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Centre

Moorepark

Moorepark Research Report 2012

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Agriculture and Food Development Authority

Moorepark Research Report 2012

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Introduction

Following two very good years, the agri-food sector had a challenging time in 2012. Adverse weather dominated the farming environment in 2012 with heavy rainfall and below average sunshine and temperatures during the summer months resulting in reduced pasture growth, difficult grazing conditions and impaired silage harvesting. Annual forage production as well as silage quality were impaired resulting in increased concentrate feed usage in grassland enterprises, particularly on dairy farms. While feed, fertiliser and fuel prices all increased in 2012 the greatest impact on costs for dairy enterprises was the increase of 50% in concentrate feed usage in the second half of 2012 compared with the same period in the previous year Lower milk prices, lower milk supplies and increased input costs led to an estimated 24% decline in dairy farm incomes.
The following are the main highlights from the 2012 programme:

Low-cost genomic selection
Genomic selection was launched for Irish dairy cattle in Spring 2009. Retrospective analysis of how the bulls genomically tested in 2009 and 2010 compare with their daughter proofs in 2012 clearly show that the accuracy of identifying the best bulls for Ireland is 10-20% greater with genomics. Moreover, the accuracy is improving year-on-year. Genomic technology has been used for several decades for parentage verification. However, this technology cannot be used for genomic selection implying duplication in costs for farmers who require both parentage verification and genomic proofs. Having two concurrent systems also necessitates the procurement of at least two biological samples of the animal. In 2013 Teagasc, in collaboration with the ICBF, Weatherbys and the USDA developed a world-first national genotyping platform for both dairy and beef animals that will facilitate both parentage verification (and aid in solving any pedigree discrepancies like who the actual sire is) and genomic selection thereby reducing duplication and therefore costs. The new genotyping platform also facilitates screening of (breeding) animals for known lethal genetic defects, congenital defects and other major genes like the A1/A2 beta-casein mutation. This genotyping platform will develop further as new mutations and their effects are discovered both in Ireland and internationally. The outcome is access to state-of-the-art genomic technologies for the Irish Agri-Food industry at a low cost and inconvenience.

Energy Use in Irish Milk Production Systems
Reducing energy consumption in Irish milk production is a topical issue for two reasons. First, electricity costs are expected to increase because of the introduction of a dynamic pricing system with peak and off-peak prices, which might impact farm profitability. Second, electricity consumption is identified to contribute to about 25% of energy use along the life cycle of pasture-based milk. The objective of this research is to document electricity use per kg of milk sold and to identify strategies that reduce its overall use while maximizing its use in off-peak periods. We therefore, assessed average daily and seasonal trends in electricity consumption on 22 Irish dairy farms, through detailed auditing of electricity consuming processes. In order to determine the potential of identified strategies to save primary energy, we also assessed total primary energy use along the production chain of Irish milk. Total energy use was 31.73 Mega Joules per kg of Milk Solids. Electricity use accounted for 12% of total energy use (range 8-21%). On average 31% of this electricity was used for milk cooling, 23% for water heating, and 20% for milking. Other major energy consuming processes were application of chemical fertilizers (57% of total energy use, range 40-80%), purchase of concentrate feed, (21% of total energy use, range 8-36%) and fossil fuel use, (8% of total energy use, range 1-15%). Analysis of the electricity consumption temporal trends revealed that the introduction of a dynamic pricing system could increase energy costs for dairy farmers. Combining technology that decouples energy use from milking times (e.g. timer controlled water heating systems or chilled water cooling systems) with energy efficient technology (e.g. variable speed drive vacuum pumps and ground water plate heat exchangers), therefore, has potential to improve the economic and environmental competitiveness of Irish milk production.

Sward structural effects on intake and milk performance
Sward structure differences are known to influence intake animal performance. The stem proportion of a sward has been shown to act as a barrier to intake. Stem is also lower in quality when compared to leaf or pseudostem proportions. Swards with increased stem

proportions have been shown to have a negative effect on milk yield of lactating dairy cows. In order to determine if the differences observed in previous studies were likely to be true effects or as a result the individual cultivar effects, four perennial ryegrass cultivars were selected based on results from Distinctiveness, Uniformity and Stability trials (DUS Trials). Two Tetraploids (Astonenergy and Delphin) and two diploids (Glenroyal and Tyrella) were selected based on their reported differences in leaf length, leaf width, digestibility within the DUS trials. The objective of the study was to examine if these differences resulted in differences in animal performance in favour of the cultivars with the larger leaf sizes. The cultivars were sown in August 2011 as monocultures. Three replicates of each cultivar were sown totalling 2.86 ha (approx.) per cultivar. In April 2012, forty spring calving lactating dairy cows were blocked according to a number of pre experimental variables and randomly assigned to one of the four grass cultivars. The study was a 4 × 4 latin square design. Each period within the square lasted 3 weeks (2 weeks adaption and 1 week measurement). Two full latin squares were completed (April – June and June – September). Animals were offered 17 kg DM/cow per day. Herbage mass, post grazing sward height and growth rates were similar for all cultivars. Pre grazing sheath height was lower for Delphin and highest for Glenroyal. Leaf proportion above 4 cm was greater for the two Tetraploids than the two diploids. Milk yield and milk solids yield was 1 kg and 0.1 kg greater per cow per day on the tetraploid swards compared to the diploids. These results indicate that tetraploids can support higher animal performance and further strengthen the argument for increased leaf and reduced stem proportion to increased milk production per cow.

Supplementary feeding spring calving dairy cows in spring and autumn

Grazed grass is the cheapest source of nutrition for dairy cows in Ireland. During times of grass deficit, supplementary feeds are offered to fill the deficit and maintain milk yield. Different supplementary feeds can be offered and the choice includes grass silage, other silages and concentrate feeds. Milk protein concentration is affected by dietary intake of crude protein (CP) and macro-minerals such as phosphorus (P). Milk protein is an important component in the manufacture of dairy products. Dairy cows in early lactation in spring 2012 were offered grass, and concentrate feeds differing in CP and P concentration. Results suggest that supplementing a grazed grass diet for 8 weeks with 4 kg of a low CP supplementary feed did not significantly reduce milk yield or milk composition. It did however significantly reduce MUN concentration, which is desirable from a milk processing perspective. Supplementing a grazed grass diet for 8 weeks with 4 kg of a low P supplementary feed also did not significantly reduce milk yield or milk composition, but by the end of the study, blood P concentration was below the recommended level. Dairy cows in late lactation in autumn 2012 were offered a high grass allowance, low grass allowance (LG), LG and baled grass silage, LG and pit grass silage or LG and concentrate. Offering concentrate significantly increased milk yield and milk solids yield compared to all other treatments. Offering a low allowance of grass reduced milk yield and milk solids yield compared to all other treatments. The high allowance of grass and the LG supplemented with silage gave results intermediate to the previously mentioned results, but similar to each other. Future work will investigate the effects of other supplementary feeding regimes on dairy cow production performance and will test the processability of milk from these different nutritional regimes.

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ANIMAL RESEARCH PROGRAMME

Genetic Improvement of Animals

Genetic parameters of energy status predicted using the mid-infrared spectrum of milk

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Introduction

Animal energy status is associated with animal health and fertility (Beam and Butler, 1999). McParland *et al*. (2012) showed that the mid-infrared spectrum (MIR) of milk, collected nationally during routine milk recording is an accurate predictor of both energy balance (EB) and energy intake (EEI). The objective of this study was to estimate genetic parameters for these MIR-predicted energy status traits.

Materials and Methods

Data for this study originated from two separate research institutes: the Teagasc Animal and Grassland Research & Innovation Centre (MPK) comprising seven research herds located in the south of Ireland, and the Scottish Agricultural College Langhill herd (SAC) located in the west of Scotland. Individual morning and evening milk samples from both research herds were analysed using an MIR spectrometer (FOSS Milkoscan FT6000, Hillerod, Denmark) located at MPK. Midday milk samples from SAC cows were also available. Samples from MPK animals were analysed weekly, while samples from SAC were analysed on a monthly basis. Spectral data were transformed through a $\log_{10}$ transformation of the reciprocal of the wavelength value and the first derivative of the transformed values was obtained for use in the prediction equations. Principal component analysis of all spectra was undertaken and outliers removed leaving 22,459 MPK and 2,884 SAC spectra available for energy status predictions.

Equations previously developed using a subset of these data to predict EB and EEI with respective prediction accuracies of 0.65 and 0.78 (McParland *et al.,* 2012) were applied. "True" EB and EEI were also computed by applying random regression models to intake, milk production, live weight and body condition score, using the method described by Banos and Coffey (2010). In total, up to 627 and 2,605 true EB and EEI records were available for MPK and SAC animals, respectively.

Univariate animal linear mixed models were applied using ASReml software (Gilmour *et al.,* 2006) to estimate variance components for both true and predicted EB and EEI. All models were adjusted for the fixed effects of herd-year-season of calving, age at calving, year-month of record, and the interaction between parity and the cubic effect of days in milk. All fixed effects were fitted separately for each country. A random additive genetic effect for animal and a random permanent environmental effect of animal within parity were fitted in both models. The covariance between predicted and true EB and EEI was also estimated using bivariate animal models. A pedigree file, at least four generations deep, where available, was generated for all MPK and SAC animals included in the analysis and comprised 4,475 individual animals.

Results and Discussion

Mean true and predicted EB (SD in parenthesis) was 27.43 (23.74) and 4.96 (30.52) MJ for MPK animals respectively; corresponding values for SAC animals were -9.03 (32.74) MJ and -8.13 (21.26) MJ, respectively. Mean true and predicted values of EEI for MPK and SAC animals (SD in parenthesis) were 154.18 (23.34), 143.61 (29.75), 169.36 (46.55) and 170.04 (34.79) MJ, respectively. The heritability of true and predicted EB was 0.11 (SE=0.03) and 0.20 (SE=0.02), respectively, across data sets. The heritability of true and predicted EEI was 0.25 (SE=0.03) and 0.15 (SE=0.01), respectively. Genetic correlations between true and predicted EB and EEI as well as milk, fat and protein content are provided in Table 1. The genetic correlation between true EB and true EEI was 0.36 (not shown; SE=0.11) which was similar to the correlation between predicted EB and predicted EEI (r = 0.25; Table 1).

However a correlation of 0 between true EB and predicted EEI was observed. A moderate genetic correlation between true and predicted EB indicates genetic similarity between the EB calculated from the research data and that predicted from the MIR spectrum. This indicates that selection for improved EB using routinely available MIR data will improve true EB. Similarly the genetic correlation between true and predicted EEI was strong at 0.76 (SE=0.06) promoting the feasibility of using predicted EEI as indicator to improve true EEI.

Table 1. Genetic correlations[1] between true energy balance (True EB) and predicted energy status (Pred EB, Pred EEI[2]) and milk, fat and protein content

	True EB	Pred EB	Pred EEI
Pred EB	0.59 (0.10)	-	0.25 (0.07)
Pred EEI	0.00 (0.14)	0.25 (0.07)	-
Milk (kg)	-0.15 (0.13)	-0.66 (0.04)	0.33 (0.07)
Fat (%)	-0.21 (0.13)	0.45 (0.05)	0.31 (0.06)
Prot (%)	-0.22 (0.12)	0.19 (0.06)	0.41 (0.05)

[1]Standard error in parentheses, [2]Effective energy intake

Conclusion

Energy balance and EEI predicted using the MIR spectrum are both heritable and genetically similar to true EB and EEI computed using research data. Genetic selection for EB and EEI using the MIR spectrum is possible.

Acknowledgements

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RMIS Project Number 5791

Genetics of linear type traits in Irish dairy cattle

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Introduction

Linear type traits describe the physical characteristics of individual animals and are based on visual assessments scored on a linear scale. Physical characteristics assessed include body size, mammary system, and feet and legs conformation. The objective of this study was to generate a genetic evaluation statistical model for linear type traits in Ireland that can subsequently be used for national genetic evaluations.

Materials and Methods

Data on 192,423 Irish classification records on 27 type traits taken between the years 1983 and 2011, inclusive were available. Of the 27 type traits, 22 traits were scored on a linear scale of 1 to 9, with the remaining 5 composite traits (overall, dairy, body, legs and udder) scored on a scale of 40 to 100. Only the first record in time from first parity animals scored between 1 and 330 days post-calving was retained. Furthermore only records from animals calving for the first time between 20 months and 38 months of age were retained. Animals born more than 8 years after their sire's date of birth were discarded. All traits, with the exception of temperament and ease of milking, were standardised to a common variance within field officer-by-year. For temperament and milking speed, only herds with variation recorded for these traits were retained. Contemporary groups were formed as a two-way interaction between herd and date of classification; contemporary groups containing <5 records were discarded. Following all edits, 46,378 records from 1,553 herds remained. Variance components for each type trait were estimated using a linear animal mixed model in ASReml (Gilmour *et al.,* 2008). Fixed effects included in the model were contemporary group, calving month, days in milk, age at first calving, heterosis and recombination loss. Covariances among the type traits were estimated using a series of bivariate sire linear mixed models. Correlation analyses were undertaken between sire breeding values estimated using the statistical model developed here and estimated using the previous genetic evaluation model.

Results and Discussion

The body-related traits were the most highly heritable, and feet and leg-related traits were the most lowly heritable (Table 1). The coefficient of genetic variation varied from 0.21 to 0.40 indicating that considerable exploitable genetic variation existed for all traits. Strong genetic correlations were observed between the type traits describing similar characteristics of an animal. The body-related type traits were weakly to strongly correlated with each other (0.02 to 0.66) and with the overall conformation composite trait (0.01 to 0.77). Correlations indicate that taller animals were wider, deeper and more angular with less condition. Similarly udder-related type traits were all moderately genetically correlated with each other (0.11 to 0.79) and with the udder composite trait (0.32 to 0.87). The genetic correlations between the body-related type traits and udder and teat-related traits suggest that taller, deeper and wider animals had better udder and teat conformation. The correlations between bull estimated breeding values calculated using the previous statistical model and the statistical model developed here ranged from 0.946 (rear legs set) to 0.996 (angularity).

Conclusions

A new and pertinent statistical model for linear type traits that is more appropriate for the Irish dairy production system was developed. As a consequence of the correlations between the bull estimated breeding values not being unity, re-ranking of some sires is inevitable in the next national genetic evaluation of linear type traits.

Acknowledgements

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Table 1. List of type traits, co-efficient of genetic variation for each trait (CV_g), and heritability estimates[1] (h^2).

Traits	***CV_g***	***h^2***
Stature	0.28	0.45
Chest Width	0.30	0.23
Body Depth	0.24	0.27
Angularity	0.26	0.28
Rump Angle	0.29	0.31
Rump Width	0.26	0.21
Body Condition Score	0.40	0.18
Rear Legs Set	0.21	0.09
Foot Angle	0.34	0.09
Fore Udder Attachment	0.27	0.17
Udder Support	0.23	0.11
Udder Depth	0.24	0.30
Rear Udder Height	0.27	0.21
Rear Teat Placement	0.26	0.21
Teat Placement rear view	0.38	0.26
Teat Placement, side view	0.24	0.19
Teat Length	0.29	0.34
Temperament	0.24	0.02
Ease of Milking	0.26	0.01

[1] The standard errors ranged from 0.005 to 0.018 for all heritability estimates.

RMIS Project Number 5889

Genome-wide associations for carcass traits in Irish Holstein-Friesian cattle

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Introduction

Carcass traits are critical to the biological and economical efficiency of cattle production and as such there is great interest in understanding the underlying genetic architecture influencing animal performance. Genome-wide association (GWA) approaches allow unbiased examination of a large number of genetic variants spread across the entire genome to detect regions associated to a trait of interest. The aim of the study was to identify regions of the genome associated to carcass performance using phenotypes of four economically important carcass traits; carcass weight (CWT), carcass fat (CFAT), carcass conformation (CONF) of progeny as well as cow carcass weight (CULL).

Materials and Methods

Genotypes of 54,001 single nucleotide polymorphisms (SNPs) and predicted transmitting abilities, (*i.e.* measure of genetic merit), were available for 5,706 Holstein-Friesian sires. These animals were representative of the genetic composition of Irish herds. Quality control was performed on both the genotypic and phenotypic data. Following quality control, 44,265 SNPs and 941 (CWT), 768 (CFAT), 936 (CONF) and 763 (CULL) animals remained. Two statistical methods were used to quantify associations between SNP genotypes and phenotypes. The first method was a single SNP regression model (SSR) that associated each SNP individually with each phenotype in a linear mixed model while accounting for pedigree structure between animals. Association P-values were adjusted to correct for errors arising from multiple testing using the false discovery approach described by Storey and Tibshirani (2003). The resultant q-values were used to determine significance of each SNP (q-value < 0.05 (CWT, CFAT, CULL) and q < 0.005 (CONF)). The second statistical approach used was a Bayesian mixture model. This was a modified version of BayesB that allowed incorporation of prior knowledge such as the proportion of SNPs, π, assumed to have no effect on the trait of interest. SNP posterior probabilities (*i.e.* probability of association) (PP) for each trait were calculated using alternative values of π. SNPs with a PP>0.5 were considered high PP SNPs. The occurrence of each high PP SNP across all priors was estimated and used to get an average occurrence rate of SNPs for each prior. High PP SNPs in the prior with the highest average occurrence rate were deemed associated to a trait. All bovine genes (Btau4.0) within a 500kb region up and downstream of SNPs found significant using the Bayesian approach were identified. These genes were mapped to their human orthologs using the mapping available from hg19. The R package GOseq, without the correction for gene length bias, was used to identify significantly (P<0.05) over-represented KEGG pathways.

Results and Discussion

Significant associations using the SSR approach were detected on all autosomal chromosomes. A total of 2, 25, 27 and 48 SNPs were significantly associated to CWT, CFAT, CONF and CULL, respectively. A total of 44 unique SNPs were found significant using the Bayesian approach; 12, 6, 12, and 15 SNPs for CWT, CFAT, CONF and CULL, respectively. From the pathway analysis, twenty-five different pathways were found significantly over-represented across all analyses. The most significantly over-represented pathways for each trait were the Jak-STAT signalling pathway (CWT), peroxisome proliferator-activated receptor (PPAR) (figure 1) signalling pathway (CFAT), Inositol phosphate metabolism (CONF) and Glutathione metabolism (CULL). The most significantly over-represented pathway was the PPAR signalling pathway ($p=9.58 \times 10^{-4}$). PPAR is a signalling pathway known to be involved in animal growth, in particular growth related to fat metabolism and proliferation.

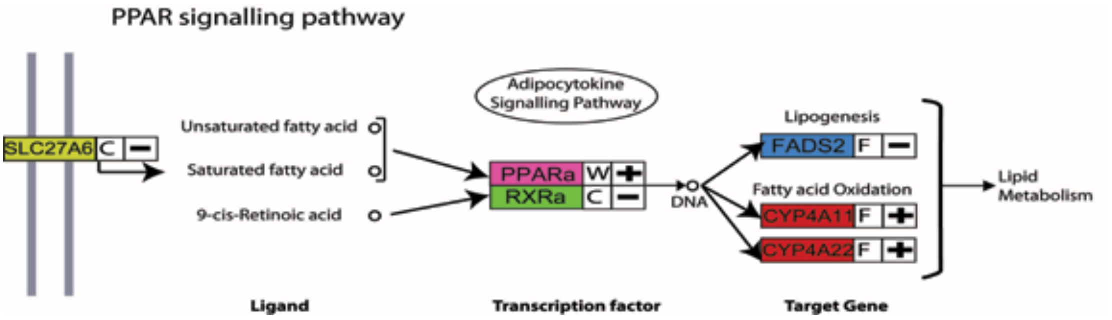

Figure1. Genes in regions surrounding significant Bayesian SNPs that are in the PPAR signalling pathway. Colours indicate different chromosomes that the significant SNP was found on. Trait that SNP was significant for; $\boxed{W}$ = carcass weight, $\boxed{C}$ = carcass conformation, $\boxed{F}$ = carcass fat. SNP effect; $\boxed{+}$ = positive, $\boxed{-}$ = negative.

Conclusion

A number of regions across the genome were found to be associated with each trait using two different statistical methods. A number of genes and key molecular processes involved in growth and carcass traits have been identified. Future research will involve exploiting high-throughput sequencing to identify causative mutations in these regions that may be responsible for variation in these phenotypes.

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RMIS Project Number 6018

Additive genetic, non-additive genetic and permanent environmental effects for female reproductive traits in seasonal calving herds

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Introduction

Traditional measures of fertility traits for dairy cows have low heritability resulting in a low reliability for genetic merit in cows (Berry et al., 2012). Incorporating non-additive genetic effects and permanent environmental effects into genetic evaluations of fertility traits could provide measures of expected cow performance more reflective of phenotypic performance. The objective of this study was to estimate genetic and environmental components for fertility traits in seasonal calving dairy cows. Such information could be useful in the development of a cow production index, whereby a ranking order for cow production traits are established from genetic and permanent environmental effects.

Materials and Methods

Calving dates, pregnancy diagnoses, service information, as well as animal movements including death and slaughter events between the years 2005 and 2012 were available. Submission (SR21) was defined as the animal being bred within the first 21 days of the breeding season (SR21=1), or not (SR21=0). Only calving to first service (CFS) records between 10 and 250 days were retained. Number of services (NS) up to a maximum of 10 per lactation was used. Pregnancy to first service (PFS) and six-week pregnancy rate (PR6) was defined, using insemination data, pregnancy diagnosis data and, where available, subsequent calving dates. Cognisance was taken of timing of the insemination relative to the end of the AI breeding season, the culling date of the animal, and the date of data extraction. Calving in the first 42 days of the calving season (CR42) was assumed to have happened if the cow calved in the first 42 days of the herd calving season (CR42=1), otherwise not (CR42=0). Only calving intervals (CIV) between 300 and 600 days were retained. However, where a CFS record <150 days existed, a CIV record up-to 800 was permitted within the analysis. Data on estimated foetal gestational age were available from 83,275 reproductive tract ultrasound measures. Assuming a full term gestation of 278 days, predicted calving date was estimated. Predicted calving interval (pCIV) was subsequently calculated, where possible. An additional calving interval trait, pcCIV, which combined predicted and actual calving interval data, with actual calving interval data taking precedence, was also derived. Contemporary groups were defined as herd-year-season of calving and only groups with at least 5 records were retained. A random sample of contemporary groups was retained for variance component estimation. Following editing 764,333 records from 373,877 cows in 10,669 herds remained. Variance components were estimated using repeatability animal models in ASREML (Gilmour et al., 2009). Fixed effects included in the model were contemporary group, parity, heterosis and recombination loss. An additive genetic and a permanent environmental effect across lactations were both included as random effects.

Results and Discussion

Summary statistics for the fertility traits are in Table 1. Heritability estimates for each trait was less than 0.04 which is consistent with the literature (Veerkamp and Beerda, 2007); therefore less than 4% of the phenotypic variation is attributed to additive genetic effects. The repeatability estimates of the fertility traits were all greater than 5% indicating a large permanent environmental contribution. Heterosis effects and recombination loss effects were all greater than zero. As much as 6% of the phenotypic mean of some fertility traits were attributed to heterosis effects, while the respective estimates for recombination loss effects accounted for up to 2% of the mean.

Table 1: Summary statistics including the heritability (h^2) and repeatability (r) of the fertility traits

Trait	***N***	***Mean***	***h²***	***r***
SR21 (%)	118481	63	0.02	0.09
CFS (d)	141624	78	0.04	0.08
NS	144841	1.7	0.02	0.07
PRS (%)	105177	46	0.02	0.05
PR6 (%)	107419	59	0.03	0.11
CR42 (%)	89052	62	0.001	0.08
CIV (d)	137641	399	0.03	0.07
pCIV(d)	15550	398	0.03	0.07
pcCIV(d)	145119	399	0.04	0.07

Heritability standard errors were all <0.004; repeatability standard errors were all <0.007

Conclusions

Repeatability estimates for the fertility traits suggest a significant contribution of permanent environmental effects to phenotypic differences among cows. Coupled with the significant heterosis and recombination loss effects this suggests that a cow production index should account for both non-additive genetic and permanent environmental effects to aid in culling decisions.

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RMIS Project Number 6027

Developing a model of dairy cattle to predict milk production across lactations

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Introduction

Developing experiments to test the effects of various management practices at farm level is difficult and requires significant resources. Modelling biological systems presents significant opportunities to simulate the possible interactions within systems while not realising the costs associated with conventional experiments. However there are many interacting components in biological systems which make the modelling of them difficult and complex (Shalloo et al., 2004). The overall objective of this study was to develop a dynamic, mechanistic and stochastic simulation model of a dairy farm.

Materials and methods

The model described in this paper simulates the milk production of each animal individually, with a daily time step. The dairy cows are represented in the model through a number of complex interactions which include intake, body condition score change, milk production, growth, annual culling and mortality, which is represented by the genetic make up of the herd. The genetics of the animals is included in the model at the start of the simulation with a stochastic component included in order to simulate genetic variation within the herd. Animal intake and performance is simulated based on the French nutrition system (Faverdin et al., 2011). The model is stochastic, dynamic and mechanistic in nature allowing it to react to changing conditions at farm level. Model simulation requires an initial description of the cattle (age, body weight, body condition score, etc) and management rules around the farm (drying, culling, feeding) as well as the length of time in which the simulation is being carried out (e.g. 1 month, 1 year, etc). In this study the model has been evaluated and validated by simulating data from Curtin's farm over the period 2009 to 2011. The model was parameterised with the initial Curtins data and was simulated over a three year period. The model was simulated 50 times to ensure that the overall model was in a steady state. The Curtins experiment measured the effect of three stocking rates (SR) SR1 3.28 $cow.ha^{-1}$, SR2 2.92 $cow.ha^{-1}$, SR3 2.51 $cow.ha^{-1}$ (McCarthy et al., 2012). The outputs from the model were compared to the recorded weekly data to compare model accuracy at the herd level. A number of statistical procedures were used to determine model accuracy which included root mean square error (RMSE) and the relative predicted error (RPE) for milk production. The model outputs and the actual data was compared across 4 periods, namely, whole year (2-40 weeks), spring (2-16 weeks), summer (17-25 weeks and autumn (26-40 weeks), with the analysis carried out for primi- and multi- parous cows separately.

Results and Discussion

A general guide for model usefulness centres on an RPE of less than 10% (Delagarde et al., 2011): In this analysis daily milk production across the four different periods had an RPE of less than 10% except for primiparous cows on SR1 in spring (Table 1). The model adjusted to the different stocking rates by predicting a higher average daily milk production for cows stocked at lower stocking rates (21.68kg/cow fat and protein corrected milk) over the whole year for multiparous cows with a corresponding figure for the higher stocking rate (19.70 kg/cow fat and protein corrected milk). The RPE of the model for primiparous cows in higher stocking rates in early lactation is below requirement, it is anticipated that this is associated with a feed deficit in early lactation and the partition of feed for maintenance, growth and milk production during this period of deficit.

Conclusion

This model accurately predicted milk production at the herd level across parities, years and stocking rates. Further research is required to validate the model across international studies and to improve the model accuracy for primiparous cows in early lactation.

Acknowledgement

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Table 1: Comparison between the average real (R) and simulated (S) daily milk production of the dairy cattle for the stocking rate 3.28 (SR1), 2.92 (SR2) and 2.51 (SR3) for the multiparous and primiparous cow.

		SR1				SR2				SR3			
	lactation week	mean R (kg)	mean S (kg)	RMSE (kg)	RPE (%)	mean R (kg)	mean S (kg)	RMSE (kg)	RPE (%)	mean R (kg)	mean S (kg)	RMSE (kg)	RPE (%)
multiparous	2-40	20.27	19.70	**1.03**	**4.00**	20.11	19.94	**1.39**	**5.40**	21.90	21.68	**1.40**	**5.21**
	2-16	25.63	24.87	**1.35**	**5.26**	24.75	25.38	**1.46**	**5.68**	26.81	27.59	**1.43**	**5.35**
	17-25	19.59	19.71	**0.29**	**1.36**	19.58	20.20	**0.89**	**4.28**	21.69	21.94	**0.73**	**3.15**
	26-40	15.33	14.52	**0.92**	**5.26**	15.79	14.34	**1.54**	**8.37**	17.12	15.61	**1.63**	**8.39**
primiparous	2-40	15.73	15.12	**1.90**	**9.51**	15.96	16.05	**1.40**	**7.36**	17.07	17.59	**0.94**	**5.39**
	2-16	19.76	17.25	**2.69**	**13.47**	19.21	18.01	**1.70**	**8.91**	19.75	19.73	**0.64**	**3.65**
	17-25	14.93	14.63	**1.08**	**6.58**	15.38	15.89	**0.98**	**5.82**	16.96	17.36	**0.77**	**4.29**
	26-40	12.18	13.28	**1.20**	**9.50**	13.06	14.19	**1.28**	**9.28**	14.46	15.59	**1.24**	**7.58**

RMIS Project Number 6159

Risk factors associated with reproductive tract status

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Introduction

Ultrasound of the reproductive tract is a non-invasive procedure that is routinely carried out to assess reproductive tract status (Mee *et al* 2009). The objective of this study was to identify the risk factors associated with fertility phenotypes derived from reproductive tract ultrasound measures in dairy and beef cattle.

Materials and Methods

Data were available on 148,990 reproductive tract ultrasound records from 75,966 cows in 843 Irish herds between March 2008 and October 2012. All ultrasound measurements were preformed by a single company (Reprodoc Ltd., Fermoy, Co. Cork, Ireland; http://www.cowsdna.com/). Ultrasound was performed transrectally using a real-time B-mode ultrasound scanner with a 5MHz transducer. A measurement of the right ovary, left ovary and a cross section of the uterine horns were taken and a reproductive classification was determined. Cycling was defined as the presence of a corpus luteum (CL) in non-pregnant animals on either ovary at the time of examination; the absence of a CL was defined as not cycling. Early ovulation was defined if the ultrasound scan was within 15 days of calving and a CL was present on either ovary. Delayed ovulation was only defined in cows examined greater than 40 days post calving that were not pregnant at the time of examination. If no CL was present then delayed ovulation had occurred otherwise delayed ovulation had not occurred. Cystic ovaries were defined as the presence of a fluid filled structure greater the 30 mm in diameter present on either ovary. Any data collected after a previous ultrasound scan that indicated treatment was required was discarded. After editing 136,212 records on 72,954 animals from 806 herds remained. Not all records available had measures for all the traits.
Factors associated with the logit of the probability of a positive outcome for each of the fertility traits were determined using separate multivariate logistic regression in PROC GENMOD (SAS 2009). A binominal distribution of the data was assumed. Factors considered for inclusion in the model included parity, dystocia, herd type, days since calving, year of examination, month of examination, breed of dam, heterosis and recombination loss of the dam. Animal was included in the model as a repeated measure.

Results and Discussion

The incidence of cycling (n=38,207), early ovulation (n=1,315), delayed ovulation (n=37,033) and cystic ovaries (n=53,515) were 88.3%, 25.0%, 7.9% and 3.9% respectively. Cows in beef herds were less likely to be cycling at the time of scan (OR=0.51, 95% CI=0.36-0.92, P=0.0001) than cows in dairy herds. Beef cows were more likely to have delayed ovulation (OR=2.60 95% CI=1.66-4.07, P<0.0001) than dairy cows. There was no association between herd type and early ovulation and cystic ovaries. Parity 5+ cows had a lower likelihood of cystic ovaries than parity 1 (OR=0.52 95% CI=0.44-0.61, P<0.0001) and parity 2 cows (OR=0.70 95% CI=0.59-0.82, P<0.0001). Parity was not associated with delayed ovulation, early ovulation or cycling. As days post calving increased, the likelihood that the cow had resumed cycling increased (P<0.0001). Days post calving was also associated with delayed ovulation (P<0.0001), the further the ultrasound scan was from 40 days postpartum the less likely the cow was to have delayed ovulation. Days post calving did not have an association with either cystic ovaries or with early ovulation. Holstein (P=0.0002) and Belgian Blue (P=0.0043) animals were less likely to have resumed cycling at the time of the scan than other breeds. Holstein (P=0.0002) and Belgian Blue (P=0.004) were also more likely to have a delayed ovulation. The month of examination and year of examination was associated with cycling (P<0.0001), delayed ovulation (P<0.0001) and cystic ovaries (P<0.0001). Month of examination was associated with early ovulation (P=0.0003) but year of examination was not. There was no association with the fertility traits and dystocia, heterosis or recombination loss.

Conclusions

Beef cows were more likely to have poorer fertility than dairy cows. First and second parity cows had a lower likelihood than parity 5+ animals to have cystic ovaries which has an adverse effect on fertility. The Holstein and Belgian Blue breeds had poorer fertility than other breeds, both taking longer to resume cycling post calving.

Acknowledgements

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RMIS Project Number 6160

Twinning and multiple ovulations in Irish dairy and beef cows

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Introduction

Incidence of twinning and multiple ovulations in Irish cattle is unknown. Furthermore, the risk factors associated with both traits is not extensively known internationally. The objective of this study was to quantify the incidence of both twinning and multiple ovulations in Irish dairy and beef cows, and the risk factors associated with each.

Materials and Methods

Information on dam and calf identification as well as calving date, parity of the dam, breed of dam, calf gender, dystocia and stillbirths was extracted from the Irish Cattle Breeding Federation database. Dystocia was coded on a scale from 1 to 4 (1 = no assistance/unobserved; 2 = slight assistance; 3 = severe assistance; and 4 = veterinary assistance/including caesarean). Stillbirths were coded as a binary variable (0 = not stillborn; 1 = stillborn). Where the calving resulted in twins, dystocia for that calving was the most severe record for either calf, and stillbirth was assumed to have occurred if either of the twins died.

Only calving events resulting in either a singleton or twin birth between the years 2002 and 2012 were retained. A total of 17,665,889 calving events from 102,543 herds remained. This dataset was used to quantify the incidence and sex ratio of twin calves born. In order to examine the risk factors associated with twin calves born, a subset of the main dataset was used for the years 2011 and 2012, which contained only records from years where herds recorded at least one twin birth. This dataset consisted of 2,389,302 calving events from 36,323 herds. Data were also available on 148,990 ultrasound records of the reproductive tract of 75,966 cows in 843 Irish herds between March 2008 and October 2012. Multiple ovulations were described as the presence of two corpora lutea (CL) either on one ovary or one CL on each ovary during the diestrous stage of the cycle. While a single ovulation was defined as the presence of one CL during the diestrous phase. After data editing 42,801 records from 29,882 cows remained. Factors associated with the logit of a twin birth or multiple ovulation were determined using multivariate logistic regression in PROC GENMOD (SAS, 2009) assuming a binomial distribution of the data. Factors considered for inclusion in the models were herd-type (i.e., beef or dairy), year, month of calving or scanning, parity of dam, and breed proportion of the dam. The association between the occurrence of a twin birth and both dystocia and stillbirth was quantified using ordinal and logistic regression, respectively in PROC GENMOD (SAS, 2009); a cumulative logit link function was used for the ordinal regression as well as accounting for the multinomial distribution of the data.

Results and Discussion

The incidence of twinning in the entire data was 1.75% and varied by year from 1.64% (2010) to 1.93% (2007) with no obvious trend. Of the twin births, 28.13% were both heifer calves, 27.37% were both bull calves and 44.50% of twins were mixed. In herds that recorded at least one twin birth, factors associated with the likelihood of a twin birth were herd-type (i.e., dairy or beef), parity, breed, year and month of calving. The incidence of twin births increased consistently with parity where incidences of 1.38%, 2.94%, 3.60%, 4.01% and 4.92% were observed for parity 1 to 5 respectively. The likelihood of twinning increased ($P<0.0001$) consistently with increased parity with an odds ratio relative to fifth parity animals of 0.31, 0.67, 0.79 and 0.86 for parity one to four, respectively. The predicted probability of a twin birth in a parity 1 to 5 Holstein cow calving in March was 1.1%, 2.4%, 2.8%, 3.0% and 3.4%, respectively. The odds of a twin birth in a beef herd was 1.67 times (95% CI: 1.62 to 1.73) that of a dairy herd. The incidence of twinning peaked between July and September, where the highest incidence of twin births occurred in July (5.79%). Twinning rate was greatest in Angus, Charloais and Simmental bloodlines.

The incidence of multiple ovulations in cycling cows was 6.71%. Factors associated with the likelihood of a multiple ovulation were parity, days calved, breed, month and year of scan. The likelihood of multiple ovulations increased ($P<0.0001$) as parity increased with an odds ratio relative to fifth parity animals of 0.69, 0.68, 0.81 and 0.87 for parity one to four, respectively; the respective incidence of multiple ovulations was 5.82%, 6.01%, 7.05%, 47.02% and 7.83% for parity 1 to 5. The odds of multiple ovulations did not differ between dairy and beef herds, however, within breeds, cows with Simmental bloodlines had the highest rate of multiple ovulations compared to all other breeds investigated ($P<0.05$). Additionally, the likelihood of multiple ovulations increased with interval from calving ($P<0.0001$).

The incidence of stillbirths was 2.17%. Twin births had a 3.7 times (95% CI: 3.56 to 3.87) greater odds of having at least one stillborn calf compared to singletons. The odds of a more difficult calving was almost twice (OR=1.87; 95% CI 1.81 to 2.80) for twin births compared to singletons.

Conclusions

The overall incidence of twin births (1.75%) and multiple ovulations (6.71%) in Ireland is low. The likelihood of twin pregnancies and multiple ovulations occurring in cows increased both with increasing parity and in Simmentals, indicating a relationship between the two traits. The probability of stillbirths and dystocia increased with the incidence of twin births

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RMIS Project Number 6160

Genetic parameters of novel fertility traits derived from reproductive tract ultrasound

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Introduction

Traditional fertility traits are lowly heritable (Berry et al., 2012) thereby requiring large progeny group sizes to achieve high accuracy of selection and rapid genetic gain. The fertility breeding goal trait currently included in the Irish national dairy cattle breeding objective, the economic breeding index, is calving interval. Calving interval is a complex fertility trait and is a function of several fertility sub-traits such as the ability to resume cyclicity early post-partum, express oestrus, conceive and establish pregnancy as well as gestation length. Some of these traits are antagonistically genetically correlated (Berry et al., 2012). Genetic evaluations for the individual component traits of fertility could help resolve genetic antagonisms and achieve more rapid genetic gain for fertility. The objective therefore of this study was to estimate genetic parameters for novel fertility traits derived from ultrasound examination of the reproductive tract.

Materials and Methods

Data were available on 148,990 reproductive tract ultrasound records from 75,966 cows in 843 Irish herds both dairy and beef, between March 2008 and October 2012. All ultrasound measurements were preformed by a single company (Reprodoc Ltd., Fermoy, Co. Cork, Ireland; http://www.cowsdna.com/). Ultrasound was performed transrectally using a real-time B-mode ultrasound scanner with a 5MHz transducer. To identify reproductive classifications, a measurement of right ovary, left ovary and a cross section of the uterine horns were taken**.** The presence of a corpus luteum (CL) in non-pregnant animals at the time of the ultrasound scan was defined as cycling; the absence of the CL was defined as not cycling. Delayed ovulation was only defined in cows which were examined greater than 40 days postpartum and were not pregnant. The absence of a CL was defined as delayed ovulation, otherwise ovulation was assumed to have previously occurred. Multiple ovulation was defined as the presence of two or more CLs present on one or both ovaries at the time of the ultrasound scan. Ovarian cysts were defined as the presence of a fluid filled structure greater the 30 mm in diameter present on either ovary. Only cows with a known sire were retained. Contemporary groups of herd-year-season of calving were defined for each of the traits. Only contemporary groups with at least 5 records for each of the traits were retained.

Variance components for each of the fertility traits were estimated using repeatability animal linear mixed models in ASREML (Gilmour et al., 2009). Fixed effects included in the model were contemporary group, parity, and days since calving. The random effects in the model were direct additive effect for animal, the permanent environment effect within lactation and the permanent environmental effect across lactation.

Table 1. Number of records (N), mean incidence, heritability (h^2 (standard error)), repeatability (r^2 (standard error)) and genetic standard deviation (σ_g).

Trait	***N***	***Mean***	***h^2 (se)***	***r^2 (se)***	***σ_g***
Cycling	32543	86.90%	0.11 (0.01)	0.85 (0.01)	0.10
Delayed ovulation	27152	8.18%	0.10 (0.01)	0.80 (0.01)	0.09
Mulitple ovulation	36661	5.69%	0.02 (0.01)	0.05 (0.02)	0.03
Cystic	36661	4.00%	0.07 (0.01)	0.27 (0.01)	0.01

Results and Discussion

Summary statistics for the different fertility traits are in Table 1. Heritability estimates for the fertility traits, with the exception of multiple ovulation, were greater than generally observed for most traditional measures of fertility (Berry et al., 2012). The repeatability of these traits was also larger than observed for traditional measures of fertility (Kelleher et al., 2013). Moreover, considerable genetic variation existed for these traits implying that genetic selection for these traits will be fruitful. The genetic correlation with calving interval for cycling, delayed ovulation, multiple ovulations and cystic ovaries was -0.22 (0.14), 0.30 (0.13), 0.02 (0.18) and 0.32 (0.44), respectively. These correlations indicate selecting for these novel fertility traits could improve the accuracy of selection for calving interval.

Conclusions

Heritable genetic variation for these novel fertility traits exist. Because these data are now being routinely collected and uploaded into the national database, breeding values for these traits can be routinely estimated and incorporated into national breeding strategies for improved fertility.

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RMIS Project Number 6160

Mathematical modelling of lamb growth rate

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Introduction

Mathematical models have been extensively used in different species to summarise and predict live-weight (Goonewardene et al., 1981; Gbangboche et al., 2008). Growth curves may be broadly classified into functions with a given form or polynomials. The objective of this study was to compare different mathematical models fitted to lamb live-weight data with particular emphasis on the ability to predict futuristic live-weight.

Materials and Methods

The data analysed were obtained from the Athenry Research Demonstration flock for the year 2012. The animals form part of a stocking rate x genotype study that was run across a selection of breeds commonly used in Irish commercial sheep population. A total of 6,594 weight records were collected on 556 lambs ranging in age from 0 to 205 days of age. Several growth functions (Table 1), as well as, polynomial regressions models were fitted to the live-weight data of each animal individually.

Table 1. Growth functions

Growth Function	***Equation***
Von Bertalanffy	$Y_t = A\,(1-Be^{-kt})^3$
Gompertz	$Y_t = A\,\exp(-Be^{-kt})$
Richards	$Y_t = A\,(1-Be^{-kt})^m$
Logistic	$Y_t = A\,/\,(1-Be^{-kt})$
Brody	$Y_t = A\,(1-Be^{-kt})$

[1]Y_t = *live-weight,* A = *asymptotic mature weight,* B = *constant of integration,* k = *maturing rate,* m = *inflection parameter*

The model was then progressively built up to a linear mixed model where the parameters A and k (described above) were included as both fixed and random effects. Random regression polynomial functions (RRM) were also fitted.

The goodness of fit for each growth function to the data was quantified using the R^2 and the root mean square error (RMSE) statistic. To test the accuracy of each model to predict futuristic live-weight, live-weight data post 100 days of age in 25% of the animals were masked. Three different models were used to predict the masked weights: 1) the Von

Bertalanffy growth function, 2) Von Bertalanffy with asymptotic weight, constant of integration and maturing rate included as random effects and 3) a linear random polynomial regression. The correlation between the predicted and actual weight of the masked weights was used to determine the accuracy of prediction for the different models.

Results and Discussion

Table 2 outlines the summary statistics of the fit of the different models to the live-weight data, when all were fitted with no random components except for the polynomial model. The mean R^2 and RMSE values ranged from 0.90 to 0.99 and 1.39 kg to 11.04 kg, respectively for the different models. The R^2 and RMSE values, within animal, for the Von Bertalanffy growth function with asymptotic mature weight, constant of integration and maturing rate individually included as random effects ranged from 0.98 to 0.99 and 1.46kg to 2.39kg, respectively. A linear random regression fitted the growth data (R^2= 0.98) better than the lower order polynomial.

Table 2. Growth functions with corresponding R^2 values and RMSE values.

Function	***R^2 value***	***RMSE (kg)***
Von Bertalanffy[1]	0.99	1.39
Gompertz[1]	0.93	11.04
Richards[1]	0.94	8.34
Logistic[1]	0.90	7.17
Brody[1]	0.99	1.52
Polynomial	0.98	1.57

[1] Non-linear fixed effects models.

The Von Bertalanffy fixed effect model predicted the masked weights least accurately (0.67). The Von Bertalanffy mixed model equation, with maturing rate included as a random effect, and the random regression polynomial, had correlation values between actual and predicted weights of 0.90 and 0.89, respectively. The Von Bertalanffy mixed model equation, with asymptotic mature weight included as a random effect had the strongest correlation (r= 0.97), indicating that it was the best model for the prediction of futuristic weights. The RMSE value for this model was 1.53kg, signifying 68% of predicted live-weight records were within ± 1.53kg of the actual weights.

Conclusions

The Von Bertalanffy mixed model growth function with asymptotic mature weight included as a random effect had the highest accuracy when it came to predicting weights throughout all stages of growth. This result in the prediction of live-weight is extremely promising in striving to produce a growth prediction tool for farmers.

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RMIS Project Number 6195

Development of a new management sub-index for the Irish dairy cattle economic breeding index

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Introduction

Consultation with the Irish dairy industry clearly highlighted the necessity to generate estimates of genetic merit on individual animals for management traits, especially milking speed and temperament. The objective of this study was to use information generated from DIY milk recording meters in Ireland to derive milkability traits for inclusion in the Irish national dairy cattle breeding program.

Materials and Methods

Milk flow data were available from 235,036 milking events from 74,607 cows in 1,075 Irish dairy herds between September 2011 and July 2012. All records were from cows milked twice daily between 5 and 305 days post-calving. Milk yield was recorded for both morning and evening milkings but only one milk sample was taken for the quantification of milk composition. The $\log_{10}$ of somatic cell count was used to calculate somatic cell score (SCS). Milk flow rates and total milking duration data were available for all milkings. Information on cow temperament and incidence of mastitis were available from the national Dairy Efficiency Program. Herd-owners were asked to score each cow for temperament, on a scale of 1 ("very good") to 5 ("very poor"). Herds retained had to report at least one incidence of mastitis and some variation in cow temperament to be considered for inclusion in the analysis. A total of 326,081 records from 5,137 herds remained. Only Holstein-Friesian cows with a known sire were retained.Variance components for each of the milking characteristic traits were estimated using repeatability animal linear mixed models in ASREML (Gilmour et al., 2009). Fixed effects included a two-way interaction between herd and test-date, together with the main effects of parity, stage of lactation, milking session (AM or PM). Two-way and three way interactions between parity, stage of lactation and milking session were also included. The random effects included in the model were the direct additive genetic effect for animal, a permanent environmental effect within lactation, and a permanent environmental effect across lactations. Residual milking duration (RMD) was defined as milking duration genetically independent of milk yield; residual milking duration including SCS (RMDS) was also defined, at the genetic level, as milking duration genetically independent of both milk yield and SCS. Covariances between the milkability traits and both temperament and mastitis were estimated using a series of bivariate sire models.

Economic values for milkability and temperament were calculated assuming a labour cost of €12.44/hour. For milking duration twice-a-day milking for 305 days in a 100 cow herd with 12 milking units was modeled. The impact of animal temperament on the likelihood of injury or death derived from national statistics was included in the derivation of the economic value for temperament.

Results and Discussion

The duration of each milking was, on average, 393 seconds (i.e., 6.55 minutes) although considerable variation (standard deviation of 116.8 seconds) was observed. The heritability of milk yield and milk composition varied from 0.17 to 0.35; the repeatability varied from 0.36 to 0.51. The heritability of milking duration, average milk flow (AMF), and maximum milk flow (MMF) varied from 0.17 and 0.21 while the repeatability varied from 0.31 to 0.50. The heritability of RMD and RMDS was 0.21 and 0.18, respectively. The genetic standard deviation of RMD and RMDS was 40.6 seconds and 37.6 seconds, respectively. The heritability of temperament was 0.10 (se=0.01) which is consistent with international estimates.

Milking duration was not genetically correlated with milk yield (r=0.01) but was negatively genetically correlated (r=-0.38) with SCS. When milk yield was included as a covariate in the statistical model of milking duration, the genetic correlation between milking duration and both milk yield and SCS was 0.01 and -0.32, respectively. Milk yield was positively genetically correlated with AMF (0.69) and MMF (0.43) as were the genetic correlations between SCS and both AMF (0.18) and MMF (0.30).

Milking duration was negatively correlated with mastitis (-0.17). The genetic correlation between RMD and RMDS with mastitis was -0.17 and 0.14, respectively. Milking duration was positively genetically correlated with cow temperament score (0.25) indicating that temperamental animals had longer milking duration. The genetic correlation between RMD and RMDS with temperament was 0.25 and 0.40, respectively. The economic weight for RMD and temperament was -€0.25/second and -€33.69, respectively. Within the economic breeding index RMD and temperament would receive a relative emphasis of 2.20% and 2.05%, respectively.

Conclusions

Considerable exploitable genetic variation in milking duration independent of milk yield and SCS exists. Milking duration and temperament traits are of economic importance constituting 4.22% of the relative emphasis within the economic breeding index for the selection of profitable Irish dairy cattle.

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RMIS Project Number 6195

The relationship between milk yield and predicted transmitting ability for maternal weaning weight across four cow breed types

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Introduction

Predicted transmitting ability (PTA) is the average genetic value for a given trait that an animal transmits to its offspring. Milk yield, is an important trait in determining lifetime live-weight performance in spring-calving suckler calf-to-beef systems (Murphy *et al.*, 2008). At present breeding values for maternal weaning weight are generated using maternal weaning weights and on-farm milk scoring. Low levels of sire ancestry recording in the beef suckler cow population coupled with a lack of weight recording in commercial suckler herds has unfavorable implications for genetic evaluation of maternal weaning weight (Evans and Pabiou, 2012). This study aimed to examine the relationship between the cow milk yield and estimated PTA for maternal weaning weight.

Materials and Methods

Data from the Derrypatrick research herd comprising 105 progeny of spring-calving (mid-March) first-parity, Limousin × Holstein-Friesian (25) (LF), Limousin × Simmental (LS) (25), Charolais × Limousin (CL) (30) and Charolais × Simmental (CS) (25) beef suckler cows was used. Intake, milk yield and performance of the cow breed types, and pre-weaning growth of their calves was presented previously (Minchin and McGee, 2011). Milk yield was estimated once during the grazing season (July 2010) using the weigh-suckle-weigh procedure (McGee et al., 2005). Suckling was prevented by using a calf muzzle so that calves were present with the dam at all times to minimise alterations in the grazing behaviour of the dam. Following an initial suckling-prevention period of 8 h and a preliminary suckling out, calves were re-muzzled and weight changes before and after suckling were recorded 16.5 to 17 h later. The difference between the pre- and post-suckling weights was adjusted to a 24-h basis providing an estimate of daily milk production. Calf live weight was also recorded every three weeks during the grazing season. Predicted transmitting ability coefficients for maternal weaning weight from the April 2012 Irish domestic genetic evaluations were calculated for the 105 females included in the study. The correlation between milk yield and the dams PTA for maternal weaning weight was examined. Animals were ranked into 5 categories representative of the beef "€uro-star" ratings based on milk yield: 5 star (Top 20 % (mean 5 star for all breeds: 11.96); 4 star (80-60 %); 3 star (60-40 %); 2 star (40-20 %) and 1 star (0-20 %) (mean 1 star for all breeds: -7.24).

Results and discussion

Average estimated milk yield was 6.92 kg day^{-1} across all breeds and ranged from 1.38 to 13.18 kg day^{-1}. Distribution of milk yield across the four cow breed types is presented in Figure 1. Milk yield was highest for LF with 40 % of records in excess of 10 kg day^{-1} and lowest for CL with 53 % of records less than 6 kg day^{-1}. The PTA for maternal weaning weight across the 5 categories ranged from 20.95 to -11.06. Cows with the highest ranking PTA category for maternal weaning weight had the highest recorded milk yield (Table 1). A difference of 8.2 kg in recorded daily milk yield was observed between the highest and lowest ranking PTA category for milk yield. This difference in milk yield corresponded to a difference of 42 kg in calf live-weight between cows ranked in the top 20% versus the bottom 20% (Table 1). A strong positive correlation (0.56) was recorded between milk yield and the dams PTA for maternal weaning weight.

Table 1. Ranking of milk yield and corresponding PTA for maternal weaning weight

	Milk yield (kg)		***Calf weight (kg)***
Ranking	Recorded	PTA	03/08/2010
100-80%	10.7	12.03	197
80-60%	8.1	4.88	186
60-40%	6.8	4.65	179
40-20%	4.6	1.89	176
20-0%	2.5	-3.17	155

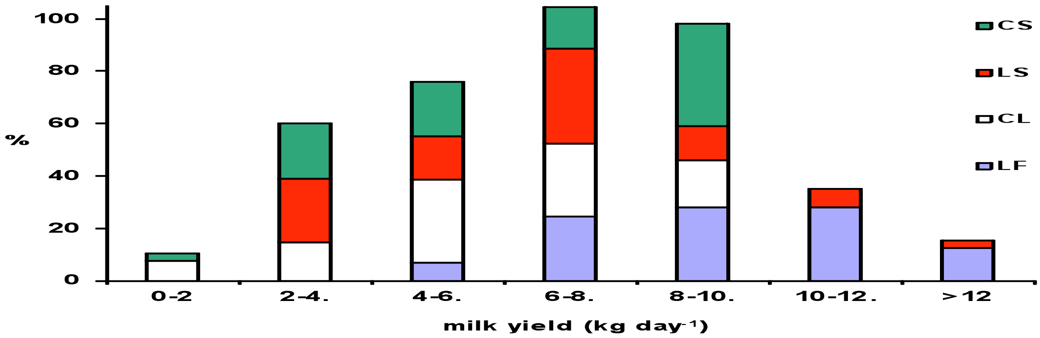

Figure 1. Distribution of estimated milk yield across the four cow genotypes.

Conclusions

The strong correlation recorded between milk yield and the dams PTA for maternal weaning weight indicates that selecting for maternal weaning weight will result in cows with higher milk yields and heavier calves at weaning.

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Genetic parameters for the Irish sheep population

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Introduction

A new genetic evaluation programme was launched for the Irish sheep population in 2009. These evaluations allow farmers to select animals across a range of performance traits including lambing, growth, and maternal traits. Although international studies have demonstrated ample genetic variation in performance traits (Safari et al., 2005), the genetic variation in such traits in Ireland has not been quantified. The objective of this study was to estimate genetic parameters for Irish sheep data for a variety of traits.

Materials and Methods

Data from 339,809 animals between the years 1988 to 2012, across a variety of traits were obtained from the Sheep Ireland database. The data were divided into three distinct trait groups: lambing traits (lambing ease and lamb survival), growth traits (weaning weight, ultrasonic fat and muscle measurements) and a reproductive trait (number of lambs born; NLB). Lambs, or ewe in the case of NLB were discarded if sire, dam, maternal grandsire, flock of birth or date of birth were unknown. For lambing traits, only lambs with a recorded birth type of 1 (singleton) to 4 (quadruplet) and a rearing rank of 1 to 3 were retained. Only lambs with a known lambing ease (1=no assistance, 2=some assistance, 3=severe assistance and 4=veterinary assistance) were retained when lambing ease was the dependent variable. Similarly when lamb survival was the dependent variable only lambs with recorded lambing survival (1= dead at birth and 2= alive at birth) were included. For weaning weight only lambs with live weights records between 20 and 55 kg and aged between 66 and 130 days were retained. Ultrasonic scan records were retained on lambs 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. For NLB only one record per year was retained for each ewe. Contemporary groups were defined as flock-year-season of birth, or lambing in the case of NLB. Only records from contemporary groups with at least 4 other records were retained. Phenotypic and genetic variance components for all traits were estimated using linear animal mixed models in ASREML (Gilmour *et al.,* 2011). For the lambing and growth traits, the univariate animal model was progressively built up to include a maternal genetic effect and a permanent environmental maternal effect across parity. The log likelihood ratio test between nested models was used to determine whether the addition of extra random components improved the fit to the data. For the lambing traits the fixed effects considered for inclusion in the model were contemporary group, gender, birth type, parity of dam, dam age nested within parity, and the main breed of both sire and dam. Fixed effects included in the model for the growth traits included contemporary group, age at weighing or scanning (linear and quadratic effect), and gender. When muscle and fat score were the dependent variables, weight at scanning was also included as a fixed effect. For NLB, parity, age of animal nested within parity, animal breed and contemporary group were included as fixed effects.

Results and Discussion

The proportion of ewes that experienced severe lambing difficulty (lamb ease score >2) was 12% and the proportion of lambs reported dead was birth was 11%. Lambs weighed on average 33 kg at weaning and were on average 96 days of age. The proportion of ewes with multiple lambs at birth (NLB >1) was 51%.

Table 1. Number of records (n), direct heritability (h^2_d), maternal heritability (h^2_m), and the maternal repeatability (R_m) for all traits[†]

Trait	*n*	h^2_d	h^2_m	R_m
Lambing Ease	14,829	0.16	0.04	0.22*
Lamb Survival	11,578	0.07	0.004	0.09*
Weaning weight	9,992	0.21	0.06*	0.24*
Muscle score	39,017	0.25	0.02*	0.05*
Fat score	39,005	0.19	0.004	0.04*
NLB	70,999	0.07	-	-

[†] s.e. of heritabilities varied from 0.004 to 0.03. *Maternal heritability and maternal repeatability different (P<0.05) from zero

The direct heritability of all traits ranged from 0.07 (number of lambs born) to 0.25 (muscle score; Table 1). The coefficient of genetic variation across all traits ranged from 3.75 (muscle score) to 20.75 % (fat score). The estimated maternal heritabilities ranged from 0.004 (lamb survival and fat score) to 0.06 (weaning weight). Significant maternal heritabilities were observed for weaning weight and muscle score indicating the importance of milk yield for growth traits. The maternal repeatability was significant across all lambing and growth traits and ranged from 0.05 (muscle score) to 0.24 (weaning weight).

Conclusions

Significant genetic variation existed for lambing, growth and reproductive traits within the Irish sheep population. Selection of such traits as part of a breeding programme will allow for genetic gain to be achieved across all traits.

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Improvements in the health sub-index for the Irish dairy cattle economic breeding index

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Introduction

The health sub-index in the economic breeding index (EBI) includes the goal traits mastitis, somatic cell score (SCS), and lameness. Currently, the economic values for mastitis and lameness are applied to SCS and the linear type classified locomotion, respectively, via an assumed respective genetic correlation with mastitis and lameness of 0.70 and -0.40. This is not optimum but was undertaken originally because of the lack of routine data on both mastitis and lameness. However, mastitis and lameness data are now collected through farm software packages, animal events, and the national Dairy Efficiency Programme (DEP). The objective of this study was to attempt to improve the health sub-index of the current EBI through the use of cow health data routinely collected nationally.

Materials and Methods

Data on mastitis and lameness were available from the DEP between the years 2011 and 2012 on 501,888 dairy cows from 6,194 herds. Mastitis was recorded by farmers, on a per lactation basis, as 1) no case, 2) one case or 3) at least two cases; lameness was recorded using the same approach. For the purposes of this study, both traits were dichotomised as 1) no case or 2) at least one case. Data from herds that failed to report any mastitis or lameness were discarded and only Holstein-Friesian cows with a known sire were retained. Contemporary groups of herd-year-season of calving were generated and only groups with at least 5 records were retained.

A total of 539,841 health records recorded by farmers through either farm software packages or the Animal Events system were also available. Only records on mastitis, lameness, grass tetany, milk fever, left and right displaced abomasums and retained afterbirths were retained. Recorded mastitis and lameness events were used to update the DEP data. All other diseases were merged into a single variable “other diseases”. Linear type trait information was available on 151,077 first parity Holstein-Friesian cows scored between the years 1993 and 2012. Only the first record in time per cow scored between 5 and 330 days post-calving was retained and only cows with a known sire, and calving for the first time between 20 months and 38 months of age were retained. All traits were standardised to a common variance within field officer-by-year. Contemporary group was defined as herd-date of classification and only contemporary groups with at least five records were retained. A random sample of herds was taken to facilitate the estimation of variance components. A total of 96,678 records were available for both mastitis and lameness, 10,688 were available for “other diseases”, and 51,039 were available for type traits. Variance components were estimated using animal linear mixed models in ASREML (Gilmour et al., 2009). Covariances were estimated using a series of bivariate sire linear mixed models. Fixed effects included in the model for the animal health traits were contemporary group, parity, heterosis and recombination loss. Breed proportion was accounted for through the use of pedigree groups. Economic values for mastitis, SCS, and lameness were calculated as outlined in detail by Berry et al. (2007).

Results and Discussion

The incidence and heritability of mastitis was 0.12 and 0.02 (se=0.004), respectively. The incidence and heritability of lameness was 0.11 and 0.04 (se=0.006), respectively. The incidence and heritability of 'other diseases' was 0.05 and 0.01 (se=0.01), respectively. The low heritability of these traits is consistent with the generally low heritability estimates reported internationally for health measures from field data (Berry et al., 2011). The genetic correlation between mastitis and lameness was 0.69 (se=0.07) while the genetic correlation of 'other diseases' with mastitis and lameness was -0.03 (se=0.24) and -0.33 (se=0.20), respectively. The genetic correlation with SCS for mastitis and lameness was 0.73 (se=0.07) and 0.20 (se=0.10), respectively. Genetic correlations between mastitis and the udder type traits varied from -0.12 to 0.19 with the exception of a negative correlation (-0.32; se=0.10) with udder depth and a positive correlation (0.31; se=0.09) with teat length. Genetic correlations between the feet and legs related type traits and lameness were all weak varying from -0.13 (locomotion) to 0.14 (foot angle). The economic values on mastitis, lameness and SCS were -€77.10, -€54.26 and -€43.49, respectively. The standard deviation of the health subindex for AI bulls, with reliability >70% for the sub-index, was €5. A correlation of 0.944 existed between high reliability (i.e., >70%) bull EBI values based on the current EBI and the EBI with the new proposed health sub-index.

Conclusions

The goal traits of mastitis, SCS, and lameness are now included in the EBI with an emphasis of 3.35%. Research is underway on new health traits to include in future revised versions of the health sub-index.

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Accuracy of Irish beef genetic evaluations

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Introduction

National genetic evaluations provide information for selection decisions to increase long-term performance of the national herd. The usefulness of genetic evaluations, however, is a function of how accurately they reflect actual phenotypic performance. Previous assessments of the accuracy of the terminal genetic evaluations (Campion et al., 2009) have shown that differences in genetic merit are reflected in differences in phenotypic performance. No Irish study, however, has attempted to evaluate how estimates of genetic merit for maternal traits are reflected in phenotypic differences. The objective of this study was to quantify, using national data, the difference in phenotypic performance in maternal-related traits among animals differing in genetic merit.

Materials and Methods

Predicted transmitting ability (PTA) of all male animals from the March 2011 Irish domestic genetic evaluations were available. Traits considered included age at first calving, calving interval, survival, and both direct and maternal weaning weight. Phenotypic performance data from beef herds recorded between April 2011 and June 2012 were also available; these data therefore did not contribute to the genetic evaluations. Calving dates from 924,427 calving events were available across 36,040 beef herds. Age at first calving was defined as the number of days between birth and first calving. Calving interval was defined as the number of days between two consecutive calving events for the same cow; only calving intervals between 300 and 800 days were retained. Survival was defined as whether a cow survived from one lactation to the next. A total of 160,062 weaning weight records were available. Weanlings were defined as animals aged between 6 and 9 months of age and only weanlings weighing between 150 and 600 kg were retained. Across all traits, only animals with a known sire or maternal grandsire were retained. Herd-year-season contemporary groups were generated separately for each trait. With the exception of survival the association between PTA for each of the traits and phenotypic performance for the corresponding trait was quantified using a fixed effects model in PROC GLM (SAS, 2012). For survival the logit of the probability of an animal surviving to the subsequent lactation was modelled using logistic regression in PROC GENMOD (SAS, 2012). For all traits the estimated breeding value (EBV) for each animal was defined as the sum of the sire PTA and half of the maternal grandsire PTA. For weaning weight the maternal genetic merit effect was defined as dam's sire PTA for maternal weaning weight. As well as including the fixed effect of genetic merit for the dependent variable under investigation, the other fixed effects considered for inclusion in the model were contemporary group, heterosis and recombination loss, and breed of dam (beef or dairy); when the dependent variable was calving interval, parity was also included as a fixed effect in the model. For weaning weight the interaction between calf gender and age, heterosis and recombination loss of the calf and dam parity, were included as fixed effects.

Results and Discussion

A positive association was observed between genetic merit with age at first calving (P=0.003), calving interval (P=0.002), direct weaning weight (P<0.001) and maternal weaning weight (P<0.001). The regression coefficients for each trait are in Table 1. The regression coefficients for both fertility traits (age at first calving and calving interval) were low but positive indicating that selection of animals based on genetic merit for both traits will result in an improvement phenotypic performance. For weaning weight the regression coefficients for both the direct and maternal effect were not different from one indicating that each increase in EBV unit will increase phenotypic performance by 1 kg.

Table 1. Number of records (n), effect (direct or maternal) and regression coefficients (standard error in parenthesis) for age at first calving, calving interval and weaning weight

Trait	*n*	*Effect*	*Regression coefficient*
Age at first calving	7,981	Direct	0.32 (0.15)
Calving interval	38,619	Direct	0.58 (0.16)
Weaning weight	7,263	Direct	1.15 (0.24)
		Maternal	0.97 (0.38)

For survival the logit of the probability increased by 0.21 (s.e. =0.05) per unit increase in the EBV for survival. Across all traits no significant association was found between the interaction breed of the dam (beef or dairy) and the EBV for the trait and the phenotypic performance of the progeny indicating that breed of dam is accounted for in the genetic evaluations.

Conclusions

Genetic merit for maternal traits was associated with phenotypic performance in the national population, although the association was lower than expected for some traits. This highlights the importance of genetic evaluations for selection of maternal bulls or selection of replacements within the suckler herd.

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Characterisation of contrasting spring milk production systems

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Introduction

Grass-based milk production systems predominate in Ireland with the season of calving coinciding with the initiation of grass growth (Dillon *et al*., 1995). The proportion of grass and grass silage in the diet of Irish dairy cows varies considerably between farms (National Farm Survey, 2011). Little is known about the genetic, production or financial characteristics of Irish farms operating different systems of production. The objective of this study was to characterise the performance of Irish herds differing in production system.

Materials and Methods

Genetic, milk production, grassland management and financial data were extracted on a herd basis from the Irish Cattle Breeding Federation and Teagasc databases and merged for 2,736 herd years from 1,707 spring milk herds for the years 2008 to 2011. Hedley and Bird (2006) constructed five different systems of production based on the proportion of grass utilised in the diet. Using the data available in the present study, herds were also allocated to production systems where: the proportion of purchased feed accounted for <10% of total dry matter (DM) intake (system 1); between 10 and 20% (system 2); between 20% and 30% (system 3); >30% (system 4). Herd average genetic merit for Economic Breeding Index (EBI), milk sub-index (SI), fertility SI and predicted transmitting ability (PTA) define for milk (kg) were also available. Furthermore, herd average yield and fat and protein yield (kg/cow) was also accessed. Measures of grassland management available included proportion of purchased feed in the diet and grass consumed (t DM/ha). Measures of financial performance available included gross revenue output, total variable and fixed costs and net margin. A series of analyses were undertaken to characterise the physical, genetic and financial data for each system of production using mixed models in PROC MIXED (SAS, 2005). Each model included the effect of year, region of the country and system of production and the interaction between system and year; herd was included as a repeated effect. The dependent variables included EBI, milk SI, fertility SI, milk PTA, yield, stocking rate, percentage purchased feed, grass utilised, gross output, variable and fixed costs and net margin.

Table 1. Genetic characteristics, milk and grass production and financial performance of spring milk farms with different production systems

	System of production				***SE***	***Significance***
	1	2	3	4		
EBI (€)	74.4^{a}	73.8^{a}	73.2^{a}	69.1^{b}	0.77	P<0.001
Milk SI (€)	23.2	23.3	23.5	24.2	0.52	NS
Fertility SI (€)	43.5^{a}	43.2^{a}	42.7^{a}	38.8^{b}	0.70	P<0.001
Milk PTA (kg)	49.5^{a}	50.8^{a}	52.1^{a}	65.9^{b}	2.90	P<0.01
Yield (litres/cow)	4811^{a}	4971^{b}	5093^{c}	5407^{d}	31.2	P<0.0001
Milk solids yield (kg/cow)	366^{a}	376^{b}	383^{c}	405^{d}	2.4	P<0.0001
Stocking rate (LU/ha)	1.99^{a}	2.02^{a}	2.05^{b}	2.09^{b}	0.020	P<0.01
Purchased feed (% of total fed)	8.2^{a}	14.9^{b}	23.8^{c}	34.3^{d}	0.16	P<0.0001
	8.25^{a}	7.96^{b}	7.37^{c}	6.80^{d}	0.073	P<0.0001
Grass utilised (tonnes DM/ha)						
Gross output (€/ha)	2991^{a}	3134^{b}	3238^{c}	3482^{d}	40.9	P<0.0001
Variable costs (€/ha)	837^{a}	1005^{b}	1187^{c}	1424^{d}	11.0	P<0.0001
Fixed costs (€/ha)	874^{a}	918^{b}	956^{c}	1003^{c}	16.1	P<0.0001
Net margin (€/ha)	1276^{a}	1218^{b}	1105^{c}	1069^{c}	28.3	P<0.0001

Results and Discussion

Summary statistics for a range of genetic, grassland performance and financial performance characteristics are summarised in Table 1. Herd EBI was lower ($P<0.001$) for system 4 farms than for farms with other systems of production; fertility SI and milk PTA followed a similar trend. Milk SI was similar for all systems. Milk PTA was higher ($P<0.01$) for system 4 farms than for farms in other production systems. Milk yield was lowest ($P<0.0001$) on system 1 and highest on system 4 farms; yield of fat and protein followed a similar trend. Stocking intensity was highest ($P<0.01$) on system 4 farms and lowest on system 1 farms. Dairy farms operating at system 1 had the earliest start ($P<0.0001$) and finish ($P<0.01$) to the grazing season while system 4 farms had the latest start and earliest finish (data not presented). Grass utilisation was highest ($P<0.0001$) on system 1 farms. Gross output hectare was lowest ($P<0.0001$) on system 1 farms. Variable and fixed costs per hectare followed a similar trend. Net margin was highest ($P<0.0001$) on system 1 farms and lowest on system 3 and 4 farms.

Conclusions

These results suggest that greater emphasis is placed on genetic merit for milk yield on higher input farms and associated higher milk production levels. Such increases in production are associated with higher financial output, higher costs and lower margin measured on a unit area basis.

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Physiology of Reproduction, Growth & Lactation

The effect of genetic merit for fertility traits on dry matter intake, milk production and uterine health

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Introduction

A lactating dairy cow model of fertility has been established composed of two groups of cows with similar genetic merit for milk production traits, but with extremes of good (Fert+) or poor (Fert-) genetic merit for fertility traits. Previous work has shown that dry matter intake (DMI) was greater in Fert+ cows compared with Fert- cows (Moore et al., 2012). The objectives of this study were to determine DMI during the transition period, milk production and uterine health in Fert+ and Fert- cows.

Materials and Methods

The estimated breeding values (EBVs) for 15 Fert+ and 10 Fert- cows enrolled in the study are summarised in Table 1. The average (± SD) parity was 3.4 ± 0.7 and 3.4 ± 0.8 for Fert- and Fert+, respectively.

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

	Fert-	***Fert+***
Milk BV (kg)	222 (70)	204 (80)
Calving Interval BV (days)	4.0 (1.5)	-3.2 (0.6)
Survival BV (%)	-1.7 (0.6)	1.9 (0.4)

The prepartum diet consisted of grass silage (76%), straw (14%) and concentrate (10%) with precalver minerals and the postpartum diet consisted of grass silage (34%), maize silage (31%), lactation ration (14%) and soya (11%). Dry matter intake was recorded daily from weeks -2 to 5 relative to parturition (0) using the Griffith-Elder Mealmaster feeding system (Griffith-Elder & Co Ltd, Suffolk, UK). Body weight (BW) and body condition score (BCS) were recorded weekly. Milk yield was recorded twice daily after calving. Postpartum uterine health was assessed by scoring vaginal mucus weekly on a scale 0 (clear, no pus) to 3 (≥ 50% purulent material) and by examining uterine cytology at wk 3 and 6 to record the polymorphonuclear neutrophil (PMN) count.

All data were analysed using SAS. Normality was checked and data was transformed where required. Mixed model procedures with repeated measures were used where appropriate. Genotype and parity were included as fixed effects. Cow nested within genotype was included as a random effect. The NPAR1WAY procedure was used to analyse vaginal mucus score data. The postpartum interval required to achieve a vaginal mucus score of 0 was determined by the LIFETEST procedure. The FREQ procedure was used to examine the proportion of each genotype classified as endometritic (PMN > 6%).

Results and Discussion

Dry matter intake tended to be greater in the Fert+ cows compared with the Fert- cows (17.9 ± 0.63 vs. 16.3 ± 0.78 kg DM/day, P = 0.1; Figure 1). There was no genotype by week interaction.

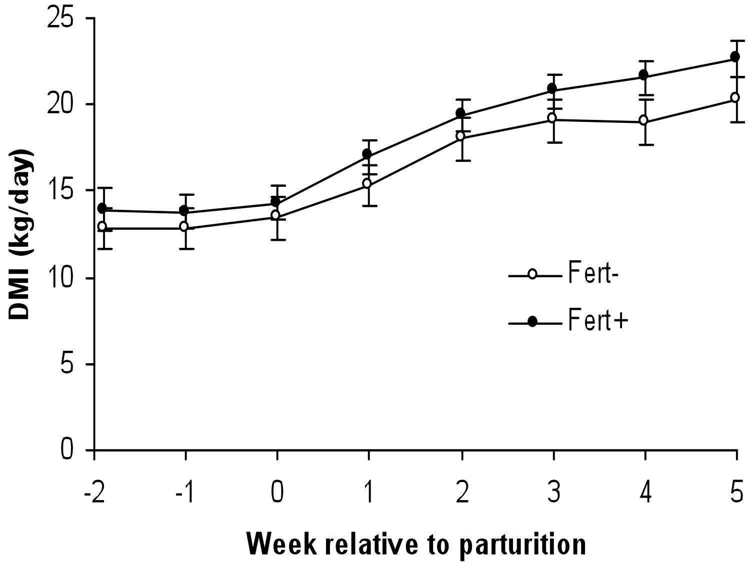

Figure 1. Effect of genetic merit for fertility traits on postpartum DMI

Mean BCS at calving was similar for both genotypes (3.12 vs. 2.98 units, P = 0.14). Mean BCS and BCS nadir were greater for the Fert+ cows compared with the Fert- cows (3.01 vs. 2.75 units, P = 0.0001 and 2.71 vs. 2.44, P = 0.007, respectively). There was no effect of genotype or genotype x week on BW during the first 4 weeks of the study. Mean BW was 547.0 ± 17.9 and 582.0 ± 12.4 kg (P = 0.12) for the Fert- and Fert+ cows, respectively.

During the first 35 weeks of lactation, milk solids production was greater in the Fert+ cows compared with the Fert- cows and the fat:protein ratio tended to be greater in the Fert- cows (Table 2).

Table 2. Milk production variables during weeks 1-35

	Fert-	Fert+	SEM	P-value
Milk Yield (kg)	22.5	24.2	0.85	0.1
Milk solids (kg)	1.7	1.9	0.05	0.0006
Fat:Protein ratio	1.33	1.26	0.02	0.01

Fert- cows had greater vaginal mucus score than Fert+ cows on weeks 1 (3.0 vs 2.0, P = 0.06), 3 (2.3 vs. 1.1, P = 0.02) and 6 (1.0 vs. 0.0, P = 0.01) post partum, but the survival distribution function indicated no difference between genotypes in the time required to achieve a vaginal mucus score of 0 (P = 0.26). Cytology results indicated similar proportion (0.77) of each genotype was classified with endometritis on wk 3. At wk 6 a greater proportion of the Fert- cows were still classified as endometritic compared with the Fert+ cows (0.75 vs. 0.22, P = 0.06).

Conclusions

The results indicate that genetic merit for fertility traits tended to have a positive effect on DMI during the transition period. Also, these results indicate that good genetic merit for fertility traits is associated with better uterine health status and greater BCS after parturition, without antagonizing milk production.

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RMIS Project Number 6075

The effect of genetic merit for fertility traits on the follicular fluid metabolome of dairy cows

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Introduction

The follicular fluid metabolome has been previously shown to be different in non-lactating heifers and postpartum cows (Bender et al., 2010) and to be predictive of pregnancy outcome in humans (Wallace et al., 2012). A lactating cow model of fertility has been established composed of two groups of cows with similar genetic merit for milk production traits, but with extremes of good (Fert+) or poor (Fert-) genetic merit for fertility traits (Moore et al., 2012). The objectives of this study were to examine the metabolome of follicular fluid (FF) from the first dominant follicle on day 7 of the oestrous cycle in Fert+ and Fert- cows.

Materials and Methods

Twenty-seven dairy cows (20 lactating and 7 non-lactating) with good (n=16, Fert+) or poor (n=11, Fert-) estimated breeding values (EBV) for calving interval (Table 1) were enrolled in the study. The average (± SD) parity and days postpartum of the lactating cows were 2.7 ± 0.5 and 2.2 ± 0.4, and 61±13 and 62±13, for Fert+ and Fert-, respectively. The average (± SD) parity and days postpartum of the non-lactating cows were 1.7±0.6 and 1.5 ± 0.6, and 682 ± 38 and 586 ± 100, for Fert+ and Fert-, respectively. Cows were managed indoors as one group. The lactating cow diet consisted of maize silage (35%), lactation ration (29%), grass silage (24%) and soya (12%).The non-lactating cow diet consisted of grass silage (76%), straw (14%) and concentrate (10%).

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

	Fert-	Fert+
Milk BV (kg)	238 (69)	175 (72)
Calving Interval BV (d)	4.1 (1.1)	-3.0 (0.6)
Survival BV (%)	-1.4 (1.1)	1.9 (1.1)

Cows were enrolled on an ovulation synchronisation protocol as described previously (Moore et al., 2012). On day 7 of the oestrous cycle, FF of the first wave dominant follicle was collected by transvaginal follicular aspiration and snap-frozen in liquid nitrogen. Samples were stored at -80 °C. Metabolites were extracted from FF and analysed by gas chromatography mass spectrometry (GC-MS). Statistical analysis was performed on the data using univariate and multivariate techniques.

Results and Discussion

A total of twenty-seven fatty acids were identified and quantified in the FF collected on day 7 of the oestrous cycle. Analysis of the FF revealed that there were 8 fatty acid (FA) metabolites significantly different between the Fert+ and the Fert- cows (Table 2).

Table 2. Effect of genetic merit for fertility traits on fatty acid metabolites of day 7 follicular fluid. Values are expresses as percentage (%) ± SD

Fatty Acid	Fert+	Fert-	P-value
C14.1	0.049 ± 0.02	0.075 ± 0.03	2.32×10^{-2}
C14.0	0.562 ± 0.06	0.635 ± 0.12	4.99×10^{-2}
C17.1	0.538 ± 0.11	0.671 ± 0.14	1.41×10^{-2}
C18.3n6	0.637 ± 0.17	1.055 ± 0.31	2.32×10^{-4}
C20.1	0.051 ± 0.02	0.147 ± 0.07	2.12×10^{-5}
C20.0	0.078 ± 0.02	0.081 ± 0.02	8.49×10^{-3}
C21.0	0.004 ± 0.00	0.008 ± 0.00	2.98×10^{-3}
C24.1	0.082 ± 0.02	0.114 ± 0.04	1.2×10^{-2}

Partial least squares-discriminant analysis (PLD-DA) was carried out and as illustrated in Figure 1, there was clear separation between the Fert- and Fert+ cows based on the FF fatty acid results.

Random Forest (RF) classification models were used to predict fertility outcome in FF samples by producing models with error rates of 12% indicating that 88% of FF samples were classified to the correct cow genotype.

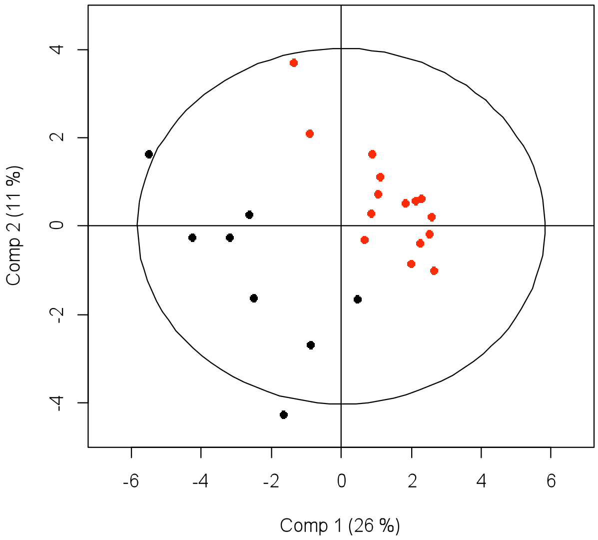

Figure 1. PLS-DA score plot of Fert- (black circles) vs. Fert+ (red circles) follicular fluid. R^2 = 0.93, Q^2 = 0.74

ROC analysis was performed and the area under the curve (AUC) was used as an estimation of the predictive accuracy of the panel of fatty acid biomarkers. Using the statistically significant FA (Table 2) an AUC of 0.89 was obtained highlighting high predictive ability.

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RMIS Project Number 6075

Differential gene expression and alternative transcription in endometrial tissue of a lactating cow model of fertility

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Introduction

A lactating Holstein cow model of fertility has demonstrated significant phenotypic variation between animals with good (Fert+) and poor (Fert-) genetic merit for fertility traits. Fert+ cows have shorter calving to conception interval, fewer services per conception, greater body condition score (BCS), and greater circulating concentrations of circulating insulin-like growth factor 1 (throughout lactation) and progesterone (during the luteal phase) (Cummins et al. 2012a,b). Using RNA sequencing data, our aims were to examine the endometrial transcriptome of Fert+ and Fert- animals on day 7 after a synchronised oestrus in non-pregnant animals and to compare gene expression and alternative transcription between the two groups. Typically day 7 marks the arrival of the pre-embryo into the uterus in pregnant animals. The embryo does not begin signalling its presence in the uterus until ~day 17. The null hypothesis of no difference in uterine gene expression between animals with divergent genetic merit for fertility was tested.

Materials and Methods

Endometrial tissue biopsies were collected from 13 animals (6 Fert+, 7 Fert-) on day 7 after synchronized oestrus. Ovulation was verified by subsequent progesterone profiling. RNA was extracted using a Trizol-based method and cDNA libraries were prepared for sequencing. Sequence data was aligned to the UMD3.1 reference genome for *Bos taurus*. Count data normalised using a trimmed mean of M-values (TMM) were used in the analysis of differential gene expression (DGE) between Fert+ and Fert- conditions. Using the Bioconductor package edgeR, the biological coefficient of variation was estimated and the data modelled as a negative binomial (over-dispersed Poisson) distribution. Differential expression was determined using an exact test adapted for over-dispersed data that calculated Benjamini-Hochberg false discovery rate (FDR) adjusted P-values at a level of 10% ($P < 0.1$). Analysis of physiological pathways over-represented in the set of significantly differentially expressed genes, again using FDR correction with adjusted $P < 0.1$, was conducted using KEGG pathways and GOseq, which accounts for gene-length biases. Signatures of alternative transcription were detected using a subset of six animals (3 Fert+, 3 Fert-; paired-end sequence available) with software written in-house. SpliceGrapher was used to visualise and further analyse the genes found to produce alternative transcripts.

Results and Discussion

We have found that: (i) 467 genes were significantly differentially expressed (adjusted $P < 0.1$) in the endometrium between Fert+ and Fert- cows on day 7 of the oestrous cycle; (ii) of these 467 genes, 49 (10%) were found in pathways by over-represent analysis, and the top three pathways identified were: neuroactive ligand-receptor pathway (15 genes), calcium signalling pathway (12) and focal adhesion pathway (10); (iii) alternative transcription events occurred in 10 genes, all of which were differentially expressed.

Multiple genes already implicated in fertility that show significant DGE were found. Genes involved in cytoskeleton and extracellular membrane, potentially functional in uterine remodelling and supporting the focal adhesion KEGG pathway include: actins *ACTA2, ACTB, ACTC1*; actinins *ACTN1, ACTN2, PDLIM3*; myosins *MYH11, MYLK*; calponin *CNN1*; filamins *FLNA, FLNB*; fibrinogens *FGA, FGB, FNBP1*; thrombospondin *THBS4*; R-spondins *RSPO1, RSPO3*; ponsin *SORBS1*; and tropomyosins *TPM1, TPM2*.

Several DEG products may play functional roles in the uterine lumen as histotroph to maintain the pre-embryo: serpins *SERPINA1, SERPINA3-7, SERPINA12, SERPINB12*; aquaporin *AQP5*; osteopontin *SPP1*; mucins *MUC1, MUC16, MUC20*; and vitronectin *VTN*.

Many ion, especially calcium, signalling genes appear frequently: *ACCN1, ACCN2*; *ATP2B2, ATP2B3, ATP2B4*; *CADPS, CAP2, CAPS, CAPSL*; gaba receptors *GABRB3, GABARD*; junctophilins *JPH2, JPH3*; purinergic receptors *P2RX1, P2RX2*; 16 potassium voltage-gated channels and 5 solute carriers.

These three broad physiological groupings may result in dynamic endometrium function at both the structural and signalling levels.

Alternative transcription at genes involved in the above pathways (*TPM4, CNN1, MYH11, MYLK, ACTB, PDLIM3*) lends support to the divergence at the gene level between the Fert+ and Fert- groups.

Conclusion

The null hypothesis of no difference in endometrial gene expression between Fert+ and Fert- animals is rejected. Divergence between the groups manifests itself as differentially expressed genes leading to intrinsic physiological differences. These indicate a set of genes and biological processes that may underlie the phenotypic differences observed between Fert+ and Fert- cows and could be targets for future research into improve the fertility of Irish dairy cattle.

Acknowledgements
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RMIS Project Numbers 6075

Effect of pasture based systems on reproductive performance, sub-clinical endometritis and immune status

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Introduction

The dairy sector is forecast to expand in Ireland after the end of the milk quota regime. In order to increase output and improve efficiency, many farmers will increase stocking rate (SR). This study was conducted to assess the effects of SR and calving date (CD) on reproductive parameters in lactating dairy cows on a grass based system of production.

Materials and Methods

One hundred and forty Holstein-Friesian (North American or New Zealand ancestry) or Jersey crossbred cows were used in this study. Cows were assigned to three different SRs: LOW (2.52 cows/ha); MED (2.92 cows/ ha); or HIGH (3.3 cows/ha). Within each group, cows were separated into EARLY (mean calving date 12th Feb) and LATE calving (mean calving date 25th Feb). Blood samples were collected from a subset of cows (n=37) at weeks -1, 1, 3, 6, 12, and 24 relative to calving for haematological analysis. Milk progesterone (P4) concentrations were measured in one a.m. milk sample per week. Variables calculated include the postpartum interval to commencement of luteal activity (CLA; first milk P4 sample ≥ 3ng/ml), proportion of P4 values >3ng/ml (PLA) and proportion of cows having resumed oestrous cyclicity by 28 d postpartum (CYC28) and by mating start date (CYCMSD). Endometrial cytology samples were collected from 121 cows at six weeks post-calving using the cytobrush technique. Cows were classified as endometritic if the polymorphonuclear neutrophil count was >6%. Herd breeding records and ultrasound scanning results at the end of the breeding season were collated and reproductive variables calculated. Continuous variables were checked for normality using the univariate procedure in SAS, and transformed as necessary. The milk P4 variables CLA and PLA were analysed using mixed models procedures (SAS Institute Inc., Cary, NC). All binary variables were analysed using logistic regression (GENMOD). The models for both MIXED and GENMOD included SR, CD, parity (1, 2 and ≥3) and the interaction between SR and CD as fixed effects. Cow was included as a random effect in the mixed models.

Results and Discussion

There were no significant differences between the SR or CD treatments on the postpartum interval to CLA. The CLA decreased with increasing parity (Table 1). There was an interaction (P=0.045) between SR and CD for PLA during first 60 days after calving. This occurred because the late calving cows for both the HIGH and LOW SR treatments had lower PLA values than EARLY calving cows, but the opposite occurred for cows in the MED SR treatment. A tendency was observed for a greater proportion of cows in the high SR treatment to have resumed cyclicity by MSD (P = 0.07; Table 1). The incidence of endometritis determined from cytology results at 6 weeks postpartum was not affected by either SR (P = 0.9) or CD (P = 0.9). There was, however, a significant effect of parity on endometritis (P=0.002; Figure 1). Haematology profiles were broadly similar for the SR and CD treatments.

Table 1. Effects of SR and CD treatments on milk P4 and phenotypic fertility variables.

	Stocking Rate			Calving Date		Parity			P-values			
	High	Med	Low	Early	Late	1	2	3	SR	CD	PARITY	SR*CD
No.Cows	45	41	47	69	64	31	33	69	-	-	-	-
CLA(d)	37.9	41.8	41.2	40.0	40.6	48.6	37.7	34.7	0.53	0.85	0.002	0.27
PLA	0.36	0.28	0.30	0.32	0.31	0.25	0.34	0.36	0.055	0.55	0.013	0.045
CYC28	0.27	0.27	0.27	0.22	0.33	0.10	0.24	0.36	0.99	0.15	0.01	0.42
CYCMSD	0.98	0.90	0.85	0.91	0.91	0.97	0.88	0.90	0.07	0.89	0.35	0.47
Sub Rate	0.80	0.87	0.96	0.91	0.84	0.91	0.83	0.88	0.07	0.20	0.64	0.42
CRFS[1]	0.63	0.43	0.69	0.51	0.65	0.59	0.56	0.59	0.04	0.10	0.92	0.38
6WKICR[2]	0.70	0.57	0.80	0.63	0.74	0.72	0.61	0.71	0.05	0.18	0.53	0.29

[1] Conception Rate to First Service; [2] Six Week In Calf Rate

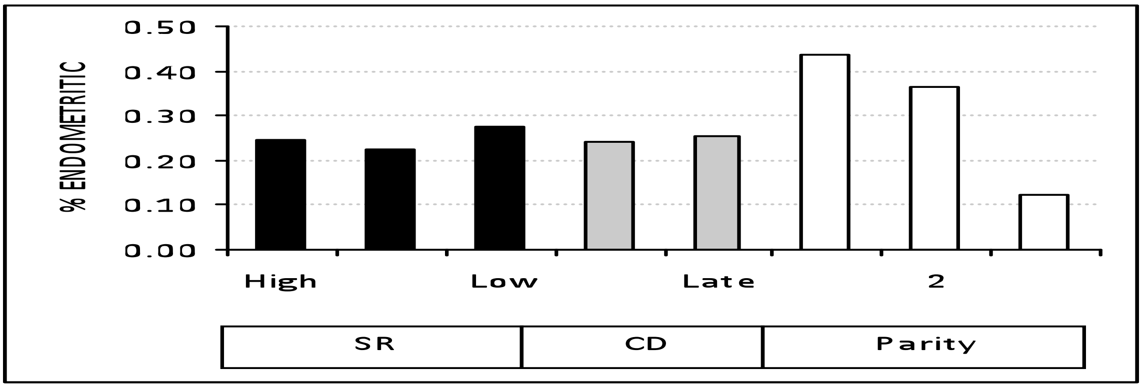

Fig. 1. Rate of endometritis at six weeks post calving.

Conclusions

The milk P4 results indicate that the cows on the HIGH SR treatment tended to have a greater proportion of cows cycling by MSD. The LOW SR had the best overall fertility performance, but the HIGH SR treatment had better fertility than the MED group. Cows in their first lactation were more likely to be endometritic at six weeks post-calving, highlighting the importance of postpartum monitoring and management of primiparous cows

RMIS Project Number 6076

Expanding the dairy herd in pasture-based systems: the role for sexed semen use on virgin heifers

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Introduction

Flow cytometry is currently the only reliable method of sorting populations of X- and Y-chromosome bearing sperm. The technology consistently produces approximately 90% gender bias amongst resulting offspring (Garner and Siedel, 2008), but likelihood of conception after insemination is reduced with sexed semen compared with conventional semen (Seidel et al., 1999). The removal of the EU milk quota regime in 2015, coupled with Food Harvest 2020 targets for a 50% increase in milk output by 2020 (DAFF, 2010) presents a real opportunity for Irish dairy farmers to increase milk output and herd size for the first time in over 30 years. This study examines the potential for using sexed semen in virgin heifers to accelerate herd expansion.

Materials and Methods

A bio-economic model was developed to examine the effects of sexed semen use on replacement heifer numbers and rate of herd expansion in a seasonal dairy production system. Three separate herds were established according to the type of semen used on virgin heifers: conventional frozen-thawed (Conv), sexed fresh (SFre), or sexed frozen-thawed (SFro). In the model, sexed semen was used for the first and second inseminations in heifers only. Conception rates achieved with sexed fresh and sexed frozen-thawed semen were assumed to be 94% and 75% of those achieved with conventional frozen-thawed semen, respectively. The price of semen was €21 and €47 per straw, for conventional and sexed (fresh and frozen) semen, respectively. Initial herd size was 100 cows, which was maintained for the first two years of the 15-yr simulation, after which all available replacement heifers were retained to facilitate herd expansion. Two different scenarios of land availability were examined for each of the three herds using different semen types: land available allowed expansion to a maximum herd size of 150 cows (S1); or land available allowed expansion to a maximum herd size of 300 cows (S2). Once maximum herd size was reached, sexed semen use was discontinued and all excess heifer calves were sold at one month old. All capital expenditure associated with expansion was financed with a 15-yr loan. Each of the different options was evaluated in terms of annual farm profit, annual cash flow and total discounted net profit. The analysis was completed at a milk price of €0.27/L, and sensitivity analyses was carried out at €0.22/L and €0.32/L.

Results and Discussion

The use of fresh sexed semen generated more replacement heifers leading to faster herd expansion compared with frozen-thawed sexed semen and conventional frozen-thawed semen (Figure 1). Total discounted net profit under S1 for the SFre herd was €19,929 greater compared with the SFro herd and €41,852 greater compared with the Conv herd. Under S2, discounted net profit for the SFre herd was €138,587 greater compared with the SFro herd and €239,987 greater compared with the Conv herd. At a milk price of €0.27/L, cashflows remained positive throughout the simulation under S1. Under S2, however, the SFre, SFro and Conv herds experienced negative cash flows in Yr 3, 7 and 7 of the simulation, respectively. All 3 herds suffered negative cash flows for extended periods of time under both S1 and S2 at the lower milk price of €0.22/L, although cash flows were most negative in the SFre herd.

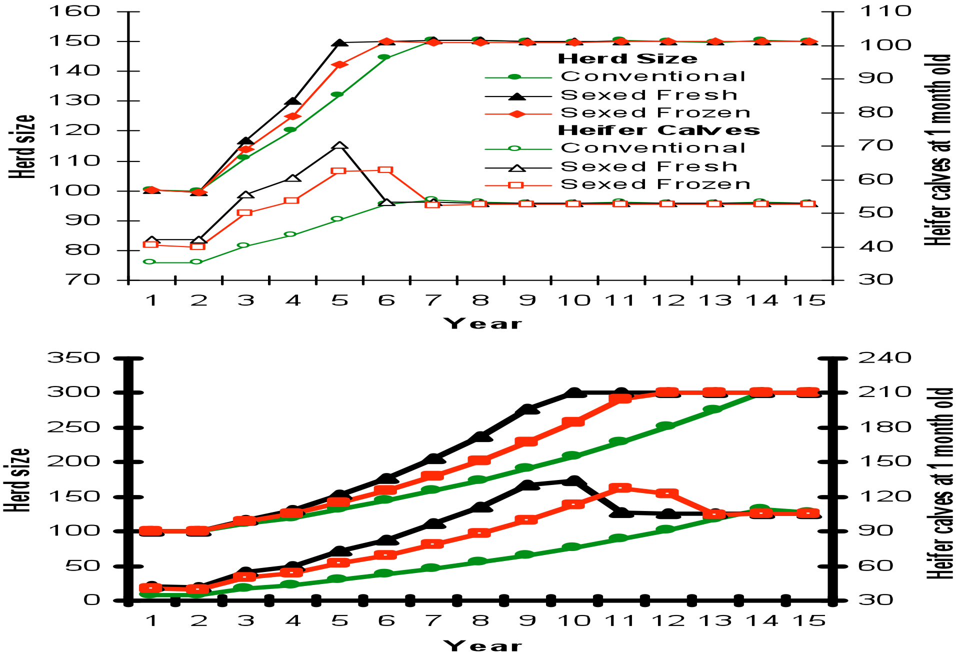

Fig. 1. Herd size and number of heifer calves born in the first 6-wks of the calving period surviving to 1 month old in herds using either fresh sexed, frozen-thawed sexed or frozen-thawed conventional semen in virgin heifers only, under Scenario 1 (upper panel) or Scenario 2 (lower panel).

Conclusions

The use of sexed semen, and in particular fresh sexed semen, in dairy heifers facilitates faster, more profitable expansion compared with conventional frozen-thawed semen use, despite marginal reductions in fertility. Financial pressures arising from low milk price were greatest when rate of expansion was highest.

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RMIS Project Number 6222

Expanding the dairy herd in pasture-based systems; the role for sexed semen use on virgin heifers and lactating dairy cows

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Introduction

The development of semen sorting technology presents dairy producers with the opportunity to increase the number of female calves born in a herd. The technology is capable of delivering a 90% gender bias in resulting offspring, but the fertility of the sexed semen product is reduced compared with conventional semen (Norman et al., 2010).

The use of sexed semen on virgin heifers facilitates faster, more profitable herd expansion in seasonal calving production systems (Hutchinson et al., 2013) This study investigates the potential for extending sexed semen use to both virgin heifers and lactating dairy cows to accelerate herd expansion.

Materials and Methods

A bio-economic model was developed to examine the effects of sexed semen use in virgin heifers and lactating cows on replacement heifer numbers and rate of herd expansion in a seasonal dairy production system. Five separate herds were established according to the type of semen used: conventional frozen-thawed (Conv); sexed fresh semen used in lactating cows for the 1st 3-wk of the breeding season only (SFre1); sexed frozen-thawed semen used in lactating cows for the 1st 3-wk of the breeding season only (SFro1); sexed fresh semen used in lactating cows for the 1st 6-wk of the breeding season (SFre2); or sexed frozen-thawed semen used in lactating cows for the 1st 6-wk of the breeding season. In all herds using sexed semen, it was used for the 1st and 2nd AI in virgin heifers. Conception rates achieved with sexed fresh and sexed frozen-thawed semen were assumed to be 94% and 75% of those achieved with conventional frozen-thawed semen, respectively. The price of semen was €21 and €47 per straw, for conventional and sexed (fresh and frozen) semen, respectively. Initial herd size was 100 cows, which was maintained for the first two years of the 15-yr simulation, after which all available replacement heifers were retained to facilitate herd expansion. Two different scenarios of land availability were examined for each of the five herds: land available allowed expansion to a maximum herd size of 150 cows (S1); or land available allowed expansion to a maximum herd size of 300 cows (S2). Once maximum herd size was reached, sexed semen use was discontinued and all excess heifer calves were sold at 1 month old. All capital expenditure associated with expansion was financed with a 15-yr loan. Each of the different options was evaluated in terms of annual farm profit, annual cash flow and total discounted net profit.

Results and Discussion

The use of fresh sexed semen generated more replacement heifers leading to faster herd expansion compared with frozen-thawed sexed semen and conventional frozen-thawed semen (Figure 1). Total discounted net profit under S1 for the SFre2 herd was €4,130, €38,869, €47,231 and €52,089 greater compared with the SFre1, SFro1, Conv and SFro2 herds, respectively. Under S2, discounted net profit for the SFre2 herd was €44,204, €255,524, €280,373 and €325,815 greater compared with the SFre1, SFro1, SFro2 and Conv herds, respectively. Under S1, the SFre2 and SFro2 herd both experienced negative cash flows in Yr 3 of the simulation. Under S2, cash flow was negative in Yr 7 for the Conv herd, Yrs 1 and 3-5 in the SFre1 herd, Yr 3 and 7 for the SFro1 herd, Yrs 1-5 for the SFre2 herd, and Yrs 3-5 and 7 for the SFro 2 herd. The use of sexed frozen-thawed semen had a negative effect on the herd calving pattern, with a greater proportion of the herd calving later in the year compared with herds using sexed fresh or conventional frozen-thawed semen.

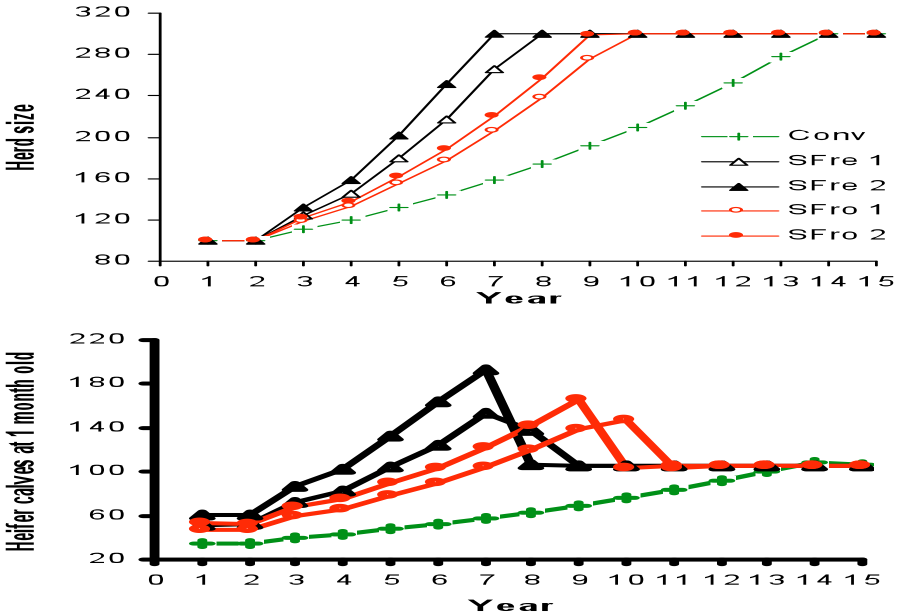

Figure 1: Herd size (upper panel) and heifer calves born in the 1st 6-wk of the calving period surviving to 1 month old (lower panel) in herds using either sexed fresh, sexed frozen-thawed or conventional frozen-thawed semen in virgin heifers and lactating cows under Scenario 2 (land available limits maximum herd size to 300 cows).

Conclusions

Sexed fresh semen use in lactating cows in addition to virgin heifers can facilitate faster, more profitable expansion of Irish dairy herds. The faster expansion, however, resulted in liquidity issues during the most rapid expansion, placing the viability of the farm business at risk. The reduced fertility of sexed frozen-thawed semen reduced farm profitability and will prevent its widespread use in lactating cows.

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RMIS Project Number 6222

Animal Health & Well-Being

The use of a targeted selective treatment approach to parasite control in first season dairy-to-beef calves

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Introduction

With increasing reports of anthelmintic resistance in cattle (Soutello *et al.*, 2007) there is a need to use anthelmintic treatment regimes that are both practical and effective at controlling parasitic infections in first season dairy-to-beef calves. Latterly, control of parasitic infections has focussed on treatment of the individual as opposed to the group in an effort to increase the population of parasites *in refugia* to delay the development of anthelmintic resistance. These treatment regimes are termed targeted selective treatments (TSTs). This study reports on the preliminary findings of a TST approach in a group of dairy-to-beef calves over their first grazing season to control both lungworm (*Dictyocaulus viviparus*) and gastrointestinal (GIT) nematodes.

Materials and Methods

Fifty one spring-born Holstein-Friesian (H-F) and forty seven spring-born Hereford × H-F dairy-to-beef calves with an initial mean age (s.d.) and mean liveweight (s.d.) of 130 (28.3) days and 120 (23.6) kg, respectively, were used in the study. Calves were randomly allocated by breed, age and weight to one of two treatments; Standard Treatment (control) (n=48) and TST (n=48). Each treatment group was replicated once. Control and TST calves were rotationally grazed in adjacent paddocks on a predominantly perennial ryegrass-based sward (*Lolium perenne*) from July 3rd 2012 to the end of the trial on November 2nd 2012 when calves were housed. There were 7 rounds of sampling in the study at three weekly intervals. The dates of the rounds are as follows; 3rd July (round 1), 24th July (round 2), 14th August (round 3), 4th September (round 4), 25th September (round 5), 16th October (round 6) and 2nd November (round 7). At each round of sampling calves were weighed and blood and faecal sampled. Faecal samples were taken directly from the rectum using latex gloves and placed into 180 mL collecting pots. Gloves were changed between individual samples. Once collected, dung samples were analysed for the presence of *Dictyocaulus viviparus* using the Modified Baermann technique and faecal egg count (FEC) was determined using the McMaster method (Thienpont *et al.*, 1986). Plasma pepsinogen was determined using the method described by Ross *et al.* (1967). All Calves in the standard anthelmintic regime treatment groups were treated subcutaneously with ivermectin at a dosage rate of 1.0 mL per 50 kg bodyweight (Qualimec® 10 mg/mL solution for injection, Janssen Animal Health) at rounds 1, 3, 5, and 7 (housing). Individual calves in the TST groups were treated at pasture on average ten days post sampling with the same product at the same dosage rate and based on their laboratory results as follows;

+ve Baermann result
or
+/- Baermann result with plasma pepsinogen ≥ 2 U/L tyrosine and FEC ≥ 200 eggs per gram (EPG)

All calves in the TST groups received an anthelmintic treatment at round 7 (housing). Data were analyzed using the PROC MIXED function of SAS (Version 9.1, SAS Institute, Cary, NC). Data are presented as LSmeans ± SEM. Differences between treatments were determined using a Tukey-Kramer adjustment for multiple comparisons and considered significant when $P \leq 0.05$.

Results and Discussion

There was an effect of round ($P<0.0001$), a treatment × round interaction ($P<0.0001$) and no effect of treatment ($P>0.05$) for FEC (Fig. 1). There was an effect of treatment ($P=0.004$), of round (P<0.0001), and a treatment × round interaction (P<0.0001) for plasma pepsinogen concentrations. Individual calves in the TST groups were treated post sampling from rounds 2 to 6. There were a total of 62 individual treatments in the TST groups resulting in a 57% reduction in anthelmintic use in TST groups compared to control groups at pasture. Seventy three per cent of TST treatments were due to the presence of lungworm (± GIT nematodes). Clinical signs of lungworm infection were evident in TST calves at round 4. The overall average daily weight gain (ADG) (P>0.05) for control and TST groups was 0.50 (±0.02 SEM) kg/day and 0.47 (±0.03 SEM) kg/day, respectively. The difference in ADG between the two treatments was not significant.

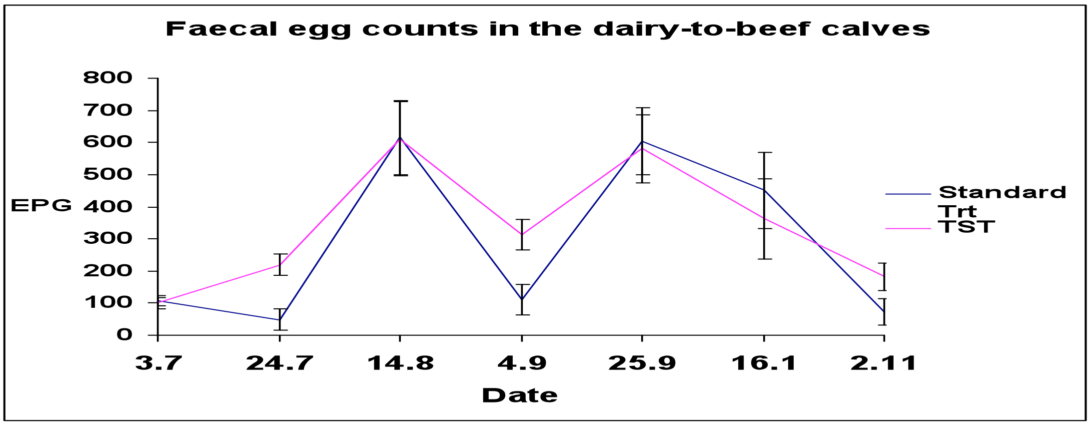

Fig. 1. Faecal EPG (Lsmeans ± SEM) in dairy-to-beef calves.

Conclusions

Parasite control in first season dairy-to-beef calves at pasture can potentially be controlled with fewer anthelmintic treatments whilst not significantly impairing performance. As a result, there will be less selection for resistant nematodes thus delaying the development of anthelmintic resistance. However, farmers must remain vigilant with respect to lungworm control given its unpredictive epidemiology.

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RMIS Project Number 5902

Effects of milk feeding volume and frequency on weight gain in dairy heifer calves

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Introduction

Traditionally calves are offered milk at 8-10% of their birth body weight (BW) per day, which limits their growth and weight gain (Jasper and Weary, 2002). Feeding milk at a daily rate of 13-15% BW should be sufficient to allow calves reach over 50% of their growth capacity (Lorenz *et al*., 2011). Gleeson *et al,* (2007) showed no significant difference in calf performance between calves offered milk at 10-12% BW either once-a-day (OAD) or twice-a-day (TAD). However, it is unknown how calves will respond to a higher volume of milk when offered once-a-day. The objective of this study was to determine the effect of feeding volume and frequency of feeding on weight gain of replacement dairy heifer calves during the pre-weaning period.

Materials and Methods

A randomised block design experiment was conducted at Teagasc Moorepark from 10 Jan to 15 June 2012 using 96 dairy replacement heifer calves. Animals were balanced based on breed, (66 Holstein-Friesian; HF, 18 Jersey-cross; JEX and 12 HF x Norwegian Red; NRX), date of birth (1 February ± 7.21 days), and BW (34.8 kg, ± 4.98 kg). Calves were then randomly assigned to one of the following three treatments for approximately 60-130 days: i) offered milk at a rate of 8-10% of BW once daily (10% OAD) ii) offered milk at a rate of 13-15% BW once daily (15% OAD) and iii) offered milk at a rate of 13-15% BW in two equal feeds until weaning (15% TAD).

All heifers were weighed at birth and fed 7.5% of their BW in colostrum within the first hour. All calves were offered 2L twice daily for 4 days and subsequently fed twice daily according to their treatment volumes until turnout at 3 weeks. OAD feeding began at this time. Within each treatment calves were sub-divided based on birth BW (heavy > 35kg and light ≤ 35 kg) to minimise differences in volumes offered. The amount of concentrates fed to each group was recorded.

Weekly weighing was carried out until all calves attained their target weaning BW (95kg HF, NRX and 80kg JEX). Once they achieved their target BW calves were removed from the group and gradually weaned during the subsequent week. Bodyweight gain (BWG) over the milk feeding period was calculated by subtracting birth weight from weaning weight and dividing by the number of days to weaning. In the fourth and eighth week following weaning, calf BW was measured to monitor any carry over effects.

Data were analysed using analysis of variance in SAS. Terms for treatment and sub-treatment (birth BW) were included in the model. The interaction was also tested but was found to be non-significant and therefore will not be reported in this paper.

Results and Discussion

Calves assigned to the 10% OAD treatment tended to take longer (+6 days) to achieve weaning weight when compared to the 15% TAD treatment calves (86 days). There was no difference in number of days to achieve weaning weight between calves assigned to the 15% OAD and 15% TAD (87 days) treatments. Calves born at a heavier BW were weaned ($P<0.001$) 12 days earlier than those born at a lighter BW (95 days).

The average daily BWG from birth to weaning tended to be greater ($P=0.08$; +0.04 kg/calf/day) for the 15% TAD calves when compared to the 10% OAD calves (0.58 kg/calf/day). There was no difference between the 15% OAD and 15% TAD (0.61 kg/calf/day) or the 10% OAD and the 15% OAD calves (0.60 kg/calf/day). There was no difference in average daily BWG between calves born at a lighter or heavier birth weight (0.60 kg/calf/day). There was no carry over effect of any treatment on weight gain at 4 (113.6 kg) and 8 (136.5 kg) weeks post weaning.

There was no difference in daily concentrate intake over the entire milk feeding period between the 15% OAD and 15% TAD treatment calves (0.91 kg/calf/day; Figure 1). The 10% OAD calves ate significantly less concentrate (-0.33 kgDM/calf/day; $P<0.01$) than the other treatment calves. There was no effect of initial calf birth weight on concentrate consumption during the milk feeding period (0.80 kgDM/calf/day). The lower weight gain in calves offered 10% OAD concurs with Jasper and Weary (2002).

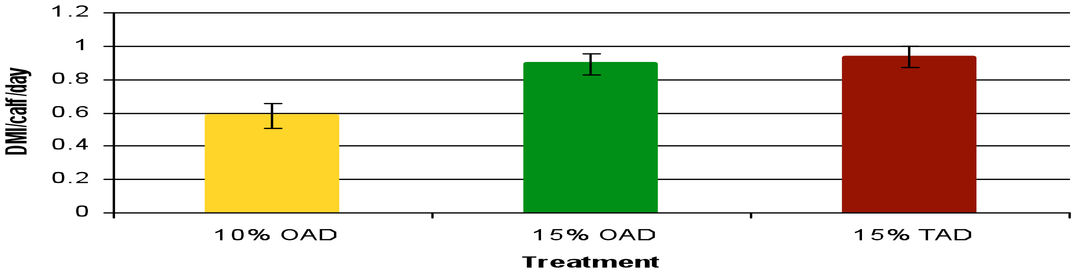

Figure 1. Mean concentrate dry matter intake/calf/day from birth to weaning with SE.

Conclusions

Feeding volume has an impact on weight gain. BWG was greater for calves offered milk at a rate of 13-15% BW resulting in a lesser number of days to weaning when compared to calves offered milk at a rate of 8-10% BW. This study has also shown that feeding frequency does not have a significant impact on calf weight gain or concentrate dry matter intake. This study suggests that offering more milk to dairy heifer replacement calves can reduce the number of days to weaning.

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RMIS Project Number 6009

Effect of pre-partum iodine supplementation of the dairy cow diet on the health status of her calves

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Introduction

Post quota abolition in 2015 the optimisation of calf health will be of greater significance than ever, particularly given the anticipated expansion of the national herd (Food Harvest Report, 2020). Currently, official figures suggest the health of Irish dairy calves is less than optimal (4.6% calves dead in the first 12 months of life excluding stillbirths: (AIM, 2011)). Thus, it is necessary to identify practices that may impact on calf health. A number of studies in sheep have demonstrated the negative effects that over-supplementation of iodine (I) in the pre-partum diet of ewes may have on the health of their offspring (Boland *et al.,* 2005), however little information is available as to whether the same phenomenon occurs in cattle. Thus, the objective of this experiment was to investigate whether excessive I supplementation of the pre-partum dairy cow has a negative effect on the health of her calves.

Materials and Methods

The experiment was carried out at Teagasc Moorepark Research Farm, Co. Cork, Ireland, from 13 December 2011 to 19 June 2012. Calves (n=129) were assigned to one of six treatment groups, based on the level of pre-partum I supplementation of their dam and the colostrum that they received. The treatments were: (1)HI I (n=22): born to dams supplemented at three times the current maximum permitted limit (15 mg/kg), fed HI I colostrum; (2) NO I (n=22): born to dams that received no I supplementation, fed NO I colostrum; (3) STD I (n=22): born to dams that received the current maximum permitted level of I (5 mg/kg), fed STD I colostrum; (4) HI I X (n=23): born to HI I dams, fed NO I colostrum; (5) NO I X (n=21): born to NO I dams, fed HI I colostrum; (6) HI-NO I (n=19): born to dams that received the high level of I supplementation for the first half of the dry period and no I supplementation for the second half, fed HI-NO I colostrum Calves continued to receive milk from their respective treatments for the first 72 hours of life after which animals were managed similarly.

Individual animal health scores were assigned to calves on a twice weekly basis by one trained observer; females were scored until weaning at twelve weeks of age, males were scored until they were sold between two and four weeks of age. Health scores were assigned using a calf health scoring system developed by the School of Veterinary Medicine, University of Wisconsin-Madison, USA. Calves were scored on four different aspects of health (Table 1). Each individual aspect received a score from zero to three; zero representing normal and three representing the most severely affected.

Statistical analysis was carried out using PROC GENMOD (SAS, 2009). A total of 1,636 individual calf health scores from 129 calves were available. For each health aspect separately, the probability of a calf having a higher health score (i.e., worse score = poorer health) within the study period was modelled by ordinal regression utilising a cumulative logit link function and a multinomial distribution. Variables considered for inclusion in the model were sex of calf, parity of dam, experimental treatment group, week of birth of the calf and age of the calf in days when assessed. A series of univariate ordinal regression analyses was initially undertaken including each variable individually in the model. Subsequently a multivariate model was created by stepwise backward elimination. Significance was declared at $P<0.05$. Odds ratios and 95% upper and lower confidence intervals were calculated.

Table 1: Calf health scoring criteria (University of Wisconsin-Madison)

Score	0	1	2	3
Nasal discharge	Normal serous d/c*	Small unilateral cloudy d/c	Bilateral cloudy or excessive d/c	Copious bilateral purulent d/c
Eye/Ear score	Normal	Small ocular d/c, or ear flick	Moderate bilateral d/c or slight unilateral ear droop	Heavy ocular d/c or head tilt/bilateral ear droop
Faecal score	Normal	Semi-formed	Loose, stays on bed	Watery, sifts through bed
Cough	None	Single induced	Occasional spontaneous	Repeated spontaneous

*Discharge abbreviated to d/c

Results and Discussion

Experimental treatment had no significant effect on the probability of the calf being assigned a worse score for any of the health aspects of interest. For all health aspects, the probability of a calf being assigned a worse score increased with age both linearly and quadratically. Respiratory incidences were greatest at 59-61 days of age; eye/ear score was greatest at 28 days of age. Faecal consistency score was highest at 20 days of age while cough score was greatest at 7 days of age. Female calves were nearly 3 times more likely to be assigned a worse nasal score than a male calf ($P<0.01$).

Conclusion

The level of pre-partum I supplementation did not affect the health parameters of calves measured in this study. However, as the age of the calf affected health parameters, particular vigilance is indicated at certain critical stages when monitoring signs of health during the calf-rearing period.

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RMIS Project Number 6009

Genome wide association study for calving performance in Irish cattle

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Introduction

Dystocia and perinatal mortality are complex quantitative traits that are known to exhibit genetic variation (Purfield et al., 2012). There is anecdotal evidence from monitoring of genomic evaluations that there may be a major gene effect for calving dystocia segregating in the Irish population. The objective of this study was to conduct a genome wide association study to identify possible genomic regions associated with calving traits in Irish dairy cattle.

Materials and Methods

Genotypes for 4,752 Holstein-Friesian AI bulls genotyped using the Bovine50K marker panel (Illumina, San Diego, CA) were available. Following the removal of single nucleotide polymorphisms (SNP) on the sex chromosome, of unknown position, and SNP with >0.5% mendelian inconsistencies between parents-offspring, 51,515 SNPs remained. Missing genotypes were imputed using Beagle Version 3.1.0 (Browning and Browning, 2007). Monomorphic SNP and those deviating ($P < 10^{-8}$) from Hardy Weinberg were removed. After edits 4,752 animals with 43,849 SNP genotypes were available. The pedigree of each animal was traced back at least four generations where available. Predicted transmitting abilities (PTAs) and their associated reliabilities were available for 3,486 animals. PTAs were deregressed before analyses. Association analyses were undertaken by fitting all SNP simultaneously using Bayesian genomic selection methods (Habier et al., 2011) on only animals with >40% reliability for each trait. The Bayesian model was implemented using methods Bayes-B and Bayes-Cπ. Bayes Cπ was initially used to formulate the estimation of π, the probability of a marker having zero effect. The Bayes B algorithm was then run using the posterior mean π from the Bayes C analysis. This method fits a different variance for every covariate (SNP) in the model. The Markov chain length for both Bayesian analyses was 50,000 iterations, with the first 10,000 excluded as the burn in period. Bayes factors and the proportion of genetic variance attributable to each SNP was calculated.

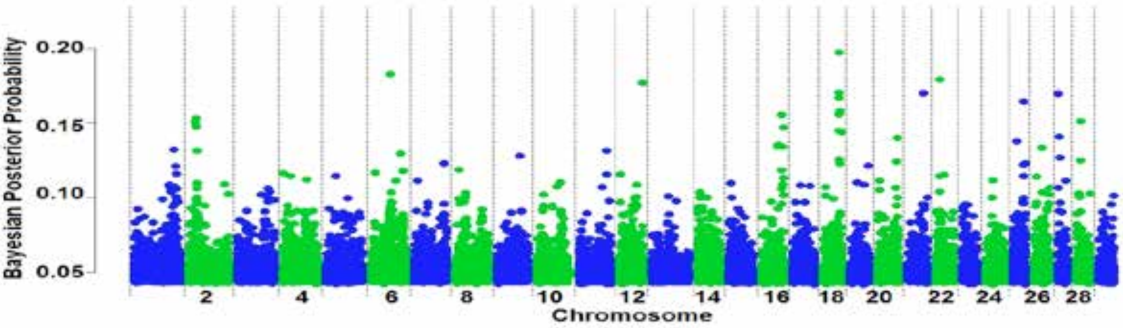

Figure 1: Bayesian posterior probability values for each SNP being associated with calving difficulty

Results and Discussion

The posterior mean π for calving difficulty was 0.9912 and for perinatal mortality 0.99973. Several different chromosomal regions were associated with calving difficulty and perinatal mortality. The Bayesian posterior probability was greatest for genomic regions associated with calving difficulty, with SNP on chromosomes 12, 18, and 23 yielding the highest posterior probabilities (Figure 1). The overall probability of SNP being associated with perinatal mortality was much lower than that for calving difficulty. However chromosomes 1, 2, and 25 displayed possible genomic regions of the highest posterior probabilities (i.e. 0.2175 to 0.2359) to be associated with mortality. The ten most significant SNP explained 0.00016 of the genetic variance in calving difficulty (Table 1).

Table 1: Posterior probability, Bayes factors (BF) and the proportion of variance explained for five SNP that were most associated with calving difficulty

Ch	Position	Posterior Probability	BF	Total variance (%)
18	56515084	0.1974	4.673063	1.62^10^{-5}
6	66383308	0.1827	4.247278	2.30^10^{-5}
22	12830183	0.179	4.142509	2.14^10^{-5}
12	80812970	0.1769	4.083465	1.87^10^{-5}
18	56812286	0.1703	3.899843	1.76^10^{-5}

Conclusions

Areas of the genome are associated with perinatal mortality and calving difficulty in Irish dairy cattle and these may play an important role in the phenotypic occurrence of these traits.

Acknowledgements

The authors gratefully acknowledge funding from Science Foundation Ireland and RSF 11/SF/311.

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RMIS Project Number 6047

Genome wide association study for body conformation in Irish dairy cattle

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Introduction

Genetic evaluations are routinely undertaken for linear type traits in Ireland (Coyne et al., 2013). Linear type traits describe the biological extremes of animal conformation. Six body-related linear type traits are scored in Irish dairy cattle which describe the body conformation of each animal. The objective of this study was to investigate if regions of the bovine genome were associated with these body-related type traits.

Materials and Methods

Genotypes from the Illumina Bovine50 Beadchip (54,001 single nucleotide polymorphisms; SNPs) were available on 1,216 Holstein-Friesian AI bulls. Following the removal of SNPs on the sex chromosome, of unknown position, and SNPs with >0.5% mendelian inconsistencies between parents-offspring, 51,515 SNPs remained. Missing genotypes were imputed. SNPs with a minor allele frequency <2% and deviating (P <10-8) from Hardy Weinburg equilibrium were removed. After edits 1,216 animals with 43,849 SNP genotypes were available. Predicted transmitting abilities (PTAs) and their associated reliabilities for several linear type traits (stature, chest width, body depth, rump angle, rump width and angularity) were available on all animals. All PTAs were deregressed using full pedigree. Association analyses between the genotype panel and each phenotype were undertaken by fitting all SNP simultaneously using Bayesian genomic selection methods (Habier et al., 2011) on only animals with >40% reliability for each trait. The Bayesian model was implemented using (n=1,216) Bayes-C. This method is less sensitive to the prior genetic and residual variances and puts more emphasis on information contained in the data. The chain length for both Bayesian analyses was 50,000 iterations, with the first 10,000 excluded as burn in.

Results and Discussion

Several chromosomal regions were associated with the six body-related type traits four of which are presented in Figure 1. Associations with rump angle had the greatest Bayesian posterior probability with putative quantitative trait loci on chromosome 1, 8, and 22. The four highest Bayesian posterior probability SNPs explained 0.0004 of the genetic variation attributable to stature. Only one out of the 20 most significant SNPs for all traits, was associated with >1 trait; the eighth most significant effects for body depth, located on chromosome 11 was also the ninth most significant for rump angle. This contrasts with recent work from Cole et al. (2011) who found that many of their most significant SNP effects overlapped for body traits, particularly those associated with body depth and stature. However, that study was also undertaken with a small dataset.

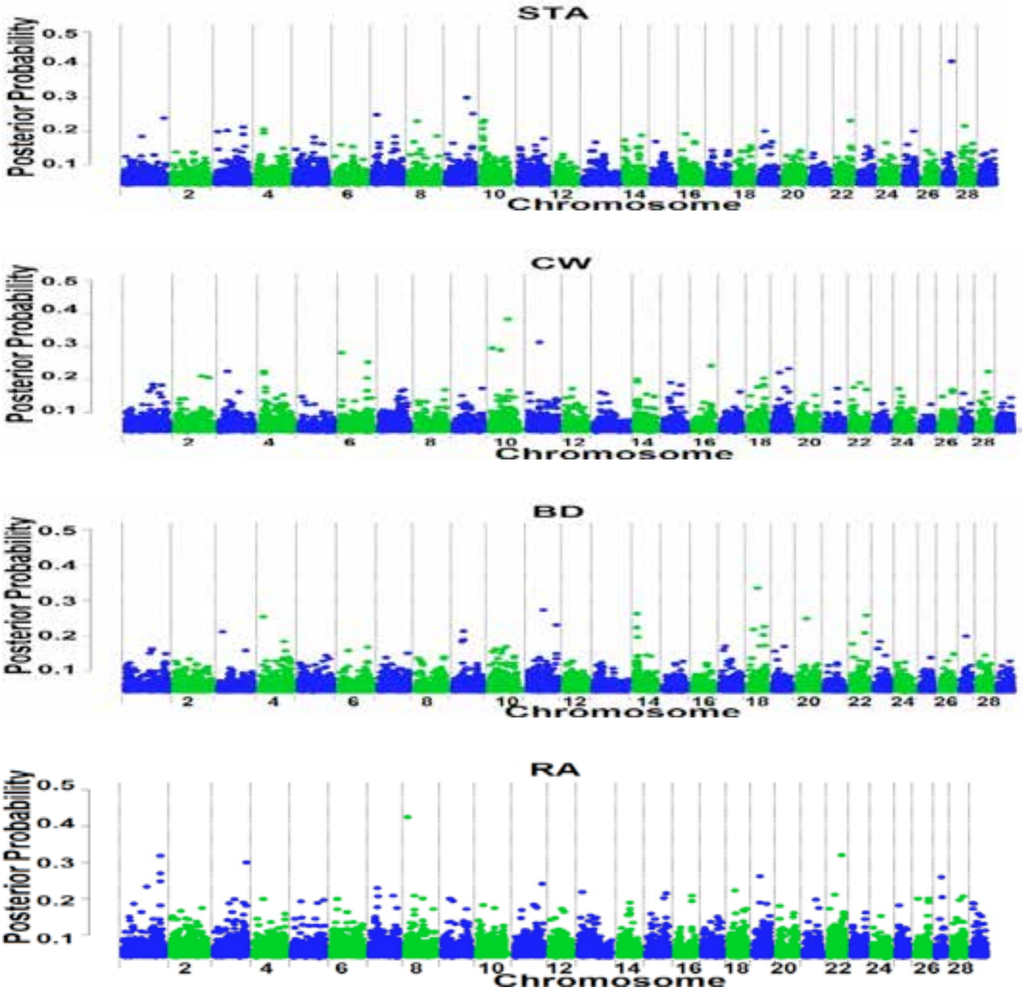

Fig 1: Bayesian posterior probabilities for each SNPs being associated with stature (STA), chest width (CW), body depth (BD) and rear angle (RA)

Conclusions

Several regions of the bovine genome were associated with the body-related type traits. However, the posterior probability of all was low, signifying a considerably larger dataset of genotyped and phenotyped animals is required.

Acknowledgements

Funding from RSF 11/SF/311 is gratefully acknowledged

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RMIS Project Number 6047

Genetic parameters for calving traits in Irish cattle

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Introduction

Dystocia, commonly known as calving difficulty, is defined as a prolonged or difficult parturition. Perinatal mortality is defined as calf mortality shortly before, during, or after parturition (Philipsson et al., 1976). Both phenomena are common problems on dairy and beef farms and impact on profitability through the direct cost of losing a calf, as well as its potential association with subsequent cow performance (Olsen et al., 2010). The objective of this study was to estimate genetic parameters of perinatal morality, calving dystocia and also perinatal mortality not associated with calving dystocia (PMND) in Irish cattle.

Materials and Methods

Data on calf, sire, dam, calving date, age and parity of dam, gender of calf, degree of calving assistance, and occurrence of perinatal mortality (recorded as calf dead at birth or within 24 hours) were available from the years 2008 to 2012, inclusive. In total 3,225,562 calving records were available where the sire and maternal grandsire of the calf were known. Of these, 2,630,037 calving events had information on the degree of calving assistance required at birth and 1,824,729 recorded the occurrence of perinatal mortality. Calving assistance is scored on a linear scale from 1 to 4, where 4 is veterinary assistance. Animals whose data were used in this analysis were from a range of different dairy and beef breeds and crossbreds. Dams of unknown parity, and parities >10 were discarded, as well as calving events where the birth of more than two calf births was recorded. Cows that calved for the first time less than 608 days of age and animals calving more than 2 years from the median, within parity, were discarded. Dam parity was divided into five classes; 1, 2, 3, 4, and ≥5. Contemporary groups (CG) were generated within trait by grouping animals calving in close proximity within a herd. CGs were defined separately for primiparous and multiparous cows. A random selection of CGs with at least five records were retained comprising of 131,168 animals from dairy and beef herds. Variance components for calving traits were estimated using a univariate animal-dam repeatability model for multiparous cows and a univariate animal-dam model for primiparous cows in ASReml (Gilmour et al., 2008). Fixed effects included in the models were CG, parity, age of cow (months) nested within parity, calf gender, whether the calf was a single or twin, and heterosis and recombination loss coefficients of both the calf and cow. Random effects were the additive genetic effect of the calf, the maternal genetic effect of the cow, and in the pluriparae model a cow permanent environmental effect. Breed was accounted for by use of founder breed groups in the pedigree.

Results and Discussion

The prevalence of dystocia (i.e., calving difficulty score ≥3), perinatal mortality and PMND was greatest ($P<0.001$) in primiparous cows (Table 1). The prevalence of dystocia was greater ($P<0.001$) in male (4.98%) than female calves (2.85%), irrespective of parity. The prevalence of twins in the dataset was 1.64%. The occurrence of a stillborn calf was greatest (22%) when “some calving assistance” was required at calving. Heritability of all traits was greater in first parity animals (Table 2), consistent with international studies (Steinbock et al., 2003). Direct and maternal heritability estimates for both primiparous and multiparous animals were statistically significant for dystocia and perinatal mortality. However, PMND had the lowest heritability estimate which was not different from zero.

Table 1 Prevalence of perinatal mortality (PM), dystocia and perinatal mortality not associated with dystocia (PMND) in primiparae and pluriparael

	PM %	Dystocia %				PMND %
		1	2	3	4	
Primiparae	5.5	74.3	19.9	3.7	2.0	2.3
Multiparae	2.8	82.1	14.5	2.1	1.3	1.2

Table 2 Direct and maternal heritability estimates for perinatal mortality (PM), dystocia and perinatal mortality not associated with dystocia (PMND)

	Dystocia		*PM*		*PMND*	
	Dir	Mat	Dir	Mat	Dir	Mat
Primparae	0.39	0.04	0.02	0.02	0.01	0.01
Multiparae	0.23	0.03	0.01	0.01	0.01	0.01

Conclusions

Genetic parameters of perinatal mortality and dystocia although low agree with previous international estimates. PMND although non significant exhibits genetic variation which could be possibly exploited to reduce incidences.

Acknowledgements

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RMIS Project Number 6047

Genotypic diversity and antimicrobial susceptibility status of Irish mastitis-associated *Staphylococcus aureus*

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Introduction

Bovine mastitis is considered to be economically the most important disease of the dairy industry both globally and in Ireland. Mastitis is typically bacterial in origin with a variety of pathogens implicated in causing mastitis. *Staphylococcus aureus* is traditionally considered to be the predominant mastitis pathogen in Ireland. Molecular epidemiological studies have shown that specific genotypes of *S. aureus* are particularly suited to infecting cattle suggesting these isolates have acquired or adapted distinct virulence factors for interacting with a bovine host (Herron-Olson et al., 2007). The aim of this study was to profile the genetic diversity of Irish mastitis-associated *S. aureus* using Multi Locus Sequence Typing (MLST) and to identify the prevalent clonal complexes using the eBURST algorithm. The antimicrobial susceptibility status of the *S. aureus* isolates to a range of commonly used antibiotics was also established to determine if antimicrobial susceptibility and sequence type (ST) were associated.

Materials and Methods

Milk samples were collected over a one year period from cows displaying symptoms of clinical mastitis on 32 farms. From these milk samples a total of 137 *S. aureus* isolates were recovered. Genotypic characterization of the isolates was carried out using MLST with all PCR conditions and oligonucleotide sequences provided on the *S. aureus* MLST database (http://saureus.mlst.net/). For each isolate, a consensus sequence was generated for each of the seven loci analysed, using Bioedit. Consensus sequences were subsequently compared to those in the MLST database to assign allele numbers for each locus. For each isolate, the alleles at each of the seven loci defined its sequence type (ST). Groups of related genotypes were identified using the eBURST algorithm. Irish mastitis-associated *S. aureus* STs were also compared with all STs of bovine origin in the MLST database. Antimicrobial susceptibility profiling was performed using the Clinical and Laboratory Standards Institute (CLSI) performance standards for antimicrobial disk susceptibility testing for bacteria isolated from animals for the following antibiotics: Amoxicillin + Clavulanic Acid (AMC), Oxacillin (OX), Ampicillin (AM), Penicillin (P), Cefalexin (CN), Ceftiofur (XNL), Kanomycin (K), Neomycin (N), Clindomycin (CM), Erythromycin (E), Tetracycline (TE) and Enrofloxacin (ENR).

Results and Discussion

MLST analysis was performed for 137 *S. aureus* isolates from which 55 different STs were identified. Of these, 46 were novel STs that had never been sampled previously. The MLST results show a high level of genotypic diversity in the *S. aureus* isolates, both nationally and on individual farms. The majority of farms had a variety of STs present, suggesting that there may be multiple reservoirs of *S. aureus* on these farms. Despite the large number of novel STs only five clonal complexes (CC) were identified; CC97, CC71, CC151, CC5 and CC1 indicating a phylogenetic relationship among many of the isolates. CC97, CC71 and CC151 are all known bovine-specialised clonal types and the majority of isolates clustered into these groups with only four isolates clustering with CC5 and CC1. A small number of isolates did not cluster and remained singletons. The antimicrobial susceptibility status for the 137 isolates to twelve commonly used antibiotics was determined and results are shown in Fig. 1. Overall, low levels of antimicrobial resistance were observed although approximately 50% of the isolates were resistant to Ampicillin and Penicillin. Antimicrobial susceptibility results were compared with ST results from MLST and resistance to ampicillin and penicillin was associated with the CC71genotype.

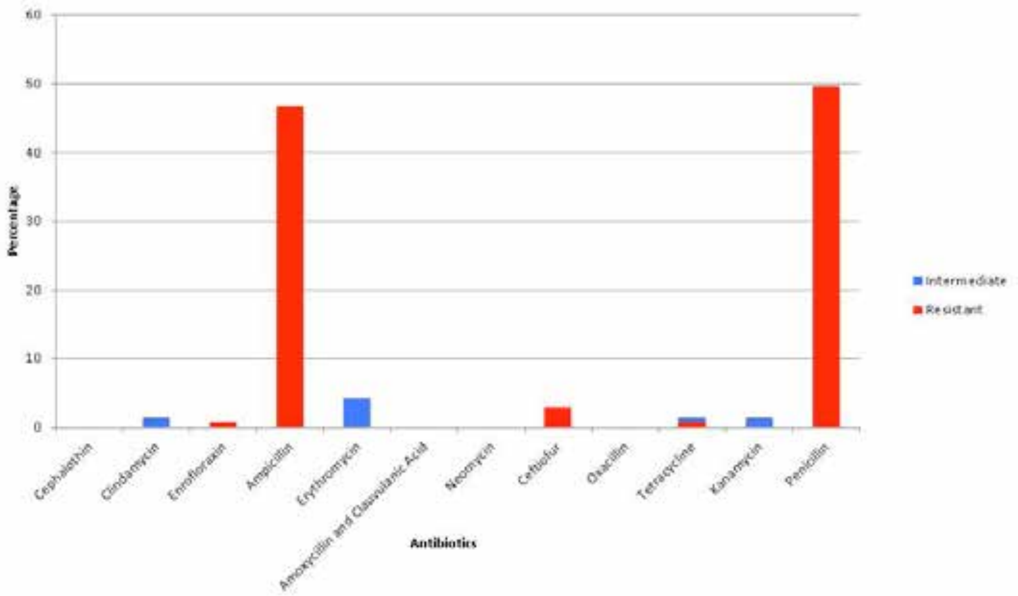

Fig. 1. Antimicrobial susceptibility status of 137 *S. aureus* isolates

Conclusions

MLST analysis showed extensive genotypic diversity in Irish mastitis-associated *S. aureus* isolates. However, the majority of isolates were highly related and belonged to 5 clonal complexes. Three of these clonal complexes are known to be bovine adapted. Antimicrobial susceptibility testing of the *S. aureus* isolates showed that many displayed penicillin and ampicillin resistance and this resistance was associated with CC71.

Acknowledgements

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Animal Facilities, Labour, Automation & Energy Efficiency

Overmilking causes deterioration in teat-end condition of dairy cows in late lactation

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Introduction

To minimise the effect of increasing herd size on labour resources, larger parlours with more milking units are being installed in an attempt to maintain short total herd milking times. However, this increases the number of clusters handled per operator. In parlours not fitted with automatic cluster removers (ACR), clusters may remain attached after milk flow has ceased, resulting in overmilking, particularly in late lactation in seasonally calved herds. Overmilking has been linked with an increased incidence of clinical mastitis and higher somatic cell count (SCC) in some studies. This may be due to altered teat condition. Lewis *et al.* (2000) reported an association between teat hyperkeratosis and subclinical mastitis. Some studies have reported no effect on teat condition with 2 min of overmilking (Gleeson *et al.*, 2003), whilst others have (Hillerton *et al.*, 2002). However, few studies have compared more than one level of overmilking in the same experiment. The objective of this study was to determine the effect of varying degrees of overmilking on teat-end hyperkeratosis, milk production variables and indicators of udder health during late lactation.

Materials and Methods

The effect of four end-of-milking criteria on teat condition of 181 spring calving multiparous Holstein-Friesian cows, at an average 217 ± 24 days in milk, over a six week period was examined. The four treatments were: remove cluster once milk flow rate fell to 0.2 kg/min plus 5 s (Ovr0), plus 120 s (Ovr120), plus 300 s (Ovr300), and plus 540 s (Ovr540). Teat-end hyperkeratosis score was determined at week 0, 3, 5 and 6. Daily measurements included individual cow milk yield, milking duration, overmilking duration and maximum milk flow rate.

Teat-end condition data were analysed using mixed models including overmilking treatment, the interaction of week and overmilking treatment. The initial teat-end score was used as a covariate. The milking data were analysed using mixed models, including the fixed effects of farm, session (AM/PM), overmilking treatment, with initial milking data as a covariate, plus cow, session and week within cow as random effects. All analyses were undertaken using GenStat 14.1.

Results and Discussion

There was an interaction between teat score and week (P<0.05). The greatest change occurred from week 0 to 3 (P<0.001), changes from week 3 to 5 and from weeks 5 to 6 were not significant (P>0.05). Teat end hyperkeratosis score increased with increasing duration of overmilking at each measurement week (Table 1). Mean teat score of the Ovr120 treatment was significantly higher than Ovr0 only at week 5 (Table 1). In comparison, mean teat score of the Ovr300 and Ovr540 treatments were greater than the Ovr0 treatment at week 3, 5 and 6 (P<0.001). However, mean teat score of the Ovr540 treatment only increased significantly beyond the Ovr300 treatment at week 6 (P<0.001). Milk production variables and SCC were not different between treatments, except milking duration.

Table 1. Effect of four overmilking treatments (Ovr0, Ovr120, Ovr300 and Ovr540) on mean teat end condition score

	Treatment					
Time	Ovr 0	Ovr 120	Ovr 300	Ovr 540	SED[‡]	P-value
Wk 0	1.7	1.7	1.7	1.7		
Wk 3	1.8	1.9	2.1	2.1	0.07	***
Wk 5	1.7	1.9	2.0	2.1	0.06	***
Wk 6	1.8	1.9	2.1	2.3	0.07	***

[†] Wk = week; [‡] Standard error of the difference; *** = P≤0.001.

The results of this overmilking study have important implications for milking management in dairy parlours. The effect of overmilking on teat-end hyperkeratosis can be rapid, with changes detected in three weeks. Overmilking of greater than 2 min (120 s) is likely to occur in two scenarios; (a) single operator swing-over parlours (≥14 units) utilising a full pre-milking routine, without the use of ACR, during any stage of lactation, or (b) when applying no pre-milking routine (i.e. immediate cluster attachment) if parlour size is greater than 26 and 22 units at peak and late lactation lactation, respectively (O'Brien *et al*., 2012). Thus, when constructing a new swing-over parlour the ideal number of units should be determined based on the anticipated cow milking duration and operator work routine time to ensure maximum utilisation of clusters, minimum operator idle time and avoidance of overmilking. In existing parlours, if overmilking is likely to occur then either the work routine must be streamlined, an additional operator employed in the parlour, ACR installed, or an appropriate number of units deactivated.

Conclusions

Overmilking should be limited to 2 min (120 s), which has implications for milking management in large parlours not fitted with automatic cluster removers.

Acknowledgements

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RMIS Project Number 6202

The association between Udder hygiene score and the *Bacillus cereus* count in raw bulk tank milk

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Introduction

Ireland currently produces 10-15% of the global export market for infant formula (Danone, Pfizer and Abbott). The market typically grows by an average of 15% year on year (DAFM, 2011). A significant threat to this growing industry is the food borne pathogen *Bacillus cereus.* The pathogen can grow in contaminated infant milk formula. Under storage abuse conditions of reconstituted infant formula (>20°C for 24hrs) *Bacillus cereus* counts can reach hazardous levels (>10^3CFU/g) (Haughton *et al*., 2010).

While reported cases are rare, the potential to cause illness in contaminated infant formula is especially important. Infants have greater susceptibility to the organism and therefore are at a higher health risk than other people (Becker *et al.,* 1994). However an initial count must be present for there to be a potential risk. This initial count can be introduced at farm level. *Bacillus cereus* is ubiquitous in nature and is present in large numbers in the soil. During the grazing period Christiansson et al. (1999) reported that the *Bacillus cereus* spore content of milk was strongly associated with the degree of contamination of the teats with soil. The effect of udder hygiene on the *Bacillus cereus* count in milk has not been previously studied. The objective of this study was to investigate the association between udder hygiene score and *Bacillus cereus* counts in raw bulk tank milk.

Materials and methods

Sixty-three herds were visited once during milking from July to Sept 2012 in Co. Cork. The mean herd size was 66 cows. Herds were categorised based on their *Bacillus cereus* count for the previous four bulk tank milk results prior to a farm visit. Low-count herds (n=21) had *Bacillus cereus* counts of less than 10cfu/ml for at least three out of four tests. Average-count herds (n=25) had *Bacillus cereus* counts of between 10 and 100cfu/ml for at least three out of four tests. High-count herds (n=17) had *Bacillus cereus* counts of greater than 100cfu/ml for at least two out of four tests.

Using the udder hygiene scoring (UHS) system developed by Shreiner and Ruegg (2003) udder hygiene was scored on an average of fifty cows in each herd. An UHS of one identified udders completely free of dirt, scores 2 and 3 indicated udders that were slightly or moderately covered with dirt, while an UHS score of four identified udders where >30% of the surface area was covered with caked-on dirt. The association between herd-type and UHS was analysed using ordinal regression (PROC GENMOD, SAS, 2003) with herd as a random effect and herd-type as a fixed effect.

Results and Discussion

No impact of herd-type (*Bacillus cereus* category*)* on UHS was identified (P>0.05).The number of cows within each of the 4 hygiene scores were similar regardless of herd-type (Table 1). The lack of difference among categories could be due to similar housing conditions for all herds. Cows were out on pasture and experienced similar weather conditions. Shreiner and Ruegg (2003) found a significant association between UHS and environmental mastitis pathogens. In that study the eight herds investigated were all housed in free stalls and so experienced different housing conditions.

Using the same scoring system Krawczel *et al.* (2012) studied the effect of increased stocking density indoors on udder hygiene. In this study cows were housed in free stalls with mattresses and sawdust. Increasing the stocking density to 142% by various conditions did not affect udder hygiene. This suggests that the variance in stocking densities on pasture may have no effect on udder hygiene score.

Comparing cow cleanliness using a 20 point scale on organic and conventional farming systems in the UK, Ellis *et al.* (2006) concluded that farming system had no effect on cow cleanliness when cows were on pasture. However when cows were housed organic cows tended to be cleaner. This suggests that herd variability is more apparent when cows are housed compared to when at pasture.

Table 1 The percentage of cows in each category for udder hygiene scores

	Udder hygiene score			
Herd-type	1	2	3	4
Low count	25%	30%	26%	20%
Avg. count	25%	33%	24%	18%
High count	21%	29%	24%	26%

Conclusion

For Irish cattle, during the pasture season, there was no association between udder hygiene score and *Bacillus cereus* in raw bulk tank milk samples. This could be due to similar housing and weather conditions experienced by all herds.

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RMIS Project Number 6237

Efficacy of post-milking teat disinfection products in reducing bacterial numbers on teats

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Introduction

The concentration of bacteria recovered from teat skin has been shown to be lower when teats are disinfected compared to untreated teats (Fox and Norell, 1994). The type of post milking disinfectant product can have varying degrees of success in reducing the microbial count on teats (Gibson *et al*., 2008). Iodophor and Chlorohexidine have been shown to be effective against *Staphylococcus* and *Streptococcus* bacteria (Pankey *et al.,* 1983). A range of newly formulated teat disinfectant products are now available on the market. The objective of this study was to investigate the effectiveness of ten post-milking teat disinfection treatments on *Staphylococcal* and *Streptococcal* bacterial numbers on teat skin, at two time periods after disinfection.

Materials and Methods

Ten disinfectant treatments were chosen based on contrasting chemical composition. These treatments were applied post-milking to the teats of 20 Friesian dairy cows (2 groups of 10 cows) over a 10 day period. Two different disinfectant treatments were applied to the two cow groups on each day. Treatments applied: T1=lactic acid (Hyprid), T2=biguanide hydrochloride (Vita teat foam), T3=chlorohexidine (Deosan Teat Foam), T4=polyhexamethylene biguanide (Super cow teatfoam), T5=Biocide (experimental), T6=ammonium lauryl sulphate (Helodip), T7=iodine (Deosan super iodine), T8=chlorohexidine (Deosan teat care plus), T9=lactic acid (Viralac), T10=iodine (Deosan super iodine). Teat preparation (wash + dry with paper) prior to milking was carried out for T10 only. Teats were swabbed after milking and before disinfection using one sterile swab for the teats on the right hand side of the udder and one sterile swab for the two teats on the left hand side of the udder to establish the number of *Staphylococcus* and *Streptococcus* bacteria present. All disinfectant treatments were applied at the morning milking to all four teats of each cow, within each group, on one occasion. The teats from the right hand side of the udder were swabbed 5 minutes after the application of disinfectant and the teats on the left hand side of the cow were swabbed one hour after disinfection. Immediately after swabbing, swabs (n=800) were placed in individual sterile bottles containing 5mls of Tryptic Soy Broth and frozen (-20^{O}C) until analysed. The swabs were subsequently plated on two selective agars: Baird parker (*Staphylococcus)* and Edwards *(Streptococcus)* and following incubation at 37 ºC for 24 hours, colony counts (cfu/ml) were manually counted. Plates with numerous (NS) colony counts were assigned a count of 100 for statistical analysis. The statistical analysis used a factorial structure to examine main effects and interaction of time and treatment. The analysis used the NLMIXED procedure of SAS 9.2 (2009). Adjustments for multiplicity of treatment comparisons were made with the MULTEST procedure of SAS using a step-down Bonferroni adjustment.

Results and Discussion

The mean reduction in *Staphylococcal* and *Streptococcal* bacterial numbers on teats, 5 minutes and 1 hour after disinfection, for ten disinfectant treatments, are presented in Figures 1 and 2, respectively. Treatment 2 had the largest numerical reduction in *Staphylococcal* counts and had significantly greater reductions than treatments 1, 5, 6, and 7 (P<0.01). Treatment 4 had the largest numerical reduction in *Streptococcal* bacteria and had significantly greater reductions than treatments 1, 3, 5, 6, 7 and 10 (P<0.01). The level of reduction may be influenced by the initial bacterial levels on teats. *Staphylococcal* bacteria were present on ninety four percent of teats and *Streptococcal* bacteria were present on sixty nine percent of teats post-milking and before disinfection. The percentage of teats with no

Staphylococcal and *Streptococcal* bacteria present 5 minutes after disinfection ranged from 25 to 89% and from 67 to 100%, respectively. The high bacterial populations observed on teats highlights the importance of post-milking teat disinfection since teat skin colonized by *Staphylococcus aureus* is more likely to result in mastitis (Roberson and Fox, 1994). There was no interaction for time (5 minutes v 1 hour) or a treatment x time interaction for either *Staphylococcal* or *Streptococcal* bacteria.

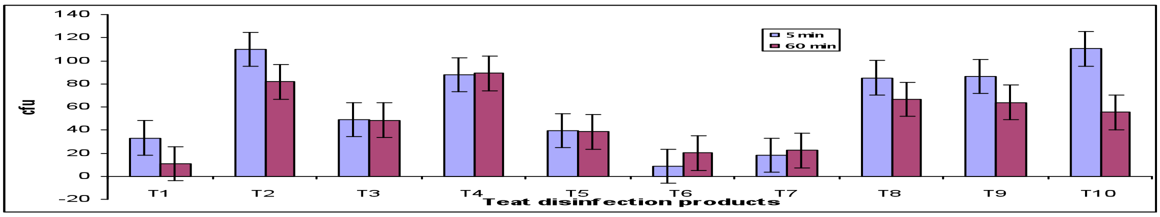

Figure 1. Mean reduction in *Staphylococcal* counts on teats, 5 min and 1 hour after post-milking disinfection

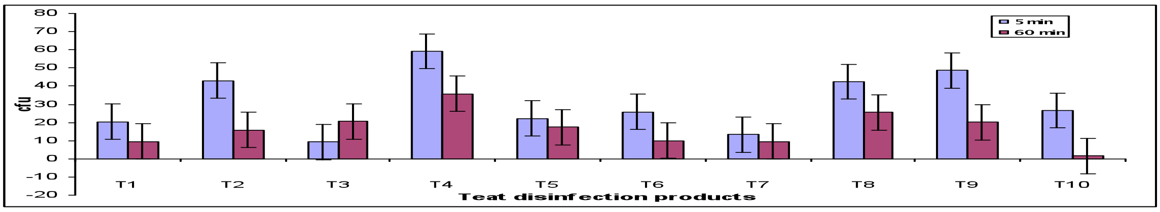

Figure 2. Mean reduction in *Streptococcal* counts on teats, 5 min and 1 hour after post-milking disinfection

Conclusions

A high level of *Staphylococcal* and *Streptococcal* bacteria was observed on teats post-milking and this highlights the importance of post milking disinfection. Some products were more effective in reducing specific bacteria types.

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RMIS Project Number 6237

Animal Nutrition and Product Quality

The effect of offering concentrate feeds differing in crude protein and Phosphorus concentration to spring calving dairy cows on milk yield and composition and animal N and P status in early lactation

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Introduction

Milk composition is affected by the dietary concentration of crude protein (CP) (Kung Jr and Huber, 1983) and minerals such as Phosphorus (P) (Wu and Satter, 2000). Milk composition has consequent effects on milk processability (Dillon *et al.,* 1997). The objective of this study was to determine the effects on milk yield and composition, and animal nitrogen (N) and P status, of offering supplementary concentrate feeds differing in CP and P concentration to grazing, dairy cows in the early lactation period (Feb – May).

Materials and Methods

The 8-week study took place at Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co Cork, between 29 February and 9 May 2012. Forty eight lactating dairy cows were blocked on calving date, lactation number, milk yield, milk fat and protein concentration, milk solids yield, bodyweight and body condition score. From within block the cows were randomly assigned to one of four treatments: high protein high Phosphorus (HPrHP), medium protein high Phosphorus (MPrHP), low protein high Phosphorus (LPrHP) and low protein low Phosphorus (LPrLP). The treatment groups were offered 13 kg DM grass per cow/day. Four kg per cow daily of concentrate feeds were offered, at morning milking. The HPrHP concentrate contained 240 g/kg CP and 5.7 g/kg P; MPrHP 160 g/kg CP, 5.7 g/kg P; LPrHP 80 g/kg CP, 5.7 g/kg P and LPrLP 80 g/kg CP, 0.096 g/kg P. Milk yield was recorded daily and milk composition was recorded weekly. Faecal samples were collected from each cow during week 5 of the study for analysis of P concentration. Blood samples were taken prior to, during week 4 and at the end of the study for analysis of P and blood urea nitrogen (BUN) concentration. Data were analysed using covariate analysis and the PROC MIXED statement of SAS, with terms for week, treatment and the interaction between treatment and week included in the model.

Table 1. Effect on milk yield and milk composition of offering supplementary concentrate feeds differing in crude protein and Phosphorus concentration to dairy cows in early lactation

	HPrHP	MPrHP	LPrHP	LPrLP	S.E.	P-Value
Milk yield (kg/d)	27.6	27.0	26.2	27.0	0.73	NS
Milk fat (g/kg)	44.5	45.4	46.1	42.7	1.41	NS
Milk protein (g/kg)	34.0	33.5	33.7	33.9	0.53	NS
Milk solids (kg/d)	2.15	2.12	2.07	2.03	0.052	NS
Milk urea (mg/100ml)	60.3^{a}	56.8^{a}	47.8^{b}	46.9^{b}	0.92	<0.001
Milk casein (g/kg)	26.6	26.0	26.0	26.1	0.30	NS

HPrHP – High Protein, high Phosphorus; MPrHP – Medium protein, high Phosphorus; LPrHP – Low protein, high Phosphorus; LPrLP – Low protein, low phosphorus; $^{a-b}$ Means within a row not sharing a common superscript differ significantly ($P<0.05$)

Results and Discussion

Milk yield, milk fat concentration and milk protein concentration were not affected by treatment and there was no treatment*week interaction (Table 1). This agrees with work carried out by Mulligan *et al.* (2004) who offered supplementary concentrate feeds differing in CP concentration and Wu and Satter (2000) who offered feeds differing in P concentration. Milk urea nitrogen (MUN) concentration was significantly effected ($P<0.001$) by treatment and there was a significant ($P<0.001$) interaction between treatment and time (Table 1). Milk urea is an indicator of non-protein nitrogen, a component of bovine milk not used in the manufacture of cheese and whey dairy products (Dalgliesh, 1993). Therefore increased MUN is undesirable from a processing perspective. The BUN concentration of HPrHP, MPrHP and LPrHP (3.87 ± 0.174; 3.49 ± 0.164; 3.15 ± 0.157 mmol/L) were all greater ($P<0.001$) than LPrLP (2.45 ± 0.159 mmol/L). In week 8 of the study, blood P was lower ($P<0.001$) in the LPrLP treatment (0.95 ± 0.065 mM) than in the HPrHP, MPrHP and LPrHP treatments (1.28 ± 0.063; 1.23 ± 0.071; 1.33 ± 0.062 mM). Faecal P was also lower ($P<0.001$) in the LPrLP treatment (4.9 ± 0.678 g/kg) than in the HPrHP, MPrHP and LPrHP treatments (6.48, 6.22 and 6.29 ± 0.678 g/kg respectively).

Conclusions

The results suggest that supplementing a grazed grass diet with 4 kg of a supplementary feed containing 80 g/kg CP and 0.096 g/kg P, did not significantly reduce milk yield or milk composition. However, it did significantly reduce MUN concentration, which is desirable from a milk processing perspective. Increasing P and N efficiency at farm level can have positive economic implications, as well as reducing their environmental impact (Oenema, 2004).

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RMIS Project Number 6095

The effect of offering different supplementary feeds to grazing dairy cows in late lactation on milk yield and milk composition

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Introduction

Grazed grass is the cheapest source of nutrition for dairy cows in Ireland (Dillon *et al*., 1997). During times of grass deficit, supplementary feeds are offered to maintain milk yield (Burke *et al*., 2004). Different supplementary feeds can be offered and the choice includes grass silage, other silages and concentrate feeds. The objective of this study was to investigate the effects of offering different supplementary feeds to grazing dairy cows in late lactation on milk yield and composition.

Materials and Methods

The study was conducted at Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co Cork from 13 August to 7 October, 2012. Sixty spring-calving lactating dairy cows were blocked by calving date, lactation number, milk yield and composition, bodyweight and body condition score. From within block, the cows were randomly allocated to one of five treatments: high grass allowance (HG), low grass allowance (LG), LG and baled grass silage (GB), LG and pit grass silage (GP) and LG and concentrate (GC). The average DMD of the baled and pit grass silage was 740 and 670 g/kg respectively. The concentrate was a 160 g/kg CP dairy concentrate. All treatment groups were offered 13 kg DM grass per cow/day, apart from the HG treatment, which was offered 17 kg DM grass per cow daily. The HG and LG treatments did not receive any supplementation. Treatments GB, GP and GC were offered 4 kg DM per cow daily of the appropriate feed. These feeds were offered at morning milking. Milk yield was recorded daily and milk composition was recorded weekly. Data were analysed using covariate analysis and the PROC MIXED statement of SAS, with cow used as a random effect and week as the repeated measure Lactation number, treatment, week and the interaction of treatment and week were included in the model.

Results and Discussion

Table 1 presents the milk performance results of the study. Milk yield was significantly (P<0.001) affected by treatment, and there was a significant (P<0.001) treatment by week interaction. Milk yield was greater (P<0.05) in the supplemented treatments than in the non supplemented treatments. There was a significant effect of treatment (P<0.001) and treatment by week interaction (P<0.001) on milk solids yield.

Table 1. The effects on milk production of offering different supplementary feeds to grazing dairy cows in late lactation

	Grass only		13 Kg DM grass plus 4 kg DM supplementary feed				
	High Grass	Low Grass	Bailed Grass-Silage	Pit Grass-silage	Concentrate	S.E.	P-Value
Milk Yield (kg/d)	12.4^{b}	11.5^{a}	13.3^{c}	13.3^{c}	15.3^{d}	0.27	<0.001
Milk fat (g/kg)	49.1	50.8	49.8	46.7	47.9	1.31	NS
Milk protein (g/kg)	38.8	37.6	3.7.5	37.8	3.88	0.50	NS
Milk lactose (g/kg)	41.9	41.5	41.9	41.8	42.8	0.03	NS
Milk solids (kg/d)	1.08^{b}	1.01^{a}	1.12^{b}	1.09^{b}	1.29^{c}	0.02	<0.001

In all weeks of the experiment, GC had a greater milk solids yield than LG. There was also a greater increase in milk solids in GC than in HG in weeks 3, 4, 5 and 7. This agrees with Burke *et al*. (2004) who found that supplementation gave rise to increased milk yield and milk solids yield compared to grazed grass alone. In weeks 2, 3 and 4, GC also had greater milk solids yield than GB and GP. Milk fat concentration, milk protein concentration and milk lactose concentration were not affected by treatment (P>0.05). The results agree with similar studies (Kennedy *et al*., 2008; McEvoy *et al*., 2008). However, there is a need for more detailed analyses as the suitability of milk for processing is of key importance to the dairy industry. Milk processability tests should be conducted to establish if differences exist between supplementary feeding strategies.

Conclusions

In this study offering grass silage increased milk yield and milk solids yield in the late lactation period with no negative effect on milk protein or milk fat concentration. The processability of milk from different nutritional regimes in late lactation should be tested to ensure it is of the highest quality.

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RMIS Project Number 6095

Investigation of the persistence of triclabendazole residues in bovine milk following lactating-cow and dry-cow treatment

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Introduction

Triclabendazole (TCB) is one of the most important anthelmintic drugs because it is the only one that shows activity against fluke from the earliest stage of infection onwards. A maximum residue limit (MRL) of 10 µg/kg was recently set for TCB residues in milk (EU, 2012). The objective of this research was to investigate the metabolism and persistence of TCB residues in milk (of recently calved cows), resulting from a preventative flukicidal treatment (dry cow) and the presence of residues in milk resulting from potential flukicidal reactionary treatment (lactating animals). The measurement of TCB included the metabolites TCB-SO, TCB-SO_2 and keto-TCB.

***Mate**rials and Methods*

Lactating cow study

Six lactating dairy cows (3 Holstein-Friesian, 2 Montbeliarde, 1 |Norwegian Red) were weighed and administered TCB orally using 12 ml of Fasinex 10% (containing Triclabendazole) per 100 kg live weight. Milk samples were taken twice daily for 23 days post treatment. All samples were stored for a maximum of 1 week at -20˚C until analysed using multidimensional chromatography coupled with mass spectrometry (LC-MS/MS).

Dry cow study

A total of 36 Holstein-Friesian dairy cows, were weighed and TCB administered orally using 12 ml of Fasinex 10% (containing Triclabendazole) per 100 kg live weight at the start of the dry period. Animals calved at 44 to 65 days post-treatment. Milk samples were collected from the cows during the first 10 days in milk. All samples were labelled on collection and stored at -20˚C until analysed within 2 weeks using multidimensional chromatography coupled with mass spectrometry (LC-MS/MS).

Results and Discussion

Lactating cow study

TCB-SO_2 constituted >87% of marker residues with TCB-SO being the second major metabolite in milk, followed by lower concentrations of keto-TCB, at ≥3.5 days post drug administration. Measured as the sum of TCB residues, a mean of 1621 µg/kg, was the highest concentration detected, at 1.5 days post-treatment (Figure 1). The TCB concentration was below the new MRL of 10 µg/kg in the milk in all animals at 18.5 days post-treatment. These results highlight that caution should be applied when using TCB in lactating cows because long withdrawal periods would be required to ensure that milk samples comply with EU MRLs.

Dry cow study

Summed TCB marker residues were detected in the first milking of only two out of the 36 cows at the concentrations of 0.21 and 0.46 µg/kg (both animals calved at 57 days post-treatment). Residues were non detectable at later time-points.

Following treatment at drying off, TCB residues can be detected in milk post calving, but residue levels detected were well below the new MRL of 10 µg/kg. The results show that, products containing this triclabendazole product can potentially be applied as dry cow treatments if withholding periods are observed. In addition, this research highlighted the importance of including TCB-SO_2 in future analysis for TCB residues in milk samples.

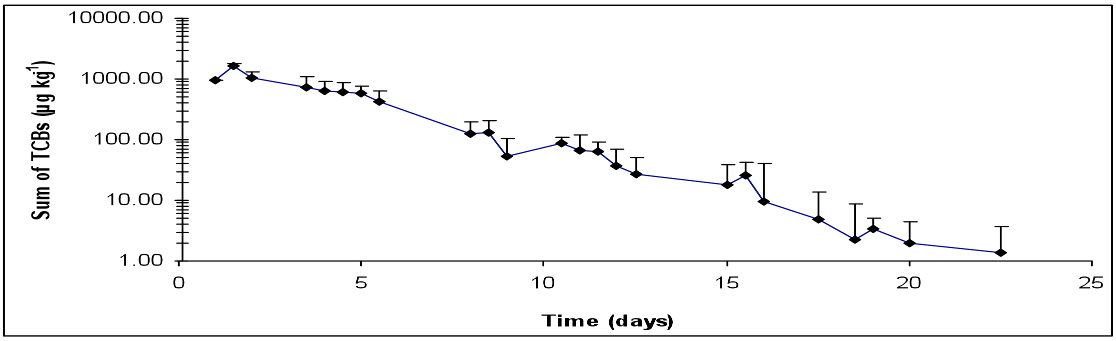

Figure 1 Plot of the sum of TCB residues in cow milk as a function of time (days) post treatment

Conclusions

TCB residues persisted in the milk of lactating cows for almost 20 days post-treatment. This means that this drug is not suitable for application to dairy cows during lactation. When pregnant cows were treated at drying off, residues were detectable in 2 out of 36 cows once they returned to lactation post-calving. Thus, Triclabendazole may be used as a dry-cow treatment.

Acknowledgements

This research was supported by the Walsh Fellowship Programme and the Dairy Levy Research Trust.

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RMIS Project Number 6203

Animal and herd factors associated with somatic cell count of Irish Holstein-Friesians

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Introduction

Milk quality is of increasing importance to the Irish dairy industry as milk processors seek to add value to their products. Somatic cell count (SCC) refers to quantity of leucocytes per mL of milk and is an indicator both of udder health, particularly mastitis, and milk quality. The objective of this study was to identify animal and herd factors associated with somatic cell count in lactating Irish Holstein-Friesian dairy cows.

Materials and Methods

Milk recording data on individual cows together with cow and herd-level information were obtained from the Irish Cattle Breeding Federation. Only records from days 5 to 305 of lactation obtained between the years 2007 and 2011 from Holstein-Friesian cows were retained. Spring calving herds were defined as herds where at least 80% of calvings occurred between December and April, otherwise herds were classified as year-round calving herds. Age at calving within parity was defined as a class variable with animals classed either as 1) less than, 2) greater than or 3) within one standard deviation of the median age at calving for each parity. Stage of lactation was defined with 10 classes in 30 day intervals from 5 to 300 days in milk. Geographical location of herds was classified according to province (Leinster, Munster, Ulster, Connaught). Parities greater than four were grouped for the analyses (5+) and test day records from animals greater than tenth parity were removed. Animals which moved herd during lactation were removed from the analyses and contemporary group of herd-year-season of calving (HYS) was generated and HYS with less than five records were removed. A random sample of 30% of herds were retained for analysis. The final data set contained 2,854,690 test-date records from 656,924 lactations on 282,143 animals in 2,390 herds.

Somatic cell count was normalised to somatic cell score (SCS) using the transformation: SCS = $\log_{10}$ (SCC). Test day SCC was recorded (td_SCS) and three additional SCS traits were defined: the maximum SCS recorded per cow lactation (peak_SCS), the minimum SCS recorded per cow lactation (min_SCS), and the average SCS recorded across cow lactation (avg_SCS).

Factors associated with each of the variables were determined using a repeatability animal linear mixed model in ASReml (Gilmour et al., 2006). Fixed effects considered for inclusion in the model were parity, age at calving centered within parity, geographical location, herd type (spring or mixed calving herd), heterosis and recombination and the random effects of animal and HYS. Where the dependent variable was recorded on a test-day basis, ie, td_SCS, lactation stage and test month were included as fixed effects and the random effect of the animal within lactation was also included. Least squares means for all fixed effects were extracted assuming no heterosis or recombination loss.

Results and Discussion

Of the herds used in the analyses, 69% were classified as spring calving herds, whilst 65%, 24%, 6% and 5% of herds were located in Munster, Leinster, Ulster and Connaught, respectively. Parity groups were evenly represented with 24%, 21%, 17%, 13% and 25% of the data from first to parity 5+ animals.

Unadjusted average td_SCS was 115,095 cells/mL while avg_SCS, peak and minimum SCS within lactation were 111,226, 239,112, and 54,973 cells/mL, respectively. Animals in Connaught herds had the highest td_SCS (147,775 cells/mL) whilst animals in Leinster herds had the lowest td_SCS (126,038 cells/mL; $P<0.01$). The highest peak was observed in Munster (294,239 cells/mL; $P<0.01$), the min_SCS was observed in Leinster (49,023 cells/mL; $P<0.01$). Spring calving herds had lower td_SCS than year-round calving herds (130,287 v 144,544 cells/mL; $P<0.01$) and a lower peak (222,383 v 344,905; $P<0.01$).

Test day SCS ranged across stage of lactation from 93,218 cells/mL between days 30 and 60 of lactation to 206,681 cells/mL between days 270 and 305 of lactation ($P<0.01$). Heterosis had a negative effect on SCS, reducing td_SCS, avg_SCS, min_SCS and peak_SCS by up to 0.03 (se = 0.004) SCS units. Recombination had a positive effect on SCS increasing td_SCS, avg_SCS, min_SCS and peak_SCS by up to 0.06 (se = 0.008) SCS units. The oldest animals (parity 5+) had the greatest td_SCS, avg_SCS, min_SCS and peak_SCS when compared to younger animals ($P<0.01$). Animals calving at a young age respective to their parity had the greatest td_SCS, avg_SCS, min_SCS and peak_SCS ($P<0.05$). Predicted values of td_SCS across test month are shown in Figure 1. A clear non-linear association between td_SCS and month of the year exists ($P<0.01$) with lowest td_SCS occurring during the spring and summer months when the majority of Irish dairy animals will be out at grass. System of production was not available for analysis in this study.

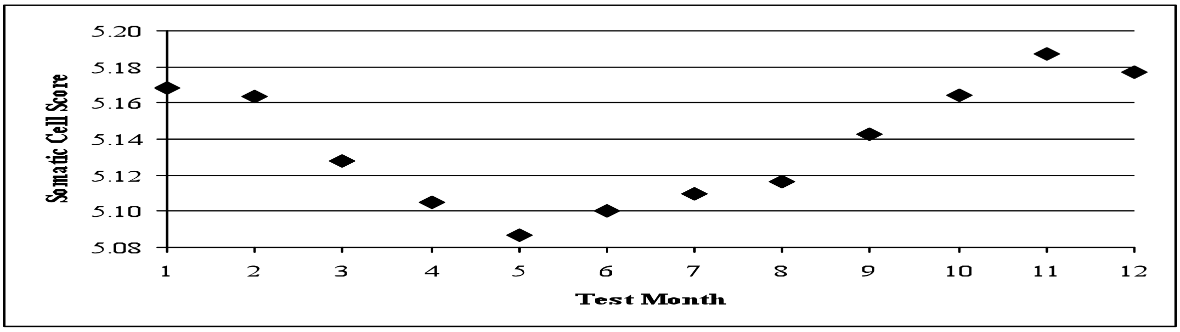

Figure 1. Predicted test day SCS across test month

Conclusion

SCC was significantly influenced by all herd, animal and time of year effects investigated in this study.

Acknowledgements

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RMIS Project Number 6260

GRASSLAND RESEARCH PROGRAMME

Grass Growth, Sward Dynamics & Utilisation under Grazing

Validation of a parameterised mechanistic model at Teagasc, Animal and Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork

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Introduction

In temperate regions although grass growth occurs throughout much of the year, there are marked seasonal variations. For grass based dairy farmers, maximising grass supply in the cows' diet minimizes the quantity of purchased feed required. Budgeting grass supply allows more control of the feed budget. Currently, grass budgeting is limited by the lack of a suitable model to simulate and forecast grass growth. Many grass growth models exist but most have limitations in terms of their suitability for use in Ireland (Hurtado-Uria *et al.,* 2013a) as they were developed at other locations, or are site specific. Existing models can be paramaterised for use in new areas/regions. Hurtado-Uria *et al*. (2013a) evaluated three grass growth models and showed that the model developed by Jouven *et al*. (2006) (hereafter referred to as the Jouven Model) had the greatest potential to simulate grass growth in Ireland, but concluded that the model would require adaptation and parameterization to improve its grass growth simulation. Therefore, the objective of this study was to validate the adapted Jouven Model for Moorepark conditions.

Material and Methods

The Jouven Model was parameterised for Moorepark using meteorological and grass growth data for Moorepark from 2005 to 2009 (Hurtado-Uria *et al*., 2013b not published). The model uses a daily time step. The model was parameterized using Solver in Excel with the objective being to minimise the root mean square error (RMSE). Constraints, such as ensuring that none of the parameters could be negative and that the nitrogen (N) index (NI) had to be less than or equal to one, were included to ensure the new parameters were sensible. Adjusted parameters included initial biomass, NI, bulk densities, temperature thresholds, senescence, abscission and seasonal parameters (details of each in Jouven *et al*., 2006) Moorepark data from 2010 and 2011 were used to validate the new parameterized model (Adapted Model). The Jouven Model and the Adapted Model were compared against 2010 and 2011 grass growth measured at Moorepark using the mean square prediction error (MSPE) as a measure of fit.

Results and Discussion

Predictions of grass growth were improved with the Adapted Model (Figure 1). The MSPE was reduced from 476 to 183 kg dry matter (DM)/ha/day, and the R^2 increased from 0.72 to 0.91 with the Adapted model compared to the Jouven (Table 1). In spring, the Adapted Model reduced MSPE from 134 to 25 kg DM/ha/day and R^2 increased from 0.18 to 0.98 with the Adapted Model (Table 1). In mid-season, the Adapted Model reduced MSPE from 720 to 279 kg DM/ha/day, a good line bias was found (0.000) and R^2 was improved from 0.06 to 0.55 (Table 1). In autumn, random variation was the greatest component of the MSPE (0.625) and R^2 was improved from 0.74 to 0.81 (Table 1) for the Adapted Model compared to the Jouven Model.

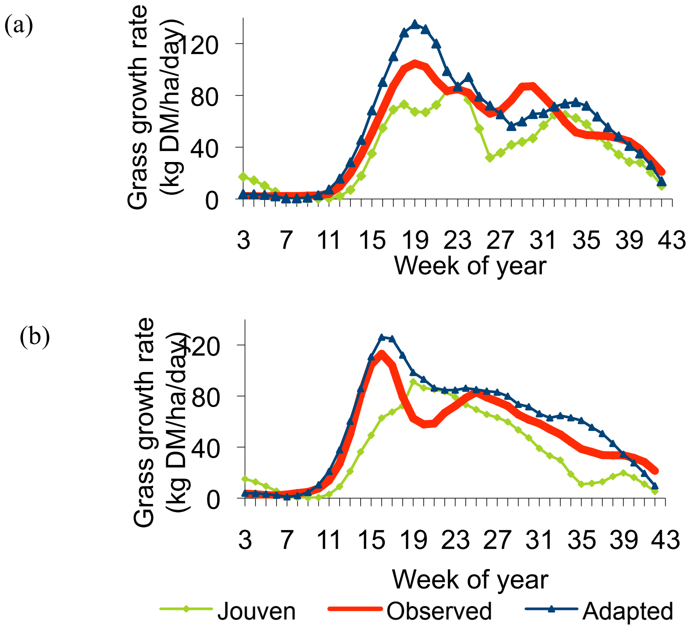

Figure 1. Grass growth (kg DM/ha/day) simulated by the Jouven Model, the Adapted Model and grass growth measured at Moorepark for (a) 2010 and (b) 2011

Table 1. Precision of the Jouven Model and the Adapted Model in simulating total production and seasonal production - spring (Jan–Apr, weeks 1–13), mid-season (Apr–Aug, weeks 14–30), autumn (Aug–Nov, weeks 31–45) using mean square prediction error (MSPE) and R^2 for the years 2010-2011

Period	Model version	Proportion of MSPE			MSPE	R^2
		Mean bias	Line bias	Random		
Total	Jouven	0.269	0.115	0.617	476	0.72
	Adapted	0.317	0.146	0.537	183	0.91
Spring	Jouven	0.023	0.181	0.796	134	0.18
	Adapted	0.169	0.719	0.113	25	0.98
Mid-season	Jouven	0.376	0.247	0.378	720	0.06
	Adapted	0.535	0.000	0.465	279	0.55
Autumn	Jouven	0.563	0.013	0.424	229	0.74
	Adapted	0.267	0.108	0.625	113	0.81

Conclusions

The Adapted Model improved grass growth simulation at Moorepark. This improvement was achieved with changes to the parameters (e.g. NI increased to 1; adjustments to seasonal parameters such as temperature required for start and end of reproductive phase, and initial biomass) used by the model, thus suggesting that adaptation is possible for other locations.

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RMIS Project Number 5903

Effect of perennial ryegrass (Lolium perenne) cultivar on milk production and dry matter intake of Holstein Friesian cows during the early summer period

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Introduction

In Irish grass-based production systems, eighty percent of the dairy cows' diet consists of grazed grass. O'Donovan & Delaby (2005) and Gowen *et al* (2003) reported that late heading cultivars resulted in increased milk yield, Wilkins & Humphreys (2003) reported a positive effect of increasing sward digestibility on dry matter intake (DMI). The objective of this study was to examine the effects of four perennial ryegrass cultivars, on milk production and DMI of spring calving Holstein Friesian cows, during the early summer period.

Materials and Methods

The study commenced on 2nd April 2012 and was continued until 22nd June. A 4x4 Latin square design was used to examine four monoculture swards, which were sown in September 2011. The cultivars selected for the study were: Astonenergy – tetraploid (heading date 31st May), Delphin –tetraploid (heading date 01st June), Glenroyal –diploid (heading date 03rd June), Tyrella –diploid (heading date 03rd June). The swards were rotationally grazed, using four herds of 8 cows. Cows were blocked based on parity (3; s.d. 1), milk yield (26.7; s.d. 3.0 kg), fat (52.9; s.d. 3.10 g/ kg), protein (39.2; s.d. 2.09 g/ kg) and lactose (46.6; s.d. 1.08 g/ kg), calving date (3rd March; s.d. 13 d), body weight (506; s.d. 59.5 kg) and body condition score (3; s.d. 0.25) prior to the experiment commencing. Each Latin square period lasted 21 days. The first 16 days were used for the acclimatisation to treatment, and the final five days were used for measurement. Cows were offered a daily herbage allowance of 17 kg DM/cow/d (>4cm). Fresh herbage was offered each morning after milking. Pre and post grazing sward heights were measured daily and herbage mass was measured twice weekly. Samples of herbage were taken twice during each measurement period to measure dry matter digestibility (DMD) using Near Infra-Red Spectrometry. Milking took place at 07:00 h and 16:00 h daily. Milk data were collected at each milking; six successive milk samples were analysed for milk fat, protein and lactose concentrations during the measurement period. Herbage DMI was estimated using the N-alkane technique during each measurement period. The data were analysed using the mixed procedure (PROC MIXED) of SAS (2011). The model included cultivar and experimental period. Cow was included as a random effect.

Results and Discussion

The Astonenergy and Delphin had a higher pre grazing herbage mass ($P<0.001$; 1288 kg DM/ ha) and sward height ($P<0.01$; 8.1 cm) than Glenroyal or Tyrella (1161 DM/ha and 7.2 cm). Post grazing sward height was highest in Delphin (3.9 cm) and was lower ($P<0.05$) in Astonenergy and Tyrella swards (3.6 cm). The effects of perennial ryegrass cultivar on milk production and DMI are presented in Table 1. Although not statistically significant ($P=0.10$), the Astonenergy sward resulted in a higher milk yield (+0.9 kg/cow/d) than the Tyrella sward. Astonenergy also led to a higher concentration of milk protein than Delphin or Tyrella. There was no difference in the proportions of milk fat, lactose or total milk solids content between the four cultivars. This is contrary to the results reported by Wims *et* al (2011), which showed Abermagic resulted in a significantly lower milk yield and milk solids when compared to other varieties examined. The DMI was similar for all cultivars (17.1 kg DM). This contradicts Gowen *et al* (2003) who reported that cultivar had an effect on grass DMI. The DMD tended to be different between cultivars ($P=0.08$). The highest DMD was observed in the Astonenergy sward. The overall digestibility of the herbage offered was high (798 g / kg).

Conclusion

The four cultivars examined in this study did not demonstrate a difference in milk production or DMI during the early summer period. However it was evident that DMD may influence milk and protein yield, as the highest herbage yield was attained with most digestible cultivar and the lowest yield with the least digestible cultivar. Further investigation is required, in order to examine the effect of season on the results, by repeating the experiment further into the summer and autumn.

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RMIS Project Number 6091

The effect of white clover on the competitive hierarchies in perennial ryegrass mixtures

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Introduction

There is increasing interest in the role of forage legumes in ruminant production systems particularly white clover (WC) (*Trifolium repens*) due to rising input prices. White clover has the potential to reduce nitrogen (N) input from purchased chemical fertiliser through the fixation of atmospheric N. White clover is usually sown with multiple perennial ryegrass cultivars (*Lolium perenne* L.) (PRG). Gilliland *et al.* (2011) reported changes in the established sward canopy relative to the sown proportions in PRG seed mixtures. The changes can affect dry matter (DM) and sward quality. These results only relate to competitive hierarchies of PRG cultivars in the absence of WC. Therefore, the effect of WC on the competitive hierarchies of PRG cultivars in the sward canopy under animal grazing warrant investigation. The aim of the study was to establish the effects of WC on the competitive hierarchies in PRG seed mixtures.

Materials and Methods

Eighteen plots (5 m × 3 m) were sown in May 2009. Two cultivars of PRG were sown (37 kg/ha) - one diploid: Tyrella (TY) and one tetraploid: Dunluce (DL). Two medium leaf WC cultivars (Chieftain and Crusader) were sown (4.9 kg/ha) as a 50:50 mixture. A randomised complete block design was used (three (TY:DL ratio) × two (clover contents) factorial arrangement of treatments), and plots were replicated three times. Three of the binary mixtures were sown as PRG swards and three were sown as PRG+WC swards. The cultivar proportions on a seed number basis in the PRG and PRG+WC swards were 86:14 TY/DL, 64:36 TY/DL and 37:63 TY/DL. Plots were grazed from February to October in 2010 and 2011. The plots were sampled for cultivar proportion using a starch gel electrophoresis method three times in each year. The methodology of the starch gel electrophoresis process was described by Kennedy *et al.* (1985). The genotype frequency of each mixture was compared with those of its constituent cultivars in monoculture to determine the composition. Equations described by Gilliland and Watson (1987) were used to determine proportions. Cultivar proportions were analysed in PROC Mixed in SAS (2003) using repeated measure analysis period (repeated measure), treatment and their interactions were included in the model.

Results and Discussion

Dunluce increased its proportion in the sward when sown as a minority of the seed mixture (Table 1). The increases are likely due to the larger plant size of the tetraploid plants. However, TY was not completely suppressed. This suggests the cultivars reached a competitive equilibrium. As the sown proportion of DL increased, there maybe more intra-cultivar plant competition which negated further increases in the proportion of DL. The presence of WC in the sward did not affect the competitive hierarchies in the sward canopy. The mean sward composition over the two years of the study was similar across all mixtures, regardless of the presence or absence of WC. White clover has a prostrate growth habit which would not influence the structural attributes (seed size, leaf size and plant structure) of PRG cultivars that are the main drivers of change in canopy composition between diploids and tetraploids (Gillliland *et al.,* 2011).

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

	Sown ratios	October 2010	October 2011	Mean§
Tyrella Dunluce	86:14^{1}	69:31^{2}	68:32^{2}	62:38^{2}
	64:36^{1}	55:45^{12}	62:38^{12}	54:46^{12}
	37:63^{1}	36:64^{1}	34:66^{1}	42:58^{1}
Tyrella Dunluce + White clover	86:14^{1}	50:50^{ad2}	60:40^{2}	62:38^{2}
	64:36^{1}	60:40^{1}	57:43^{12}	54:46^{12}
	37:63^{12}	30:70^{1}	48:52^{2}	46:54^{12}
		P value		SED
Period		0.001		4.9
Treatment		0.001		1.4
Treatment*Period		NS		3.4

^{123} values denote significant differences (P<0.05) between cultivar proportions within rows; § Mean values relates to the sward composition across the six sampling periods of the study; SED standard error of the difference

Conclusion

The results suggest that previously reported work on the competitive hierarchies of PRG cultivars in PRG only swards can be extrapolated to swards where WC is present. White clover appears to have no effect on the competitive hierarchies between PRG cultivars.

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RMIS Project Number 6091

Sward structural differences between cultivars of perennial ryegrass (*Lolium perenne*) during the early summer period

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Introduction

Sward canopy structure has an affect on the intake potential (Forbes *et al.* 1988) and milk production of dairy cows (Flores-Lesama *et al.* 2006). Phenotypic variation between cultivars results in a difference in sward structure (Smit *et al.* 2005). Wims *et al.* (2011) found that cultivars with a high proportion of stem negatively affected milk production. The objective of this study was to investigate the differences in sward structure between cultivars of perennial ryegrass, under grazing, during the early summer period.

Materials and Methods

In September 2011, four perennial ryegrass cultivars were sown as monocultures with three replications. The cultivars selected for the study were: Astonenergy – tetraploid (heading date 31st May), Delphin –tetraploid (heading date 1st June), Glenroyal –diploid (heading date 3rd June), Tyrella –diploid (heading date 3rd June). Each cultivar was sown in three blocks, which totalled 2.9 ha per cultivar, at a sowing rate of 32 kg/ha for diploids and 40 kg/ha for tetraploids. The experiment began in April 2012 and continued for 12 weeks. The swards were grazed by four groups of eight cows, which were randomly assigned one of the four cultivars. Cows were offered 17 kg DM of herbage per day. Rotation length was similar for all cultivars. Measurements were taken during weeks 3, 6, 9 and 12 The following measurements were conducted twice during each measurement period: pre and post grazing herbage mass; extended tiller height and leaf sheath height were measured on 100 tillers pre and post grazing; herbage was sampled to ground level and a 40 g sub-sample was separated into leaf, pseudostem, stem and dead components between 4 and 8 cm and above 8 cm before drying at 90^{o}C overnight; tiller and leaf DM weight were measured on 100 tillers and leaves; pre and post grazing sward heights were taken daily. The data were analysed using the mixed procedure (PROC MIXED) of SAS (2011). The model included cultivar, experimental period and day within period as the repeated measure.

Results and Discussion

The effects of cultivar on sward structural characteristics are presented on Table 1. Astonenergy and Delphin had the highest herbage mass ($P<0.01$), tiller weight ($P<0.001$) and leaf weight ($P<0.001$). Both cultivars also expressed a higher growth rate ($p<0.001$; 65.5 kg DM/ha/d) than Tyrella and Glenroyal (57.5 kg DM/ha/d $p<0.001$). There were no differences in tiller height or post-grazing sheath height, however Glenroyal tended to have a greater pre-grazing leaf sheath height than Delphin. Leaf, pseudostem and stem proportions were similar for all varieties. Astonenergy and Delphin tended ($P=0.06$) to have the lowest proportion of dead material above 8 cm. The differences in sward structure did not affect the milk production or herbage intake during the early summer period (Lawrence *et al.,*2013).

Table 1. The differences in sward structural characteristics between four perennial ryegrass cultivars

	Astonenergy	Delphin	Glenroyal	Tyrella	S.E.	P-value
Pre-grazing height (cm)	7.8^{ab}	8.3^{b}	7.3^{ac}	7.1^{c}	0.19	<0.001
Post-grazing height (cm)	3.6^{a}	3.9^{b}	3.7^{ab}	3.6^{a}	0.07	<0.05
Pre-grazing herbage mass (kg DM/ha/d)	1282^{a}	1293^{a}	1185^{b}	1138^{b}	31.4	<0.01
Growth (kg DM/ha/day)	65^{a}	66^{a}	59^{b}	56^{b}	1.8	<0.001
Tiller weight (g DM)	0.08^{a}	0.08^{a}	0.06^{b}	0.06^{b}	0.005	<0.001
Leaf weight (g DM)	0.02^{a}	0.02^{a}	0.01^{b}	0.01^{b}	0.001	<0.001
Pre-grazing extended tiller height (cm)	24.5	24.4	22.3	22.4	0.83	NS
Pre-grazing leaf sheath height (cm)	6.6^{ab}	6.1^{a}	7.4^{b}	6.7^{ab}	0.32	0.08
Post-grazing extended tiller height (cm)	7.4	7.4	7.6	7.2	0.24	NS
Post-grazing leaf sheath height (cm)	5.3	5.3	5.4	5.3	0.18	NS
4-8 cm leaf proportion	0.53	0.48	0.49	0.53	0.036	NS
4-8 cm pseudo-stem proportion	0.26	0.28	0.23	0.20	0.023	NS
4-8 cm stem proportion	0.07	0.05	0.05	0.07	0.018	NS
4-8 cm dead proportion	0.15	0.19	0.23	0.20	0.025	NS
>8 cm leaf proportion	0.87	0.88	0.84	0.84	0.027	NS
>8 cm pseudo-stem proportion	0.07	0.05	0.06	0.06	0.012	NS
>8 cm stem proportion	0.02	0.02	0.01	0.03	0.011	NS
>8 cm dead proportion	0.05^{a}	0.05^{a}	0.09^{b}	0.07^{ab}	0.011	0.06

SE= Standard error. $^{a-b\,=}$ Means with a different subscript, within a row tended to be different ($p<0.08$)

RMIS Project Number 6091

Conclusion

The differences reported between cultivars in the sward structural characteristics were small. Both of the tetraploid cultivars expressed larger pre-grazing herbage mass, daily growth and tiller weight. Further work is necessary to measure the effect of season on the sward structure of the varieties measured.

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Herbage production and sward clover content in grazed grass + white clover plots: effect of N fertiliser application rate

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Introduction

There is interest in the inclusion of white clover in grazed grass swards due to the potential of grass + clover swards to improve the sustainability of grazing systems (Peyraud et al., 2009) and to increase nitrogen (N) availability for herbage production. This potential is related to the ability of clover to fix atmospheric N; however, the amount of N fixed is influenced by a range of factors including N fertiliser application (Andrews et al., 2007). Nitrogen fertiliser application can reduce sward clover content (Ledgard and Steele, 1992) as the clover is out-competed in terms of growth rate by the grass and shading reduces the persistency of the clover. The objective of this experiment was to investigate an appropriate N fertilisation rate to maximise herbage production without compromising sward clover content in fertilised grass + clover swards.

Materials and Methods

A series of grazing plots (8 m × 8 m) were established at the Dairygold Research Farm, Teagasc, Fermoy, Co. Cork in May 2009. The experiment had a 2 × 5 factorial arrangement of treatments with three replicates, and measurements were made in 2011 and 2012. Treatments were two swards: grass only (GO) and grass + clover (GC), and five fertiliser N rates: 0, 60, 120, 180, 240 kg N/ha/year. Both swards were sown with a grass mixture (50:50 Dunluce and Tyrella cultivars; 37 kg/ha) and the GC had a 50:50 mixture of Chieftan and Crusader clover cultivars (5 kg/ha). Dairy cows grazed the swards 10 times per year in 2011 and 2012. Pre-grazing herbage mass in each plot was estimated by cutting a strip with an Etesia lawn mower (Etesia UK. Ltd., Warwick, UK). Harvested herbage was weighed, and sub samples removed to determine herbage DM content. Sward clover DM content was estimated by removing a herbage sample (approx. 70 g) and separating into grass and clover components. Target post-grazing sward height was 4 cm. Data were analysed using Proc Mixed (SAS, 2005) with year, treatment (2 × 5), rotation, and the interactions included in the model.

Results and Discussion

Cumulative herbage production tended to be lower in 2011 than in 2012 (12.6 and 13.1 t DM/ha, $p=0.09$) and was lower for GO compared to GC (12.1 vs. 13.6 t DM/ha, $p<0.001$). Herbage DM production was also affected ($p<0.001$) by N fertiliser rate; plots receiving 240 kg N/ha produced more herbage (14.7 t DM/ha; $p<0.05$) than the plots receiving 120, 60 and 0 kg N/ha (13.2, 11.6, 11.1 t DM/ha, respectively); however, there was no significant difference between plots receiving 240 and 180 kg N/ha, or between plots receiving 180 and 120 kg N/ha. There was an interaction between sward type and N application rate in terms of cumulative herbage production ($p<0.01$; Fig 1). The overyielding of the GC swards declined as the rate of N fertilizer increased; this is in agreement with a previous study (Nyfeler et al., 2009). Average clover content across GC plots was 26.0% and was higher in 2011 than in 2012 (37.7% and 19.2%, respectively: $p<0.001$). Clover content declined as the rate of N fertiliser application increased (Fig. 1 and 2; $p<0.001$). This is a common response in mixed swards (Andrews et al., 2007); however, the average sward clover content was above 12% in all treatments. Clover content was relatively low until June and then increased until a plateau was achieved from August until the first rotation in October; then it decreased again (Fig. 2).

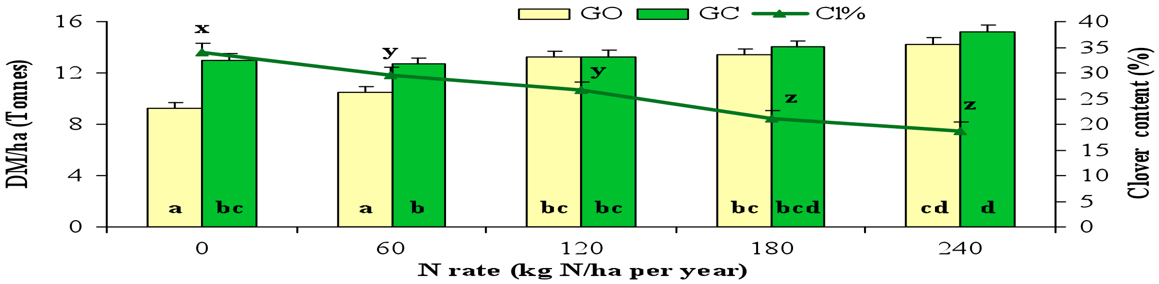

Fig. 1. Effect of sward type and N fertiliser rate on herbage production and clover content. Values with different letters differ (Herbage production: a to d; clover content: x to z; $p<0.05$) among treatments.

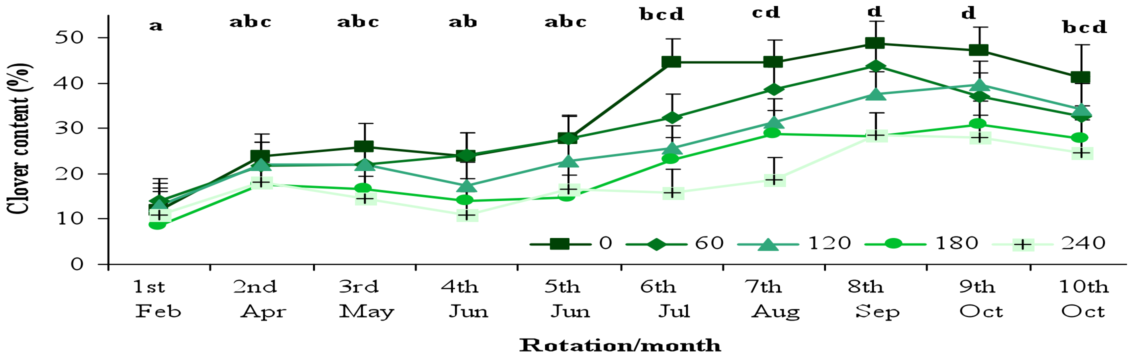

Fig. 2. Effect of N fertiliser rate and rotation on sward clover content. Different letters differ ($p<0.05$) among rotations.

Conclusions

Clover inclusion in grass swards increased total herbage production regardless of N fertiliser application rate; however, increasing N application rate reduced sward clover content.

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The influence of white clover inclusion in perennial ryegrass swards on milk and herbage production in a high N fertiliser system

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Introduction

White clover (WC) is the most important forage legume in temperate regions (Frame and Newbould, 1986). In the past Irish dairy production has relied heavily on perennial ryegrass (PRG) swards with high nitrogen (N) fertiliser application. Grass WC swards have not been widely used despite a low average national stocking rate (1.9 LU/ha; O'Donovan *et al.,* 2011). Recently, there is increased interest in including WC in PRG swards as the cost of fertiliser N continues to increase. Milk yield of cows grazing PRG WC swards can be increased by 15 to 25% compared with pure PRG swards (Ribeiro Filho *et al.,* 2003). The objective of this study was to compare milk and herbage production on a PRG WC sward and a PRG sward at a high N fertiliser input.

Materials and Methods

A PRG only sward and PRG WC sward were sown at Moorepark Dairygold Research Farm in May 2010. Swards were grazed by dairy cows randomly allocated to each treatment (n=20) from 6 February to 31 October 2012. Swards received 260 kg inorganic N fertiliser/ha. Daily herbage allowance (>4 cm) was 17 kg dry matter (DM)/cow/day. Cows received 1 - 2 kg concentrate/day when herbage supply was below requirements. Pre grazing herbage mass (>4 cm) was determined twice weekly using an Etesia mower (Etesia UK. Ltd., Warwick, UK). Pre and post grazing sward height were measured daily using a rising plate meter (Jenquip, Feilding, New Zealand). Sward WC content was estimated twice weekly by cutting 8 random grab samples to 4 cm with a Gardena shears and separating the sample into grass and WC fractions and drying at 40°C for 48 hrs (Enríquez-Hidalgo *et al*. 2012). Milk yield/cow was recorded daily (Dairymaster, Causeway, Co. Kerry, Ireland) and milk composition weekly (Milkoscan 203, Foss Electric DK – 3400, Hillerød, Denmark). Data were analysed using PROC MIXED in SAS with terms for treatment, time (week or rotation) and associated interaction. Fixed terms were week and rotation, and random terms were cow and paddock.

Results and Discussion

Cows grazing the Cl treatment had higher cumulative milk yield (P<0.01) and milk solids (P<0.05) than cows grazing the Gr treatment (Table 1). There was a significant treatment × week interaction (P<0.001). Daily milk production and milk solids was similar for both treatments in the first half of lactation, in the second half (week 19 onwards) the Cl treatment resulted in increased daily milk yield and daily milk solids compared to the Gr treatment. Both treatments had similar pre grazing sward height (10.59 cm), total herbage production (14158 kg DM/ha) and post grazing sward height (3.98 cm). Sward WC content increased from 0.084 g/kg DM in February to 0.229 g/kg in October, peaking in June at 0.29 g/kg (Fig 1). Average sward WC content (0.216 g/kg).was similar to that reported by other authors (e.g. Humphreys *et al*., 2009). Previously, at the same site, Enríquez-Hidalgo *et al*. (2012) reported no significant effect of sward type on milk yield or milk solids yield. However, in that study, the sward WC content (average 0.13 g/kg) was lower than in the current study.

Table 1. Effect of grass only (Gr) and grass clover (Cl) swards on milk yield and milk composition per cow

	Gr	Cl	SEM[1]	Trt[2]	Week	Week×Trt
MY[3] (kg/day)	17.01	18.60	0.45	**	***	***
MS[4] (kg/day)	1.41	1.53	0.03	**	***	***
Milk fat (g/kg)	4.90	4.70	0.07	*	***	***
Milk protein (g/kg)	3.63	3.62	0.03	NS	***	***
Cumulative MY[3] (kg/cow)	4788	5048	34.27	**	-	-
Cumulative MS[4] (kg/cow)	388	400	1.87	*	-	-

[1]SEM = standard error of the mean; [2]Trt = treatment; [3]MY = milk yield; [4]MS = milk solids; *** = P<0.001; ** = P<0.01; * = P<0.05; NS = Not significant

Conclusions

Cows grazing Cl swards had higher cumulative milk and milk solids yield than Gr swards. The sward WC content remained high throughout the experiment despite high N fertiliser application.

Acknowledgements

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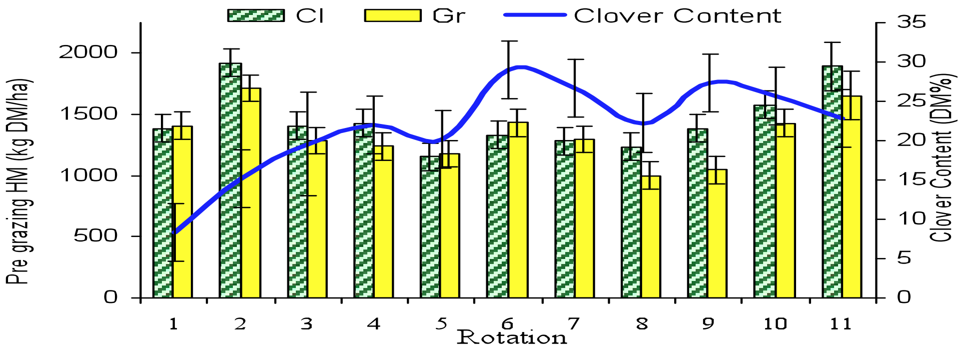

Figure 1. Pre-grazing herbage mass and clover content

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RMIS Project Number 6120

A comparison of the effect of grass + clover and grass only swards on dairy cow grazing behaviour on three occasions during the grazing season

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Introduction

Future dairy sector trends (N fertiliser price will increase at a higher rate than milk price) will make mixed swards more common (Humphreys et al., 2012) as white clover fixes N in the sward making it available for grass growth. Cattle show a partial preference for clover compared to perennial ryegrass (Rutter, 2006) and clover has faster rumen passage rate than grass (Beever et al., 1986). Previous work had shown that clover preference and grass intake are affected by sward clover content (Harris et al., 1997; Rutter, 2006). The objective of this experiment was to determine the effect of sward type on the grazing behaviour of dairy cows on three occasions during the grazing season.

Materials and Methods

A grass only (GO) and a grass clover (GC) sward were sown at the Dairygold Research Farm, Teagasc, Fermoy, Co. Cork in May 2010. Swards were rotationally strip grazed and fresh herbage offered daily (17 kg DM/cow/d). Pre-grazing herbage mass was estimated twice weekly using an Etesia mover (Etesia UK. Ltd., Warwick, UK). Grass and clover components of a herbage sample from the GC sward were separated to estimate sward clover content twice weekly. Eight rumen-fistulated dairy cows were arranged into four 2 × 2 Latin squares and allocated to each treatment for one period of 14 days in three time stages (TS): May (TS1), July (TS2) and September (TS3). Each period had a 10 day acclimatisation phase and grazing behaviour data were collected on days 11 and 12 of each period by fitting the cows with IGER behaviour recorders (Rutter et al., 1997). Data were analysed individually for each TS using PROC MIXED (SAS, 2005) including sward type, period and cow in the model.

Results and Discussion

There was no effect (p>0.05) of sward type on pre-grazing herbage mass (TS1 = 1454, TS2 = 1551, TS3 = 2189 kg DM/ha). Average clover proportion on GC was 6.5%, 11.3% and 21.4% for TS1, TS2 and TS3, respectively. In TS1, there was no effect (p>0.05) of sward type on the time that cows spent grazing, ruminating or idling (Fig. 1) and there was no difference in the number of grazing (5834 bites/d) or ruminating (37106 bites/d) bites between treatments. In TS2, cows spent a similar amount of time ruminating (p>0.05) on both treatments, while GO cows spent 7% more time grazing and tended (p=0.08) to spend less time idling (13%) than GC cows (Fig. 1). However, in TS2, GO cows had 27.3% fewer grazing bites than GC cows (6461 vs. 8890 bites/d), while there was no difference in the number of ruminating bites between treatments (22382 bites/d). In TS3, cows spent similar time grazing on both treatments, GO cows spent 19.2% more time ruminating and 14.8% less time idling than GC cows (Fig. 1), similar to Phillips et al., (2000). In TS3, there was no difference in the number of grazing bites between treatments (5823 bites/d); however, GO cows had 23.6% more ruminating bites than GC cows (30446 vs. 24630 bites/d). Differences in grazing behaviour observed are related to sward clover proportion, as sward clover content increases ruminating time decreases (Harris et al., 1997; Rutter, 2006) due to the faster passage rate of clover through the rumen.

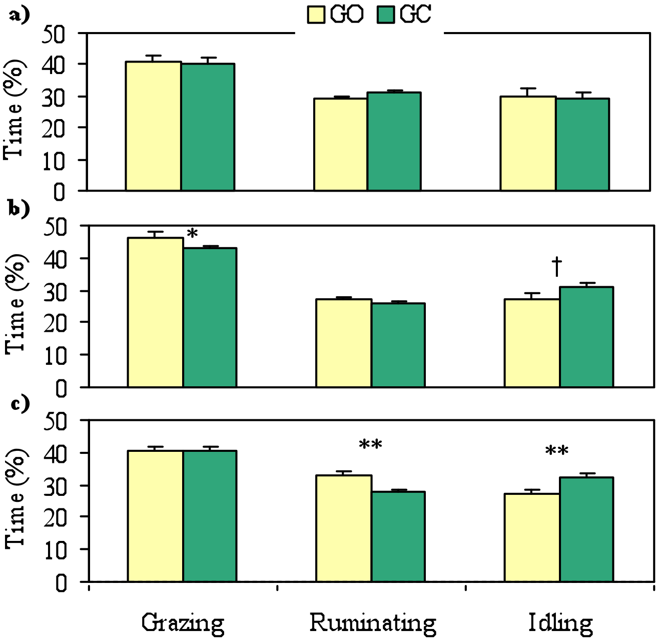

Fig. 1. Effect of sward type on dairy cows grazing behaviour in a) TS1, b) TS2 and c) TS3. † = p < 0.1; * = p < 0.05; ** = p < 0.01

Conclusions

Clover inclusion in grass swards influenced the grazing behaviour of dairy cows; however, this effect was only evident when higher clover proportions were measured.

Acknowledgements

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RMIS Project Number 6120

Modelling the surface of a paddock affected by urine deposition by dairy cows during grazing

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Introduction

Nitrogen (N) fertilizer is highly effective at increasing grass growth (Murphy, 1977) and hence farm productivity, but it also contributes to nitrate (NO_3^-) leaching to groundwater (Decau and Delaby, 1997). In grazed grass swards, urine deposition from grazing animals augments the N added through fertilization, increasing N availability for grass growth, but also the losses of N (leaching, volatilization of ammonia (NH_3)) on a small portion of a paddock surface (urine patch). Traditional soil models (STICS (Brisson *et al.*, 2003); SOIL-N (Jansson, 1991)) dilute urine patches across the whole paddock. This study models the heterogeneity of urine deposition on a paddock in order to avoid diluting the effects of urinary N deposition.

Materials and Methods

In the present study the calculation of the surface area affected by urine deposition during any grazing day depends on the number and type of animals grazing. The effects of variables such as diet or weather on the number of daily urinations per cow or on the surface area affected by urine were not investigated in this study. Each animal type has a specific number of urine depositions per day, which affect a specific area of the paddock. It is assumed in this model that within any given grazing event urine deposition will be random and without overlap. Overlap can occur between grazing events. Figure 1 illustrates the areas influenced by urine deposition over three grazing rotations (not to scale). Each surface has homogeneous soil N concentration.

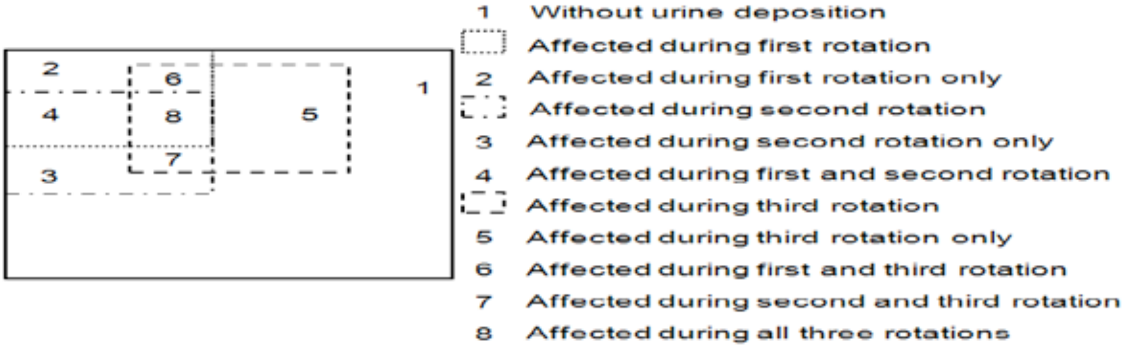

Fig. 1. Schematic representation of area covered by urine during three successive grazing events (areas not to scale).

Each urine deposition is randomly located. The probability of overlap of depositions from two grazing events depends on the size of the first affected surface. The larger the surface, the higher the probability of overlap. This model uses a mean number of urinations on the paddock per cow per day of 10 (Decau and Delaby, 1997; Dennis *et al.*, 2011). The surface affected by each urine deposition varies in the model (as in the literature), from 2 m² (Decau and Delaby, 1997) to 0.81 m² (Dennis *et al.*, 2011).

The model was evaluated by comparing the predictions of the model with the area affected by urine as reported by Dennis *et al.* (2011). The assumptions used for the comparison were area affected by urine deposition of 0.81 m², 7.5 urine depositions cow^{-1} day^{-1} at a stocking rate of 2.5 cow ha^{-1}.

Results and Discussion

A simulation was run over a 160 day period. The surface area affected by urine deposition was set at 2 m². There were three grazing rotations with numbers of days of animal residence in the paddock of 4, 6 and 4 days for the 1st, 2nd and 3rd rotations, respectively. The stocking rate was 2,5 cow ha^{-1} year^{-1}. At the end of the 160 days, 33% of the paddock area was unaffected by urine deposition, 8.24% was affected only in first rotation, 18.76% was affected during second rotation only, 8% was affected during the first and second rotations, 12.88% was affected during the third rotation only, 3.88% was affected during first and third rotations, 7.36% was affected during second and third rotations, and 7.88% was affected during all three rotations.

The same model, using an area of 0.81 m² affected by urine deposition as reported by Dennis *et al.* (2011) (less diffusion of urine in the soil) and 7.5 urine depositions cow^{-1} day^{-1} at a stocking rate of 2.5 cow/ha, predicts a cumulative affected surface of 24%, while Dennis *et al.* (2011) measured a value of 23.7%.

Conclusion

The model allows the partitioning of a grazed paddock into several surfaces depending on the quantity of urinary N received throughout a year. Therefore, a more precise account can be made of the total paddock surface area influenced by urinary N per year allowing more accurate modelling of N within a paddock.

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RMIS Project Number 6334

Nutrient Management

Nitrous oxide emissions from white clover based grassland used for dairy production

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Introduction

Nitrous oxide (N_2O) emissions from grazed grassland contributes 16 to 33% of global N_2O emissions (deKlein et al., 2008). Nitrous oxide is a potent greenhouse gas (IPCC, 1995) produced by multiple processes in soil, which are affected by factors such as nitrate content, soil moisture, temperature, soil carbon, soil oxygen and pH. Changes in these controlling factors over time create considerable variation in emissions of N_2O making it difficult to acquire accurate estimates of annual N_2O emissions. The objective of this study was to measure and assess annual N_2O emissions from white clover based grassland.

Materials and Methods

The study was conducted at Solohead Research Farm (52˚51'N, 08˚21'W). The soils have a clay loam texture and are seasonally wet. Nitrous oxide emissions from (i) white-clover based dairy production system (WC) and (ii) white clover-ryegrass plots (WC_B) were measured between October 2008 and November 2011. The WC consisted of six paddocks (1.42 to 2.07 ha) used primarily for grazing and were also cut for silage. Annual average stocking density was 2.35 cows ha^{-1} and annual fertilizer N input was 100 kg ha^{-1}. There were three WC_B plots (11 × 3m area) distributed across the farm that received no external input of N or grazing. Herbage on WC_B plots was harvested at monthly intervals and discarded. Herbage mass and N content was measured on WC plots to calculate annual N uptake in herbage dry matter (DM). N_2O emissions were measured using five static chambers per paddock in WC and one per WC_B. The N_2O sampling strategy consisted of weekly sampling with increased frequency following N fertilization. Rainfall was recorded at the site. Data were analysed using analysis of variance and the PROC GLM statement of SAS. The model included year, treatment and the interaction between year and treatment as sources of variation.

Results and Discussion

All annual totals (365 days) presented coincide with the commencement of N_2O sampling in October 2008. There was relatively high annual surplus rainfall (Fig 1a) in 2008/09 and 2009/10 compared with 2010/11. There was higher (P <0.001) annual N uptake in 2010/11 (Fig 1b), attributable to lower rainfall, aerobic soil conditions and higher mineralization of N in the soil compared to the previous two years. With regard to N_2O emissions there was an interaction (P<0.05) between year and WC treatment. There was no difference in N_2O emissions between WC and WC_B in 2008/09 or in 2009/10, whereas there was a difference (P <0.001) between them in 2010/11. While there was no difference in emissions from WC_B between years, emissions from WC in 2010/11 was higher (P<0.001) than in each of the previous two years (Fig 1c).

Conclusion

Differences between years in surplus rainfall impacted directly on soil moisture content and the mineralization of N. The extent of these differences was reflected in uptake of N in herbage DM and in N_2O emissions from the soil.

Acknowledgements

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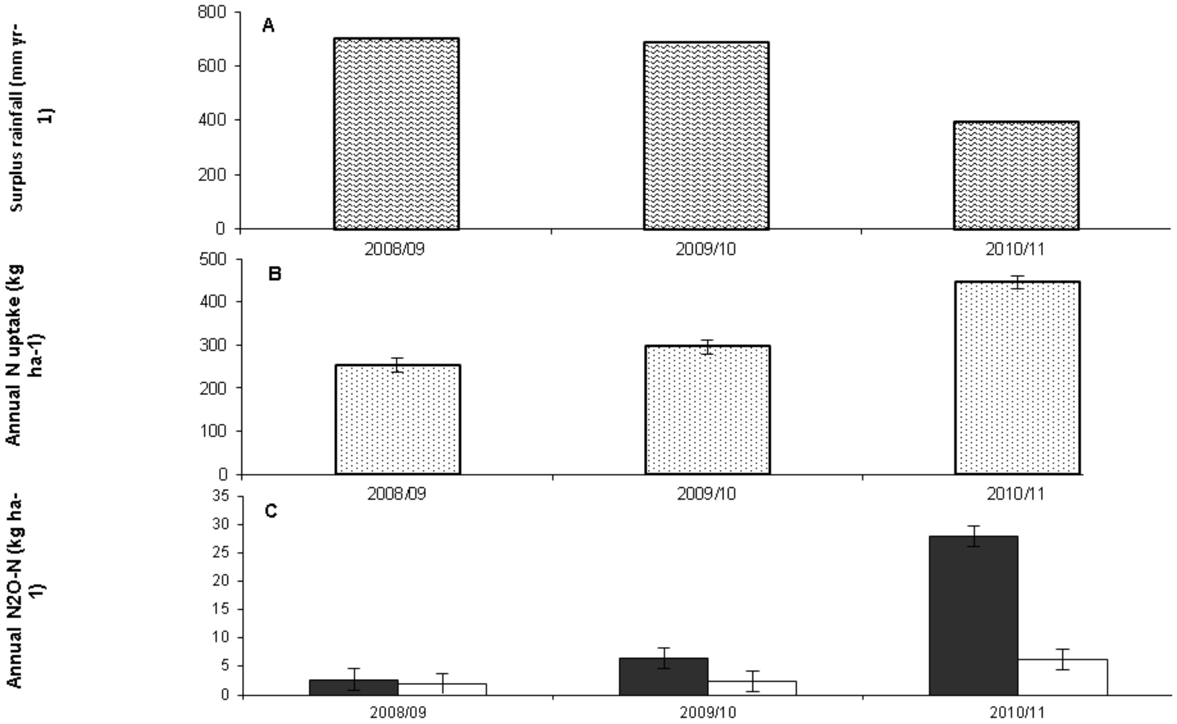

Figure 1. Annual surplus rainfall (A), annual N uptake in herbage DM (B) and annual N_2O emissions (C), from white clover based dairy production system (WC ■) and background white clover plots (WC_B □), between 2008/09 and 2010/11 (*P*<0.001). Error bars represent the standard error of the mean.

Saturated soil conditions in 2008/09 and 2009/10 are likely to have caused the predominance of complete denitrification and hence relatively low N_2O emissions. In contrast the aerobic soil conditions in 2010/11 were more favourable to incomplete denitrification and the production of N_2O, which combined with high rates of N mineralization in the soil led to the very large emission of N_2O in 2010/11.

RMIS Project Number 6045

Grass Feed & Value

Seasonal variation in organic matter digestibility and fibre content of the morphological components in perennial ryegrass cultivars

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Introduction

The grass plant comprises a number of leaf blades (L), leaf sheath (PS), true stem (TS) and dead material (D) (Stakelum and Dillon, 2007). Their proportions vary throughout the year and between cultivars (Beecher *et al*., 2012). The PS is often not separated from the TS when determining sward morphology despite the PS being more digestible than the TS (Terry and Tilley, 1968) and differences in their relative proportions can impact sward quality. The objective of this study was to determine the change in organic matter digestibility (OMD) and fibre content of L, PS, TS and D components of four perennial ryegrass cultivars throughout a grazing season.

Materials and Methods

Details of the swards and sampling process are detailed by Beecher *et al*. (2012). Immediately prior to grazing, herbage morphological composition was determined on four monoculture grazing swards. The grass cultivars were: Bealey and Astonenergy (intermediate heading tetraploids), Spelga and Abermagic (intermediate heading diploids). Grass sampling took place prior to eight grazing rotations from May 2011 onwards and two rotations prior to, and including, March 2012. Due to insufficient sample quantity the PS, TS and D replicate samples were bulked by morphological component for the first four rotations of 2011, the last four rotations of 2011 and the two rotations in 2012 giving three samples in total. A similarly-bulked L sample and a whole sample that was not separated into morphological components were analysed for comparison. There were four replicates of each of these samples. *In vitro* OMD using the method of Morgan *et al.* (1989), neutral detergent fibre (NDF) and acid detergent fibre (ADF) (Van Soest *et al.,* 1991) content were determined. Data (whole samples) were analysed using PROC MIXED in SAS with terms for replicate, rotation number, cultivar and the interaction of cultivar and rotation number. Rotation number was a repeated measure. The bulked L, PS, TS and D samples were not statistically analysed.

Results and Discussion

There was a rotation effect and cultivar effect for OMD in the whole samples. Organic matter digestibility in the whole samples was higher in mid May (738 ± 13.1 g/kg), start June (766 ± 13.1 g/kg), end June (765 ± 13.1 g/kg), end July (731 ± 13.1 g/kg) and mid Aug (748 ± 13.6 g/kg) than in mid October (671 ± 13.1 g/kg) and start February (654 ± 13.1g/kg) ($P<0.05$). Bealey had the highest OMD (752 ± 10.4 g/kg) and Spelga the lowest (696 ± 10.4 g/kg) ($P<0.05$), Astonenergy and Abermagic were intermediate. Astonenergy and Bealey had the highest combined L and PS proportions (0.93 and 0.92, respectively) ($P<0.05$) which helps explain Bealey having the highest OMD and Astonenergy the second highest OMD. Astonenergy had a low NDF and ADF content (501 and 246 g/kg, respectively), contributing to its high OMD. Results from the present study indicated that OMD of the plant fractions were biologically different. Leaf had the highest OMD and the D fraction had the lowest, following the order L > PS > TS > D (Fig 1) agreeing with Wilson (1994). There were no TS samples from end July onwards.

Conclusions

Organic matter digestibility differs between morphological components of the plant and between cultivars. Therefore, for an accurate description of a sward in grazing studies, PS should be separated from TS, especially during the reproductive period when TS is present, if accurate values for PS and TS are to be determined.

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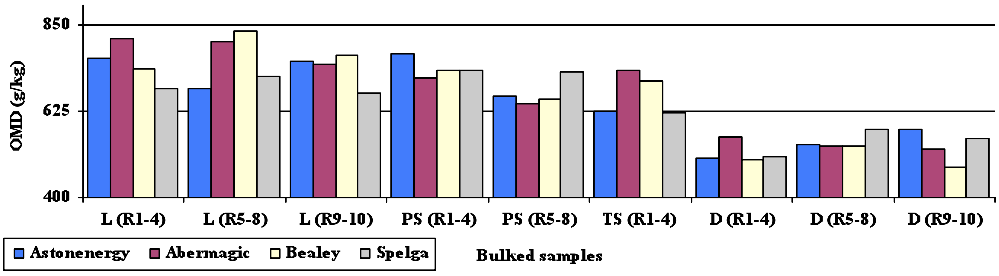

Fig 1. Organic matter digestibility (OMD) of leaf (L), pseudostem (PS), true stem (TS) and dead (D) morphological components of four perennial ryegrass cultivars bulked for rotations 1 (mid May) to 4 (mid July) (R1-4), rotations 5 (end July) to 8 (mid Oct) (R5-8) and rotations 9 (start Feb) to 10 (end Mar) (R9-10).

RMIS Project Number 5893

A comparison of Jersey, Holstein-Friesian and Jersey×Holstein-Friesian dairy cows in their ability to digest perennial ryegrass

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Introduction

Currently the increased interest in crossbreeding with Jerseys (J) in Ireland is driven primarily by the needs to combat declining fertility and to improve milk solids production on dairy farms. Grass-based dairying in Ireland is based on achieving large intakes of high quality grass and efficiently converting this into high value milk solids (Prendiville *et al.,* 2009). Differences have been identified between Jersey and Holstein-Friesians (HF) regarding production efficiencies (Prendiville *et al.,* 2009). They found that J had higher milk solids output per 100 kg bodyweight than HF. The objective of this study was to identify if J, HF and Jersey×Holstein-Friesian F_1 (J×HF) cows differ in their ability to digest perennial ryegrass.

Materials and Methods

During the summer of 2010, *in vivo* digestibility trials on a total of 48 lactating cows; 16 HF, 16 J and 16 J×HF (197 days in milk, SD 27); were conducted over four consecutive measurement periods (MP) balanced for genotype. There were 12 cows used per MP. Cows were housed in individual stalls that allowed for the total collection of urine and faeces. Holstein Friesian and J×HF were offered a high (20 kg DM/d) or low (16 kg DM/d) allowance of fresh cut perennial ryegrass twice daily from an established sward. The corresponding grass allowances for the J were 17 and 14 kg DM/d, respectively. Following a 6-d acclimatisation period, the 6-d MP (MP1: 8 Aug, MP2: 21 Aug, MP3: 4 Sep, MP4: 18 Sep) began during which total daily intake and faeces produced were recorded. A representative sample of grass offered and faeces voided from each cow were collected daily. Dry matter digestibility (DMD), organic matter digestibility (OMD), neutral detergent fibre digestibility (NDFD), acid detergent fibre digestibility (ADFD) and nitrogen digestibility (ND) were determined. The data were analysed using PROC MIXED in SAS (2002) with cow as a random variable, and genotype, measurement period, grass allowance and all interactions as fixed effects in the model.

Results and Discussion

There were no significant interactions on any of the digestibility variables examined. There was no effect of grass allowance. There was, however, a significant genotype and measurement period affect (P<0.05). Jerseys had a higher DMD than both HF and J×HF, with no significant difference between HF and J×HF. For all other variables digestibility was higher in J compared to HF (P<0.05), while J×HF were intermediate (P>0.05) (Table 1). The greater mastication of ingested herbage (Prendiville *et al.,* 2010) and a proportionally larger rumenoreticulum (Lewis *et al.,* 2011) likely contribute to the consistently higher digestibility values observed with J compared to HF. A MP affect was observed for all digestibility variables (P<0.05). The highest DMD, OMD and ND values were recorded during MP 2 and MP 4. The highest NDFD and ADFD occurred during MP 2. Grass chemical composition results (not presented) generally concurred with these findings.

Conclusion

The J and HF breeds do differ in their ability to digest perennial ryegrass, with J able to digest more of the perennial ryegrass than HF. The results of this study suggest that a proportion of the production efficiency differences reported by Prendiville *et al.* (2009) are attributable to small differences in the propensity to digest herbage.

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RMIS Project Number 6194

Grazing Management and Conservation

Short-term milk yield adaptation to changes in post-grazing sward height

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Introduction

Grazed grass is the cheapest source of nutrients for dairy cows (Finneran *et al.*, 2010) and its utilisation should be maximised throughout the grazing season to increase enterprise profitability (Shalloo *et al.*, 2004). The low availability of grazed grass in spring may be partially overcome by grazing pastures to low post-grazing sward height (PGH) to maximise the quantity of grazed grass in the diet of dairy cows. When farm grass supply meets grass demand, PGH may be increased to allow a greater allowance of grass in the cow's diet. Quantifying the variation in production with changes in PGH will inform such decisions. No information has been published on the milk output response to changes in PGH, over a short period of the lactation. Therefore, this experiment aimed to identify the short term variation in milk yield and yields of protein, fat and lactose in response to changes in PGH around the tenth week of the spring calving dairy cow lactation.

Materials and Methods

Ninety spring calving Holstein Friesian dairy cows were balanced in a randomised block design (Ganche *et al.*, 2012) and randomly assigned pre-calving to one of three (n=30) PGH treatments: 2.7 cm (severe - S), 3.5 cm (low – L) or 4.2 cm (moderate – M) from February 14 to April 24, 2011. From April 25, animals were re-randomised within each treatment to graze across two PGH: 3.5 or 4.5 cm. Animal production measurements were made from April 4 to 24 (period 1; P1) and from April 25 to May 15 (period 2; P2). This resulted in six treatments (n=15): S3.5, S4.5, L3.5, L4.5, M3.5 and M4.5. Herbage was allocated daily. Pre- and post-grazing heights were measured daily, using a pasture plate meter (Jenquip, Fielding, NZ). Milk yield (MY) was measured daily; milk composition was recorded weekly. Data on animal variables were analysed using covariate analysis using the PROC MIXED statement (SAS) with terms for parity, treatment and the interaction of parity and treatment. Days in milk and pre-experimental milk data were used as covariates for the analysis of P1 variables. For P2 variable analysis, days in milk and the averaged P1 milk output were used as covariates. The differences in milk, milk protein, fat and lactose yields between P1 and P2 were calculated per cow, by the difference of mean P1 yield and mean P2 yield. Analysis of covariance on individual MY differences between P1 and P2 showed no interaction between P1 and P2 PGH treatment effects. This allowed the calculation of the differences in MY and yields of milk protein, fat and lactose between P1 and P2, using multiple linear regression analysis with two independent parameters: P1 PGH and P2 PGH.

Table 1. Milk yield variations (Δ) to changes in post-grazing height (PGH) between P1 (April 4 to 24) and P2 (April 25 to May 15): coefficients of linear regression.

	Intercept	Slope 1 P1_PGH	Slope 2 P2_PGH	s.e.d	R^2
Milk yield Δ, kg/cow/d	- 2.30	- 1.99	+1.76	0.235	0.97
Milk protein yield Δ, kg/cow/d	- 34.1	- 83.5	+66.7	10.79	0.96
Milk fat yield Δ, kg/cow/d	- 83.1	- 86.9	+77.5	23.62	0.87
Milk lactose yield Δ, kg/cow/d	- 81.9	- 94.9	+76.0	17.87	0.93
Milk solids yield Δ, kg/cow/d	- 0.10	- 0.17	+0.14	0.016	0.98

Results and Discussion

During P1, the S, L and M cows grazed to 2.7, 3.6 and 4.4 cm (SED 0.07 cm), respectively. Increasing PGH from S to L to M linearly increased ($P<0.001$) daily MY (21.5, 24.5 and 25.6 kg/cow/d; SED 0.53 kg). During P2, average MY ($P<0.001$) were 20.7 and 22.7 kg/cow/d (SED 0.36 kg), respectively for cows grazing to 3.6 and 4.7 cm. The MY difference associated with each treatment during P2 were as follows: S3.5, -1.68 kg/cow/d; S4.5, +0.43 kg/cow/d; L3.5, -2.79 kg/cow/d; L4.5, -0.70 kg/cow/d; M3.5, -4.86 kg/cow/d; M4.5, -2.99 kg/cow/d.

Independent of P2 treatment effect, the greater PGH imposed in P1 resulted in greater MY loss in P2: -3.92 kg milk/cow/d for the cows grazing to 4.4 cm in P1 (mean of M3.5 and M4.5), compared to -1.74 kg/cow/d (mean of L cows) and -0.62 kg/cow/d (mean of S cows). Independent of PGH imposed in P1, cows grazing to 3.5 cm during P2 suffered a greater ($P<0.001$) reduction in MY (-3.1 kg/cow/d) compared to cows grazing to 4.5 cm (-1.1 kg/cow/d). A decrease of 0.047 kg milk/cow/d is expected between lactation weeks 8 and 13 (Olori *et al.*, 1997). The MY losses to changes in PGSH in the present experiment were substantially larger. The S4.5 MY difference, however, was positive given the large increase in PGH on this treatment. The differences in MY and protein, fat and lactose yields in response to changes in PGH between P1 and P2 were established using linear regression (Table 1). For example, MY variation equated to -2.30 -1.99*P1_PGH +1.76*P2_PGH (R^2 = 0.97).

Conclusions

The results from this experiment deliver a practical decision tool for farms with fluctuations in grass availability around the tenth week of the lactation. It allows dairy farmers to quantify the milk production change resulting from a change in PGH during this period.

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RMIS Project Number 6186

Effects of imposing two post-grazing sward heights for varying lengths of time during early lactation on immediate and carryover dairy cow production

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Introduction

Grazed grass can supply nutrients to dairy cows at a lower cost than alternative feeds (Finneran *et al.*, 2011). Spring grass growth in Ireland is variable (Bereton 1995), with deficits commonly arising between February and May. Imposing a low post grazing sward height (PGSH) until grass growth and availability increases later in spring is one method of offsetting the use of expensive supplements. By imposing a low PGSH (3.5cm), grass utilisation can be maintained at a high level: without reducing cow intake and milk production significantly in comparison to grazing to 4.2 cm (Ganche *et al.*, 2012). The objective of this study was to investigate the effect of imposing two PGSH of varying severity and duration over a ten week period in early lactation and to establish the carryover effects on subsequent lactation production.

Materials and Methods

Eighty (32 primiparous and 48 multiparous Holstein Friesian and Norwegian X (Jersey X Friesian) dairy cows were balanced on the basis of breed, calving date (6 February; s.d. 1.2 days), lactation number (2.04; s.d. 0.103), previous lactation milk yield (4792; s.d. 44.1 kg/cow, body weight (BW) (466; s.d. 3.8 kg) and body condition score (BCS) (2.95, s.d. 0.015) in a randomised block design. Cows were randomly assigned pre-calving to one of four (n=20) PGSH treatments from 13 February to 22 April 2012 (10 weeks P1). The treatments were: 2.7 (2.7 cm PGSH weeks 1-10); 2.7L (2.7 cm PGSH weeks 1-5 and 3.5 cm PGSH weeks 6-10); 3.5 (3.5 cm PGSH weeks 1-10) and 3.5S (3.5 cm PGSH weeks 1-5 and 2.7 cm PGSH weeks 6-10). Following P1, cows from each treatment were managed similarly from 22 April to 4 November (P2). Fresh herbage was allocated twice daily once target PGSH was achieved. Mean concentrate supplementation for the period was 2.3 kg DM/day for all animals. Grass dry matter intake (GDMI) was estimated using the n-alkane technique during wk 5 and 10 of the experiment.

Milk yield was recorded daily; milk composition, BW and BCS were measured weekly. Data on animal variables were analysed using covariate analysis and the PROC MIXED statement of SAS with terms for parity and P1 treatments included in the model. Pre-experimental values were used as covariates.

Results and Discussion

During the experiment, all treatments achieved their target PGSH of either 2.7cm or 3.5cm. The mean daily herbage allowances (DHA) were 10.6 and 13.2 kg/day for animals on 2.7 and 3.5 cm, respectively. During weeks 1-5 both the 3.5 and 3.5S cows had similar milk solids yield but produced +0.12 kg/cow more ($P<0.05$) than the 2.7 and 2.7L cows (1.85 kg/cow). Milk solids yield during weeks 6-10 was also ($P<0.05$) higher (+0.1 kg/cow) for the 3.5 and 2.7L cows when compared to the 2.7 and 3.5S cows (1.64 kg/cow). The severe decrease in production reflected the level of restriction imposed on the S treatments as they were offered 2.7 kg DM less grass to achieve their PGSH. There was no significant effect of timing of restriction. When carryover production was analysed, treatment 2.7L and 3.5S had higher (+1.5 g/kg $P<0.002$) milk protein concentration in comparison with 2.7 and 3.5 (37.4 g/kg). There was no effect of treatment on cumulative milk (4426 kg/cow) and milk solids (369 kg/cow) production. At the end of P1, 2.7 tended to have a lower BW than all other treatments. Body condition score was higher ($P<0.05$) for 3.5 and 2.7L treatments (BCS; 2.91) when compared to 2.7 and 3.5S (2.85) over the same period. There was no difference in BCS and BW for any treatment at the end of P2 indicating that the cows can recover BCS lost in P1.

Conclusions

The results of this experiment show that duration of reduced PGSH during the first ten-weeks of lactation did not affect total lactation milk or milk solids production. This has positive repercussions for dairy farmers as when grass deficits occur in spring grazing deeper into the grazing horizon can be practiced without affecting overall lactation performance, however effects on fertility need further evaluation.

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Table 1. Immediate and carry-over effect of post-grazing height on the performance of the spring calving dairy cows

	Period 1				Carryover				P1		P2
	2.7	2.7L	3.5	3.5S	2.7	2.7L	3.5	3.5S	sed	P-val	P-val
Wk1-5 milk yld kg/cow	21.8^{a}	21.9^{a}	23.9^{b}	23.7^{b}					0.70	0.04	
Wk6-10 milk yld kg/cow	21.7	22.7	22.9	21.4	14.8	14.8	15.1	14.4	0.63	0.08	0.394
Avg milk yld kg/cow	21.8	22.3	23.5	22.6					0.42	0.07	
Milk fat, g/kg	46.5	46.7	45.6	46.3	46.7	47.6	45.4	47.4	0.11	0.71	0.205
Milk protein, g/kg	33.1	33.7	33.7	33.9	37.5^{a}	38.6^{b}	37.3^{a}	39.2^{b}	0.05	0.37	0.002
Milk lactose, g/kg	47.6	47.2	47.9	47.6	44.7	44.6	45.1	44.9	0.03	0.06	0.374
Milk solids yield, kg/d	1.73^{a}	1.76^{a}	1.85^{b}	1.80^{ab}	1.24	1.26	1.25	1.24	0.035	0.032	0.882
End BW, kg	435	452	456	447	480	491	491	482	5.6	0.125	0.298
End BCS	2.82^{a}	2.90^{b}	2.91^{b}	2.87^{a}	2.84	2.87	2.85	2.86	0.022	0.035	0.935

*Performance in P1 of animals on treatment 2.7(2.7cm; 10wks), 2.7L (2.7cm-3.5cm; 5wks), 3.5(3.5cm; 10wks), 3.5S (3.5cm-2.7cm; 5wks). **Performance in P2 of animals on 2.7, 2.7L, 3.5 and 3.5S treatments in P1

Effect of post-grazing sward height and cow type/breed during the main grazing season on milk production

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Introduction

Increasing farm profitability can be achieved by converting a greater amount of harvested grass into milk solids. Two methods of achieving this are i) increasing grazed grass utilisation and ii) introducing cow genetics more suited to grass based milk production. Low spring post-grazing sward heights (PGSH; <3.5cm) increase grass utilisation but reduce the milk production of Holstein-Friesian (HF) cows (Ganche *et al.,* 2012). However, crossbred cows may react differently to lower PGSH than HF cows. Prendiville *et al.* (2011) showed that Jersey (JE) x HF cows produced higher milk constituents in comparison to HF in similar grazing managements. Begley *et al.* (2009) also showed improved performance with the Norwegian Red (NR) x HF compared to the HF. A 3-way cross comprising NR, JE and HF (3-wayX) may have some attributes suitable for a severe grazing regime. The objective of this experiment was to establish the effect of PGSH and breed on milk production performance.

Materials and Methods

Eighty (32 primiparous and 48 multiparous) spring calving dairy cows were used. Forty-eight Holstein Friesian and 32 3-wayX cows were balanced on the basis of breed, calving date (6 February; s.d. 1.2 days), lactation number (2.04; s.d. 0.103), production variables from the three weeks prior to the commencement of the experiment: milk yield (22.6; s.d. 0.07 kg/cow per day), milk fat (42.7; s.d. 0.01 g/kg), protein (33.2; s.d. 0.08 g/kg) and lactose (47.3; s.d. 0.29 g/kg) concentrations, milk solids yield (1.71, s.d. 0.004 kg/cow per day), body weight (BW) (458, s.d. 0.1 kg) and body condition score (BCS) (2.85, s.d. 0.010). Once cows were balanced they were randomly assigned to one of two PGSH treatments: 3.5 cm (S, severe) or 4.5 cm (M, moderate) from April 23 to November 4, 2012. The difference in PGSH was achieved by maintaining approximately 2.7 kg dry matter (DM)/cow difference in daily herbage allowance (DHA). Fresh herbage was allocated daily and pre and post-grazing compressed sward heights were measured daily using a folding plate meter. Sward heights were measured daily by recording approximately 30 heights across the 2 diagonals of each group of cows using the folding plate meter. Herbage mass (HM; >3.5 cm) was calculated twice weekly by cutting two strips per grazing treatment. Milk yield was recorded daily; milk composition, BW and BCS were measured weekly. Grass DM intakes (GDMI) were measured using the n-alkane technique. Data were analysed using covariate analysis and the PROC MIXED statement of SAS, with cow as a random effect and treatment as a fixed effect with terms for treatment, parity, breed and the interaction of parity, breed and treatment Pre-experimental values were used as covariates in the model. There were no significant interactions detected.

Results and Discussion

Mean DHA were 14.7 and 17.3kg/cow/day (>3.5cm) and the mean PGSH achieved were 3.8 and 4.6 cm for the S and M treatments, respectively ($P<0.001$). The M treatment had a greater pre-grazing sward height (+0.68cm; $P< 0.01$). Treatment M cows had a greater ($P<0.001$) milk yield, and milk solids yield ($P<0.001$; Table 1). The severe decrease in production reflected the level of restriction imposed on the S treatments as their GDMI showed that grazing to 3.8 cm decreased GDMI by -1.6kg/cow/day when compared to 4.7 cm (15.6kg DM/cow/d; $P<0.05$). Treatment had no effect on milk fat, protein or lactose concentration. Breed had an effect on milk constituents with 3-wayX producing higher milk fat ($P<0.001$) and protein ($P<0.01$) yield than the HF cows. The M treatment had a higher end BCS (+0.07; $P<0.05$) and BW (+12kg; $P<0.01$) than the S treatment (2.82 BCS and 479kg). There was no difference in breed for either BCS or BW in this experiment.

Table 1. Effect of post-grazing sward height (PGSH) on dairy cow performance from April 23 - November 4

	PGSH[1]		Breed			*P*-values	
	S	M	HF[3]	JNRX[4]	sed	PGSH	Breed
Milk yield (kg/d)	14.0	15.5	15.2	14.2	0.28	0.001	0.005
Milk fat, g/kg	47.1	46.8	45.2	48.7	0.59	0.682	0.001
Milk protein, g/kg	38.0	38.4	37.7	38.7	0.35	0.289	0.015
Milk lactose, g/kg	44.6	45.0	44.8	44.8	0.21	0.114	0.709
Milk solids yield, kg/d	1.18	1.31	1.26	1.23	0.025	0.001	0.204

[1]PGSH: S (3.7 cm), M (4.7 cm),[2]s.e: standard error of the difference, [3]HF: Holstein Friesian, [4]Norwegian Red X Holstein Friesian x Jersey

Conclusion

Grazing swards to 4.6 cm during the main grazing season increased cow GDMI and resulted in higher milk and milk solids yield compared to grazing to 3.5cm. Both the HF and 3wayX had similar milk solids production throughout the experiment.

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RMIS Project Number 6186

Sustainable Production Systems & System Analysis

Genetic parameters for methane emissions in grazing dairy cows

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Introduction

Enteric methane emissions (CH_4) from dairy cattle contribute significantly to the overall greenhouse gas emissions in agriculture. Breeding for reduced CH_4 emissions could be part of a national mitigation strategy. The contribution of additive genetic variation to differences in CH_4 emissions is, however, currently unknown due primarily to a paucity of data. Some studies (de Haas et al., 2011) have attempted to estimate genetic parameters for predicted CH_4 emissions but these estimates will be influenced by the genetic parameters of the traits used in the prediction equation. Data on daily CH_4 emissions of dairy cows has been collected at Teagasc, Moorepark for several years. The objective of this study was to collate the data and estimate genetic parameters of CH_4 emissions in grazing Irish dairy cows.

Materials and Methods

Daily enteric CH_4 measures from 110 different test-days on 355 cows on Teagasc research farms between the years 2009 and 2011 were analyzed. A total of 4155 measures of daily CH_4 emissions from individual cows were available. Cows originated from 19 different treatment trials across the three years. Breed of cows included Friesian, Holstein, Jersey, Montbeliard and Norwegian Reds and crossbreds. Details of milk yield (MY), calving dates and pedigree information, including heterosis and recombination effects were available; only animals with a known sire were retained. Daily CH_4 production was estimated using the sulphur hexafluoride (SF_6) tracer gas technique (Johnson and Johnson, 1995). Cows were fitted with gas collection canisters attached to their back by a harness. A flow-restricting sampling line was fitted above the nostrils to collect the CH_4 emissions from rumen digestion and the known concentration of SF_6 gas released from a bolus in the rumen. Average CH_4 emission per cow test-period was calculated for cows with at least 4 daily CH_4 observations within the treatment period. Cow average daily milk yield was also calculated across the test-period. Days in milk between 20 and 300 days were retained. Contemporary group was defined as treatment-by-period of measurement. All contemporary groups had at least 5 records. A total of 2934 CH_4 measurements from 297 cows on 19 experimental treatments remained. Variance components for CH_4 emissions were estimated using a sire linear mixed model in ASREML (Gilmour et al., 2009). Fixed effects included in the model were contemporary group, parity, days in milk, heterosis and recombination loss. The genetic correlation between daily CH_4 emissions and milk yield was estimated using a bivariate sire linear mixed model.

Results and Discussion

Average daily CH_4 emission was 379 g/day; the standard deviation was 82g/day. Average daily MY during the test periods was 17 kg and cows were, on average, 172 days calved. Daily CH_4 emissions increased ($P < 0.001$) with parity. Least squares means daily CH_4 emissions for parity, 1, 2, and 3+ animals was 344 g/day (se = 3.95), 379 g/day (se = 4.41), and 406 g/day (se = 3.95), respectively. CH_4 emissions varied by treatment with the least squares mean varying from 259 g/day to 495 g/day. Methane emissions increased with days post-calving to a peak at day 170, after which CH_4 emissions declined. This pattern is similar to the lactation profile for energy intake of dairy cows (Berry et al., 2006). The heritability of CH_4 emissions was 0.14 (se = 0.19) suggesting that 14% of the phenotypic variation in CH_4 emissions (after accounting for systematic environmental effects) was due to additive genetic effects. However, the standard error of the heritability estimate was large. The genetic standard deviation was 0.09 suggesting a coefficient of genetic variation of 0.04. The repeatability of CH_4 emissions was 0.57 (se = 0.05) suggesting good repeatability for CH_4 measures using the SF_6 technique. It should be noted that the CH_4 emission values used in this study were an average across at least four daily measures and this is likely to improve both the heritability and repeatability estimates. Nonetheless, the difference between the heritability and repeatability estimates suggest a large potential influence of a permanent environmental effect (e.g., early nutrition) on CH_4 emissions. Methane emissions were positively genetically correlated 0.21 (se = 0.27) with MY, albeit with large standard error.

Conclusions

Daily CH_4 emissions exhibited heritable genetic variation with a coefficient of genetic variation similar to those observed for most performance traits. However the standard errors of the estimates presented here are large due primarily to the small dataset. More data is required to generate more precise estimates.

Acknowledgements

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RMIS Project Number 5781

The effect of a seasonal versus a less seasonal milk supply profile on the profitability of the farm and processing sectors

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Introduction

A dominant feature of Irish dairy farming is its reliance on low-cost grass-based systems of milk production. The associated benefits at farm level create challenges at processor level due to the seasonal supply and inconsistent composition of raw milk. Dairy processors in Ireland have developed and adapted processing facilities, production systems and marketing strategies to meet the needs of a seasonal milk production system. However with Common Agricultural Policy reform and the removal of milk quotas, the seasonality of the Irish dairy industry is being challenged as a costly industry feature with claims that greater industry returns would be yielded by less seasonal milk supply. The objective of this paper was to examine the effect of changing the current seasonal supply profile (100% spring) to a less seasonal supply profile (50% spring:50% autumn) on net industry returns (farmer and processor).

Materials and Methods

Two models, the Moorepark Dairy Systems Model (MDSM) (Shalloo et al., 2004) and the Moorepark Processing Sector Model (MPSM) (Geary et al., 2010), were used to simulate the effect of seasonality within the Irish dairy industry. The MDSM simulates dairy systems inside the farm gate while the MPSM simulates processing activities from milk collection at the farm gate to selling and distribution of intermediate and final dairy products. The outputs of one model were fed into the other as an input, this was repeated on a iterative basis until both models were solved. The seasonal supply profile was characterised by a mean calving date of mid February with 15%, 70% and 15% of cows calved in January, February and March, respectively. The less seasonal supply profile was representative of a split spring and autumn calving period with 7.5% of the herd calved in January, 35% in February, 7.5% in March, 20% in September, 25% in October and 5% in November. The seasonal milk supply profile had a peak milk supply of 14% in April while the less seasonal had a peak milk supply of 12% in April. The calving patterns were fed into both the farm and processing models and the impact on profitability was determined. The cheese and casein processing capacities were representative of the Irish dairy industry (6% of the national milk pool per month). The processing capacity for cheese and casein were filled first after which milk was diverted to a combination of butter and skim milk powder, and whole milk powder production at a ratio of

76:24, respectively. An annual investment cost of €8.9 million (Industry consultation) was incorporated in the MPSM as a monthly fixed cost in the seasonal analysis to account for higher capacity requirements at peak, no investment cost was assumed in the less-seasonal analysis.

Results and Discussion

Using the national milk pool of 5,189.9 million litres and based on average product market values (2008-2010) the less seasonal supply profile was more profitable for the processing sector with proportionately more cheese and casein produced and higher revenues generated (Table 1).

Table 1. Volume of product produced

Supply profile	***Seasonal***	***Less seasonal***
Cheese, tonnes	165,080	202,914
Casein, tonnes	31,921	38,060
Butter, tonnes	141,334	131,126

The milk prices generated by the MPSM were included in the MDSM for both supply profiles. Based on a 40 hectare farm the seasonal supply profile was more profitable for the farm sector with lower concentrate, labour and overall costs (Table 2).

Table 2. Farm system financial outcomes

Supply profile	***Seasonal***	***Less seasonal***
Milk sales, €	178,538	195,227
Livestock sales, €	28,848	32,049
Total costs, €	149,221	177,786
Net farm profit, €	58,450	47,968

At industry level the seasonal milk supply profile resulted in higher net industry returns than the less seasonal supply profile (Table 3).

Table 3. Processing sector, farm sector and net industry returns for both supply profiles

Supply profile	Seasonal	Less seasonal	Differential
Processor net milk value, €m	1,474.9	1,540.7	-65.8
Dairy farm margin per litre, €/L	0.101	0.085	+0.016
Net industry returns, €m	524.2	441.1	83.0

Conclusion

From a national perspective, while including processor and farm sector interests, the seasonal milk supply profile was more profitable. With the less seasonal milk supply profile the difference in costs at farm level outweighed the increased milk price at processor level. Maintaining seasonal milk production, while investing in additional processing facilities is more profitable for the Irish dairy industry.

Acknowledgements

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RMIS Project Number 5794

The effect of stoking rate and calving date on the dry matter intake and feed efficiency of three pasture based systems of milk production

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Introduction

The efficiency of milk production in Ireland is dependent on systems based upon the extensive use of cheap high quality grazed grass (Horan et al., 2005). At a national level, such systems would be greatly enhanced through a combination of higher stocking rates and an earlier and more compact calving pattern to maximise grass utilisation (McCarthy et al., 2012). The primary objective of the study was to quantify the impact of stocking rate (SR) and calving date (CD) on the dry matter (DM) intake of spring calving pasture-fed dairy cattle.

Materials and Methods

In each of 3 years (2009, 2010 and 2011), 138 spring calving HF dairy cows with an average Economic Breeding Index of €148 were randomly assigned to one of two mean calving date treatments: Early calving (mean calving date: 14th of February) and Late calving (mean calving date: 1st of March). Within each calving group, a total of 46 animals were allocated to one of three SR treatments, Low (2.51 cows/ha), Medium (2.92 cows/ha) and High (3.28 cows/ha). In total there were 6 individual farmlets in each year, with 23 cows in each. Once allocated, all animals remained on the same treatment for the duration of the study. Cows were turned out to pasture in early February with SR treatments managed separately and calving date treatments within each SR managed similarly. Different grazing intensities were imposed on each SR, with target post-grazing residual heights of 4.5-5.0, 4.0-4.5, and 3.5-4.0 for the low, medium and high SR respectively. Individual animal intakes were estimated using the n-alkane technique (Mayes et al., 1986) on three occasions in each year at pasture; in April, May and September. During each intake period, all cows were dosed twice daily for a 12 day period with 500 mg of C32. Faecal grab samples were collected twice daily from each cow in the last 6 days of each period and bulked for analysis. Herbage samples were collected manually to represent herbage grazed after both the morning and evening milking on day 6 to 11 of each measurement period. The ratio of herbage C33 to dosed C32 was used to estimate intake. Milk yield was recorded each day during the study and live-weight weekly. The animal production data for the measurement periods were analysed using PROC Mixed of SAS (SAS, 2002). Cow was included as a random effect while year, stocking rate, calving date, and period were included as fixed effects.

Results and Discussion

There was a significant effect of stocking rate on milk production, bodyweight and DM intake (Table 1). The Low SR treatment achieved the highest daily milk and MS yield and also had a higher daily grass and total DM intake while the High SR was lowest and the Medium SR was intermediate. Calving date also had a significant effect on milk production and approached significance for grass and total DM intake. The late calving date group achieved higher milk and milk solids yields per cow. The interaction of SR and calving group for grass and total DM intake approached significance due to the comparably higher intakes of the Medium and High SR treatments in the late calving group.

Table 1. Effect of stocking rate and herd mean calving date on milk production and DM intake

Calving group	Early			Late			SIGNIFICANCE[1]			
Stocking rate	Low	Medium	High	Low	Medium	High	SE[2]	SR	CD	SR x CD
Milk yield (kg/cow/d)	21.8	19.5	19.3	22.7	20.7	20.9	0.31	***	***	
MS[3] yield (kg/cow/d)	1.6	1.5	1.5	1.7	1.6	1.5	1.57	***	*	
Bodyweight (kg)	515	496	494	514	506	500	4.0	***	0.13	
Daily intake (DM/cow)										
Concentrate	1.0	1.0	1.0	1.0	1.0	1.0				
Grass	14.9	14.3	12.8	14.9	14.3	13.5	0.21	***	0.12	0.13
Total	15.9	15.3	13.8	15.9	15.3	14.5	0.19	***	†	0.10

[1]Significance: ***= P<0.001, **= P<0.01, *=P<0.05, †=P<0.10; [2]s.e. – standard error; [3]MS = Milk solids (fat plus protein)

Conclusions

This study shows that in a grass-based system, milk production and individual animal bodyweight will be reduced as stocking rate increases due to a reduction in grass DM intake. The presence of a SR by calving group interaction for grass and total DM intake also indicates that the reduction in individual animal intake and milk production performance at higher SR can be effectively reduced by delaying calving date.

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RMIS Project Number 5891

Comparison of feeds offered during the winter on replacement dairy heifer bodyweight and weight gain

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Introduction

Substantial costs are involved in rearing replacement heifers (Shalloo *et al.,* 2012) which contribute significantly to the overall expense of dairy production systems (Heinrichs, 1993). Forage brassicas are considerably cheaper as a winter feed than grass silage and concentrates and can offer a suitable alternative where drier soil types prevail (Kennedy *et al.*, 2011). However, there are many types of brassicas (e.g. kale, rape) available for winter feeding and it is unclear if heifer weight gain is similar from all diets. The objective of this study was to compare three forage brassica diets to grass silage and concentrate diets with respect to the bodyweight (BW), BW gain and body condition score (BCS) of replacement dairy heifers during the winter feeding period.

Materials and Methods

One hundred and seventy five replacement dairy heifers were balanced on the basis of breed (90 Holstein Friesian (HF), 60 Jersey x HF (JEX) and 25 Norwegian Red x HF (NRX)), age (265 ± 19.9 days), BW (214 ± 20.5kg) and BCS (2.81 ± 0.192) and randomly assigned to one of five feeding treatments. The treatments were i) indoors offered grass silage and 1 kg dry matter (DM) concentrate/day (S1), ii) indoors offered grass silage and 2 kg DM concentrate/day (S2), iii) outdoors grazing forage kale in conjunction with grass silage bales which were offered as 300g/kg of the diet on a DM basis (K), iv) outdoors grazing forage rape in conjunction with grass silage bales which were offered as 300g/kg of the diet on a DM basis (R) and v) outdoors grazing a rape x kale hybrid forage in conjunction with grass silage bales which were offered as 300g/kg of the diet on a DM basis (H). The feeding treatments were imposed from 14 November 2011 until 22 February 2012.

The S1 and S2 animals were offered the same pit silage. The K, R and H animals were offered baled silage which was harvested at a similar age of regrowth as the pit silage. The forage crops were grazed *in situ*. Prior to the commencement of the experiment all animals received one Allsure® bolus to provide iodine, selenium, cobalt and copper supplementation.

All animals were offered fresh feed daily; the refusals of the S1 and S2 animals were removed and weighed daily, the outdoor animals were offered a fresh allocation of feed each morning by moving a temporary electric fence. During the experimental period all animals were weighed every second week and condition scored every three weeks. All animals were turned out to pasture on 22 February and offered *ad libitum* grazed grass. All animals were weighed at turnout and again two weeks later to calculate weight gain during the winter period. All data were analysed using PROC MIXED in SAS. Animal was used as the experimental unit.

Terms for treatment and breed were included in the model. Pre-experimental values for BW and BCS were used as co-variates in the model.

Results and Discussion

The concentrate fed during the winter period contained 0.33 barley, 0.33 citrus pulp and 0.33 distillers grains. The DM digestibility of the silage was 710 (±32.2) g/kg, DM was 284 (±34.9) g/kg and crude protein (CP) was 122.2 (±26.13) g/kg on a DM basis.

There was no interaction between breed and winter feeding treatment. At turnout the S2 heifers were heavier (+26 kg; $P<0.001$) than heifers from all other treatments. This equated to a weight gain during the winter period of 0.65 kg/heifer/day for the S2 heifers. There was no difference in winter weight gain between heifers from the other four treatments (0.42 kg/heifer/day). However, differences in gut fill may have existed due to the varying diets offered. Thus, heifers were weighed again two weeks post turnout and winter weight gain was recalculated. This measurement showed that there was no difference between heifers from the S2, K, R and H treatments (279 kg) but all treatments were heavier ($P<0.001$) than the S1 heifers (261 kg). Thus, weight gain calculated when heifers were all on similar diets was least ($P<0.001$) for the S1 heifers (0.38 kg/heifer/day) when compared to all other treatments which were similar (0.53 kg/heifer/day).

Two weeks after turnout the JEX heifers were lighter ($P<0.01$) and also had a lower BW gain (270 kg and 0.45 kg/heifer/day) when compared to the NRX and HF heifers, which were similar (278 kg and 0.52 kg/heifer/day, respectively).

There was no difference in the turnout BCS for the five winter feeding treatments (Figure 1). There was no difference in the BCS of the NRX and HF heifers (3.13) but they were in greater body condition ($P<0.01$) than the JEX heifers (3.02).

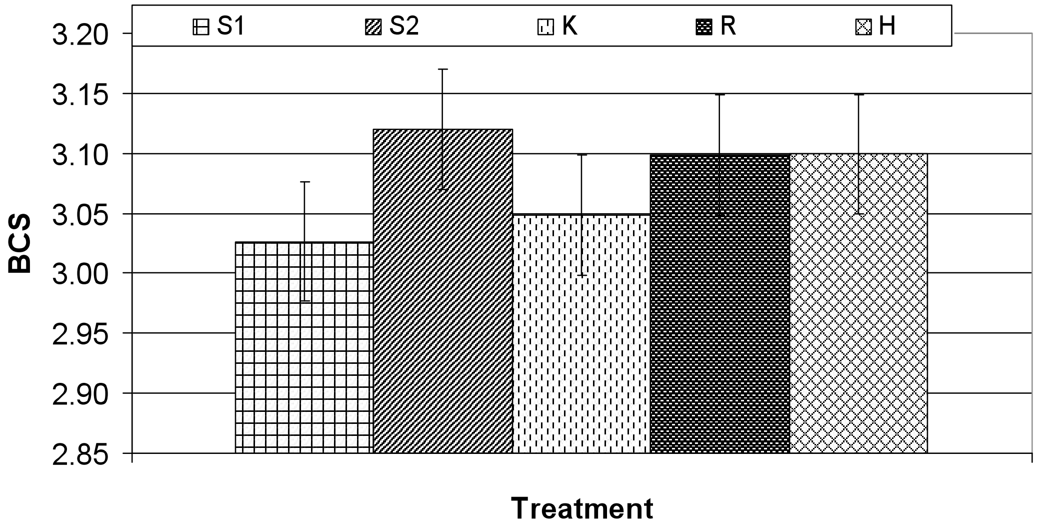

Fig. 1. Effect of winter feeding treatment on BCS at turnout

Conclusion

This study has shown that similar BW gain over the winter period can be achieved with grass silage and 2 kg DM concentrate and forage crop-based diets and that similar BW gain can be achieved from kale, rape and kale x rape hybrid forage crops.

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RMIS Project Number 5892

The effect of cow live-weight and stocking-density on soil quality

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Introduction

Rotational grazing systems involve a high stocking-density (SD) of cows in small areas for short periods. As such, the risk of soil and sward damage is high when soil and climactic conditions are unfavourable. Surface deformation coupled with compaction at shallow depth (down to approx 0.2 m) can result in increased soil resistance and decreased aeration, affecting shoot and root growth rates (Menneer et al., 2005). Both soil type and soil moisture content (weather) are fixed characteristics for a particular farm. As such, any reductions in the magnitude and intensity of soil damage will have to be brought about by changes in stock management such as changes to SD, animal live-weight (LW) and grazing management. The objective of the current study was to determine the effect of grazing by a large and small cow type on soil physical properties and poaching damage. The impact of treading by a number of different cow LW and SD was examined across two grazing seasons (Table 1).

Table 1. Cow live-weight and imposed stocking- densities

	Mean live-weight* (kg/cow)	Stocking-Density (Cow/Ha)	
		2011	2012
HF-L	573	2.35	2.45
HF-H	567	2.56	2.67
JX-L	501	2.39	2.49
JX-H	497	2.64	2.75

**P<0.001, Standard error of mean (S.E.M.) = 5.6kg*

Materials and Methods

Two breeds of dairy-cow were selected, Holstein Friesian (HF) and crossbred Jersey (JX). Both breeds were split into two herds from groups balanced for lactation number (1,2,3,≥4), calving date, and a low and high SD was imposed (Table 1). The experimental area was divided into six blocks each containing four paddocks, one of which was assigned to each system in a randomized complete block design from the start of the 2011 grazing season. Between February and April, cows were managed in two herds (i) HF and (ii) JX. When all cows had calved in April, the full treatments were imposed. The cows were turned out to graze after calving in spring and generally remained outside until November. Exceptions to this were made when herbage availability was too low or when soils were deemed to be too wet The mean number of grazing days was 232 in 2011 and 198 in 2012. Soil properties (soil bulk density, total porosity, macroporosity, gravimetric moisture content, volumetric moisture content, air-filled porosity, penetration resistance and shear strength) were measured on four occasions per year using standard methods (Herbin, 2011). Throughout the grazing season poaching depth and surface deformation were measured (Saleh, 1994). The size of the back left hoof of a subset of animals from each herd was measured and taken to represent that of the four hooves of the cow (Herbin, 2011). Data was subjected to an ANOVA analysis.

Results and Discussion

Cow LW and SD had no effect on bulk density (BD), (P>0.05) or air-filled porosity (AFP), (P>0.05) over the course of the experiment. BD (mass of soil per unit volume, g cm^{-3})at 5-10 cm depth ranged from 0.86 g cm^{-3} to 1.11 g cm^{3}, and was correlated to soil moisture content (R^2=0.91). AFP (proportion of soil volume occupied by air, %) was typically 14.5%. Poaching damage was much greater in 2012 than 2011 due to the much higher rainfall during the grazing season (784 mm compared to 588mm during the period from March 1st to October 31st). Soil surface deformation was 6.6 ± 4.2 cm m^{-1} (Mean ± standard deviation) in 2011 compared with 14.1 ± 5.6 cm m^{-1} in 2012 (P<0.001). Hoof depth was 27.9 ± 11.9 mm in 2011 and 47.5 ± 17.1 mm in 2012 (P<0.001). Surface deformation and hoof depth were greater at high SD (P<0.05) but were not affected by breed. The lack of any significant breed effect on soil physical properties was most likely due to the similar static loading pressures of both breeds. Cow hoof-print measurements were compared with cow LW for a subset of animals. While the HF cows are heavier (580 vs. 506 kg, $P<0.001$) than their JX equivalents they also have larger hoofs (273 vs. 234 cm^2, $P<0.001$) (Fig. 1). As such the mean surface loading pressure under both breeds is approximately the same ($P=0.6$).

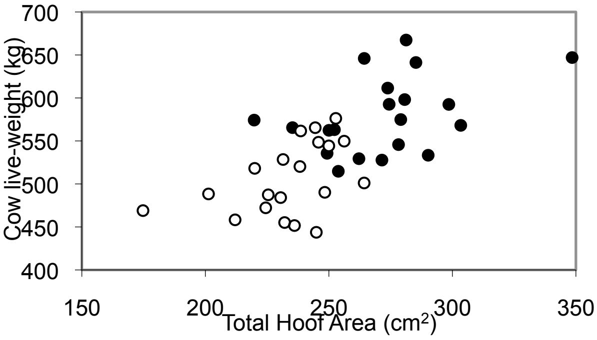

Fig. 1. *Cow live-weight(Y) and total hoof-area (X) for HF (•) and JX (o) cows. HF cows are heavier ($P<0.001$) and have larger hoofs ($P<0.001$) than their JX equivalents.*

Conclusions

Differences in cow LW did not affect soil-properties or poaching damage. Surface loading pressure and SD, rather than LW, were the factors most affecting the soils response to treading. These factors can support management decisions to reduce damage on wet soils.

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RMIS Project Number 6012

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

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Introduction

An objective of Irish production systems in the absence of milk quotas will be to increase milk solids production by maximising grass utilisation and milk productivity per unit of available feed (McCarthy et al., 2007). Recent studies have reported significant milk productivity gains when both stocking rate (SR) and supplementation rate are increased simultaneously within the grazing farm system (Coleman et al. 2010). Such a strategy may be particularly useful on dairy farms with fragmented holdings and with limited capacity for expansion from grazing systems alone. The objective of this experiment was to investigate the impact of two pasture based systems of milk production differing in overall SR and feed supplementation level on grass production and utilisation on a wetland drumlin soil.

Materials and Methods

Performance data were obtained from 120 dairy cows (60 per feed system,) in a 4 year (2008-2011) systems comparison study at Ballyhaise College, Co. Cavan. Animals were randomly allocated to one of two feed systems (FS) based on calving date, genetic potential (EBI) and parity. Once randomised, all animals remained on the same FS for the duration of the experiment. The two FS being evaluated were: a low input high pasture utilisation system (HG) and a high input high pasture utilisation system (HI). The HG FS had a stocking rate of 3.1 cows per ha, a concentrate input of 551 kg DM per cow. The HI FS system had a stocking rate of 4.5 cows per ha, a concentrate input of 872 kg DM per cow. Cows were turned out to pasture in early February with SR treatments managed separately. The pre-grazing herbage mass (HM) was estimated above 35 mm on each paddock before grazing or silage harvest based on the average yield of five quadrant samples. The post grazing height was also measured after each grazing or silage cut using a folding pasture plate meter and grazing intensity was measured based on the proportion of available herbage that was harvested. Grazing efficiency was calculated on each paddock in each rotation as the proportion of the available HM which was removed by grazing or silage harvest. Total annual pasture production for each farmlet was also calculated using the methodology of O'Donovan (2000). Animal and herbage data were analysed using Proc MIXED (SAS, 2006). Feed system, year and parity were included as fixed effects in the final animal model. Grass production and utilisation were analysed using mixed models with block and block*FS included as random effects.

Results and Discussion

Feed system had a significant effect on MS yield per cow and per ha. The higher total lactation MS yield per cow and per ha achieved with the HI FS is expected, given the large increase in energy supply within this system due to increased concentrate plus silage supplementation. Feed system had no significant effect on total average herbage production over the four years of the study (P=0.394). Over the entire grazing season pre-grazing yield was higher (P-value 0.014) for the HG FS due to the higher pre-grazing herbage masses achieved with this FS during autumn when the lower overall feed demand facilitated an increase in overall farm grass cover to extend the grazing season. Post grazing sward height (38.6 mm) and grazing efficiency (95%) were similar for both FS. There was no significant FS effect on total herbage (P=0.49) or grazed herbage (P=0.22) utilisation. However, FS had a significant effect on herbage utilized as silage with significantly more herbage conserved within the HG FS (1,704 kg DM/ha/yr) compared to HI FS (644 kg DM/ha/yr). Neither FS produced sufficient winter feed resulting in a feed deficit of 53% and 90% for the HG FS and HI FS, respectively.

Table 1. Effect of feed system on milk production, feed inputs and herbage utilised.

System	HG	HI	se	Sig.
Milk solids (fat + protein) production				
kg/cow	377	390	4.3	*
kg/ha	1,153	1,786	17.2	***
Feed inputs (kg DM/cow)				
Concentrate	551	872	9.1	***
Silage	1,168	1,431	19.4	***
Grazing characteristics (kg DM/ha)				
Grass growth	13,558	12,893	542.1	ns
Pregrazing HM	1,422	1,356	19.1	*
Feed utilisation (kg DM/ha/year)				
Grazed grass	8,445	9,139	390.2	ns
Silage	1,704	644	171.9	***
Total	10,155	9,788	366.8	ns

*=P≤0.05, **= P≤0.01, ***= P≤0.001,

Conclusion

Increasing SR and feed supplementation can significantly increase milk productivity per ha on Irish dairy farms post EU milk quotas. However, such systems will not lead to increases in home grown forage production or utilisation and consequently will reduce winter feed production. These results indicate that further significant increases in herbage production are required to justify higher SR systems.

Acknowledgements

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RMIS Project Number 6015

Evaluating expansion strategies for startup Irish dairy farm businesses

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Introduction

To encourage new dairy enterprises, the Irish government initiated a New Entrant Scheme in 2009. Over 300 new entrants have already received 200,000L of milk quota each to set up a new dairy enterprise (McDonald et al., 2012). The immediate challenge facing these new farmers is to plan farm expansion through the period in advance of and beyond milk quota abolition in 2015. The objective of this study is to examine alternative expansion strategies in terms of farm profit and net worth change taking cognisance of capital investment costs and milk quota super levy exposure using the Moorepark Dairy Systems Model (MDSM; (Shalloo et al., 2004).

Materials and Methods

The new entrant dairy farm data used in the model was based on the actual business plans of applicants (McDonald et al., 2012). Six alternative expansion strategies were investigated from 2012-2026: a static scenario whereby no expansion is undertaken (S1), a natural growth scenario where expansion is achieved only based on the natural growth of herd size over time (NG2), a wait and expand scenario where producers remain within quota until after milk quota abolition and expand to full capacity thereafter (WE3), a full scale immediate expansion scenario based on purchased animals (FNQ4), a full scale immediate expansion scenario where super levy fines are incurred during the 3 quota years (FQ5) and finally a once-a-day (OAD) milking scenario whereby OAD milking is used to increase stock numbers and avoid super levy fines in advance of quota abolition and where full scale expansion with twice-a-day milking is employed thereafter (OAD6).

The MDSM is a stochastic budgetary simulation model which combines the main segments of the dairy farm structure (Shalloo et al., 2004). The financial implications of each scenario were measured annually over 15 years based on discounted (2.6%) net profit and cumulative net worth change (excluding own labour).

Results and Discussion

At average capital investment costs and interest rates (€2,450/cow and 5.5% p.a., respectively (Teagasc, 2011)) and while increasing debt and reducing cash flows, all expansion strategies exhibited a positive discounted net profit and net worth over the 15 year period investigated when compared to S1 (Table 1). The low overall profitability of S1 reflects static and low milk receipts over the entire period of the project while costs increased. Similarly, the NG2 option also realised low overall discounted profitability due to low milk output during the initial years of expansion coupled with increased capital costs to facilitate the growing herd thereafter. The FNQ4 scenario achieves the greatest cumulative discounted net profit over the 15 year period as high levels of profitability are realised early in the lifetime of the project and no super levy fines are incurred. The FNQ4 scenario is indicative of the potential financial rewards from full scale milk production expansion post EU milk quotas. Where super levy fines exist, OAD6 achieves the greatest profit (€421,497) while WE3 is the next most profitable strategy (€342,026) as both strategies avoid super levy fines for the first three quota years and achieve maximum output thereafter. In contrast, the low overall profitability of FQ5 is a consequence of incurring large super levy penalties in advance of milk quota removal and indicates the detrimental impact of full scale milk production expansion within the current milk quota system.

Table 1. The effect of capital investment cost and interest rate on the profitability and net worth of six alternative expansion scenarios[1] over a 15 year period

Scenario	Total receipts (€)	Variable costs (€)	Fixed costs (€)	Net profit (€)	Net worth (€)
S1	1,009,014	245,568	697,981	65,465	190,590
NG2	1,615,079	503,884	1,072,934	38,261	327,595
WE3	3,152,249	1,049,130	1,761,093	342,026	792,476
FNQ4	3,849,268	1,294,041	1,964,889	590,339	1,040,789
FQ5	3,849,268	1,821,427	1,964,889	62,953	513,403
OAD6	3,267,121	1,071,302	1,774,322	421,497	871,947

Scenarios investigated[1]: S1 = Static; NG2 = Natural Growth; WE3 = Wait and Expand; FNQ4 = Full scale no quota superlevy; FQ5 = Full scale with quota superlevy; OAD6 = OAD

Conclusions

This study indicates that dairy farm expansion will protect the future profitability of the farm business. While the choice of expansion strategy will be dictated by individual farmers attitude to risk in addition to the potential return from alternative expansion strategies, these results indicate that avoiding super levy fines using OAD milking and increasing to full capacity thereafter once milk quotas are removed will maximise net farm profit and net worth on expanding dairy farms.

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RMIS Project Number 6090

Effects of production system on early maturing dairy cross heifers

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Introduction

Currently, in the quota phase out period, approximately 60% of dairy cows are bred to dairy bulls. The remainder are mated to beef breeds and the Aberdeen Angus and Hereford are the dominant beef breeds used by dairy producers. This is largely attributed to their ease of calving and short gestation traits compared with other beef breeds. Previously, Keane et al. (2009) identified a 19 month production system for early maturing dairy cross heifers. This system focused on maximising performance from pasture with limited concentrate supplementation. However, less than 2% of the national population of early maturing dairy cross heifers are slaughtered in this system while approximately 23% are over 30 months of age at slaughter. Such systems greatly reduce the stocking rate and increase housing requirements. Hence, the objective of this experiment, conducted at the Johnstown Castle Research Centre, was to investigate the performance of Aberdeen Angus × Holstein-Friesian (AAX) and Hereford × Holstein-Friesian (HEX) heifers, slaughtered off pasture, in 19 month (19MO) and 21 month (21MO) production systems.

Materials and Methods

Thirty-two February born early maturing heifer calves; 16 AAX and 16 HEX were purchased at approximately three weeks of age in spring 2011 and artificially reared on milk replacer until weaning. A 2 (19MO and 21 MO of age at slaughter) × 2 (breed type) factorial experiment was established. During the first season at pasture calves were rotationally grazed and supplemented with 1.5 kg of concentrate dry matter (DM) per day. Animals were housed on 1 December 2011 and offered silage *ad-libitum* (710 g/kg DMD) with 2 kg of concentrate DM. Animals were turned out to pasture 13 February 2012 and grazed as a single herd until the finishing period commenced. Average pre-grazing sward height was 113.0 (s.d. 14.8) mm and 43.6 (s.d. 10.99) mm post grazing, measured using a rising plate meter. Heifers were separated on 27 July 2012 and animals in the 19MO production system commenced their finishing period. Heifers in the 21MO production system remained on a pasture only diet until 4 September 2012. Heifers were allocated 2.5 kg of concentrate DM daily for 56 days before slaughter and were group fed during the finishing period. The concentrates offered consisted of 580 g/kg barley, 260 g/kg pulp, 100 g/kg soya bean meal, 40 g/kg molasses and 20 g/kg minerals. Animals were weighed fortnightly throughout the study. Heifers in the 19MO and 21MO production systems were slaughtered in September and November 2012, respectively. Data were analysed using the Generalized Linear Model (Proc GLM) statement of SAS. Fixed effects for production system and genotype were used to analyse the data. Least square means was used in the procedure to discern the difference between the production systems and breed groups. The interaction between production system and genotype was tested and found not to be significant so it was removed from the model.

Results and Discussion

Average daily gain at pasture and during the finishing period were similar for heifers in the 19MO and 21MO production systems (Table 1). No significant difference was observed for live weight at slaughter, carcass weight, kill out proportion, conformation score and fat class for heifers in the two production systems. With the exception of fat class, which was greater with the HEX compared with the AAX (P<0.05), no difference in performance was observed between the breeds.

Table 1: Performance of early maturing heifers in 19 and 21 month production systems

	Production system				Breed group			
	19 months	21 months	s.e.[1]	P-value	AAX	HEX	s.e.	P-value
ADG[2] at pasture (kg)	0.80	0.75	0.021	0.129	0.77	0.79	0.021	0.486
ADG during finishing (kg)	0.83	0.72	0.040	0.066	0.75	0.80	0.040	0.390
Slaughter weight (kg)	454	474	9.0	0.116	455	473	9.0	0.152
Carcass weight (kg)	228	240	4.9	0.085	229	239	4.9	0.146
Kill out proportion (g/kg)	502	507	2.6	0.221	503	505	2.62	0.530
Conformation score (1-15)	5.00	5.25	0.202	0.389	5.13	5.13	0.202	1.00
Fat class (1-15)	7.94	8.31	0.384	0.495	7.56	8.68	0.384	<0.05

[1] weighted standard error of the mean, [2] ADG=average daily gain

Conclusion

Results from this study indicate similar animal performance from the 19MO and 21MO production systems. The data presented also suggests no difference in performance between Aberdeen Angus and Hereford breeds at pasture. However, further research is warranted with the use of larger numbers to discern differences between the breed types.

Acknowledgements

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RMIS Project Number 6164

How does co-product allocation affect the carbon footprint of a high performing grass-based milk production system?

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Introduction

In the aftermath of the FAO (2006) "Livestock's Long Shadow" report there has been an increasing policy focus on quantifying greenhouse gas (GHG) emissions from milk and meat production. Consequently, there has been a widespread industry interest in determining the GHG emission from the life cycle (carbon footprint) of livestock products. The recent focus on product carbon footprints has resulted in a number of initiatives on developing standards to harmonise carbon footprint calculations (ISO, 2006; BSI, 2008; IDF, 2010). However, the standards do not agree on methods to allocate GHG emissions between co-products of multifunctional systems, which may significantly affect product carbon footprints. Therefore, the purpose of this study was to assess the effects of a number of allocation approaches on the carbon footprint of a high performing grass-based milk production system.

Materials and Methods

The carbon footprint of a high performing grass-based milk production system was calculated using a dairy farm GHG model (O'Brien et al., 2011). The data used to model the grass-based system was based on the 5-yr research study of Horan et al. (2005) conducted at Moorepark. The grass-based system consisted of New Zealand Holstein Friesian cows that were turned out to grass in early February and housed in mid-November. On average cows received 325 kg concentrate DM and were stocked at 2.74 cows/ha with N fertiliser applied at 250 kg/ha.

The GHG model was used to estimate all GHG emissions from the grass-based system: carbon dioxide (CO_2), nitrous oxide (N_2O), methane (CH_4) and F-gases. The model operates in combination with the Moorepark Dairy System Model (Shalloo et al., 2004), which provides the key parameters (e.g. feed rations) required for the GHG model to estimate emissions. The GHG model quantifies emissions of dairy systems using the life cycle assessment (LCA) method, which calculates emissions from all on and off-farm activities associated with milk production up to the point where milk is sold from the farm e.g. includes emissions from the manufacture of purchased inputs such as fuel. The model estimates emissions in terms of their 100-yr global warming potentials (CO_2-eq), which on a weight basis relative to CO_2 was set to a factor of 25 for 1 kg of CH_4 and 298 for 1 kg of N_2O (IPCC, 2007). The main output of the GHG model is a static account of dairy systems annual emissions, and the carbon footprint of milk production expressed per kg of energy corrected milk (ECM). In addition to producing milk, dairy farms also produce meat from culled cows and surplus calves. Therefore, GHG emissions should be distributed between these outputs. The following six approaches were used to allocate GHG emissions between milk and meat; 1) Milk – all to milk, 2) Mass – to the mass of milk and meat, 3) Economic – to the value of milk and meat (BSI, 2008), 4) Energy – the feed energy needed to produce milk and meat based on IDF (2010), 5) Emission – emissions from surplus calves, dairy females <2 yrs and from finishing culled cows were attributed to meat with the rest assigned to milk, 6) System Expansion – emissions from suckler beef are subtracted from the GHG emission generated by milk and the equivalent quantity of meat from a dairy system (ISO, 2006). The meat from a dairy system for system expansion includes surplus dairy calves raised for beef.

Results and Discussion

The result show, when the 100% allocation to milk scenario was excluded, that Mass and Economic allocation attributed the most GHG emissions directly to milk production (94-98%) followed by Energy and Emission approaches (87-88%). System Expansion attributed the least emissions to milk production (60%), because the emissions associated with producing beef from the dairy herd (13.1 kg CO-eq/kg carcass weight (CW)) were significantly lower than the suckler herd (20.4 kg CO_2-eq/kg CW). The large differences between the results shows that comparisons of product carbon footprints are confounded when different allocation procedures are followed.

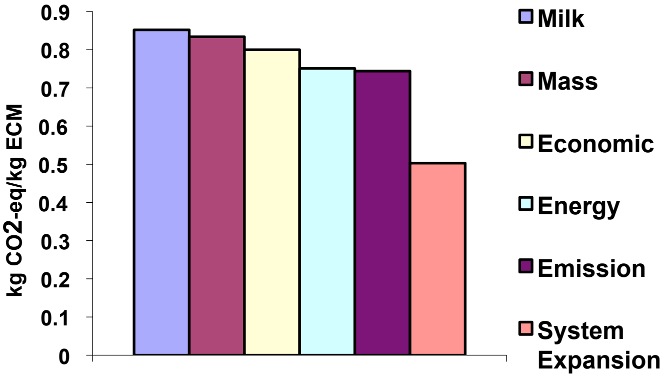

Fig. 2. The effect of allocation method on the carbon footprint of a high performing grass-based dairy system.

Conclusion

This study shows that the carbon footprint of milk production cannot be compared when different allocation methods are used. Therefore, a single procedure needs to be agreed to facilitate a valid comparison of the carbon footprint of milk.

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RMIS Project Number 6241

The impact of mastitis on the profitability of Irish dairy farms

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Introduction

Mastitis has been identified as one of the most economically relevant diseases in dairy cattle for Irish dairy farmers by Animal Health Ireland. The economic losses associated with mastitis are often underestimated at the farm level due to the returns that the farmer fails to realise, like reduced milk production and lower herd growth potential. Internationally, a large body of work has been completed estimating the costs associated with mastitis at farm level but this research has not been undertaken in Ireland. The objective of this study was to estimate the impact of mastitis on the profitability of Irish dairy farms.

Materials and Methods

The cost components associated with mastitis accounted for in this analysis were (1) reduced milk production, (2) culling, (3) treatment of clinical and (4) treatment of subclinical mastitis cases, (5) veterinary visits, (6) discarded milk, and (7) milk price penalties. These cost components were incorporated into the Moorepark Dairy Systems Model (MDSM) (Shalloo et al., 2004). The MDSM estimated the total costs, total milk receipts, and net farm profit for an average dairy farm of 40 ha across 5 somatic cell count (SCC) categories, ≤100,000, 100,001–200,000, 200,001–300,000, 300,001–400,000, and >400,000 cells/ml. The impact of SCC on milk production used in this analysis was based on a study completed by Kelly (2009). Kelly (2009) examined the association between SCC and milk yield across parities with 237,695 test day records. The estimated milk production loss per cow over the length of the lactation (280 days) for each SCC category was 177, 351, 485, 544 and 601 litres for ≤100,000, 100,001–200,000, 200,001–300,000, 300,001–400,000, and >400,000 cells/ml, respectively. The clinical and subclinical mastitis cases treated and treatment practices across each of the SCC categories were estimated from a number of data sources: Herd Ahead Survey, ICBF database and the Mastitis Farm Practice Survey. Using this data it was estimated that at a SCC of <100,000 cells/ml, 11% of the herd were treated for clinical mastitis increasing to 38% of the herd at a SCC of >400,000 cells/ml. Treatment for subclinical mastitis was low at 1% of the herd at a SCC of <100,000 cells/ml and >400,000 cells/ml. Treatment costs including intramammary tubes, injectable antibiotics, pain relief and veterinary attention were accounted for in the analysis. The culling rates due to mastitis were estimated from the Mastitis Farm Practice Survey and the ICBF database. The proportion of the herd culled due to mastitis increased as SCC increased, increasing from 3% of the herd at a SCC of <100,000 cells/ml to 13% of the herd at a SCC of >400,000 cells/ml. All costs included in the analysis were based on up-to-date industry costs and prices.

Results and Discussion

Physical outputs

As SCC increased, milk sales decreased from 532,122 kg at a SCC of <100,000 cells/ml to 513,596 kg at a SCC of >400,000 cells/ml. Cull cow sales increased from €6,990 at a SCC of <100,000 cells/ml to €11,497 at a SCC of >400,000 cells/ml. When both the voluntary and involuntary culling rates were included in the analysis the replacement rate was 19% at a SCC of <100,000 cells/ml increasing to 28% at a SCC of >400,000 cells/ml with an associated heifer replacement cost of €25,550 and €40,709, respectively.

Financial outputs

As SCC increased milk receipts decreased, reflecting the decrease in milk sales and replacing high producing multiparous cows with primiparous cows. Livestock receipts increased due to the increased replacement rate and the associated cull cow value. However, overall there was a decrease in total farm receipts of €3,056 as SCC increased from <100,000 to >400,000 cells/ml. As SCC increased from <100,000 to >400,000 cells/ml total farm costs increased by €16,258; this increase in costs was associated with increased purchasing of replacement heifers and treatment costs. This resulted in a decrease in total farm profitability of €19,504 as SCC increased from <100,000 to >400,000 cells/ml. Culling and purchasing of replacement heifers accounted for 46% of the total costs of mastitis, reduced milk production 36%, penalties 10% and diagnostic testing, treatment and veterinary attention accounted for 8% of the costs of mastitis.

Table 1. Impact of SCC on farm receipts, farm costs and net farm profit

	SCC (,000 cells/ml)				
Financial Outputs	<100	100-200	200-300	300-400	>400
Total farm receipts, €	192,147	191,617	192,342	190,431	189,091
Total farm costs, €	161,085	164,994	172,749	173,536	177,343
Net farm profit, €	31,252	26,771	19,661	16,936	11,748

Conclusion

Mastitis resulted in a considerable reduction in net farm profit. Quantifying the costs of mastitis to demonstrate the losses occurring on Irish dairy farms is an important step in motivating farmers to acknowledge the scale of the problem and implement effective management practices.

Acknowledgements

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RMIS Project Number 6283

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