without financial cost**.** The large difference between methods was because the IPCC method attributes the abatement from some mitigation measures to sectors or regions other than the Irish agriculture sector.

Table 4. Annual abatement potential in Mt of CO_2 equivalents of cost effective (measures that cost less than the forecasted price of carbon), and cost prohibitive mitigation measures for Irish agriculture compared to a Food Harvest 2020 reference scenario.

Measure	IPCC Method		LCA method	
	Cost effective	Cost prohibitive	Cost effective	Cost prohibitive
Total annual abatement potential	2.49	0.18	2.81	0.62
Abatement accredited to Irish agriculture	1.10	0.02	2.81	0.62

Conclusions

The comparison between GHG accounting methods showed that the IPCC and LCA methods did not agree on the abatement potential of several mitigation measures. This finding has demonstrated that it will be difficult to incentivise farmers to adopt mitigation measures where the abatement may not be accredited to the Irish agricultural sector.

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RMIS Project Number 6241

A case study of the carbon footprint of milk from high performing confinement and grass-based dairy farms

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Introduction

Globally greenhouse gas (GHG) emissions will have to be cut by up to 80% (relative to 1990 levels) before 2050 to prevent adverse climate change (IPCC, 2007). Internationally dairy production is responsible for 4% of GHG emissions, but demand for milk is projected to grow by 1.1% per annum from 2006 to 2050 (FAO, 2013). Thus, the focus on reducing GHG emissions (carbon footprint) per unit of milk is increasing. Previous life cycle assessment (LCA) studies (e.g. Flysjö *et al.*, 2011) report grass-based farms have a lower carbon footprint of milk than farms where cows are housed full-time (confinement farms). However, these studies have only considered national or regional average performing farms. Thus, our aim was to compare the carbon footprints of milk from high performing confinement and grass-based dairy systems across several regions.

Materials and Method

Case study farms located in regions accustomed to grass-based and confinement milk production were selected to represent the upper quartile of USA and UK confinement systems and Irish grass-based systems. The aim of the Irish system was to maximize milk from consumed grass through a combination of extended grazing (early February to late November), compact calving patterns and rotational grazing. In contrast, the goal of the UK and USA systems was to maximize milk yield/cow. Physical data (Table 1) for the Irish and UK systems were obtained from research herds (O'Brien *et al.*, 2011; Garnsworthy *et al.,* 2012); and data for the USA system was from the top 5% of herds recorded by DairyMetrics. The performance of these herds was compared to national statistics, which showed that they represented top performing herds in each nation A "cradle to farm" gate LCA model was applied to estimate carbon footprint of milk (O'Brien *et al.,* 2011). Thus, GHG emissions from all processes associated with dairy production until milk was sold from the farm were quantified. Emissions estimated by the model were converted to carbon dioxide-equivalents (CO_2-eq), using conversion factors of 1 for CO_2, 25 for methane (CH_4) and 298 for nitrous oxide (N_2O; IPCC, 2007). The annual GHG emissions output of the model was allocated between milk and meat using a physical allocation method (IDF, 2010). This method related GHG emissions to the cow's use of energy to produce milk and meat. Carbon footprint of milk was calculated by expressing GHG emissions attributed to milk per t of energy corrected milk (ECM).

Table 5. Annual technical description of high performance Irish, UK and USA dairy systems

Item	Irish	UK	USA
Livestock units/ha	2.53	3.74	2.79
Milk yield, kg/cow	6,262	10,892	12,506
Fat, %	4.47	3.95	3.58
Protein, %	3.55	3.14	3.17
ECM[a], kg/cow	6,695	10,602	11,650
Replacement rate, %	18	34	38
Live weight, kg	543	613	680
Concentrate, kg DM/cow	320	2,905	3,355
N fertilizer, kg N/ha	250	106	53

.[a] Energy corrected milk

Results and Discussion

Carbon footprint per t of ECM was lowest for the Irish grass-based system, was 4% greater for the UK confinement system, and was 6% greater for the USA confinement system (Table 2). Enteric CH_4 was the main source of GHG emissions for grass-based and confinement systems (42-51%) followed by manure (23-31%). The remaining GHG emissions of the Irish grass-based system were from fertilizer (22%), but for the UK and USA systems concentrate (12-19%), electricity and fuel (7-8%) were the next most important GHG sources. Carbon sequestration had a little or no effect on emissions of the UK and USA systems (0, -1%), but had a large effect on the Irish system (-9%).

Table 6. Dairy systems carbon profiles and footprints of milk in kg of CO_2-equivalent/t of energy corrected milk

Emission and source	Irish	UK	USA
Enteric fermentation	381	329	327
Manure	191	179	241
Fertiliser	161	35	29
Concentrate	28	148	93
Other inputs	47	91	96
Carbon sequestration	-69	-9	0
Carbon footprint of milk	739	772	787

Conclusion

High performance grass-based systems are capable of having a lower carbon footprint of milk compared to top performing confinement systems.

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