



Moorepark Research Report 2011

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***Teagasc Animal & Grassland Research and
Innovation Centre,
Moorepark,
Fermoy,
Co. Cork***

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INTRODUCTION

The worldwide demand for dairy products is expected to increase by 2.5% per annum as a result of global population growth and projected increases in per capita disposable income. The gradual expansion and ultimate removal of milk quotas in 2015 gives Ireland the opportunity to claim a disproportionate share of this growth. To ensure success Irish dairy farmers must act now to develop their farm systems by planning for increased milk production while at the same time cushioning against the potential volatility that is expected in milk price. The Food Harvest 2020 document predicts a 50% increase in milk production deliveries by 2020. A rise from an average of 5.1 billion litres over the 2007 to 2009 period, to 7.66 billion litres in 2020 is anticipated. In addition to productivity increases, this will necessitate an increase in the size of the national herd from its current 1.1 million to about 1.4 million dairy cows. This additional production, combined with value added at the processor level, is expected to be worth in excess of €1 billion to the Irish agri. economy. Any expansion in the dairy farm business should only be undertaken if it increases profit and provides a better lifestyle to the farm family. When EU milk quota is abolished farm profitability will be dependent on profit per hectare being maximised.

In 2011, there were over 1.1 million dairy cows producing milk on 18,548 Irish dairy farms. Total Irish milk output amounted to around 5.6 billion litres of milk with an estimated farm gate value of €1.8 billion. Exports of Irish dairy products and ingredients were valued in the order of €2.7 billion, making Ireland the 10th largest dairy export nation in the world. 2011 was a very successful year for the Irish dairy industry driven by relatively high milk price and favourable climatic conditions. Based on the National Farm Survey, there were approximately 15,600 specialist dairy farms with an average Family Farm Income of €68,570, a 36% increase on 2010. The income increase was entirely market driven with market gross output up 15% on dairy farms as the annual milk price increased by 15%. The value of direct payments on dairy farms comprised just 13% of total output and 34% of income. Direct costs on dairy farms increased by 9%, mainly due to increases in fertiliser, hire of machinery, vet and AI costs. Total overhead costs were unchanged, while some components increased, especially energy based costs, charges associated with buildings depreciation declined in line with the reduction in construction/building replacement costs. Just over 23% of dairy farms earned €30,000 or less, while 22% earned €100,000 or more.

The following are the main highlights from the 2010 programme:

Curtins Stocking Rate Farm Systems Research Study

A two-year whole-farm system study compared the accumulation, utilization and nutritive value of grass in spring-calving grass-based systems differing in stocking rate (SR) and calving date (CD). Six treatments (systems) were compared over two complete grazing seasons. Stocking rates used in the study were low (2.5 cows ha⁻¹), medium (2.9 cows ha⁻¹) and high (3.3 cows ha⁻¹) respectively, and mean CD were 12 February (early) and 25 February (late). Each system had its own farmlet of 18 paddocks and one herd that remained on the same farmlet for the duration of the study. Stocking rate had a small effect on total herbage accumulation (11,860 kg DM ha⁻¹ year⁻¹) and but had no effect on total herbage utilization (11,700 kg DM ha⁻¹ year⁻¹). Milk and milk solids (MS; fat + protein) production per ha increased by 2 580 kg ha⁻¹ and 196 kg ha⁻¹ as SR increased from 2.5 to 3.3 cows ha⁻¹. Milk production per ha and net herbage accumulation and utilization were unaffected by CD. Winter feed production was reduced as SR increased. Increased SR, associated with increased grazing severity, resulted in swards of increased leaf content and nutritive value. The results indicate that, although associated with increased milk production per ha, grazed grass utilization and improved sward nutritive value, the potential benefits of increased SR on Irish dairy farms can only be realized if the average level of herbage production and utilization is increased.

Study of New Entrants to the Irish Dairy Industry

As part of the gradual expansion and abolition of EU milk quotas, the Irish government has approved the allocation of milk quota to a small number of new entrants to dairy production. The objective of this study was to describe the characteristics of new entrant dairy farm businesses developing within the Irish dairy industry in terms of geographical distribution, planned production system characteristics and intended operational scale and expected profitability based on an analysis of successful applications and business plans to the Irish New Entrant Dairy Scheme over a 3 year period. A total of 230 applications and business plans of entrants who received up to 200,000 litres of milk quotas through the New Entrant Scheme from 2009-2011, were analysed for the effects of region, age, household income, previous dairy experience, and education on overall business plan expectations. The results show that a youthful and highly educated group of new farmers are using the New Entrant Scheme to enter the Irish dairy industry. Ninety-three percent of new dairy entrants have at least two years of formal 3rd level agricultural education and have detailed plans to become relatively large scale and efficient milk producer's post-EU milk quota abolition. Region, education and dairy experience had no effect on the expectations and intentions of new entrants to dairying. In contrast, applicant age has a significant impact on business plans and expectations, as younger entrants have less owned resources, are increasingly reliant on additional borrowing and have significantly increased expectations for the productive capacity of their potential farm businesses when compared to older entrants.

The results provide a further indication that quota abolition is likely to result in an increased regional polarisation of milk production within Ireland with increased intensity of production within traditional milk production areas in the south.

Colostrum studies

Provision of good quality colostrum is a fundamental part of rearing healthy calves. Colostrum quality is determined by the quantity of IgG (immunoglobulins) present. Literature has deemed high quality colostrum as that which has an IgG concentration greater than >50mg/ml. In a study completed at Teagasc Moorepark IgG concentration of colostrum (i.e. first milking) was determined from 704 dairy cows of varying breed and parity. Samples were collected from a further group of cows to look at the deterioration of IgG concentration in colostrum over time. The average IgG concentration was 112 mg/ml, with a range of 13 to 257 mg/ml. This means that almost 96% of the samples were classified as high quality colostrum (>50mg/ml) which has good implications for Irish dairy farmers. Cows in later lactations produced colostrum with higher IgG concentration than those in earlier lactations even when differences in milk yield at the time of milking were accounted for. The highest quality colostrum was obtained from cows in their fifth lactation, however the quality of colostrum from the majority of heifers was also deemed to be high quality and should not be automatically discounted. IgG concentration increased as time interval from calving to milking decreased which implies that colostrum should be collected from the cow as soon as possible post-calving in order to maximise colostral IgG concentration. In general, higher yielding cows also tended to have poorer quality colostrum due to dilution of colostrum IgG. Month of calving was also associated with colostrum quality, cows that calved later in the spring (April and May) produced colostrum with a lower IgG concentration than cows that calved in the earlier months (January to March) and cows that calved from August to December. IgG concentration in milk declined rapidly with each successive milking post-calving, the concentration at least halving between first and second milking. Only the colostrum from the first milking had an IgG concentration above the threshold of 50mg/ml IgG which is used to classify colostrum as good quality which highlights the importance of using only the colostrum obtained at the first milking as a source of colostrum for newborn calves.

National genetic evaluations and the EBI

A major revision of the national genetic evaluations for fertility in Irish dairy cattle was completed in 2011. This revision saw the expansion of the number of lactations included in the genetic evaluation from 3 to 5 as well as the incorporation of insemination data (i.e., calving to first service and number of services). These insemination traits replaced milk yield as predictors of calving interval thereby facilitating the identification of high yielding, fertile cows. The end result was more accurate genetic evaluations for female fertility. Research for the first ever implementation of a national male fertility and AI technician fertility evaluation was completed in 2010 and implemented in 2011. This evaluation provides up-to-date knowledge on bull fertility as well as the performance of individual AI technicians after accounting for confounding effects including the inherent fertility of the cow herself and her days since calving. Research on the genetic of calf price based on mart data was completed in 2011 which will be implemented in the EBI in 2012. Calf price at 28 days is more reflective of the future reality in Irish dairy herds and therefore the EBI will become more pertinent to the Irish dairy farm of the future. Research on the exploitation of the digital images taken of all Irish carcasses for use in national genetic evaluations was also completed in 2011 which will be implemented into national genetic evaluations in 2012. These images are used to more accurately define the value of the carcass thereby increasing the accuracy of genetic evaluations. A national breeding programme strategy through Gene Ireland was developed. Algorithms developed to derive contract matings were further refined and re-implemented in 2011. The overall outcome of this research is to increase long-term genetic gain in Ireland through retention of genetic diversity. The first ever national genetic evaluation for linear type traits was also completed and sent to INTERBULL for validation in 2011. These proofs were released nationally through ICBF in 2012. Research on improving the genetic evaluation through a superior statistical model and genetic parameters based on Irish data was completed in 2011. A validation exercise was undertaken in 2010 relating herd average EBI to Profit monitor data. The results showed that the difference in profit per lactation per unit change in EBI was within the expectation of €2 profit per lactation per 1 unit increase in EBI.

Trichloromethane (TCM) levels in milk

Trichloromethane (TCM) levels in butter are an important market-driven concern for the dairy industry at present. TCM residue develops in milk (concentrated in the fat fraction) due to interaction between chlorine (in the milking machine/bulk tank cleaning process) and milk. TCM levels in Irish butter have always been well within legal requirements but European competitors and consumers are requiring a minimum level of 0.03mg/kg. To maintain a position of dominance in the butter market, it is necessary to reduce TCM levels in butter to 0.03mg/kg, which effectively means reducing TCM levels in milk to <0.002mg/kg. An industry-funded project at Teagasc has addressed this issue in recent years and significant progress has been achieved. TCM levels in Irish butter were reduced from 0.07 mg/kg in 2007 to 0.03 mg/kg in 2011. This was achieved through farm visits to identify incorrect practices, advice on the correct practices allied with a vigorous advisory campaign through Teagasc and the dairy companies and, most importantly, an intensive analysis programme. The most influential factors on milk TCM level included the detergent product type,

correct volume of detergent product used, sufficient rinse water volume used both before and after wash cycle, not re-using detergent solution more than once and taking similar precautions in washing the bulk tank as milking machine. Routine screening for TCM in both tanker milks and individual suppliers' milk resulted in analysis of approximately 25,000 milk samples during 2011.

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ANIMAL RESEARCH PROGRAMME

Genetic Improvement of Animals

Characterisation of the sequence variation in genes of the somatotrophic axis in DNA pools from cattle divergent for carcass weight

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Introduction

The somatotrophic axis is well established as central to post-natal growth and development in mammals. In domestic livestock the influence of this axis on traits of commercial importance such as body size, carcass weight, milk yield and fertility has been widely published. While there is evidence from our own research (Mullen et al. 2010; 2011) that variation in genes of the somatotrophic axis are associated with production traits in cattle, there is a dearth of information on the effect of causal polymorphisms in genes of this axis and its regulators on animal performance. Sequencing large numbers of complete genomes would prove an invaluable resource for causal polymorphism identification; however this is currently not feasible primarily due to the costs involved. A DNA pooling approach coupled with targeted genome enrichment, prior to high throughput sequencing is a cost effective alternative. The accuracy of allele frequency estimates generated using this approach has recently been demonstrated (Mullen et al. 2012). The aims of this study were: (1) to identify putative coding and regulatory DNA sequence polymorphisms in candidate genes of the somatotrophic axis, and (2) to estimate allele frequency differences at these loci between dairy bulls divergent for genetic merit for carcass weight, using DNA pooling, target enrichment and high-throughput sequencing approaches.

Materials and Methods

DNA from semen samples of 150 Holstein-Friesian (HF) bulls, available through artificial insemination, were divided into two groups divergent for genetic merit for carcass weight while also simultaneously minimising the co-ancestry within each group.

Targeted genes ($n = 83$) included hormones, transcriptional regulators, binding proteins and genes involved in gluconeogenesis and insulin nutrient partitioning-related pathways.

For both sample groups, DNA was pooled using equimolar DNA quantities from each individual animal. The Agilent SureSelect® Target Enrichment System was used to selectively capture whole gene and regulatory DNA sequences for the 83 somatotrophic axis genes, followed by sequencing using the Illumina GAII platform. All DNA sequence data were aligned using the *B. taurus* UMD3.1 reference genome and the BWA aligner software package. DNA sequence polymorphisms were identified using the SAMtools package. A minimum of four non reference allele reads was required to identify polymorphisms across both groups.

Results and Discussion

In total, ~ 10 million reads spanning ~ 2 Megabases (Mb) of sequence data were generated. A total of 4,132 SNPs and 756 indels with on average 53-fold coverage were identified across the 83 genes. Thirty-one percent ($n=1288$) of SNPs identified were located within putative regulatory regions in the 5' and 3' UTR. Fifty-eight percent ($n=2,414$) were intronic and the remaining 7% ($n=313$) were exonic, of which 4% ($n=172$) were non-synonymous (NS) substitutions. In total, 196 SNPs showed a greater than two-fold allele frequency differential between the low and high carcass weight cattle groups. Table 1 shows four examples of this SNP category.

Table 1. Four SNPs in Holstein-Friesian cattle divergent for carcass weight (CWT). The frequency of the second allele is shown for each SNP

Entrez Gene ID	Chr.	Location within gene	SNP	High CWT freq	Low CWT freq
<i>GHR</i>	20	Intron	A / G	0.60	0.14
<i>IGF1</i>	5	Intron	A / T	0.44	0.20
<i>GH1</i>	19	Exon (NS)	G / A	0.72	0.35
<i>IGF2R</i>	9	Intron	T / C	0.71	0.21

We previously observed associations between carcass weight and variants in *GHR* and *IGF1* (Waters et al. 2012). Our previous studies encompassed sequence analysis of limited regions of each gene investigated

but the polymorphisms presented herein were identified across entire genes and regulatory regions. Therefore it is probable that a subset of these polymorphisms underlie heritable variation in carcass weight.

Conclusions

This study has identified novel variation and allele frequencies of key genes involved in growth and development in cattle. Future work will include genotyping, association analyses as well as *in vitro* testing to identify candidate causal polymorphisms affecting performance in cattle. The ultimate objective will be to validate in independent populations including beef breeds and determine their contribution to genetic variation for carcass weight.

Acknowledgements

M.P.M. was funded through an SFI grant (07/SRC/B1156).

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RMIS Project Number 5666

Predicting energy balance of Holstein-Friesian cows using mid-infrared spectrometry of milk

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Introduction

The main hindrance to the inclusion of energy status (ES) in multi-trait genetic evaluations as a predictor of health and fertility is the difficulty and expense of energy intake data collection on large numbers of animals. Recently, the mid-infrared spectrum (MIR) of milk, the method of choice worldwide to routinely predict milk composition, was proposed as an indicator of ES (McParland et al., 2011). The objective of this study was to test the robustness of the equations developed to predict ES across independent populations of indoor-fed and grazing Holstein-Friesian dairy cows.

Materials and Methods

Performance data collected between 1990 and 2011 from two separate research herds were used in this study; data from the Scottish Agricultural College research herd (SAC) and data from the Teagasc Moorepark research herd (MPK). The SAC herd comprised 1,218 cows divided into two dietary treatments, high concentrate and low concentrate. The MPK data set comprised 1,586 animals of differing strains of Holstein-Friesian on a predominantly grazed grass diet with periodic concentrate supplementation. Random regression models were fit, within parity, and within country, to routinely collected dry matter intake (DMI) (SAC only), milk production, body weight (BW) and body condition score (BCS) records to generate daily solutions for each trait and ultimately calculate ES for each day of lactations 1 to 4. Energy status was computed for MPK animals only during periods of lactation where actual DMI was recorded. Energy balance (EB; MJ/d), was computed as a function of milk yield, fat and protein content, DMI, BW and BCS. Energy content (EC; MJ) was computed as a function of BCS and BW predicting body lipid and protein weight.

Morning (MPK(am)) and evening (MPK(pm)) milk samples from MPK animals were analysed weekly using a Foss MIR spectrometer. Morning (SAC(am)), midday (SAC(md)) and evening (SAC(pm)) samples from SAC animals were analysed monthly using the same MIR spectrometer. The Foss MIR spectrum contains 1,060 data points which represent the absorption of infrared light by the milk sample at wavelengths in the 900 cm⁻¹ to 5,000 cm⁻¹ region. Only spectral data with an actual phenotypic record for all component variables of EB within 7 days of the corresponding milk sample were retained. Spectral data were transformed from transmittance to linear absorbance through a log₁₀ transformation of the reciprocal. In total, 820 MPK(pm) and 844 MPK(am) spectral records from 244 MPK cows with EB data were available together with 2,989 SAC(pm), 2,992 SAC(am) and 2,742 SAC(md) records from 337 SAC cows.

Partial least squares regression was used to predict ES from the MIR linear absorbance data. Predictor variables included a subset of wavelengths from the spectrum of 1,060 correlated wavelengths, together with

milk yield. All prediction equations were undertaken using am, md (where available), and pm samples, separately. Accuracy of all equations was tested using both split sample cross-validation and external validation. Two types of analyses were undertaken: 1) prediction equations were calibrated within the SAC data set and externally validated on the MPK data set, and 2) the two research data sets were combined and equations calibrated and validated using the combined data set. When equations were calibrated and externally validated using the combined data set, the data were sorted according to ES and every fourth record removed from the calibration data set for inclusion in the external validation data set. This was done to optimise the robustness of the prediction equation, since samples contained in the calibration data set should represent the variation observed in the phenotype to be predicted.

Results and Discussion

Prediction equations calibrated using data from SAC only, were not useful to predict either EB or EC of MPK animals. External validation accuracies ranged from 0 to a maximum of 0.15 for both sets of equations. The slope between true and predicted EB was close to 0 while the bias was greater than 40 MJ for all equations tested across research data sets. Similarly, the slope and bias between true and predicted values of EC was poor across all equations tested. Prediction equations developed using pooled data from SAC and MPK research data sets were more robust than equations tested across research data set. Combined prediction equations had an accuracy of prediction of EB of 0.69, and had a slope (se) from the regression of true on predicted values of EB of 0.98 (0.03), whilst the mean bias (se) between true and predicted values of EB was 1.12 (0.88) MJ. Very high accuracy of prediction was not expected given the inherent errors in calculation of “true” energy balance. The accuracy of prediction of EC was lower than that of EB, however was more robust when equations were tested across research data set.

Conclusion

Equations have been developed which give accurate predictions of energy balance across lactation using the MIR spectrum of milk. Although equations developed on one production system are not robust to predict energy balance of animals on a different production system, when a combined data set across production systems was used, results were greatly improved.

Acknowledgements

The RobustMilk project is financially supported by the European Commission under the 7th Research Framework Programme, Grant Agreement KBBE-211708

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RMIS Project Number 5791

Multi-breed beef genomic selection

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Introduction

Genomic selection was officially included in the Irish national dairy cattle genetic evaluations in spring 2009, with an increased accuracy of selection anticipated (Berry et al., 2009). Since 2009 approximately 40% of semen sold annually was from genomically selected sires. Retrospective analysis clearly shows an increased accuracy of selection using genomic selection in Irish dairy cattle (Cromie et al., 2011). The objective here was to evaluate the potential of genomic selection to increase the accuracy of selection in Irish beef cattle.

Materials and Methods

Genotypes of 777,962 single nucleotide polymorphisms (SNPs) were available on 2,544 Holstein-Friesian, Charolais, Limousin, Angus, Hereford and Simmental beef bulls. Only animals and SNPs with a genotype call rate >95% were retained. Also, both autosomal SNPs and animals with >2% Mendelian inconsistencies between parent-offspring pairs were discarded. Non-autosomal SNPs, as well as SNPs with a minor allele frequency <2%, poor call clustering, and those deviating from Hardy-Weinberg equilibrium ($P < 0.1 \times 10^{-7}$) were discarded. Following all edits 533,463 SNPs from 1,834 beef animals remained, consisting of 587 Limousin, 559 Charolais, 237 Simmental, 236 Angus and 215 Hereford bulls.

The pedigree of each animal was traced back at least four generations, where available. Estimated breeding values (EBV) and associated reliability estimates, for all animals and their parents were obtained for carcass weight, carcass conformation and carcass fat score from the Irish domestic genetic evaluation in August 2011. Estimated breeding values were de-regressed and parental contribution was subtracted from the reliability of each animal. Only bulls with at least 40% reliability (following removal of parental contribution) for the trait under investigation were retained for inclusion in the estimation of SNP effects. A random sample of animals, within breed, was chosen for validating the SNP effects and are referred to as the “validation animals”; the remaining animals, referred to as the “training animals”, were used to estimate the SNP effects. An additional group of animals with a reliability of <40% were used to quantify the expected reliability of direct genomic values as well as the weighting on genomics within their genomic breeding value. The genomic relationship matrix was estimated, within breed, by regressing Z'Z on the numerator relationship matrix and scaling the Z'Z matrix with the resulting intercept and regression coefficient from the model; the Z matrix (number of animals by number of SNPs) contained the alleles for each locus as -1 (homozygous), 0 (heterozygous) and +1 (homozygous). Direct genomic values were subsequently estimated as $D\hat{G}V = G * (R + G)^{-1} \tilde{y}$, where G is the genomic relationship matrix among the training animals and G* is the genomic relationships between the validation animals and the reference animals; R is a diagonal matrix containing one divided by the animal's reliability from his daughters less one and $\tilde{y}$ is the deregressed EBV for the trait under investigation.

Results and Discussion

The number of animals in the training population for Charolais, Limousin, Hereford, Angus and Simmental were 371, 393, 124, 151, and 157, respectively. The correlation between the pairwise expected relationships (i.e., from the numerator relationship matrix) and the actual genomic relationships (i.e. from the genomic relationship matrix) varied across breeds from 0.65 to 0.83, most likely suggesting a combination of discrepancies in the recorded pedigree but also the ability of the genomic relationship matrix to capture Mendelian sampling. The mean genomic reliability per breed varied from 17% in the Angus to 27% in the Simmental; the mean weighting on genomics in the genomic breeding values varied from 6% (Angus) to 14% (Simmental). The contribution of genomics to the genomic breeding value of an animal was not only dependent on the size of the training population but also on the relatedness of the young animals to the training population, signifying that genomic selection in the present study at least, was more than likely more accurately tracing relationships rather than quantitative trait loci *per se*. Sufficient validation bulls for Angus, Simmental and Hereford did not exist to generate a meaningful analysis of the accuracy of genomic selection. The correlations between direct genomic values, with a reliability >40%, and traditional estimated breeding values, with a reliability >80%, for the different carcass traits varied from 0.39 to 0.66 in the Charolais and between 0.31 and 0.47 in Limousin. However there were few animals in the comparison.

Conclusions

Genomic information can contribute to the accuracy of selection in beef animals. However, the increase in accuracy in the present study was modest, predominantly due to the relatively small size of the training populations. More genomic information on phenotyped animals is required.

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RMIS Project Number 5883

Genes associated with angularity in dairy cattle are associated with obesity in humans

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Introduction

Despite substantial research into the genetic basis for variation in traits of importance to human populations much less research has been undertaken in identifying the functions of bovine genes. Through comparative genome analysis, the research undertaken to understand the functions of human genes can be exploited by cattle breeders. The aim of this study was to identify bovine genes associated with angularity, a genetically similar trait to body condition score (BCS) and to identify novel genes for future obesity studies of mammals.

Materials and Methods

Angularity, a linear type trait classified on dairy animals refers to the “angle and openness of the ribs, combined with flatness of bone”. The strong negative genetic correlation between angularity and BCS (Berry

et al., 2004) indicates that these traits are genetically similar. Estimated breeding values, and associated reliability, for angularity were provided by the Irish Cattle Breeding Federation (ICBF). Parental contribution to the reliability of each breeding value was removed. Only bulls with an adjusted reliability for any type trait greater than 30% were included in the analysis. Breeding values were de-regressed to be independent of the relationship between animals included in the evaluations, and reverse the shrinkage of breeding values in the mixed model equations.

Holstein-Friesian bulls (n=5,736) were genotyped with the Illumina BovineSNP50 Beadchip (Illumina Inc., San Diego, CA). All genotyped bulls were previously, or are currently available for widespread use through AI in Ireland. A total of 230 single nucleotide polymorphisms (SNPs) were removed due to an observed Mendelian inconsistency rate greater than 0.50%. SNPs with a minor allele frequency <5% (n=7,947), or where greater than 5% of calls were missing (n=1,073) or deviated from Hardy-Weinberg equilibrium (n = 1,755) were removed from the analyses. All SNPs were bi-allelic and were recoded as 0, 1 or 2 according to the number of alleles present at each locus. The final data set comprised 42,996 SNPs from 1,396 bulls with a breeding value for angularity. Single SNP regression analysis was performed in ASReml (Gilmour et al., 2006) using a linear mixed animal model to detect the regions of the genome associated with angularity. Fixed and random effects accounted for in the mixed model were the SNP genotype of the animal and the animal, respectively. A pedigree file, five generations deep, was generated using data obtained from the ICBF national database and contained 6,320 animals. The dependent variable was weighted by its adjusted reliability. The Bonferroni correction was applied.

The Ensembl SNP identifier and gene location of SNPs were obtained using the BioMart interface to the Ensembl database. SNPs located in inter-genic regions were discarded from the analyses. Orthologous genes in *Homo sapiens* were also obtained from BioMart. Due to the strong association between angularity and BCS in cattle, the literature was reviewed and online data bases (eg. OMIM) used to identify a) genes in *Homo sapiens* associated with obesity and bone quality traits and b) biological associations between human orthologs of angularity-associated bovine genes and phenotypic variation in humans.

Results and Discussion

The Bonferroni correction resulted in lowering the statistical significance threshold for the P-value to $P < 0.000001$. 262 SNPs within 78 genes across the bovine genome were associated with angularity (Figure 1). SNP rs110342629 (b=-0.99), located on chromosome 19 had the highest probability of association ($P = 3.15 \times 10^{-15}$) with angularity.

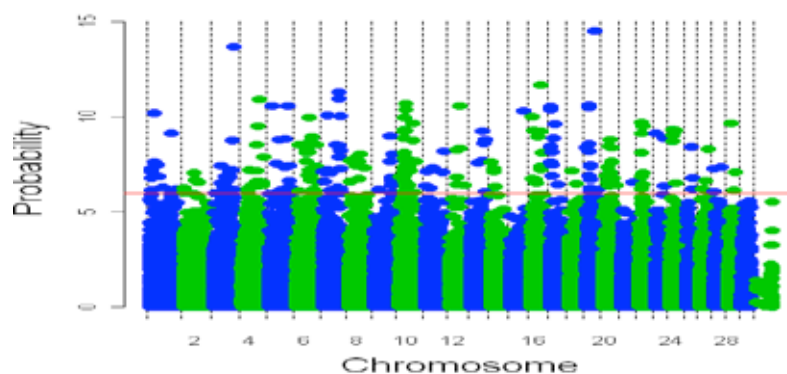


Figure 1. Manhattan plot of the probability ($-\log_{10}(\text{p-value})$) of SNP associations with angularity

Of the 23 genes most strongly associated with angularity ($-\log_{10}(\text{p-value}) > 8.5$), orthologs of 8 of the genes are known to be associated with variation in obesity, obesity linked traits and bone quality traits in mammals. Obesity traits associated with mammalian orthologs identified in this study include obesity (*ARID5B*, *CHCHD3*), fat tissue in mice (*ARID5B*), adipogenesis (*ARID5B*), fatty acid metabolism (*HADH*), insulin resistance (*PDZD2*), diabetes (*CHCHD3*, *RASPG1*), pancreatic function (*PDIF1*), uric acid (*SLC2A9*) and back fat in pigs (*ANO10*). Bone quality traits associated with mammalian orthologs of bovine genes which in turn were associated with variation in angularity include skeletal dysplasia, bone bowing and reduced bone mineral density (*NF1*) and bone erosion (*SLC2A9*). The SNP with the strongest angularity association in this study was located within *FTSJ3*, a gene homologous to the rRNA methyltransferase *FTSJ* involved in growth rate regulation (Ching et al., 2002).

Conclusions

Orthologs of bovine genes associated with angularity, a genetically similar trait to BCS are associated with obesity linked traits and bone traits of mammals. A potential candidate gene for further obesity work in mammals, *FTSJ3*, was identified.

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RMIS Project Number 5883

The effect of dystocia on subsequent performance in dairy cows

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Introduction

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

Materials and Methods

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

Results and Discussion

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

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

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

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

Conclusions

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

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RMIS Project Number 5889

Factors associated with selling price and live weight of Italian calves

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Introduction

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

Materials and Methods

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

Results and Discussion

The vast majority (i.e. 82%) of calves sold were males, and half the calves were sold between 15 and 25 days of age. The correlation between live-weight and price was 0.46 and between live-weight and value was 0.64; both correlations were different ($P < 0.001$) from zero. Herd-year was included ($P < 0.001$) in all models. Male calves were heavier ($P < 0.001$) than females (67 kg vs. 63 kg) and sold for a greater ($P < 0.001$) value (€292 vs. €252). The association between gender and live-weight, price and value (Figure 1), however, differed ($P < 0.0001$) by breed. PR male purebred calves were heaviest (69.6 kg) while BI purebred females were lightest (59.4 kg). Calves destined for beef production were, on average, heavier (69 kg; $P < 0.001$) and

received a greater ($P<0.001$) price and value at sale (€4.60 per kg and €291), compared to those destined for veal production (62 kg live-weight; €3.90 per kg and €253). However, the association between destination and live-weight, price and calf value also differed by breed ($P<0.001$). The majority of beef crossbred and calves from dual purpose dam breeds were destined for beef production while the majority of purebred calves from dairy dams were destined for veal production system. The association between age at sale and live-weight differed by breed ($P<0.001$); age was not associated with either calf price or calf value but both price and value increased ($P<0.001$) at a decreasing rate with live-weight. The association between age and live-weight of calves at sale differed by breed type ($P<0.0001$). Live weight, price and value of calves at sale varied by month of sale due to different supply and demand of calves during the year. Calf price was lowest during the autumn and winter months, when many calves were sold. Calves sold in June were heaviest (66 kg) and received the greatest price and value (€4.60 per kg; € 291) while those sold in December were lightest (64 kg) and received the lowest price and value (€4.00 per kg; € 259) at sale.

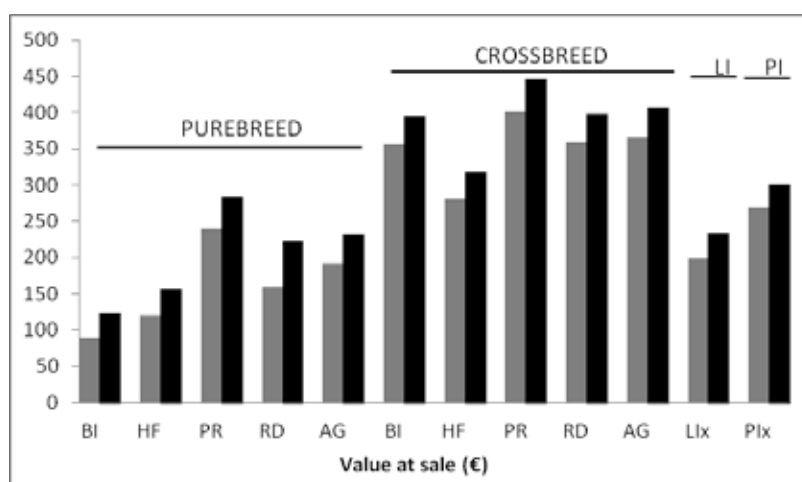


Figure 1. Least squares means of calf value for different breed1 and breed crosses2 by gender (male=black bars; female=grey bars)

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

Conclusions

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

Acknowledgements

The authors thank the Breeders Federation of Trento province for providing the data and the Trento province for funding the research.

RMIS Project Number 5889

Identifying profitable beef bulls for use in Irish dairy herds

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Introduction

Considerable transfer of germplasm occurs between Irish dairy and beef herds. In 2010 approximately 40% of dairy cows were bred to beef bulls, with Angus (14%), Hereford (10%) and Limousin (6%) being the most used breeds. When using beef bulls on their herd, dairy farmers wish to produce an easy calved, good quality, live calf that has little effect on the subsequent lactational performance of its dam. To date, however, dairy farmers have no specific tool to facilitate selection of the most profitable beef bull for use in their herd. The aim of this study was to develop a new breeding index for dairy farmers that will aid in the selection of beef bulls.

Materials and Methods

For the development of any breeding goal, knowledge of three key components is required: 1) traits that influence the breeding goal, 2) genetic parameters of traits included in the selection index; and 3) the optimum economic values for each trait. The traits of interest included in the new index were: calving difficulty, calf mortality, gestation length, and calf price. Heritability estimates for these traits have been calculated using Irish data previously (Berry et al., 2011; McHugh et al., 2011). The economic value for calving difficulty was derived from the costs associated with an increase in the incidence of difficult calvings from 6 to 7%. The economic cost includes the costs of increased stockman hours, veterinary interventions, cow mortality, disposal and infertility as well as of loss in milk sales (McHugh et al., 2012). The economic value for calf mortality was calculated as the cost of calf disposal plus the average value of an equivalent live calf. For gestation length the economic value was calculated as the benefit of a one day shorter calving interval. For each of the three traits described above the projected or current prices and costs were used in the calculation of the economic values. As a monetary value is assigned to each calf the economic value for calf price was implicitly assumed in the breeding value of the calf. Calf price was the average price paid for a calf sold between 2 and 42 days of age within the range of €2 to €450 (McHugh et al., 2011). A proportion of resultant female progeny from the mating of a beef bull to a dairy cow are likely to subsequently become replacement females in the beef herd. Therefore, the response to selection on this new index on genetic merit of, in particular, milk yield and fertility in beef animals was of interest. Thus, the correlation between this new index and milk and fertility sub-indices of the existing suckler beef value index (SBV) was quantified by correlating each sire's EBV for both milk and fertility with the EBV calculated for each trait included in the new index.

Results and Discussion

The calculated economic weights, along with the relative emphasis on each of the four traits are presented in Table 1. Decreases in calving difficulty, peri-natal mortality and gestation length increase farm profitability and this is reflected in the negative economic weightings for these three traits. Approximately two-thirds of the relative emphasis was placed on calf price, indicating the importance of high calf price to farm profitability as well as the large genetic variation in this trait. However the genetic standard deviation (25.7 kg) was considerably higher for calf price compared the other traits included in the index.

Table 1. Genetic standard deviation (σ_g), economic weighting and relative emphasis (%) for each of the four traits included in the index

<i>Trait</i>	<i>σ_g</i>	<i>Economic weighting</i>	<i>Relative emphasis</i>
Calving difficulty	2.94	-3.84	27.04
Calf mortality	0.29	-1.78	1.24
Gestation length	1.88	-2.26	10.17
Calf price	25.7	1.00	61.55

Sire predicted transmitting abilities (PTAs) are currently available for calving difficulty, calf perinatal mortality and gestation length and PTAs for calf price will be available from the ICBF in 2012. Therefore the index value of an animal can be calculated simply as the sum of the economic weight times the respective PTA.

The correlation between the new index and the milk and fertility sub-indices of the SBV was moderately positive ($r=0.35$). This indicates that selection of beef bulls on the new index will result in indirect selection for improved milk and fertility traits in female progeny used as beef herd replacements, both of which are of key economic importance to the suckler herd. Preliminary analysis of sire breeding values clearly shows that this index favours easier calving sires with shorter gestation lengths. For example, results to date suggest that Aberdeen Angus and Hereford sires will, on average, generate €37 greater profit per calf born to a dairy dam compared to progeny of a Belgian Blue sire.

Conclusions

The formation of this new index will facilitate easy identification of the most profitable beef bulls for use in the dairy herd. It is envisaged that the new index will be launched in 2012.

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The authors gratefully acknowledge funding from ABP Food Group.

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RMIS Project Number 5889

Breeding for increased flock mean 40-day lamb weight but lower flock variance

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Introduction

Maximising growth rate at an early stage across the entire flock is the primary aim of all sheep producers. However, achieving uniformity of growth can prove difficult as there is anecdotal evidence that some paternal half-sib families exhibit large variation in performance whereas small variation can be observed in other paternal half-sib families. A proportion of the differences in animal performance across different production systems may be described as differences in the residual variance. Genetic models have been designed to account for heterogeneity of variance, or the differences in the residual variance, that allow for breeding values to be calculated based on the residual variance. Knowledge of these breeding values will allow producers to breed animals that are robust across different environments, thus producing more uniform progeny whilst reducing variation in their performance. The objective of this study was to estimate variance components for the genetic effect of mean 40-day weight as well as the genetic effects of the variance in 40-day weight.

Materials and Methods

A total of 20,699 forty day live-weight records taken between the years 2009 and 2011, across 29 commercial flocks were obtained from Sheep Ireland. Only animals aged between 20 and 65 days of age were retained. Animals were discarded if sire, maternal grandsire, or flock of birth were unknown. Animals were also removed if their 40 day weight was not between 8 and 35 kg. Furthermore, animals with 40 day weights greater than ± 4 standard deviations from the mean were discarded. Contemporary group was defined as flock by date of weighing. Only records from contemporary groups with at least 4 other records were retained. The fixed effects included in the model used to estimate variance components were contemporary group, gender, age of lamb at weighing (linear and quadratic effect), lambing difficulty, birth and rearing rank of the lamb, month and year of weighing, ewe parity, the main breed fraction of the lamb, ewe, and ram, and ewe age nested within parity. The random effect included in the model was sire. Following all edits a total of 11,099 forty day live-weight records remained.

Variance components for live weight were estimated using a double hierarchical generalised linear model described in detail by Rönnegård et al. (2010) in ASREML (Gilmour et al., 2011). In summary, a linear mixed model was used to calculate estimates for the mean and the variance of the mean with a weighting factor (**W**) equating to the identity matrix for size **n** observations. The residual variance for each animal was then used to calculate a weighted gamma generalised linear model for the calculation of the residual variance model. The mean model was rerun to obtain new residual variance estimates which were then in turn used in the residual variance model. These steps were then continually iterated until convergence was deemed to have been reached once the variance components did not change over successive iterations.

Results and Discussion

The genetic (σ_a^2) and phenotypic variance (σ_p^2) of the converged mean and residual variance models are shown in Table 1. The corresponding heritability estimates for the mean and residual variance models were 0.16 (s.e.=0.01) and 0.0001 (s.e.=0.000), respectively. The number of flocks analysed in this study was 29 which may account for the low genetic effect for the residual variance model; increasing the number of flocks analysed in subsequent studies may result in an increase in the genetic effects.

Table 1. Comparison between the genetic (σ_a^2) and phenotypic (σ_p^2) variance calculated using the mean and residual variance models

Variances	Mean model	Res variance
σ_a^2	2.71	0.001
σ_p^2	13.9	1.02

Similar to previous studies (Rönnegård et al., 2010) the calculated genetic and phenotypic variances for the residual variance model were smaller than the respective estimates for the mean model. However, the calculation of heritability, albeit low (0.0001), for the residual variance indicates that genetic variation exists which can be exploited to help reduce the variation thereby aiding management especially drafting of lambs of similar weight.

The correlation between the estimated breeding values (EBVs) for the mean model and the residual variance for sires with greater than 70 progeny was -0.49 indicating that selection on increasing the mean 40 day live-weight can occur without increasing the corresponding the residual variance. The difference in variation

between the EBVs for the mean and residual variance model allow for a genome wide association study (GWAS) to be conducted that could potentially identify recombination hotspots or regions that are associated with epigenetic effects.

Conclusions

Results from this study show that it is possible to change the mean and the variance of traits simultaneously through the genetic heterogeneity of residual variance.

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RMIS Project Number 5889

Genetics of deep phenotypes for fertility

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Introduction

Calving interval is the goal trait for fertility in the Irish dairy cattle national breeding objective, the economic breeding index (EBI). However, calving interval is lowly heritable, requires a subsequent calving to occur, requires a long-time horizon to generate an observation, but more importantly is in itself an index of the post-partum interval to oestrus, pregnancy rate, and gestation length. Access to deeper phenotypes (i.e., greater refinement of the trait) for fertility that are less influenced by non-genetic effects (e.g., unrecorded post-partum voluntary waiting period to service), may contribute to greater genetic gain. The objective of this study was to undertake a preliminary quantification of the genetic parameters for a range of deep phenotypes for fertility measured using ultrasound.

Materials and Methods

Information on 60,552 reproductive tract ultrasound scans from 43,124 cows in 531 herds, predominantly from the year 2011 were available. All scans were recorded by one skilled technician (Reprodoc Ltd.). Data included the subjective assessment of the uterus (hereon known as uterine score; lower scores were more desirable), presence of corpus lutea, gender of calf and approximate day of gestation, where available.

Only Holstein-Friesian cows from a known sire were retained. Phenotypes defined in this study were 1) health status of reproductive tract, 2) presence of ≥ 1 of corpus lutea, 3) presence of multiple ovulation, and 4) whether the corpus luteum was on the left or right ovary. Reproductive tract status was scored as described by Mee et al. (2008). Contemporary group of herd-year-season of calving was defined for each trait separately and only animals with at least four other contemporaries also with information for the trait under investigation were retained. Lactation yield and subsequent calving interval were also available. Variance components for the fertility traits were estimated using animal linear mixed models in ASREML. Fixed effects included in the models were contemporary group, days post-calving at scan, parity of the cow, and genetic group. Genetic covariances with milk yield and calving interval were estimated using a series of bivariate sire linear mixed models. The impact of selection on the EBI or either of the two main sub-indexes, the milk subindex or the fertility subindex, was estimated by correlating the sire estimated breeding value (EBV) for each of the deep phenotypes with sire genetic merit for the EBI and sub-indexes. No correction for reliability of sire EBV was undertaken.

Results and Discussion

Summary statistics for each of the traits investigated are presented in Table 1. The heritability of the different fertility traits derived in this study was consistent with (inter)national estimates for traditional measures of fertility (Berry et al., 2010). The genetic correlations between traits observed suggest that selection for milk yield alone would be expected to lead to a deterioration in the health status of the reproductive tract post-calving, reduce the probability of a cow cycling, and increase the incidence of multiple ovulation (Table 2). Inferior reproductive tract score was associated with longer calving intervals as was the probability that the cow was not cycling.

Table 1. Number of records (N), mean and heritability (h^2 ; standard error in parenthesis) for each trait			
Trait	N	Mean	h^2 (se)
Uterine score (G1,2,3,4)	11390	1.47	0.021 (0.010)
Oestrous cyclicity (Yes/No)	10312	80%	0.057 (0.016)
Multiple ovulation (Yes/No)	848	8%	0.022 (0.062)
Ovary ovulated (Right - Yes/No)	848	56%	0.049 (0.084)
Both ovaries ovulating (Yes/No)	848	7%	0.093 (0.108)

Table 2. Genetic correlations (standard error in parenthesis) between fertility traits and performance		
Trait	Milk yield	Calving interval
Uterine score	0.22 (0.21)	0.36 (0.21)
Oestrous cyclicity	-0.45 (0.14)	-0.56 (0.14)
Multiple ovulation	0.66 (0.28)	-0.45 (0.28)

Estimated breeding value for inferior reproductive tract score was associated with lower EBI ($r = -0.24$), lower fertility subindex ($r = -0.28$) and greater milk production subindex ($r = 0.11$). Estimated breeding value for cyclicity was positively correlated with EBI ($r = 0.29$) and the fertility subindex ($r = 0.37$) but negatively correlated with the milk subindex ($r = -0.17$)

Conclusions

Deep phenotypes evaluated in the present study are heritable although heritability estimates are not greater than traditional fertility traits. However, improvements in the statistical model may result in a reduction in residual variance and thus greater heritability. Selection for EBI, and in particular the fertility sub-index, is improving genetic merit for the deep fertility phenotypes investigated in this study.

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RMIS Project Number 5889

Usefulness of health and temperament data from the dairy efficiency program in genetic evaluations

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Introduction

Accurate genetic evaluations for low heritability traits, such as animal health, require routine access to large quantities of phenotypic data (Berry et al., 2011). An opportunity arose as part of Article 68(1) of Council Regulation (EC) 73/2009 to "... address specific disadvantages affecting farmers ..." and encourage efficiency gains through the adoption of best practice. This initiative was exploited to increase the quantity of individual cow information recorded on mastitis, lameness, and temperament, amongst other traits. The objective of this study was to estimate genetic parameters for mastitis, lameness, and temperament recorded in the dairy efficiency program.

Materials and Methods

Data recorded by farmers on 283,300 cows, one lactation record per cow, from 3,492 herds were extracted from the Irish Cattle Breeding Federation database in October 2011. Mastitis and lameness were recorded separately as 0, 1, or ≥ 2 cases per cow in the current lactation; temperament was recorded as "VG"-very good, "G"-good, "A"-average, "P"-poor, and "VP"-very poor. For the purpose of this study both mastitis and lameness were dichotomised separately as "no case" or "at least 1 case". In total, 299 herds recorded no cases of mastitis, 337 herds recorded no cases of lameness, and 144 herds recorded no variation in cow temperament; of these herds, 30 reported no case of either mastitis or lameness and also reported no variation in cow temperament. Cows from herds that recorded no variation were discarded for the trait under investigation. Contemporary group was defined as herd-year-season of calving and only contemporary groups with at least 5 records were retained. Following edits, 185,335 cows, 187,006 cows and 205,137 cows remained in the analysis of mastitis, lameness, and temperament, respectively. Lactation milk yield and lactation geometric mean somatic cell count data were also available. Somatic cell count was normalised using a logarithm transformation; this variable will be hereon referred to as somatic cell score (SCS). Genetic and residual variance components for mastitis, lameness, and temperament were estimated using

an animal linear mixed model in ASREML (Gilmour et al., 2011). Fixed effects included in the model were contemporary group, parity of cow and pedigree group. Animal was included as a random effect accounting for relationships among animals. Covariance components with milk yield and SCS were estimated using a series of bivariate sire linear mixed models.

Results and Discussion

Mean incidence of mastitis and lameness was 11% and 9%, respectively which is lower than estimated previously using farmer recorded event data in Ireland (Berry et al., 2010). Incidence increased ($P < 0.001$) with parity from 6% and 3% for mastitis and lameness, respectively in first parity to 20% and 18%, respectively in parity five and greater. The heritability (in parenthesis) for mastitis and lameness was 0.022 (0.003) and 0.31 (0.003), respectively; the respective genetic standard deviation was 0.44 and 0.47 units. The heritability estimates were lower than previously documented using farmer recorded event data in Ireland (Berry et al., 2010; heritability of 0.05 and 0.04 for mastitis and lameness, respectively) as well as recorded internationally (Mrode and Swanson, 1996; 0.04 for mastitis). The heritability for temperament was 0.14 (0.01); the genetic standard deviation was 0.26 units. The genetic correlation (standard error in parenthesis) between mastitis and lameness was 0.55 (0.060); the respective phenotypic correlation was 0.09 (0.003). The genetic correlation is similar to the 0.48 reported by Pryce et al., (1997) using UK farmer recorded data. The genetic correlations with milk yield and SCS are in Table 1 and are in line with previous analyses of Irish data as well as a review of international studies (Mrode and Swanson, 1996).

Table 1. Genetic correlations (standard errors in parenthesis) between the different traits		
Trait	SCS	Milk yield
Mastitis	0.84 (0.03)	-0.05 (0.06)
Lameness	0.44 (0.05)	-0.12 (0.05)
Temperament	0.01 (0.06)	-0.08 (0.04)

Conclusions

Farmer scored mastitis, lameness, and temperament as part of the Irish dairy efficiency program is heritable and genetic correlations with performance traits are in line with expectations from previous analyses of Irish data as well as other international studies. The participation in recording, as measured by the proportion of herds that reported at least some incidence of mastitis/lameness or variation in cow temperament, was high albeit the incidence of both mastitis and lameness is likely to be biased downwards. These data will be incorporated into a revised genetic evaluation module for health traits.

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RMIS Project Number 5889

Pedigree analysis of Irish sheep populations

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Introduction

Inbreeding has deleterious effects on many aspects of production, health and fertility in livestock (Mc Parland et al., 2007). The objective of this study was to undertake a pedigree analysis including the quantification of inbreeding levels in the largest sheep populations in Ireland. The sheep populations investigated included the Blackface Mountain (BM), Belclare (BR), Charollais (CL), Galway (GL), Suffolk (SU), Texel (TX) and Vendeen (VN).

Materials and Methods

Ancestry information of all sheep recorded on the Sheep Ireland data base was extracted. The pedigree file comprised 237,695 sheep and was used to compute the number of complete generation equivalents (CGE), inbreeding coefficients, and generation intervals. The number of CGEs with information was computed as:

$$\sum_{i=1}^{n_j} \frac{1}{2^{g_{ij}}}$$

where n_j = number of ancestors of animal j , and g_{ij} is the number of generations between individual j and its ancestor i . Inbreeding coefficients (F) for all animals were calculated using the Meuwissen and Luo (1992) algorithm. Individual pedigree files were constructed for the BM (n=15,090), BR (n=22,596), CL (n=22,744), GL (n=10,411), SU (n=51,488), TX (n=64,055) and VN (n=9,396) populations. Using individual pedigree files the 100 most influential sheep to the gene pool of females born in 2010 for each respective population was determined. Generation intervals for each selection pathway (i.e., sires of males, dams of males, sires of females, and dams of females) were calculated by birth year both across all sheep populations using the full pedigree file as well as for individual populations.

Results and Discussion

Sheep born in 2010 had, on average, between 1.30 (CL) and 4.88 (GL) CGE recorded (Table 1). One CGE is equivalent to one complete generation of ancestry recorded on the Sheep Ireland data base (i.e. both sire and dam known), while 2 CGEs is equivalent to all four grandparents recorded in the database. A minimum of one CGE is required to detect traditional inbreeding in an animal. Twenty four percent of SU born in 2010 had less than one CGE recorded, while 82% of CL and SU had less than two CGE recorded. Similarly, over 62% of BM, TX and VN sheep had less than two CGE recorded. The correlation between CGE and F across the entire pedigree file was 0.23. A positive correlation between these statistics was expected since the more ancestry that is recorded in the data base, the greater the capacity to detect inbreeding.

The average population F of sheep born in 2010 ranged from 0.04 (SU) to 2.00% (GL). However, given the low level of ancestry recorded for CL, SU, TX and VN populations the average F presented in this study may not be truly reflective of inbreeding in those populations. Average F of CL, SU, TX and VN sheep with a minimum of 2 CGEs was 0.80, 0.08, 0.09 and 0.45%, respectively. Genomic information may help elucidate the true degree of inbreeding in these populations as well as correct for any potential pedigree errors. Despite the poor ancestry recording, very high F was recorded for some individual animals. All populations had sheep with an F of at least 25% (i.e father-daughter mating) while one, five and four individual sheep in the CL, SU, and TX populations, respectively, had inbreeding coefficients of 50%. Inbreeding coefficients of this magnitude arise from the mating of both highly inbred and highly related animals.

Table 1. Number of records (No), mean inbreeding percent (F; SD in parenthesis) and mean number of complete generation equivalents (CGE; SD in parenthesis) for sheep born in 2010

Breed	No	F	CGE
Blackface Mountain	206	0.82(2.45)	3.58(0.86)
Belclare	2330	0.82(2.68)	2.70(1.21)
Charollais	1140	0.14(1.27)	1.30(0.67)
Galway	1112	2.00(3.54)	4.88(0.88)
Suffolk	2274	0.04(0.76)	1.82(0.83)
Texel	3413	0.07(0.84)	2.08(0.92)
Vendeen	1144	0.28(1.32)	2.28(0.76)

On average, the generation interval for sire and dam pathways was 3.2 and 4.1 years, respectively when all populations (including those not individually studied here and those of unknown breed fraction) were included. However, the average generation interval varied among individual sheep populations studied. The average generation interval of sires ranged from 1.53 years (BM) to 3.78 years (CL) whilst the average generation interval of dams ranged from 3.31 (BM) to 4.10 (SU). The average generation interval was greater for dams than for sires for all populations studied with the exception of the SU.

The 10 most prominent ancestors to the BM, BR, CL, GL, SU, TX and VN populations cumulatively contributed 50%, 39%, 47%, 42%, 25%, 21% and 38% to the gene pool of females born in each of their respective populations in 2010. The highest contributing ancestor in each of the BM, BR and CL populations contributed over 9% to the gene pool of females born in each of their respective populations in 2010.

Conclusions

The level of inbreeding in sheep varied according to the population studied and ranged between 0.04 and 2.00% for sheep born in 2010. Yet, detection of inbreeding levels are dependent on good ancestry recording which remains poor across most sheep populations investigated in this study with the exception of the GL.

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RMIS Project Number 5889

Analysis of runs of homozygosity in cattle breeds

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Introduction

Runs of homozygosity (ROH) are contiguous lengths of homozygous genotypes that are present in an animal due to parents transmitting identical sister haplotypes to their offspring. The length of an ROH can be an indication of consanguinity as the longer the ROH segment, the more likely recent inbreeding occurred in the pedigree. However, long runs of homozygosity may also persist in outbred animals, believed to be due to the existence of multiple-megabase-scale ancestral haplotypes as a result of the mutation, linkage disequilibrium (LD) and recombination rates at their genomic location (Gibson, *et al.*, 2006). The presence of more ancient relatedness, which is often unaccounted for in an animal's pedigree due to limitations of recording, can also account for shorter ROH lengths (Kirin, *et al.*, 2010). As a result, past and present breeding practices will have played an important role in determining the length of the ROHs for a particular animal. The objective of this study was to quantify the levels of ROH that exist in different breeds of cattle.

Materials and Methods

Genotypes from 891 AI bulls from eight purebred dairy (n=360) and beef cattle breeds (n=420) and one Holstein-Friesian crossbreed (n=111), generated from the Illumina Bovine high-density (HD) panel were used. Only biallelic SNPs on the 29 autosomes were retained and both animals and SNPs with genotype rates <90% were discarded. Also, monomorphic SNPs and SNPs that deviated from the Hardy Weinberg equilibrium ($P < 0.0001$) within breed were discarded. PLINK v1.07 was used to identify ROHs, by taking a sliding window of 5 Mb across the genome, and allowing no more than two missing genotypes and one possible heterozygous genotype per window. A minimum threshold length of 0.5 Mb was set for identification of ROH. The HD genotypes were used for validation of the BovineSNP50 density panel to identify ROH by retaining the 48,734 SNPs (reduced HD panel) common to both the HD and the Illumina BovineSNP50 Beadchip. To establish that this reduced density also predicted the correct ROH length category for ROH, the quantity of ROHs that were correctly assigned to the HD ROH length category was plotted. SNP involvement in a ROH was also calculated by counting the number of times each SNP appeared in a ROH. Measures of homozygosity (F_{ROH}) and the pedigree inbreeding coefficient were calculated and correlated for all animals that had all animals that had a complete generation equivalent value ≥ 6 (n=230). F_{ROH} was calculated as $F_{ROH} = \sum L_{ROH} / L_{auto}$ where L_{ROH} was calculated as the sum of all ROHs >0.5Mb in length and L_{auto} is the total length of the genome covered by SNPs (i.e., 2.51 GB). The pedigree inbreeding coefficient was calculated according to the Meuwissen and Luo (1992) algorithm.

Results and Discussion

ROHs were common and frequent across all breeds as all animals had at least one ROH present in their genome that was between 1-5 Mb in length. The dairy breeds had a greater incidence of long ROHs (>30 Mb in length) indicative of recent inbreeding, whereas the Angus and Hereford had substantially more of their genome covered in shorter ROHs (1-5 Mb) suggesting a high level of distant ancestral relatedness possibly due to their geographical isolation during breed formation. Analyses of SNP involvement in a ROH revealed that certain areas of the genome were more commonly involved in a ROH than others (Figure 1). In particular a region on chromosome 14 involving the TOX gene, an immune gene, was observed in 87.4% of the HD genotyped population in a ROH. Strong correlations existed between the pedigree-based inbreeding coefficient and F_{ROH} ($r = 0.75$; $P < 0.0001$). A total of 157,600 ROHs were identified using the HD panel, whereas only 19,078 ROHs were identified using the reduced HD panel. The majority of ROH that the reduced panel failed to recognise were between 0.5-1 Mb in length but almost all ROHs in length categories of >5Mb were recognised and assigned to the correct length category >70% of the time, validating the BovineSNP50 array panel for use.

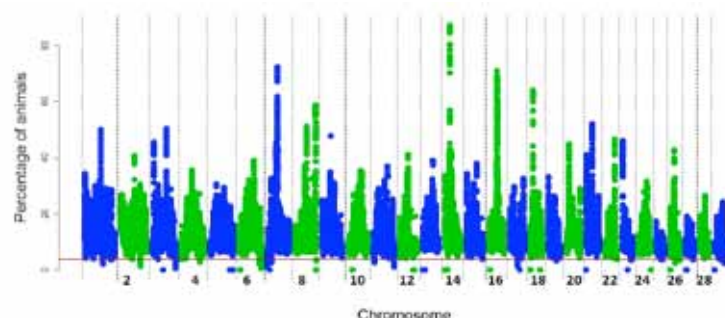


Fig. 1. Incidence of each single nucleotide polymorphism (SNP) in a run of homozygosity (ROH) in the HD panel population.

Conclusions

We show that the extent of a genome under ROH in cattle provides a sufficient predictor of the pedigree inbreeding coefficient, suggesting that in the absence of pedigree data, this method may be used to infer aspects of recent population history.

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The authors gratefully acknowledge funding from Science Foundation Ireland

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RMIS Project Number 5889

Genetic parameters for perinatal mortality in Irish dairy cattle

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Introduction

Perinatal mortality in cattle is defined as calf mortality shortly before, during or shortly after parturition (Philipsson *et al.*, 1976). Recent studies have highlighted that the prevalence of bovine perinatal mortality is on the increase, with current incidences varying between 2% and 10% internationally. The incidence in Ireland has been previously estimated as 4.29% in Ireland (Mee *et al.*, 2008). Previous heritability estimates for perinatal mortality in Holstein dairy cattle are 4% for the direct genetic effect and 3% for the maternal genetic effect (Steinbock *et al.*, 2003). The heritability of direct and maternal calving difficulty was reported to be slightly higher at 6% and 5%, respectively (Steinbock *et al.*, 2003). The objective of this study was to estimate the heritability of perinatal mortality, calving dystocia and also perinatal mortality not associated with calving dystocia in Irish dairy cattle.

Materials and Methods

Date of birth, herd of birth, gender of calf, degree of calving assistance, occurrence of perinatal mortality (recorded as calf dead at birth or within 24hrs), parity and age of dam, as well as breed of dam, calf and sire were available from the Irish Cattle Breeding Federation for the years 2002 to 2011, inclusive. In total data from 3,884,082 birth events were available, of which 2,094,359 had information on the degree of calving assistance at birth. Data for dams of unknown parity and of parities >10 were discarded (n=28,865), as well as births with more than two calves (n=4,854). Dams who calved for the first time less than 608 days of age (n=4,580) as well as dams calving greater than 2 years from the median age within each parity, were discarded (n=95,399). Dam parity was recorded as six classes; 1, 2, 3, 4, 5 and >5. Parity number of the dam in this study was the parity of the cow the day after she had calved. Only data from dairy herds were retained comprising 1,671,296 birth events. Contemporary groups were generated based on grouping animals together for each phenotype (dystocia, perinatal mortality, perinatal mortality without dystocia) within herds that had birth dates in close proximity. Only contemporary groups with at least 5 records were retained. A random selection of contemporary groups comprising 85,776 calves was retained for analysis. These animals originated from 3,523 different herds and from 7,285 and 7,539 unique sires and maternal grand sires, respectively. Factors associated with dystocia and perinatal mortality were determined using univariate repeatability animal-dam models in ASReml (Gilmour *et al.*, 2008). Fixed effects included contemporary group, twins, parity, age within parity, and calf gender. Random effects included were the additive genetic effect, the maternal genetic effect and the permanent environmental effect. Breed was accounted for through the use of founder breed groups in the pedigree.

Results and Discussion

The percentage of data from parities 1, 2, 3, 4, 5, >5 was 26%, 21%, 17%, 13%, 9% and 14%, respectively. The percentage of birth events scored as no assistance/unobserved, slight assistance, severe assistance and veterinary assistance was 72.4%, 22.0%, 3.7% and 1.9%, respectively. The prevalence of perinatal mortality in this dataset was 2.63%, with 42.38% of perinatal mortality occurring in primiparae. The prevalence of twins was 3.59%, of which 58.51% were of the same sex; some level of assistance was reported in 35.2% of twin births. The incidence of dystocia (i.e., calving difficulty score ≥ 2) was greater in male (31.82%) than female calves (23.20%). The occurrence of perinatal mortality when no dystocia occurred was 0.96%. The prevalence of perinatal mortality when not associated with dystocia was highest (9.42%) when both the sire and dam main breed component was Jersey. The direct heritability for perinatal mortality, dystocia, and perinatal mortality without dystocia was 0.01 (s.e. 0.003), 0.20 (s.e. 0.014) and 0.003 (s.e. 0.002), respectively. Maternal heritability estimates were 0.009 (s.e. 0.003), 0.006 (s.e. 0.003) and 0.004

(s.e 0.002). These heritability estimates for dystocia and perinatal mortality are consistent with previous genetic parameter estimates reported in Irish Holstein-Friesians (Hickey et al, 2007; Berry *et al.*, 2011).

Conclusions

The prevalence of perinatal mortality is still quite high in Ireland but the incidence is, nonetheless, low in the absence of dystocia. However, genetic variation clearly exists for traits which influence perinatal mortality suggesting that, if exploited, the incidence could be reduced.

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RMIS Project Number 5889

Developing a Cattle Model for Dairy Cows

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Introduction

Developing experiments to test the effects of various management practices at farm level are difficult and require a lot of time, labour and money in order to carry them out correctly. Modelling of the biological systems present opportunities to capture the complex interactions within systems while not realising the costs associated with conventional experiments. However it is important that the models developed capture the complex interactions between the various system components. The objective of this study was to develop a dynamic, mechanistic and stochastic cattle simulation model capable of modelling a number of animal categories which includes the calf, the heifer and the cows with a daily time step.

Materials and methods

The model described in this paper simulates the performance of each animal individually, with a daily time step thus allowing the model to react in a sensible fashion to management or system changes. The model is stochastic, dynamic and mechanistic which makes the simulation more realistic based on farm level conditions and allows accurate simulation of changes in the system. The dairy cows are represented in the model through a number of complex interactions which include feed intake, body condition score change, milk production, growing and death. Individual animal intake follows the French nutrition system for dairy cow (Faverdin et al., 2011). Model simulation requires an initial parameterisation of the cattle and management rules around the farm. In this analysis the model was parameterized with data from one of the Teagasc farms (Curtins) with a starting point of 1st of January 2009 and was allowed to simulate for a three year period. At the first of January 2009, there was 93 dry cows, 40 pregnant heifers and 45 weanling heifers. In the analysis presented comparisons are shown at individual and herd level by week of lactation.

Results and Discussion

At the herd level, the model simulates extremely accurately milk production throughout the lactation. The concordance correlation coefficient (CCC) is over 0.9 for the whole year and for mid and late lactation showing a very good concordance between actual and predicted data. At the animal level, the maximal mean error is at 4kg of milk in early lactation. During the whole lactation and in mid lactation the model shows a respectable level of accuracy with a CCC greater than 0.8. However the model is showing significant deviation in both early and late lactation. It is hypothesized that the difficulty in predicting milk supply in early lactation is a reflection of an inaccurate representation of the genetic potential for milk production within the model. A further evaluation of the most suitable method of describing the genetic potential for milk production is required in the model.

Table1. Comparison between the actual and predicted milk production during a whole lactation and in early (1 to 16), mid lactation (17-25) and late (+26) lactation										
Category	Actual	Predicted	Animal				Herd			
			RMSE ¹ (kg)	RPE ² (%)	CCC ³	Bias ³	RMSE ¹ (kg)	RPE ² (%)	CCC ³	Bias ³
Global	19.37	19.08	3.52	18.44	0.81	0.98	1.02	6	0.98	0.99
Early lactation	23.86	22.95	4	16.76	0.62	0.95	1.25	5.23	0.8	0.87
Mid lactation	19.18	18.66	3.04	15.85	0.81	0.98	0.53	2.77	0.91	0.91
Late lactation	13.96	13.35	3.26	23.32	0.54	0.83	1.01	8.33	0.91	0.91

¹ Root mean square error; ² Root predicted error; ³ Concordance correlation coefficient and bias

Conclusion

The model is extremely accurate at simulating milk production at herd level. However when it comes to individual animal level the model requires further modification and calibration.

Acknowledgement

The authors acknowledge the financial support of the GreenHouseMilk Marie Curie project.

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RMIS Project Number 6159

Physiology of Reproduction, Growth & Lactation

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

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Introduction

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

Materials and Methods

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

Results and Discussion

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

Conclusions

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

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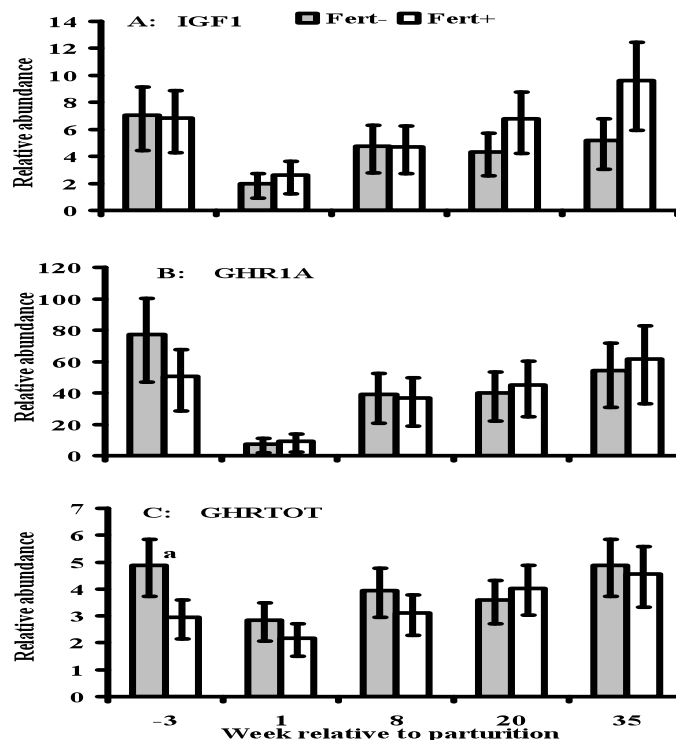


Figure 2. Relative abundance of mRNA in liver for (A) IGF-I, (B) GHR 1A, and (C) GHRtot during wk -3, 1, 8, 20 and 35 relative to parturition in Fert+ and Fert- cows. Vertical bars indicate 95% confidence intervals. (A) IGF-I: IGF-I mRNA abundance was significantly greater in Fert+ cows ($P < 0.05$)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

RMIS Project Number 5672

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

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Introduction

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

Materials and Methods

Lactating dairy cows ($n = 1,538$) across 8 commercial dairy herds were enrolled in a completely randomised block design study to evaluate synchronisation treatments. Within each herd, cows were divided into 3 calving groups based on days in milk (DIM) at MSD: early (≥ 42 DIM at MSD; $n = 1,244$), mid (21 to 41 DIM at MSD; $n = 179$), or late (0 to 20 DIM at MSD; $n = 115$). Oestrous cycles of cows in the early, mid-, and late-calving groups were synchronised to facilitate insemination after observation of oestrus or TAI at MSD (planned breeding 1; PB1), 21 d (PB2), and 42 d (PB3) after MSD, respectively. For each PB, cows in the relevant calving group were stratified by parity and calving date and randomly assigned to one of the following synchronisation protocols: 1) d -10 GnRH (10 μ g i.m. buserelin) and CIDR [Controlled Internal Drug Release, 1.38 g progesterone (P4)] administered; d -3 PGF_{2 α} (25 mg i.m. dinoprost); d -2 CIDR removed followed by artificial insemination (AI) at observed oestrus (CIDR_OBS); 2) same as CIDR_OBS,

but GnRH 36 h after CIDR removal and TAI 18 h later (CIDR_TAI); 3) same as CIDR_TAI, but no CIDR used (Ovsynch) or 4) untreated control (CTRL). Body condition score (BCS) was recorded at the time of insemination on a 1 to 5 scale (1 = emaciated, 5 = extremely fat) with increments of 0.25 as outlined by Edmonson *et al.* (1989). Cows were classified according to BCS at the time of insemination as ≤ 2.50 (Low), ≥ 2.75 and ≤ 3.00 (Medium) or ≥ 3.25 (High). Prior to assignment to treatment cows were examined by transrectal ultrasonography and the numbers of visible corpora lutea (CL) were counted. To determine conception rates, all cows on synchronisation treatments were scanned at 30 to 32 days post AI. Concentrations of P4 in plasma were determined on the day of AI and 11 days after AI. Cows were categorised according to plasma P4 at d 0 (presumptive oestrus) and d 11 after insemination (high [H] (≥ 1 ng/mL); low [L] (< 1 ng/mL). Only cows with L plasma P4 on d 0 and H plasma P4 on d 11 (LH) were considered synchronised. The following reproductive measurements were calculated and analysed: 21-day submission relative to PB1, PB2, PB3 (binary) and conception at first service (confirmed pregnant by ultrasonography at 30 to 32 days after first AI; binary). The associations between CL status, BCS, DIM and 1) synchronisation rate, 2) 21-d submission rate after PB, and 3) conception at first service for different synchronisation treatments were determined by logistic regression using the GENMOD procedure of SAS; two-way interactions between the effects listed and synchronisation treatment were also evaluated.

Results and Discussion

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

Conclusion

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

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RMIS Project Number 5672

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

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Introduction

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

Materials and Methods

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

Results and Discussion

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

Table 1. Effects of TM bolus on reproduction variables

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

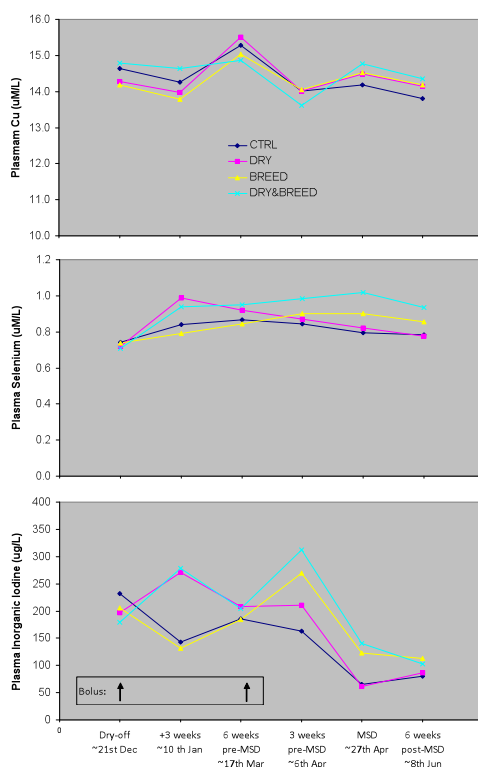


Figure 1. Temporal patterns of plasma Cu (top), Se (middle) and inorganic I (bottom) in cows administered boluses at different time points.

Conclusions

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

Acknowledgements

AllSure boluses were supplied by Animax Ltd.

RMS Project Number 5890

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

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Introduction

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

Materials and Methods

22 dairy cows with good (n=13, Fert+) or poor (n=9, Fert-) estimated breeding values (EBV) for calving interval (Table 1) were enrolled in the study. The average ($\pm$ SD) parity and days postpartum at the initiation of the study were 2.7 $\pm$ 0.48 and 2.2 $\pm$ 0.44, and 61 $\pm$ 13 and 62 $\pm$ 13, for Fert+ and Fert-, respectively. On the first day of the study, each cow received an i.m. GnRH agonist (10 ug buserelin; Receptal, Intervet Ireland, Dublin), and a CIDR was inserted per vaginum (1.38 g of P4; Pfizer Ireland, Dublin, Ireland). Seven days later, each cow received an i.m. PGF2 α injection (25 mg of dinoprost tromethamine; Lutalyse, Pfizer Ireland), and 24 h later the CIDR was removed. Each cow was again administered the GnRH agonist 36 h after CIDR removal.

Table 1. Mean EBV (SD) for milk production and fertility traits of Fert- and Fert+ genotypes.			
	Fert-	Fert+	P
Milk BV (kg)	187(114)	248(156)	0.32
Calving Interval BV (days)	3.21(1.4)	-2.55(1.2)	0.0001
Survival BV (%)	-0.65(0.5)	1.82(0.4)	0.0001

Milk yield was recorded twice daily and dry matter intake (DMI) daily starting 4 weeks before sample collection. Blood samples were collected twice daily from d 1 to 7.5 (d 0 = ovulation; confirmed by hormone values) to determine plasma P4 concentrations. On d 7, ultrasonography was used to measure CL volume and the Power Doppler function was engaged to determine CL blood flow intensity (BFI) and blood flow area (BFA). On d 7 pm and d 8 am, prostaglandin F2 α was administered to regress the CL. On d 8 am, 2 CIDRs were inserted per vaginum. Liver biopsies were collected on d 9 and hepatic mRNA abundance of genes involved in P4 catabolism was determined by RT-PCR. Genes examined were *AKr1C1*, *AKr1C3*, *AKr1C4*, *CYP2C* and *CYP3A*. On d 10, CIDRs were removed and blood samples were collected from -60 to 660 minutes relative to CIDR removal to measure P4 MCR. All data were analysed using SAS. Mixed model procedures with repeated measures were used where appropriate. Genotype and parity were included as fixed effects. Cow nested within genotype was included as a random effect. The NLIN procedure was used to estimate the decay rate coefficient of P4 for calculating the half-life and MCR.

Results and Discussion

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

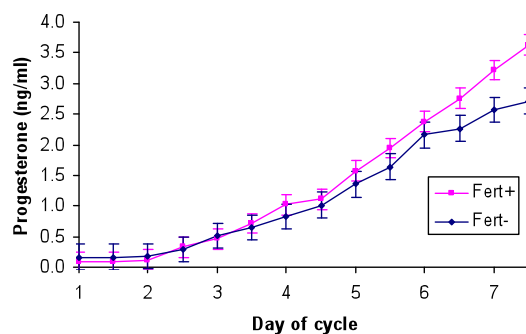


Figure 1. Temporal profile of circulating P4 concentrations from d 1 to 7.5 of the oestrous cycle of Fert+ and Fert- cows.

CL volume and BFI on d 7 were not affected by genotype, but Fert+ cows had greater CL BFA than Fert- cows (2.24 vs. 1.45 cm², $P = 0.03$). Fert+ cows had greater DMI compared with Fert- cows (24.9 vs. 23.4 kg/day, $P = 0.03$) but there was no effect of genotype on milk yield (30.1 vs. 29.9 kg/day, $P = 0.9$). Parity did not affect milk yield or DMI. Fert- cows had greater ($P = 0.03$) abundance of *AKr1C1* mRNA compared with Fert+ cows, but mRNA abundance of the other genes examined did not differ between genotypes. Genotype had no effect on the half-life (37.71 vs. 31.82 minutes, $P = 0.31$ in Fert+ vs. Fert-, respectively) and MCR of P4 (1.83 vs. 2.34 %/min, $P = 0.16$ in Fert+ vs. Fert-, respectively). The MCR was lower (1.69 vs. 2.47 %/min, $P = 0.03$) and P4 half-life tended to be greater (41.3 vs. 29.4 minutes, $P = 0.06$) in 2nd parity cows compared with 3rd parity cows.

Conclusions

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

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RMIS Project Number 6075

Animal Health & Well-Being

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

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Introduction

Seasonal increase in bulk milk somatic cell count (SCC) is of economic importance to milk processors because of decreased production efficiency, and shelf life of products, and to producers through financial penalties. For Irish dairy herds, bulk milk SCC was highest in autumn (Berry, 2006), but this occurred during summer for UK dairy herds (Green, 2006), indicating the importance of accounting for stage of lactation in order to identify times of the year that are associated with increased cow SCC, to target further investigations.

The aim of this study was therefore to describe association between time of year, and SCC at the cow level for Irish and UK herds. In particular, to identify trends, that may be masked by the effects of stage of lactation and milk yield at the herd level.

Material and Methods

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

Results and Discussion

Following adjustment for the confounding influence of stage of lactation, associations between cow SCC and calendar month were larger and more variable from February to August, and in December, for the Irish compared to the UK herds (Figure 1). This was opposite to the trends observed in bulk milk SCC for Irish herds.

At the cow level, increased SCC and variability in SCC indicate that February to August is a key time for the occurrence of new intra-mammary infections, and some of these may become chronic, and contribute high bulk milk SCC later in the year, that is a problem for Irish dairy industry. It is therefore important to monitor rates of new infections, and cures based on individual cow SCC during summer, and take farm specific action, regardless of bulk milk SCC. However, further work is needed to demonstrate the legacy of new infections from the spring and summer, and their contribution to bulk milk SCC later in the year, as well as target rates.

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

Conclusions

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

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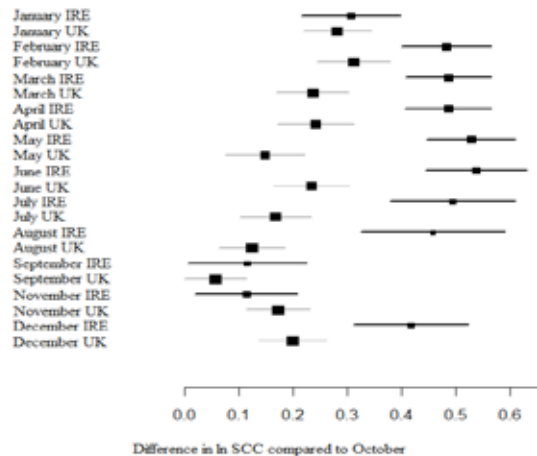


Figure 1. Model coefficients (and 95% confidence intervals) for calendar month (ln = natural logarithm)
RMIS Project Number 5894

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

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Introduction

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

Materials and Methods

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

Results and Discussion

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

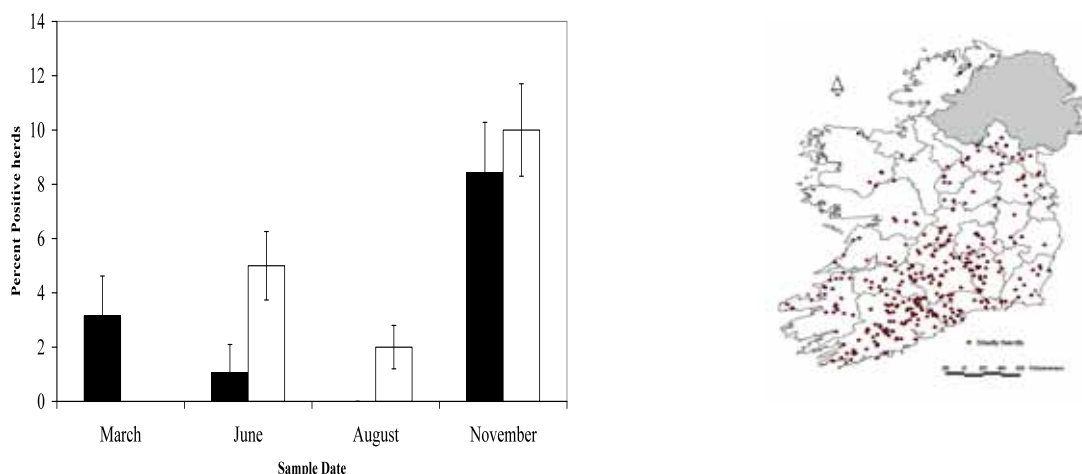


Fig. 1. True prevalence (■) and Incidence (□) of *Neospora caninum* in study herds. (Inset: map of study herd location)

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

Conclusions

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

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RMIS Project Number 5900

Periparturient calf mortality in Irish dairy herds – latest findings

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Introduction

In 2010 a prospective longitudinal study of the extent, nature and causes of calf loss in the periparturient period commenced at Moorepark; the latest results from this ongoing study in 2011 are reported here. This is a collaborative research project involving the local Cork Regional Veterinary Laboratory, the Central Veterinary Research Laboratory of DAFF, UCD, ICBF, AFBI and SAC. The objectives are to document the prevalence, risk factors and causes of calf losses in the periparturient period. Studies have shown that losses in this period are higher than in any subsequent period (Brickell et al., 2009).

Materials and methods

Between January and June 2011, 246 necropsy examinations were carried out on calves which died within 48h of calving on 30 spring-calving dairy farms (1-26 calves/farm) with high and low calf mortality. Epidemiological data were collected on carcass submission questionnaire forms and necropsies and histopathological analyses were carried out at Moorepark Dairy Production Research Centre. Additional laboratory analyses were conducted by the veterinary laboratories of the Department of Agriculture and Food in Cork (microbiological culture, fetal serology for *Leptospira hardjo* and *Neospora caninum*-Immunocomb), Limerick (maternal blood selenium) and Backweston (liver copper, cobalt and selenium and kidney selenium analysis and BVDv tissue PCR, and BVDv serum antigen and antibody assays and histopathology slide preparation), the Veterinary Sciences Division of AFBI in Stormont, Northern Ireland (maternal blood plasma inorganic iodine, copper and magnesium) and the Scottish Agricultural Colleges (SAC), Penicuik, Scotland (neonatal hepatic and serum vitamin A and E analyses).

Results and Discussion

Of the 246 calves submitted, the majority died during or within an hour after birth (69%) with the other calves dying either before (16.3%) or after calving, up to 48h (14.6%). Thus the majority (84%) of calves which die in the periparturient period are alive at the onset of calving and so represent possible avoidable losses.

A cause of mortality was assigned to each calf following the clinical history, necropsy examination and subsequent laboratory testing. The most common causes of death, in descending order, were a combination of causes (33%), dystocia (28%), eutoxia (7.3%), foetal/neonate haemorrhage (4.5%) and prematurity (3.3%). Complete histopathological analyses are outstanding. In addition, a large proportion of calves had an unassigned cause of death (16.3%). The finding that the most common cause of death involved more than one assignable cause is a novel finding. Previous analyses had included each cause of death separately (Mee and Kenneally, Research Report, 2010, 35-36). Amongst the combination cause of death category, the most common combinations were dystocia and congenital defects (22%), dystocia and premature placental separation (13.5%) and dystocia and infections (7.4%). This confirms the finding of dystocia as the most common single cause of death and highlights the high prevalence of lethal congenital defects in these dairy herds. The prevalence and risk factors for dystocia in Irish dairy herds were recently published as an additional task in this project (Mee et al., 2011). In some of these cases the accompanying cause of death, e.g. congenital defect (e.g. intestinal atresia) may have caused the dystocia, or the dystocia may have caused the accompanying cause of death, e.g. premature placental separation. These findings highlight the need for new classification criteria to assign cause of death. This has been followed up in a subsequent international Delphi survey in 2012.

The results of this Teagasc project have been used to inform current recommendations from the CalfCare Technical Working Group of Animal Health Ireland (AHI) on the care and management of the periparturient calf in Irish dairy and beef herds both through recently published farmer-focused leaflets (e.g. Lorenz et al., 2011a) and in recent peer-review publications (e.g. Lorenz et al., 2011b).

Conclusions

The results from this project in 2011 indicate that the majority of calf loss around calving may be avoidable as the majority of calves which die were alive at the onset of calving. In addition, recent results indicate that more than one cause of death may be present in a large proportion of calves which die around calving with dystocia implicated in the majority of such cases.

Acknowledgements

The authors thank the participating dairy farmers for their collaboration in this research study and the cooperation of colleagues in the Veterinary Laboratory Services of DAFM.

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RMIS Project Number 5902

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

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Introduction

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

Materials and Methods

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

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

Results and Discussion

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

However, the association between milking number and IgG levels differed ($P < 0.05$) by parity (Figure 1).

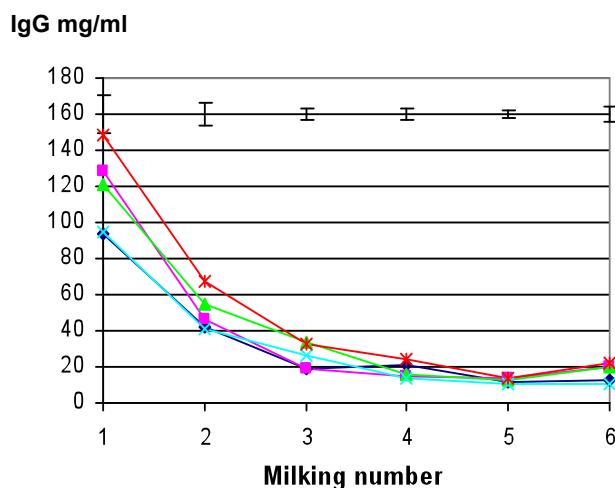


Figure 1. IgG levels for different milkings post-calving for parity 1 (blue), 2 (pink), 3 (green), 4 (turquoise) and 5+ (red); mean 95% confidence interval represented by error bars.

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

Conclusions

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

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RMIS Project Number 6009

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

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Introduction

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

Materials and Methods

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

Results and Discussion

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

Colostrum IgG concentration was positively associated ($P < 0.01$) with lactation number. Cows in later lactations produced colostrum with higher IgG concentration than those in earlier lactations even after adjustment for differences in milk yield at the time of milking. Least square means for colostrum IgG concentration (mg/ml) were 95.4 (SE 41.6), 110.2 (SE 11.6), 116.5 (SE 11.6), 114.4 (SE 12.1) and 123.7

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

Conclusions

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

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 SAS, 2009. SAS for Windows. Version 9.1. SAS Inst, Cary, NC, USA

RMIS Project Number 6009

Animal Facilities, Labour, Automation & Energy Efficiency

Heat recovery in a milk refrigeration system with variable fan speed control

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Introduction

Milk refrigeration is the largest energy consumer on dairy farms at 37% of total consumption (Upton et al 2010). Direct Expansion (DX) systems are the most popular milk cooling systems employed on Irish dairy farms. A DX milk bulk tank operates on a typical reverse-Rankine vapour compression cycle consisting of four major components; evaporator, compressor, condenser and expansion valve. Liquid refrigerant (404A) evaporates inside the bulk tank evaporator before being lifted to a higher pressure and temperature by the compressor, the super heated gas is then cooled in the condenser by externally mounted variable speed (VS) air fans and returned to liquid form, the expansion valve reduces the pressure before the evaporator in the bulk tank allowing the liquid to once again turn to vapour and thus the cycle is continued. Heat Recovery (HR) is a method of extracting thermal energy from the super heated vapour before it is dissipated into the atmosphere via the air cooled condenser. The recovered energy from the refrigeration cycle can be used to produce hot water for sterilization of milking equipment. The aim of this research is to analyse the effectiveness of a heat recovery unit and its impact on the performance of the refrigeration cycle.

Materials and Methods

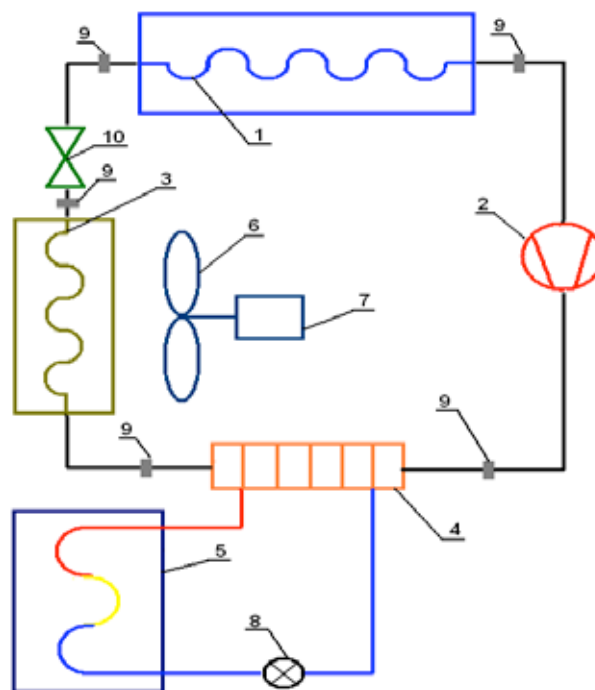


Figure 1: HR test rig: 1-Evaporator, 2-Compressor, 3- Condenser, 4-Heat Exchanger, 5-Water Tank, 6- Air Fan, 7-Variable Speed Control. 8-Water Pump, 9-Pressure-Temperature, Sensor, 10-Expansion Valve.

Two experimental protocols were followed in the testing of the system; the bulk tank was filled with 2000 litres of milk at 35°C and then cooled down to 4°C by the refrigeration system. The heat recovery unit was turned off for protocol 1 and turned on for protocol 2. The experimental test rig consisted of a typical DX bulk tank system with a HR unit. The HR comprised of a smooth plate brazed plate heat exchanger was situated on the refrigeration loop after the compressor. The HR operated on the principle of absorbing thermal energy from the super-heated vapour by pumping water through the HE from a water storage tank and back in a closed loop. Temperature-pressure sensors were placed between each major component of the DX circuit. The condenser was cooled by VS fans. The fan power was dictated by the pressure level in the condenser. To mitigate the disturbing effects of varying ambient temperature; a series of both protocols were run consecutively and the corresponding protocols with the minimum average ambient temperature percentage error were selected.

Results and Discussion

Table 1. Variation between Protocol 1 and Protocol 2

Protocol	COP	Energy Recovered (kWh)	Average Ambient Temperature (°C)
P1	3.05	0	15.2
P2	3.41	27.6	15.11

The HR unit was capable of increasing the system coefficient of performance (COP) by eliminating the super heat and a portion of the sensible heat from post compressor vapour; this in turn lowered the condensing pressure leading to a reduced work load for the compressor and air fans. The majority of available thermal energy is in the form of sensible heat at low temperatures. This low grade energy is difficult to extract from the system due the small water-vapour temperature differential. While the HR unit did remove some sensible heat from the cycle, the majority of energy came from the super-heated portion. 27.6kWh of thermal energy (34% of thermal energy in the bulk tank) was recovered through the cycle and stored in a water tank. This water can utilised for milking machine and bulk tank wash down purposes.

Conclusions

The HR Unit tested in this study is capable of lowering energy consumption in the refrigeration cycle whilst supplying a substantial amount of thermal energy for water heating. However, the effectiveness of HR relies heavily on the temperature of the milk entering the bulk tank. The introduction of a correctly configured pre-cooling system would greatly reduce the temperature lift in the refrigeration cycle, thus reducing both the impact of the bulk tank HR unit on the system COP and the amount of thermal energy available for recovery.

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RMIS Project Number 5899

Start up lactation of automatic milking at Moorepark

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Introduction

The use of automatic milking systems (AMS) is becoming increasingly popular. Recent data indicates the presence of AMS on approximately 10,000 commercial farms (De Koning, 2010). The AMS system can perform the tasks of cow identification, teat washing, milking cluster attachment, milking and cluster removal without human intervention. Automatic milking is reliant on voluntary cow traffic i.e. cows present themselves for milking while not being accompanied by a person. This is an extra challenge when cows are at pasture compared to indoors. AMS could be very relevant to dairy farming in Ireland due to labour and land being limiting while simultaneously aiming at expansion of milk production. The objective of this study was to put in place an AMS* at a Moorepark research farm and measure its production characteristics during the start up year.

Materials and Methods

The farm-let with the AMS consisted of a 24 ha milking platform. There were 63 cows in the system with a mean calving date of 15th February (range 1st February-15th March). The dairy featured one Fullwood Merlin 225 AMS unit. Extensive milking and cow information was recorded at each milking (e.g. milk yield, milking time, milk flowrate, somatic cell count (SCC), concentrate level). The grass allocation is critical to optimal cow visits to the AMS unit (it can influence too frequent or infrequent cow visits). The land area was divided into 3 grazing sections of 8 ha each (A, B and C) which are further divided into 1 ha paddocks. The greatest distance between paddock and dairy was 700m which does not deter cows from returning to the AMS for milking. Cows moved between the grazing sections A, B and C at 1:00 am, 11:00 am and 6:30 pm, respectively. Cows were diverted to the AMS for milking as they moved from one section to another. Cows were allocated 5 kg DM in each of the 3 grazing sections (A, B and C) over each 24 h period. Cows grazed to a post-grazing height of 3.5-4.0 cm. All cows received 1 kg concentrate per 24 h during the main grazing period of the lactation.

Results and Discussion

The daily milk yield profile for the start up lactation (to October) is shown in Table 1. Milk protein and fat % ranged from 3.26 and 3.93 in May/ June to 4.20 and 5.04 % in October, respectively. A milk lactose level of 4.47% was recorded in October. Milk SCC was consistently <200x10³ cells/ml between May and August, and increased to 249x10³ cells/ml during October. Average milking frequency was 1.8 milkings/cow per day/day, with 113 milkings per day, and 6 milkings per hour between 06:00 and 22:00 (Figure 1). The cows adapted relatively quickly to the AMS (within approx. 4 days). Milk output was influenced by changing cow number as

calving occurred and the fact that it was a start-up year when milk yield is expected to be reduced by 10-15% (Wade *et al.*, 2004). Sixty three cows were milked in this study, whereas, up to 112 cows is considered achievable (Jago, *et al.*, 2006) in the longer term.

Table 1. Milk yield profile		
Month	Cow no.	milk yield kg/c/d
Mar	42	21.5
Apr	56	21.9
May	60	21.4
Jun	63	23.9
Jul	63	20.9
Aug	63	16.4
Sep	62	14.3
Oct	60	8.5

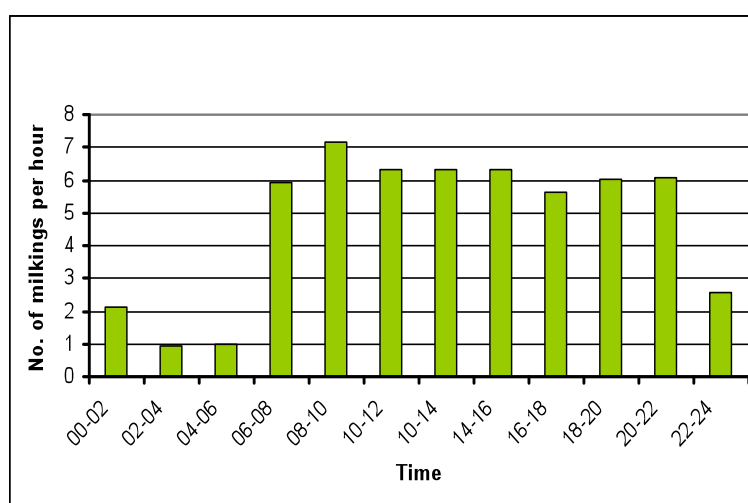


Figure 1. Average distribution of milkings/ 24 h

Conclusions

The aim of the study was achieved in that a herd of 63 cows performed satisfactorily in terms of milk production characteristics and milking frequency during the start up year within an AMS. A number of critical start-up issues were identified, which included (a) a daily data check to ensure milking and health check of all cows, (b) setting aside 0.5 h and 0.25 h at morning and evening time daily for routine maintenance checks, (c) cow selection on udder and teat conformation, (d) replacement of liners at 3-weekly intervals and (f) good backup service

*Merlin AMS supplied by Fullwood Ltd.

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RMIS Project Number 6098

Energy consumption of an automatic milking system

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Introduction

Recent data shows that there are approximately 10,000 commercial farms worldwide using automatic milking systems (AMS) to milk their cows. This figure is expected to grow rapidly in the coming years (De Koning, 2011). Therefore, the energy consumption of AMSs will become increasingly important. Studies by Bijl *et al*, (2007), and Artmann & Bohlens, (2000), showed that electricity costs were greater with AMSs compared to conventional milking systems. However these studies did not give detailed component breakdown information. The aim of this study was to document the electricity consumption of a recently installed AMS at Moorepark for the period 1st May to 31st October, 2011.

Materials and Methods

A herd of 63 spring calving cows were milked from pasture using a Merlin AMS*. Data presented here pertains to the period from 1st May to 31st of October. Cows were milked on average 1.8 times per day. Average milk yield over the period was 17 litres per cow per day. The AMS was washed with hot water 3 times per day during weeks 1-6, and twice daily, thereafter. Water heating was provided by electrical water heaters. Milk was pre-cooled using a Packo tubular cooler (model TT2) supplied with well water and subsequently, by a 5,000 litre ice bank tank. The vacuum pump was a vane pump with a 3kW motor. Vacuum level was controlled by a standard regulator from weeks 1-6, while a variable speed drive (VSD) controlled pump with 1.1kW motor was used thereafter. Compressed air was supplied by a 2.2kW compressor. The energy consumption of the AMS was monitored using Sinergy Escot energy monitoring equipment and software. The Escot data-logger can measure power consumption of multiple electrical circuits using clip-on AC current transducers. The logging software records cumulative kilowatt-hour (kWh) readings every 15 minutes. Measurement equipment was calibrated and accurate to $\pm 1\%$ of reading. This equipment allowed for measurement of the following individual components in the dairy: milking robot, vacuum pump, air compressor, milk cooling and water heating.

Results and Discussion

Water heating accounted for 37.1Wh/l (Watt hour per litre) of milk produced. The milk cooling system, air compressor, vacuum pump and robot consumed 14.8Wh/l, 14.7Wh/l, 11Wh/l and 2.9Wh/l, respectively. Miscellaneous items such as lighting and an office consumed 16.4Wh/l. The average total electricity consumed per litre of milk produced between 1st May and 31st October was 97.4Wh/l. When the relevant tariffs are applied the average cost of electricity was 1.25 Euro cent per litre of milk (c/l). The cost of electricity varied from 0.82 to 1.87 c/l as the volume of milk harvested by the AMS varied over the season from the spring-calved herd (Figure 1). Water heating was the largest consumer of electricity in this study at 38% of the total. This requirement is a consistent fixed cost irrespective of the volume of milk produced because wash cycle scheduling is time based. These average costs of 1.25 c/l were high compared to an audit of conventional milking systems (0.43c/l) on 21 commercial dairy farms (May-October 2010) (Upton *et al*, 2011). This may be due to (a) reduced milk output from the AMS due to it being the start-up year, when milk yield is expected to be reduced by 10-15% (Wade *et al*, 2004) and/ or (b) under utilization of the AMS. 63 cows were milked in this grazing based study, whereas the possibility to extend capacity to 112 is considered achievable (Jago *et al*, 2006). The change to a VSD vacuum pump in week 6 reduced vacuum pump running costs by 55% (from 0.28 to 0.13 c/l).

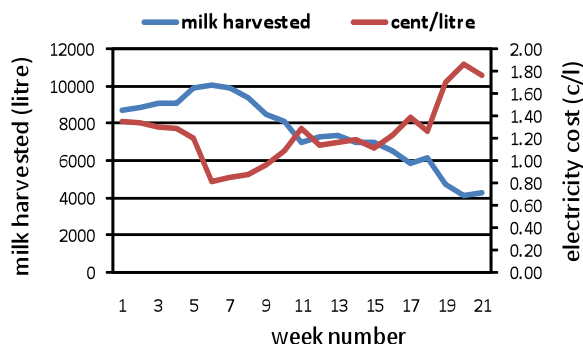


Figure 1. Seasonal variation in electricity costs per litre of milk harvested (c/l) with an AMS system

Conclusions

Average electricity costs of the AMS tested with 63 cows was 1.25 c/l. This is likely to be reduced as cows become familiar with the AMS and optimum herd size/milk output for the AMS is reached. Suitability of a

heat recovery system and cold detergent wash cycles will be investigated in 2012 to moderate running costs further.

* Merlin AMS supplied by Fullwood Ltd

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RMIS Project Number 6098

Milking performance of large Irish dairy herds milked in swing-over parlours

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Introduction

Reform of the European Union Common Agricultural Policy, to remove milk quotas in 2015 is expected to lead to expansion of dairy herds in Ireland (DAFF, 2010). Larger herd sizes exert pressure on scarce labour resources; therefore more efficient milking systems are required. Farmers need to consider capital investment, labour demand and cow health when designing an efficient milking system. Larger parlours with more units require greater capital outlay but have greater potential throughput. In herringbone parlours, this can result in an increase in the time it takes to milk a batch of cows (row time), unless additional labour is added. Longer row times result in over-milking in parlours not fitted with automatic cup removers and this has been linked with deterioration in teat health (Hillerton et al., 2002). The objective of the study was to quantify the cow throughput and udder health of herds milked in twenty herringbone parlours ranging in size from 14 to 44 units in early and late lactation.

Materials and Methods

The farms involved in this study were participants from a single discussion group, the majority of which were located in the Cork region. Average herd size was 234 (range 76 to 381) cows. Fourteen herds were spring-only calving and four calved cows in both spring and autumn. All farms maintained milking cows in a single herd and were managed so as to maximise pasture grass in the diet. One milking session was observed in September/October 2009 (late lactation) and again in April/May 2010 (early lactation). Total herd milking time (from first cups on to last cups off), number of operators and cows milked were recorded. Labour efficiency measures of cows milked per hour and cows milked per operator per hour were calculated for each herd. Operator work routine time (WRT) was calculated by dividing 3600 by cows milked/operator/h. Milking duration (individual cow cups on to cups off), milk flow duration and over-milking duration (defined as the period when cups are attached but there is no milk flow) were determined for an average of 24 cows (selected by position in row and row number) for each milking session. Teat condition including colour and hyperkeratosis were assessed for 100 teats (25 cows per milking session). Associations between efficiency measures, over-milking duration, hyperkeratosis score and parlour size (linear contrasts) were determined by using REML to fit mixed models including stage (early and late lactation), linear parlour size terms, and interactions of Stage with these as fixed effects and farm as a random effect. The interactions of parlour size and stage were not significant so only the main effects are reported.

Results and Discussion

Parlour size was positively associated with cow throughput ($P<0.001$, Figure 1a) but not cows/operator/hour ($P=0.130$, Figure 2b). Although larger parlours were able to achieve higher throughput they were not more labour efficient than smaller parlours as they required more than one operator. WRT was not associated with parlour size ($P=0.154$). The farms achieving the greatest labour efficiency had WRT of 20-21 s/operator/cow. WRT of less than this required an additional operator, and thus became less labour efficient. When the WRT $\times$ units (row time) is greater than individual cow milking time, over-milking will occur. Mean over-milking time was 1.4 ± 0.7 min (range from 0.4 to 2.7 min, early lactation) and 2.3 ± 1.2 min, (range from 0.5 to 4.6 min, late lactation). There was a positive association between parlour size and over-milking duration ($P<0.041$) and hyperkeratosis score ($P=0.049$). Over-milking was positively associated with greater hyperkeratosis in late lactation ($P=0.022$, slope 0.154 $R^2=0.24$).

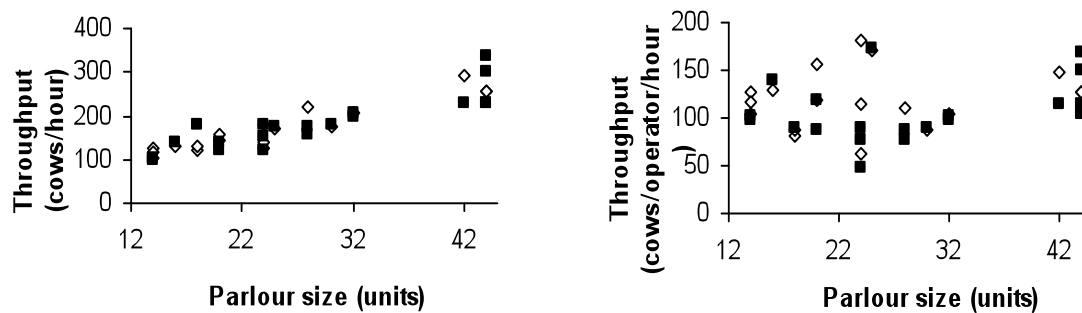


Figure 1. Throughput efficiency (a) and labour efficiency (b) of parlours ranging in size from 14 to 44 units in early (■) and late (◇) lactation.

Conclusions

Larger parlours allow more cows to be milked per hour but are not necessarily more labour efficient. Operators should ensure that row time is matched appropriately to cow milking time. As milking time decreases in late lactation, the WRT may require shortening to prevent over-milking and possible negative impacts on teat end condition and udder health.

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RMIS Project Number 6202

Animal Nutrition and Product Quality

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

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Introduction

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

Materials and Methods

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

Results and Discussion

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

Conclusions

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

Acknowledgements

This work was funded by the Department of Agriculture, Food and the Marine Research Stimulus Fund (RSF 07 526).

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

*Mean square prediction error ‡Relative prediction error

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RMIS Project Number 5793

Predicting grass dry matter intake of Irish spring calving dairy herds

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Introduction

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

Materials and Methods

A dataset of 258 herds was used in the development of the GDMI prediction equations. Grass dry matter intake was estimated using the n-alkane technique (Mayes *et al.*, 1986) as modified by Dillon and Stakelum (1989). The GDMI prediction equations were developed on a herd-basis. The dataset was divided into four periods: early spring (5 Mar-10 Apr), late spring (11 Apr-30 Apr), summer (1 May-31 Jul) and autumn (1 Aug-31 Oct). Equations were generated for each of these periods. The significant predictors of GDMI in these periods were elucidated by multiple regression analysis using SAS (2005). Forward step-wise regression

analysis was used to develop the multiple regression equations. The first GDMI equation generated contained the variables bodyweight, organic matter digestibility, pre-grazing herbage mass and concentrate consumed. Each equation after the first added a single independent variable. If the significance of the calculated F statistic was $P < 0.05$ the variable was retained in the multiple regression equation. Variables were removed from the multiple regression equation if, after the addition of a new variable, the significance of the calculated F statistic became $P > 0.05$. The multiple regression equation with the lowest residual standard deviation (rsd) and highest coefficient of correlation (R^2) in each period was chosen.

Results and Discussion

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

Table 1. Equations to predict grass dry matter intake of spring calving dairy herds during different periods of the year				
	Early spring	Late spring	Summer	Autumn
Herds	39	22	111	86
R^2 (Coefficient of correlation)	0.94	0.80	0.69	0.78
Residual standard deviation (kg)	0.74	0.86	1.08	1.08
Intercept	7.08	6.13	21.74	-13.95
Linear and quadratic coefficients for different animal, grass and supplementation factors				
Age (months)	0.12			
Weight (100 kg)			3.35	3.75
Body condition score at calving			-1.62	
Body condition score during measurement period			1.48	
Week of lactation		0.73		
Days in milk			-0.012	-0.004
Pre grazing herbage mass above 4 cm (t DM/ha)				6.99
(Pre grazing herbage mass above 4 cm) ² (t DM/ha) ²				-1.75×10^{-3}
Daily herbage allowance above 4 cm (kg DM/cow)				0.26
Fill units (0.10 FU/kg DM)			-1.71	
Neutral Detergent Fibre content (10 g per kg DM)		-0.084		
Dry matter content (10 g/per kg)	-0.17			
Post grazing sward height (cm)	1.52	1.20		
Concentrate consumed (kg DM)	-0.65	-0.55	-0.72	-0.61

Conclusions

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

Acknowledgements

This work was funded by the Irish Department of Agriculture, Food and the Marine Research Stimulus Fund (RSF 07 526).

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RMIS Project Number 5793

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

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Introduction

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

Materials and Methods

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

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

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

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

Results and Discussion

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

Conclusions

The results showed that residues of nitroxylin, levamisole and oxclozanide will be present in milk after administration, will be partitioned with the skim-milk and will be present in a subsequent powder product.

Thus, sufficient caution must be exercised with regard to withdrawal periods to ensure avoidance of risk to public health.

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RMIS Project Number 6203

The effects of milking machine wash volumes on TCM residues in milk

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Introduction

High fat dairy products, such as milk and butter can be contaminated with a residue called trichloromethane (TCM) during processing. TCM target levels of $<0.002 \text{ mg kg}^{-1}$ in milk have been set by countries importing butter products in order to achieve the required minimum levels in the finished product ($<0.03 \text{ mg kg}^{-1}$). TCM results from the use of chlorine detergent/sterilizer solutions as part of the equipment cleaning process. If chlorine comes into contact with milk TCM is formed (Tiefel and Guthy, 1997). An increase in the formation of TCM occurs in recycled detergent solutions when post rinsing is omitted from the milking machine wash procedure (Resch, and Guthy, 2000). Various volumes of rinse water are used on-farm as part of the milking machine cleaning process. A rinse volume of 14 L per milking unit has been recommended for effective cleaning. (O'Brien, 2009). The objective of this study was to investigate the effect of four rinse water volumes (7, 10, 14 and 16.5 L/milking unit) on TCM levels in milk.

Materials and Methods

A circulation cleaning procedure was conducted in a 30-unit milking machine plant. The cleaning stages included (a) an initial pre-wash rinse with cold water at a volume of 14 L per milking unit, (b) a hot (70°C) detergent/sterilizer wash at a water volume of 12 L/milking unit and (c) a post-wash rinse with cold water with different water volumes of 7, 10, 14 and 16.5 L/milking unit. The sterilizer element of the cleaning product contained a working solution of 263 ppm of chlorine. Each rinse water volume was evaluated over a 5-day period (10 milking events). Two milk samples (100 mL per sample) were obtained from the milk line during am and pm milking. The experimental dairy farm milking management procedure involved a milking interval of 17/7 (17 h between evening and morning milking and 7 h between morning and evening milking). Sample one was taken at the start of milking (first milk) as the initial milk was pumped from the receiver jar and the second sample was taken mid-way through milking (mid milk). Milk samples were analysed for TCM using head-space gas chromatography. Statistical analysis included a repeated measures model using ProcMixed in SAS 2009. The model included terms for rinse water volume (L), stage of sampling (first, mid), time (am, pm) and their interactions. Pair-wise comparisons were performed and a Tukey-Kramer adjustment was employed.

Results and Discussion

Reducing the rinse water volume from 16.5 to 7 L per milking unit resulted in an increase in TCM concentration of 0.004 mg kg^{-1} in the combined morning and evening milk samples ($P<0.001$). No statistical difference in milk TCM concentration was observed when 10 L per milking unit was employed compared to the recommended rinse volume of 14 L per milking unit. Reducing the rinse water volume from 16.5 to 14 L per milking unit resulted in an average increase in TCM concentration of 0.002 mg kg^{-1} ($P<0.05$) in the 'first milk' sample but not in the 'mid milk' sample (Table 1). Furthermore, milk TCM concentrations were highest at 'first milk' ($0.0097 \text{ mg kg}^{-1}$) with a water rinse volume of 7 L per unit compared to the three other rinse volumes ($P<0.05$). This effect was observed due to the 'first milk' sample being the first milk to come in contact with the cleaned equipment surface during the milking and TCM in the 'mid milk' sample being diluted by the larger milk volume during the main milking period. When data for am and pm milkings were compared, the average concentrations of TCM were generally higher at the pm milking compared to the am ($P<0.01$). The shorter interval prior to pm milking means reduced time for drainage of rinse water from the plant and reduced milk yield at that milking. The combined effects of rinse water in the milkline being diluted with a lower milk volume may explain the higher TCM concentrations at pm milking.

Table 1. Effect of varying the rinse water volume of a milking machine wash routine on TCM concentrations						
	Trichloromethane concentration obtained, mg kg⁻¹				sed	P-value
Rinse volume	16.5 ^b	14 ^a	10 ^a	7 ^c	0.10	***
First Milk	0.0020 ^c	0.0040 ^b	0.0044 ^b	0.0097 ^a	0.12	*
Mid Milk	0.0009 ^b	0.0013 ^{ab}	0.0006 ^b	0.0017 ^a	0.17	*
Am	0.0018 ^b	0.0019 ^b	0.0015 ^b	0.0038 ^a	0.10	**
Pm	0.0014 ^c	0.0033 ^b	0.0036 ^b	0.0076 ^a	0.10	**
Means with a common superscript are not significantly different; *** <0.001; ** <0.01; * <0.05						

Conclusions

Increasing rinse water volume will reduce TCM residue levels in bulk milk. The implementation of the recommended volume of rinse water (14L/milking unit) was highly critical in minimising the accumulation of TCM in milk. A higher rinse water volume of 16 L per milking unit will minimize TCM residues in the 'first milk' and where milk volumes are low.

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RMIS Project Number 6203

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

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Introduction

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

Materials and Methods

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

Results and Discussion

All disinfectant products resulted in a significant reduction in milk TBC (P<0.01) (Table 1). Chlorine reduced levels of thermophilic bacteria after disinfection (P<0.01). The levels of thermophilic bacteria present prior to disinfection were low for both PA treatments (<75cfu) and this may account for no significant reduction in thermophilic counts being observed after disinfection. The biocide disinfectant foamed during plant circulation to an unsatisfactory extent. All disinfectant products resulted in milk TCM levels within the acceptable target

level of 0.002 mg/kg. However, chlorine had significantly higher ($P<0.01$) TCM levels after plant disinfection. The inclusion of PA in the rinse cycle did not eliminate TCM. High numbers of bacteria are present on claw-piece internal plastic surfaces after detergent cleaning (Gleeson *et al.* 2011). The inclusion of either PA or chlorine in the rinse water reduced TBC on plastic surfaces ($P<0.01$).

Conclusions

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

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

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

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RMIS Project Number 6237

GRASSLAND RESEARCH PROGRAMME

Grass Breeding (incl establishment & renovation)

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

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Introduction

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

Material and Methods

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

Results and Discussions

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

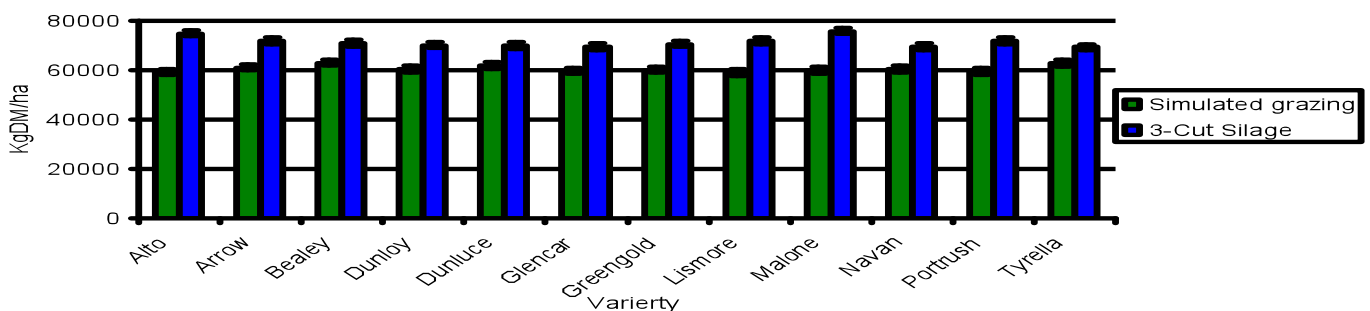


Fig 1: Cumulative DM yield for 2 Managements across 5 years

Conclusions

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

Acknowledgments

The authors wish to acknowledge funding received by the Department of Agriculture, Food and the Marine Research Stimulus Fund RSF.

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RMIS Project Number 5793

Grass Growth, Sward Dynamics & Utilisation under Grazing

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

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Introduction

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

Material and Methods

Daily data for the spring period from 1982 to 2010 at Teagasc Moorepark (January to April, weeks 1 to 17, 300 observations) were converted into average weekly data. The meteorological data analysed included minimum, maximum and mean air temperatures (°C), soil temperatures at 50 and 100 mm (°C), sunshine hours (h), solar radiation (MJ/m²), rainfall (mm), calculated evapotranspiration (ET) with Hargreaves's formula (mm) and calculated day length (h). Weekly grass growth was measured using the methodology described by Corral and Fenlon (1978). A regression analysis of weekly meteorological factors and weekly grass growth rates was performed in SPSS with the meteorological factors as the independent variables and grass growth as the dependent variable. The stepwise option was chosen to enter the significant variables at the 5% level and to remove at the 1% level. Data was also used to investigate the start date of grass growth; grass growth was considered to have actively commenced when it was 10 kg DM/ha/day.

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

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

B is the unstandardized coefficients of the variables

t and F are significant at the 0.001 level (***)

Results and Discussion

The meteorological factors having the greatest effect on spring grass growth were ET, soil temperature at 100 mm and maximum air temperature with an R² of 0.70 (Table 1). The three variables showed a positive relationship with grass growth (Figure 1). Temperature affects many physiological and growth functions of perennial ryegrass, including photosynthesis, respiration, spring growth, heading date and senescence. It took an average of 64 days from 1st January for grass growth rates to reach 10 kg DM/ha/day or greater over the 29 years; the maximum number of days required were 113 days in 1986, and the minimum was 36 days in 2008. Grass growth occurs provided soil temperatures are not lower than 5°C.

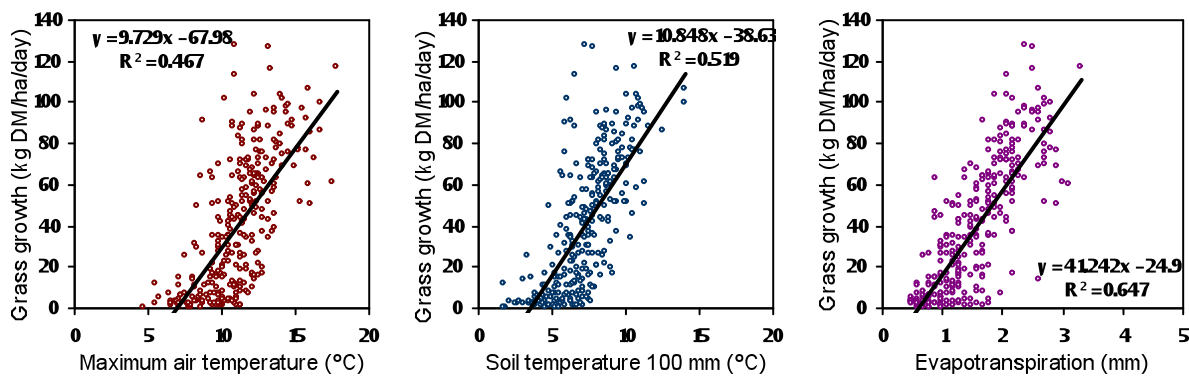


Figure 1. Relationship between grass growth and maximum air temperature, soil temperature at 100 mm and evapotranspiration in spring at Moorepark from 1982 to 2010.

Conclusions

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

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RMIS Project Number 5903

Cultivar influences milk production of grazing dairy cows

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Introduction

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

Material and Methods

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

Results and Discussion

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

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

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

SE=standard error

Conclusions

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

Acknowledgements

The authors wish to acknowledge Moorepark farm staff.

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RMIS Project Number 6091

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

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Introduction

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

Material and Methods

Four cultivars of perennial ryegrass were sown in a split plot design with 4 reps. The cultivars included 2 tetraploids: Bealey (heading date 24th May) and Astonenergy (31st May) and 2 diploids: Spelga (22nd May) and Abermagic (28th May). Cultivars were sown in 2009. From mid March to May 2011 (P1), paddocks were grazed with lactating dairy cows for an eight week period. Cows were offered 16 kg DM cow⁻¹ d⁻¹. From May to August (P2), paddocks were grazed for a 12 week period. Cows were offered 17 kg DM cow⁻¹ d⁻¹. A similar rotation length was maintained for each cultivar. During weeks 2, 4, 6 and 8 in P1, and weeks 3, 6, 9 and 12 in P2, sward measurements were completed. Within each measurement period the following was completed: pre and post grazed sward height; herbage mass; extended tiller height and sheath heights was measured on 100 tillers in the pre and posts grazed sward; herbage was sampled to ground level for each cultivar and

a sub-sample of 50g fresh weight was separated into leaf stem and dead content, before being dried at 80°C overnight. Height was measured daily, with all other measurements occurring twice during each measurement week. Data were analysed using Proc Mixed in SAS. The model included period, season, cultivar and the interaction between season and cultivar.

Results and Discussion

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

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

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

SE=standard error

Conclusions

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

Acknowledgements

The authors are grateful for the assistance of Moorepark farm staff and in particular Mr. M. Feeney for assistance with measurements.

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RMIS Project Number 6091

Sward composition dynamics in perennial ryegrass binary mixtures

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Introduction

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

Materials and Methods

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

Results and Discussion

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

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

	August 2009	October 2010	October 2011
AberMagic/Twystar	85:15	82:18	85:15
	70:30	80:20	72:28
	50:50	61:39	64:36
	30:70 ^a	21:79 ^a	58:42 ^b
	15:85	19:81	26:74
AberMagic/Greengold	85:15 ^a	47:53 ^b	60:40 ^b
	70:30 ^a	49:51 ^b	54:46 ^{ab}
	50:50	55:45	40:60
Twystar/Greengold	85:15 ^a	51:49 ^b	50:50 ^b
	70:30 ^a	46:54 ^b	31:69 ^b
	50:50	42:58	46:54
		P value	SED
	Period	0.01	1.72
	Treatment	0.001	4.22
	Treatment*Period	0.001	

SED= Standard error of the difference; ^{abc} values not sharing a common subscript within row differ significantly ($P < 0.05$).

Conclusions

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

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RMIS Project Number 6091

Effect of white clover inclusion in perennial ryegrass swards on herbage and milk production under frequent tight grazing conditions

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Introduction

White clover inclusion in swards can make an important contribution to the sustainability of ruminant production systems (Peyraud et al., 2009) due to its ability to fix atmospheric nitrogen (N). Mixed swards with high N fertiliser are highly productive but N fertiliser application can reduce sward clover content (Ledgard and Steele, 1992). However, frequent grazing can enhance clover productivity in mixed swards (Black et al., 2009). The objective of this study was to compare the herbage and milk production output from grass only and grass clover swards under frequent tight grazing conditions at a high N input level.

Materials and Methods

Two swards, grass only (GR) and grass clover (GC), were sown at the Dairygold Research Farm, Teagasc, Moorepark, Fermoy, Co.Cork in May 2010. The GR swards were a 50:50 mix of Abermagic and Tyrella perennial ryegrass sown at 37 kg/ha. The GC swards contained the same grass mix as above plus a 50:50 mix of Chieftan and Crusader white clover sown at 5 kg/ha. Swards received 240 kg N/ha/year. Thirty cows were randomly allocated to graze each treatment from 17 April to 30 October 2011. Rotational grazing was used and swards were strip-grazed, with fresh herbage offered daily (16 kg herbage dry matter (DM)/cow/d and 1 kg concentrate/cow/d). Pre-grazing herbage mass was measured three times per week using an Etesia mover (Etesia UK. Ltd., Warwick, UK). Pre- and post-grazing sward heights were recorded daily using a Rising Plate Meter (Jenquip, Feilding, New Zealand). Grass and clover components of an herbage sample were separated to estimate sward clover content twice weekly. Milk production was recorded daily and milk composition weekly. Data were analysed using General Linear Models for repeated measures in SAS (SAS, 2005). The statistical model investigated the effect of treatment and time. Covariates used were days in milk and average milk production for the three weeks prior to the start of the experiment.

Results and Discussion

Treatment effect on milk production is shown in Table 1. Cows grazing GC swards produced milk with lower fat and lactose content ($P<0.05$), but tended to have higher milk yield ($P=0.08$). Milk solids yield per day and cumulatively did not differ between treatments. The GC swards tended to have higher pre-grazing sward height (9.7 vs. 9.2 cm; sem 0.23; $P=0.06$). There was no effect of treatment on pre-grazing herbage mass (1720 kg DM/ha; sem 46.3; Fig. 1), post-grazing sward height (4.1 cm; sem 0.06) or total herbage production (12651 kg DM/ha; sem 395.9). Sward clover content on the GC swards increased from 8.8% (DM basis) in April to 19.8% in October, peaking in late August at 22.8% (Fig. 1). Average clover proportion of the GC swards (13%) was low, but was still higher than values observed (3%) in a previous experiment with similar environmental conditions and N application level (Humphreys et al., 2008).

Table 1. Effect of grass only and grass clover swards on milk production and composition (17 April to 30 October)

	Grass Only	Grass Clover	SEM	P value		
				Treat	Week	Treat*Week
Milk yield (kg/day)	19.2	19.5	0.23	0.08	***	NS
Milk solids yield (kg/day)	1.50	1.50	0.003	NS	***	NS
Milk fat (g/kg)	43.7	42.5	0.81	***	***	***
Milk protein (g/kg)	36.3	36.4	0.06	NS	***	NS
Milk lactose (g/kg)	46.1	45.9	0.14	*	***	NS
Cumulative milk yield (kg/cow)	3765	3829	113.4	NS	-	-
Cumulative milk solids (kg/cow)	294.5	293.6	9.09	NS	-	-

*** = $P<0.001$; *= $P<0.05$; NS = Non significant

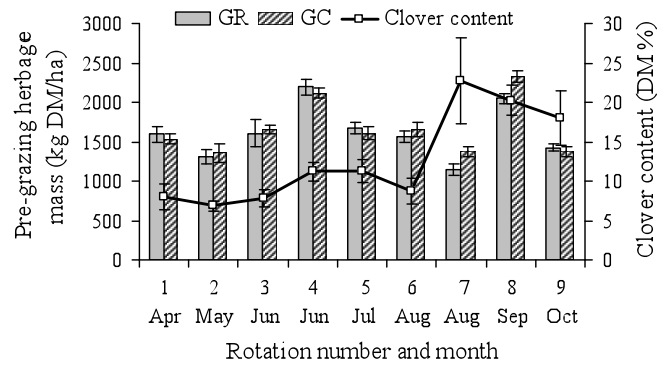


Figure 1.Pre-grazing herbage mass and sward clover content of the grass clover swards

Conclusions

Grass clover swards had similar herbage production to grass only swards, in a high N application grazing system. Clover swards supported high milk yields per cow and changed milk fat and lactose composition. Further differences between treatments could be expected if the sward clover content was higher throughout the year.

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RMIS Project Number 6120

Nutrient Management

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

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Introduction

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

Materials and Methods

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

Results and Discussion

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

Conclusion

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

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

NS, not significant; **, $P < 0.01$; ***, $P < 0.001$

RMIS Project Number 5903

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

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Introduction

Urinary N has a high potential for leaching (Haynes and Williams, 1993) and urine patches account for approximately 25% of the paddock area over the year (Haynes and Williams, 1993). Hence, urinary N leaching can be a major issue. Moir *et al.* (2007) reported that dicyandiamide (DCD) reduced nitrate (NO₃⁻) leaching under urine patches by slowing the conversion of ammonium (NH₃⁺) to NO₃⁻ in the soil, thereby increasing the quantity of available N in the soil. Dicyandiamide applied at a rate of 10 kg ha⁻¹ can reduce NO₃⁻ leaching by 45% and nitrous oxide (N₂O) emissions by 70% under dairy cow urine (1000 kg N ha⁻¹) patches in Irish soils (Selbie *et al.*, 2011). Therefore, N emissions from pastures can be significantly reduced by applying DCD to pastures. Recently there has been increasing interest in supplementing animals with nitrification inhibitors, so that the nitrification inhibitor is excreted with the urine and can work directly on the urine patch eliminating the requirement for broadcast application in the field. Ledgard *et al.* (2008) demonstrated that at least 86% of DCD infused into the rumen or abomasum of sheep was excreted in the urine. There is no published research on the effects that the infusion of DCD may have on the rumen function of dairy cows. Rumen parameters such as pH and volatile fatty acids (VFA) are an important factor in relation to animal health, performance and welfare (de Veth and Kolver, 2001). Therefore, the objective of this study was to investigate the effects on dairy cow rumen function of infusing the nitrification inhibitor dicyandiamide (DCD) into the rumen.

Materials and Methods

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

Results and Discussion

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

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

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

^a Standard error of mean

^b (acetic + butyric) / propionic

Conclusion

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

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RMIS Project Number 5903

Grass Feed & Value

Effect of closing date on dry matter yield and leaf proportion in perennial ryegrass swards during the early winter period

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Introduction

Herbage growth in Ireland is highly seasonal with peak growth rates in summer and little or no growth in winter (Brereton, 1995). During the winter period, growth of perennial ryegrass (PRG; *Lolium perenne* L.) is characterised by a reduction in leaf extension rate and an increase in leaf senescence rate (Hennessy *et al* 2008). It is common to feed livestock indoors with conserved forage and concentrate for the winter period. One alternative is to accumulate grass so that it can be grazed *in situ* thereby extending the grazing season into the autumn/winter period. The objective of this study was to investigate the effect of closing date on herbage mass (HM), sward morphology, sward chemical composition and PRG population (sward density) throughout the early winter period (October-November).

Materials and Methods

A one year old PRG sward (79% PRG) at Teagasc Moorepark, Fermoy, Co. Cork, which was previously grazed, was divided into 24 (3 x 5 m) plots. The study was a randomised block design with 2 x 4 factorial arrangement of treatments, replicated three times. Two closing dates (CLD: 8 August (E) and 15 September (L), 2011) were defoliated on four harvesting dates (HD: 3 October (HD1), 17 October (HD2), 31 October (HD3) and 14 November (HD4)). In total, the sward received 230 kg fertiliser nitrogen during the year. Plots were harvested with an Etesia rotary blade mower to a stubble height of 4 cm across all treatments. The herbage removed from each plot was weighed and sampled to determine HM. A 100 g sub-sample was dried for 48 h at 40°C to measure the dry matter (DM) content of the sample and calculate the DM yield/ha. The dried sample was then milled and analysed for dry matter digestibility (DMD) and crude protein using near infra-red spectrometry (NIRS). Prior to harvesting, tillers were sampled by cutting to ground level using a scissors and a 40 g subsample was separated into leaf, stem and dead components above and below a 4 cm stubble height. Also, three 10 cm² turves were taken from each plot. The tillers of PRG, weed grass and broad leaf weeds were counted on each sod sample to assess sward density and PRG proportion. Data were analysed using PROC MIXED in SAS 2006, CLD, HD, CLD*HD and replicate were included in the model.

Results and Discussion

There was an interaction between HD and CLD ($P < 0.05$). DM yield per ha increased with both closing dates for HD1, HD2 and HD3 however DM yield on the E-CLD plots reached its maximum earlier than the L-CLD plots (Table 1). The E-CLD plots had a significantly higher proportion of PRG tillers in the sward compared to the L-CLD, (0.85 and 0.75, respectively; $P < 0.05$). The average number of PRG tillers/m² decreased notably ($P < 0.01$; Table 1) with later harvesting dates. This suggests that PRG tiller density decreased as HM increased from HD1-HD4. Higher HM can lead to a reduction in light interception and hence shading of tillers causing tiller death. The results also showed an increase in weed grass tillers between E-CLD and L-CLD plots (947 vs. 1949 tillers/m², respectively; $P < 0.01$). There was an interaction between HD and CLD in terms of leaf proportion in the sward ($P < 0.05$; Table 1). There was a decrease in leaf proportion in the >4 cm horizon of the sward, as closing date progressed. There was a slower decline in leaf proportion >4 cm in the L-CLD plots (due to the appreciably higher leaf proportion >4 cm on HD2 and HD3). Considering these results, there was still a larger leaf yield of PRG in the E-CLD over all HD due to the higher DM yields achieved. There was no effect of CLD on sward chemical composition but as HD increased DMD declined ($P < 0.001$).

Conclusions

The earlier closing date resulted in higher overall herbage mass accumulation. As DM yield increased there was a decline in leaf proportion above a 4 cm stubble height and in PRG tiller density. Hence, as grazing date moves later into the season, herbage quality will decrease, in terms of leaf proportion and (DMD). Further investigation is required, but this study shows that swards reach a maximum DM yield during autumn irrespective of rotation length.

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Table 1. The interaction of closing and harvesting dates on DM yield and leaf proportion

CLD	08 Aug				15 Sep				Significance			
HD	3/10	17/10	31/10	14/11	3/10	17/10	31/10	14/11	SED	HD	CLD	INT
DM/ha	1925 ^a	2649 ^c	2778 ^c	2641 ^c	889 ^b	1632 ^d	1960 ^a	1977 ^a	88.0	<0.001	<0.001	<0.05
Leaf>4	0.82 ^a	0.63 ^b	0.65 ^b	0.55 ^b	0.80 ^a	0.80 ^a	0.78 ^a	0.52 ^{bc}	0.05	<0.001	<0.05	<0.05
TLR/m ²	7328	6000	4883	4644	5983	6100	5234	4584	730.4	<0.01	0.581	0.507

CLD=Closing date, HD=Harvesting date, INT=Interaction of HD*CLD, DM/ha= kg, Leaf>4, = Proportion of leaf above a 4 cm high stubble, TLR/m²=No. PRG tillers/m², SED= Standard error of difference

RMIS Project Number 5798

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

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Introduction

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

Materials and Methods

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

Results and Discussion

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

desired PGSH. The quantity of grass utilised (>2.7 cm) was, however, maximised ($P<0.001$) by grazing to 2.7 cm (918 kg DM/ha) when compared to 3.5 cm (779 kg DM/ha) and 4.2 cm (764 kg DM/ha).

Table 1. Effect of post-grazing height (PGSH) on animal performance during the early lactation period					
	PGSH treatment ¹				
	S	M	L	SED	P
Milk yield, kg/d	22.5 ^a	23.6 ^b	25.1 ^c	0.51	0.001
Milk fat, g/kg	43.9 ^a	46.8 ^b	45.9 ^b	0.91	0.015
Milk protein, g/kg	33.1 ^a	34.1 ^b	34.0 ^b	0.35	0.022
Milk lactose, g/kg	46.8	46.9	47.0	0.22	0.636
Milk solids yield, kg/d	1.75 ^a	1.91 ^b	2.00 ^c	0.046	0.001
End BW, kg	442 ^a	451 ^{ab}	464 ^b	7.3	0.019
End BCS	2.71 ^a	2.80 ^b	2.87 ^b	0.041	0.004

¹PGSH: S (2.7 cm), M (3.5 cm), L (4.2 cm); ^{a-c} Means within a row with different superscripts differ

Conclusions

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

References Format incorrect

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RMIS Project Number 5798

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

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Introduction

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

Materials and Methods

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

n-alkane technique (Dillon and Stakelum, 1989) and measured in May and August. Data were analysed using covariate analysis and the PROC MIXED statement of SAS with terms for parity, treatment and the interaction of parity and treatment. Pre-experimental values for what? were used as covariate in the model.

Results and Discussion

Mean DHA was 13.3 and 15.5 kg/cow/day (>3.5cm) and mean PGSH achieved was 3.7 and 4.7 cm for the S and M treatments, respectively ($P<0.001$). The M cows had greater pre-grazing height (+0.61 cm; $P<0.05$), and daily area/cow (+11 m²; $P<0.001$). Grazing to 3.7 cm improved grass utilisation by +0.13 compared to grazing to 4.7 cm (0.81; $P<0.001$). The M cows had a greater ($P<0.001$) milk yield (+1.6 kg/d unnecessary, can be calculated from the table!), milk fat (+54 g/d), milk protein (+68 g/d), milk lactose (+79 g/d) and milk solids (+0.12 kg/d) yields than the S cows (Table 1). Milk protein concentration was also improved (+0.6 g/kg; $P<0.01$) on the M treatment.. The first GDMI measurement period (May) showed that grazing to a PGSH of 4.7 cm increased GDMI by 1.5 kg DM/cow/d (17.1 kg DM/cow/d; $P<0.01$). The relatively low level of DHA offered to the S cows mainly contributed to the decline in GDMI which, therefore, resulted in milk and milk solids production losses. No difference in terms of end BCS was observed between treatments, the M animals however were heavier (+12 kg; $P<0.01$) than their counterparts (499 kg). Grazing pastures to 4.7 cm resulted in increasing ? unclear ($P<0.001$) cumulative milk production by 311 kg/cow and cumulative milk solids production by 22 kg/cow when compared to grazing to 3.7 cm (3236 kg milk/cow and 255 kg milk solids/cow, respectively).

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

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

¹PGSH: S (3.7 cm), M (4.7cm)

Conclusions

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

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RMIS Project Number 5798

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

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Introduction

National variety evaluation schemes for perennial ryegrass (*Lolium perenne* L.) assess the potential agronomic value of grass varieties for ruminant-based production systems based on seasonal and annual productivity, persistence and nutritive quality (Grogan & Gilliland, 2011). The use of animal production indices would greatly assist in identifying the merits of a variety. However, such indices are often unavailable

for evaluation schemes due to the scale and cost of operation required to account for animal variation (Camlin, 1997). The use of near infrared reflectance spectroscopy (NIRS) has been identified as a technique that could rapidly assess the expected intake of a grass variety (Agnew *et al.*, 2004). The near infrared spectra contain information on the underlying chemical composition of forage samples thereby providing the opportunity to predict their expected intake. This research was undertaken as a preliminary assessment of the ability to assess expected intake by NIRS.

Materials and Methods

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

Results and Discussion

The NIRS calibration model provided a disappointing estimate of expected intake ($R^2 = 0.467$; Figure 1) which can partially be attributed to error associated with the n-alkanes technique. Agnew *et al.* (2004) were able to develop a calibration model to predict the short term intake (kg DM per hour) of ryegrass dominant swards with a higher degree of accuracy ($R^2 = 0.76$).

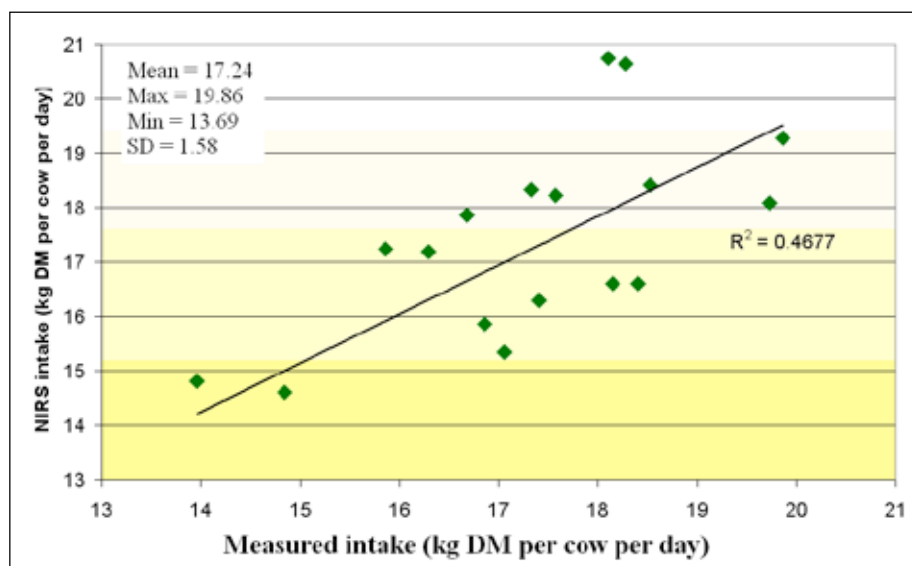


Figure 1. Scatter graph comparing the measured intake (unrestricted) as assessed by the n-alkanes technique (x-axis) to the expected intake predicted by NIRS (y-axis)

In part, the latter can be attributed to the larger calibration set ($n = 203$) that likely encompassed more variation (relative standard deviation = 27 %) than the current study (RSD = 9 %) and had a larger range in intake values. No significant correlation was found between intake and *in vitro* DMD or WSC. This may also reflect the small size of the current dataset. The n-alkanes technique provides a medium term assessment of intake (kg DM per cow per day) which may allow a wider array of factors to affect the intake. Thus, a larger calibration set that encompasses more variation in intake is required. Variety evaluation schemes normally involve mechanical harvesting which causes different sward morphology to that when grazed. Thus further study into the effect of management on the robustness of calibration models would also be required prior to implementing intake indices into national variety evaluation schemes for perennial ryegrass.

Conclusions

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

Acknowledgments

Department of Agriculture, Food and the Marine Research Stimulus Fund 07 529; field staff at Moorepark; A. Melville.

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RMIS Project Number 5893

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

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Introduction

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

Materials and Methods

Immediately prior to grazing, herbage morphological composition was determined on four monoculture grazing swards. The grass cultivars were: Bealey (intermediate tetraploid), Astonenergy (intermediate tetraploid), Spelga (intermediate diploid) and Abermagic (intermediate diploid). Swards were grazed by dairy cows to a 4 cm post-grazing height. The area for each cultivar was subdivided into 4 replicates, each measuring 361 m². Grass samples were taken once in each replicate in each rotation, from May to October, with eight rotations completed during this period. Grass samples were cut to ground level using a scissors and the vertical structure of the sward was preserved. The samples were divided into two portions: >4 cm and <4 cm stubble height. The >4 cm section was manually separated into L, PS, S and D material. The dry matter (DM) content of each fraction was determined by drying at 40°C for 48 h. Data (L, PS, S and D proportion expressed on a DM basis) were analysed using PROC MIXED in SAS with terms for replicate, rotation number, cultivar and the interaction of cultivar and rotation number.

Results and Discussion

There was a cultivar × rotation interaction ($P < 0.001$) for all four morphological fractions. In mid May Astonenergy had a higher ($P < 0.05$) proportion of L than Abermagic. At the same time Astonenergy had a lower ($P < 0.05$) S proportion compared to Abermagic and Spelga. At the start of June Astonenergy had a higher ($P < 0.01$) proportion of L than Bealey and Spelga. At this time both Astonenergy and Abermagic had a lower ($P < 0.01$) proportion of S than Bealey and Spelga. At the end of June Astonenergy had a higher ($P < 0.05$) proportion of L and lower proportion of S than the three other cultivars. At the end of July, Astonenergy had a higher ($P < 0.05$) proportion of L than Bealey. From mid August onwards for L proportion and from mid July onwards for S proportion there were no significant differences between the cultivars. High L and low S content is desirable as L is usually more digestible than S. Lewis *et al.* (2011) found that cows grazing Astonenergy spent more time with a low rumen pH ($< \text{pH} 5.2$) in the April-June period which appear to be driven by the higher L proportions as reported here, reflecting reports of Astonenergy being highly digestible (DARD, 2010).

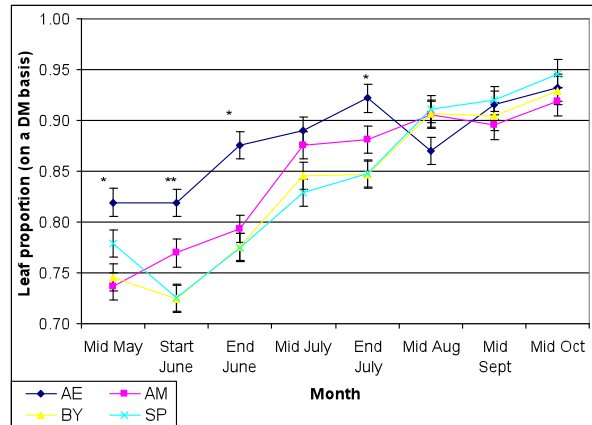


Figure 1. Leaf proportion (expressed on a DM basis) for four cultivars during eight grazing rotations

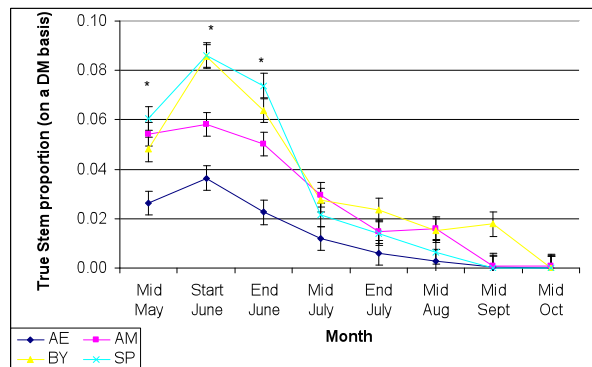


Figure 2. True stem proportion (expressed on a DM basis) for four cultivars during eight grazing rotations

Conclusions

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

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RMIS Project Number 5893

Grazing Management incl Conservation

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

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Introduction

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

Materials and Methods

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

Results and Discussion

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

Table 1: Effect of closing date and treatment on winter herbage production										
	PGSH3.5cm			PGSH4.5cm				Significance		
Closing Date	CD1	CD2	CD3	CD1	CD2	CD3	Sed	CD	PGSH	Inter
Feb DM yld (kg/ha)	668	427	321	787	635	406	35.1 1	0.0001	0.002	0.370
GR to Feb (kg/day)	1.3	0.0	1.0	2.0	0.0	0.0	0.92 1	0.364	0.927	0.747
Feb Leaf yld >3.5cm (kg/ha)	437	319	328	616	542	324	31.0 4	0.002	0.004	0.110
Feb Dead yld >3.5cm (kg/ha)	81	30	24	77	75	24	14.2 4	0.030	0.380	0.320

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

Leaf yields (>3.5) in December for all closing dates were 803, 632 and 496 kg DM/ha, for CD1, CD2 and CD3 respectively, however they were 276, 201 and 170 lower at opening in February. Both CD and PGSH had a significant effect on leaf yield (>3.5cm) at opening (15 February) with CD1 (527kg DM/ha) yielding 95kg and 200kg DM/ha more than CD2 and CD3, respectively. Imposing a PGSH of 4.5cm at closing

increased ($P < 0.01$) leaf yield $> 3.5\text{cm}$ (132.7 kg DM/ha) when compared to PGSH3.5. As CD was delayed the proportion of dead material present at opening was reduced ($P < 0.05$; Table 1).

Conclusion

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

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RMIS Project Number 6186

Sustainable Production Systems & System Analysis

Sand Filters as a tertiary treatment for dairy soiled water exiting aerobic woodchip filters

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Introduction

Washing-down parlours and standing areas following milking on dairy farms produces dairy soiled water (DSW) that contains variable concentrations of nutrients. The most common method of treatment is application to land. However, this can be associated with a pollution risk for water. Aerobic woodchip filters can remove organic matter, nutrients and suspended solids (SS) in DSW, but the effluent exiting the filters may have to be further treated before it is suitable for re-use for washing yard areas. This study looked at the performance of a single-layer sand filter (SF) and a stratified SF, to polish effluent from a woodchip filter was investigated over 82 days.

Materials and Methods

Two types of SFs were compared at laboratory-scale (three replicates): (1) stratified SFs and (2) single-layer SFs. Filters were 0.3 m in diameter; stratified SFs were 1 m deep and single-layer SFs were 0.9 m deep. The stratified SF consisted of a 0.25 m-deep layer of distribution stone (6 - 10 mm diameter), underlain by a 0.2 m-deep layer of coarse sand (effective size, D_{10} , 0.5 - 1.0 mm), a 0.075 m-deep layer of distribution stone, a 0.1 m-deep layer of medium sand (D_{10} , 0.4 - 0.8 mm), a 0.075 m-deep layer of distribution stone and a 0.2 m-deep layer of fine sand (D_{10} , 0.2 - 0.63 mm). The bottom layer of sand was underlain by a 0.1 m-deep layer of distribution stone. The stratified SF consisted of a 0.1 m-deep distribution layer (6 -10 mm in size) underlain by a 0.7 m-deep layer of fine sand (D_{10} , 0.2 - 0.63 mm) and a 0.1 m-deep layer of washed stone (6-10 mm in size). Effluent from a farm-scale woodchip filter treating fresh DSW (Ruane et al., 2011) was loaded onto the SFs at a loading rate of $20 \text{ L m}^{-2} \text{ d}^{-1}$. Effluent from each SF was collected twice weekly and analysed for SS, unfiltered chemical oxygen demand (COD) (COD_T) and filtered COD (COD_F), unfiltered Total Nitrogen (TN_T) and filtered TN (TN_F), ammonium-N ($\text{NH}_4\text{-N}$), nitrite-N ($\text{NO}_2\text{-N}$), and ortho-phosphorus ($\text{PO}_4\text{-P}$). Samples of influent and effluent from all six SFs, taken on days 62 and 75, were also analysed for total coliform (TC) content.

Results and Discussion

The influent COD concentration in this study was higher than most other studies using SFs to treat wastewater that had undergone at least primary treatment. Influent concentrations of COD_T were, on average, $1991 \pm 296 \text{ mg L}^{-1}$. The single-layer SF decreased the influent concentration by 39% and the stratified SF achieved an average decrease of 56%. An average influent COD_F concentration of $1073 \pm 221 \text{ mg L}^{-1}$ was measured and removal rates of 38 and 55% were achieved by the single-layer and the stratified SF, respectively. The removal rates achieved by the stratified SF were significantly better ($P < 0.001$) for both COD_T and COD_F . This would indicate that the stratified SFs were better at decreasing the soluble fraction of the influent as well as the fraction associated with influent SS. Therefore, both physical filtration and the oxidation of organic compounds may have contributed to the decrease in concentrations of COD_T and COD_F . Removal rates of SS for the stratified SF were significantly better than the single-layer SF ($P < 0.001$). Straining is the main mechanism of removing SS in SFs with interception, impaction and adhesion contributing to the overall reduction of solids in the effluent (Prochaska and Zouboulis, 2003). Influent concentrations of TN_T had a mean of 163 mg L^{-1} . The single-layer SF decreased the influent by, on average, 36% and the stratified SF by 57% ($P < 0.001$). Influent $\text{NH}_4\text{-N}$ concentration decreased from $42 \pm 17 \text{ mg L}^{-1}$ to $24 \pm 7 \text{ mg L}^{-1}$ in the single-layer SF and to $21 \pm 4 \text{ mg L}^{-1}$ in the stratified SF, representing a decrease of 34 and 41%, respectively ($P > 0.05$). As the SFs were aerobic, the principal mechanism for the decrease in $\text{NH}_4\text{-N}$ was nitrification. As $\text{NH}_4\text{-N}$ decreases were likely due to nitrification, it was expected that $\text{NO}_2\text{-N}$ and $\text{NO}_3\text{-N}$ concentrations might increase in the effluent. However, the single-layer SF decreased $\text{NO}_2\text{-N}$ and $\text{NO}_3\text{-N}$ by 33 and 27% and the stratified SF by 50 and 4%, respectively ($P > 0.05$). Due to the retention of Particulate N and Total Organic N within both sets of filters: mineralisation of organic N would have affected $\text{NH}_4\text{-N}$ removals, which, in turn, may have affected nitrification rates. The influent concentration of $\text{PO}_4\text{-P}$ was, on average, $27.3 \pm 6.9 \text{ mg L}^{-1}$. The single-layer SF decreased the influent concentration by 58% and the stratified SF achieved an average decrease of 74% ($P < 0.05$). For the single-layer SF, using the Langmuir isotherm, the theoretical maximum mass of P adsorbed per mass of sand was calculated to be 379 mg P kg^{-1} sand. The maximum mass of P adsorbed per mass of sand was calculated as $759.2 \text{ mg P kg}^{-1}$ for the fine sand and $1452.3 \text{ mg P kg}^{-1}$ for the coarse sand. These results are consistent with other studies showing a strong link between P sorption capacity of a filter medium and P removal. Influent TC values of $8.5 \times 10^6 \pm 7.1 \times 10^5 \text{ CFU } 100 \text{ mls}^{-1}$ were measured on days 62 and 75 of operation. Both the single-layer SFs and the stratified SFs recorded similar very high rates of removal of 96 and 95 %. Physical filtration and

adsorption, or adhesion, are believed to be the principal mechanisms for removing pathogenic bacteria from wastewater in a SF (Stevik et al., 2004).

Conclusions

Overall, the stratified SF outperformed the single-layer SF in terms of removing a significantly higher proportion of influent COD, SS, TN, and PO₄-P. The reason for this improved performance is likely the more complicated flow path and greater retention time that is likely in a stratified SF compared to a single-layer SF. In addition, a stratified SF permits the use of fine sand at a depth below the filter surface at which it would not be affected by biofilm build-up or other clogging mechanisms (Rodgers et al., 2004). This results in the provision of adsorption sites for bacteria and nutrients, and increased hydraulic retention.

Both filters, however, produced an effluent with an NO₃-N concentration greater than the maximum allowable concentration and TC concentration greater than the limits for re-use in the washing of milking parlours (IMQCS and Teagasc, 2004). In addition, stratified SFs are difficult to construct and obtaining sand of the appropriate size is often difficult (Healy et al., 2007).

Acknowledgements

The authors are grateful to Teagasc for the award of a Walsh Fellowship to the first author and for financial support provided by the Research Stimulus Fund (Department of Agriculture, Fisheries and Food).

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RMIS Project Number 5796

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

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Introduction

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

Materials and Methods

Two hundred and seventy six HF dairy cows (138 in both 2009 and 2010, respectively), comprising of two strains of HF (North American and New Zealand) were randomly assigned within strain to one of two mean CD treatments, to establish two groups of dairy cows: Early calving (mean calving date: 12th of February) and late calving (mean calving date: 25th of February). Animals within each CD were then randomly allocated to one of three SR treatments, low (2.51 cows/ha), medium (2.92 cows/ha) and high (3.28 cows/ha). Cows were turned out to grass in early February with SR treatments managed separately and CD treatments within each SR managed similarly. Different grazing intensities were imposed on each SR, with target post-grazing residual heights of 4.5-5.0, 4.0-4.5, and 3.5-4.0 for the low, medium and high SR respectively. Herbage allowance (HA) and herbage removed was measured using the method of Delaby and Peyraud (1996). Concentrate supplementation and artificial fertiliser application was the same for each SR, however late

calving treatments received less concentrate. Milk yield was recorded daily and milk composition weekly. Dietary details were analysed using mixed models in SAS. Milk production data were analysed using covariance analysis, with a model that included the effects of year, parity, strain, CD, SR, their interactions and covariates. Milk production per ha was calculated by summing the milk produced from each paddock within each treatment and dividing by the area of the paddock to give the yield per ha. Yield per ha was analysed using variance analysis with the effects of year, block, SR and CD in the model.

Results and Discussion

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

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

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

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

Conclusion

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

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RMIS Project Number 5891

The effect of stocking rate and calving date on grass production, utilisation and nutritive value

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Introduction

The Food Harvest 2020 report sets a target for a 50% increase in milk production by the year 2020 (DAFF 2010). This increase will be achieved by maximising milk production from grazed grass (Dillon et al. 2008). Stocking rate (SR), traditionally expressed as cows/hectare (ha), is acknowledged as the main driver of milk production from grass-based systems. There are conflicting reports in the literature regarding the effect of SR on grass production and utilisation (Farina et al., 2011; Macdonald et al., 2008) while little is known of the potential effects of calving date (CD) and interactions between SR and CD. The objective of this study was to investigate the impact of SR and CD on grass production, utilisation and nutritive value.

Materials and Methods

Two groups of dairy cows were established in 2008 and were randomly assigned to one of two mean CD treatments: Early calving (mean calving date: 12th of February) and late calving (mean calving date: 25th of February). Animals within each CD were then randomly allocated to one of three SR treatments, low (2.51 cows/ha), medium (2.92 cows/ha) and high (3.28 cows/ha). A separate farmlet of 18 paddocks was created for each of the 6 treatments. SR treatments were managed independently whereas CD treatments within each SR were managed similarly. Different grazing intensities were imposed on each SR, with target post-grazing residual heights of 4.5-5.0, 4.0-4.5, and 3.5-4.0 for the low, medium and high SR respectively. Concentrate supplementation (per cow) and artificial fertiliser application (per ha) was similar for each SR, however late calving treatments received less concentrate. Pre-grazing herbage mass (HM) and density were measured on each paddock before grazing by cutting and weighing two strips per paddock. Pre and post-grazing sward heights were also measured using a folding pasture platometer. A subsample was taken from each cut and samples were bulked by week and SR treatment and analysed for chemical composition. Grazing efficiency and total grass production and utilisation were determined using the method of Delaby and Peyraud (1996). Pre-grazing HM, pre and post-grazing sward height, grazing efficiency and the chemical composition of the sward were analysed using mixed models in SAS, with rotation included as a repeated effect. Total production and utilisation was analysed using Mixed models in SAS with block and block*SR included as random effects.

Results and Discussion

Stocking rate had a significant effect on the grazing characteristics as shown in Table 1. Calving date had no effect on any of the grazing characteristics analysed. There was no difference in total grass utilisation between SR treatments although there was a tendency for more grass to be utilised as silage at the low SR. Consequently, insufficient winter feed was produced for the medium and high SR (548 and 492 kg DM/cow) compared with the low SR (885 kg DM/cow). The increased grazing severity of the higher SR treatments resulted in swards of greater nutritive value. The high SR sward had a higher OMD (766 g/kg) and lower ADF and NDF (475 and 279 g/kg) compared with the medium (752, 486 and 284 g/kg) and low SR (748, 481 and 290 g/kg), respectively.

Table 1: Effect of stocking rate and calving date on grazing characteristics and total production and utilisation

	Stocking rate (SR)				Calving date (CD)		P-values		
	Low	Medium	High	s.e. ¹	Early	Late	s.e. ¹	SR	CD
Pre-grazing HM (kg DM/ha)	1349 ^a	1243 ^b	1252 ^b	18.2	1277	1286		<0.001	0.681
Pre-grazing height (cm)	8.4 ^a	8.1 ^b	8.1 ^b	0.07	8.2	8.2		0.002	0.828
Post-grazing height (cm)	4.5 ^a	4.0 ^a	3.6 ^c	0.03	4.0	4.0		<0.001	0.272
Grazing efficiency (%)	82 ^a	95 ^b	107 ^c	0.003	93	96		<0.001	0.493
Feed utilisation									
Grazed (kg DM/ha)	8,989	9,234	9,678	350.9	9,304	9,296	302.0	0.182	0.973
Conserved (kg DM/ha)	2,963	2,134	2,152	385.8	2,411	2,421	320.0	0.086	0.962
Total (kg DM/ha)	11,952	11,368	11,830	248.3	11,716	11,717	219.7	0.072	0.993
Total energy (UFL/ha)	10,281 ^{ab}	9,850 ^{bc}	10,540 ^a	206.2	10,221	10,227	182.3	0.013	0.971

¹s.e. – standard error, ^{a-c}Means with different superscript within a row are significantly different ($P < 0.05$)

Conclusions

The results of the present study indicate that increasing SR has only a small effect on herbage production but a large impact on grazed herbage utilisation. In the context of the SR used in this study, the results indicate that significant increases in herbage production are required to justify higher SR (the medium and high SR) as insufficient winter feed was produced.

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RMIS Project Number 5891

Effects of winter diet on in-calf heifer weight gain and subsequent milk production performance

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Introduction

The cost of rearing replacement heifers contributes significantly to the overall expense of milk production (Heinrichs, 1993), thus it is essential that heifers calve at the correct bodyweight (BW) at 22 to 24 months of age. Many studies have shown a positive relationship between BW at calving and first lactation milk yield (Lin et al. 1987). Forage brassicas, such as kale (*Brassica oleracea*), are considerably cheaper as a winter feed than grass silage and concentrates. The objectives of this study were to: i) investigate the effect of winter diet on pre-partum weight gain of nulliparous replacement dairy heifers and ii) to establish the effect of pre-partum feeding treatment on post-partum milk production performance.

Materials and Methods

One hundred Holstein-Friesian replacement dairy heifers were balanced on the basis of age (639 ± 20.5 days), projected calving date (23 February ± 22.0 days), BW (459 ± 43.8 kg) and BCS (3.21 ± 0.215 ; scale 0 to 5) and randomly assigned to one of four feeding treatments. The treatments were: i) indoors offered a silage only diet for the duration of the experiment (SO), ii) indoors offered silage and 2 kg concentrate for 46 days followed by a silage only diet – a total of 92 kg fresh weight of concentrate was offered to these animals (SC), iii) outdoors grazing forage kale in conjunction with grass silage bales at an inclusion rate of 30% in the diet (70K) and iv) outdoors grazing a 100% forage kale diet (100K). The over-winter experimental feeding treatments were imposed from 8 November 2010 until calving and the milk production data reported is for the first 29 weeks of lactation.

The SO and SC treatments were all offered the same silage. The 70K animals were offered baled silage. The forage kale was grazed *in situ*. The concentrate fed during the winter period was 0.33 barley, 0.33 citrus pulp and 0.33 distillers grains. The DMD of the silage was 73 (± 3.7) %, dry matter (DM) was 29.6 (± 3.49) % and crude protein (CP) was 12.0 (± 2.63) %. Prior to the commencement of the experiment all animals received one Allsure[®] bolus to provide iodine, selenium cobalt and copper supplementation. The 100K treatment animals were offered straw for the first week of the study to allow adjustment to the 100% kale diet. It was intended to offer no further fibre source after the first week to the 100K animals, however due to continuous frost 10 bales of silage were offered to 100K group 6 weeks into the experiment for a duration of one-week.

All animals were offered fresh feed daily; the indoor animals were fed using a Griffith Elder electronic feeding system. The outdoor animals were offered a fresh allocation of kale each morning by moving a temporary electric fence. All treatments were grouped individually. During the experimental period all animals were weighed weekly and condition scored every three weeks. Post parturition cows were turned out to grass directly and offered 4 kg DM concentrate for the first 40 days of lactation – all animals received the same concentrate input. Milk yield was recorded daily, while milk composition and BW were measured weekly. Body condition score was measured every three weeks. Data were analysed using PROC MIXED in SAS, terms for treatment, age and block were included in the model. Animal was used as the experimental unit.

Results and Discussion

Following the winter period daily weight gain was similar for the SC and 70K treatments (1.10 kg/heifer/day), weight gain was lower for the SO treatment (0.96 kg/heifer/day), the weight gain of the 100K heifers was significantly ($P < 0.001$) lower than all other treatments (0.78 kg/heifer/day). Figure 1 shows the profile of weight gain during the winter feeding period. At the end of the winter feeding period BCS was greatest ($P < 0.001$) for the SO and SC animals (3.47), significantly lower for the 70K animals (3.25) and lowest ($P < 0.001$) for the 100K animals (3.09).

There was no difference between treatments in cumulative milk yield or milk solids yield for the first 29 weeks of lactation (3656 and 273 kg, respectively). There was no difference between treatments in average lactation fat, protein and lactose concentration (4.10, 3.38 and 4.70%, respectively). Average BW throughout the first 29 weeks of lactation was also similar between treatments (439 kg). Average BCS of animals from the 100K treatment was lower ($P < 0.001$; 2.86) than that of the SC and SO animals (3.00) but was not different to the 70K animals (2.93). There was no difference in average BCS between the SC, SO and 70K treatments (2.98).

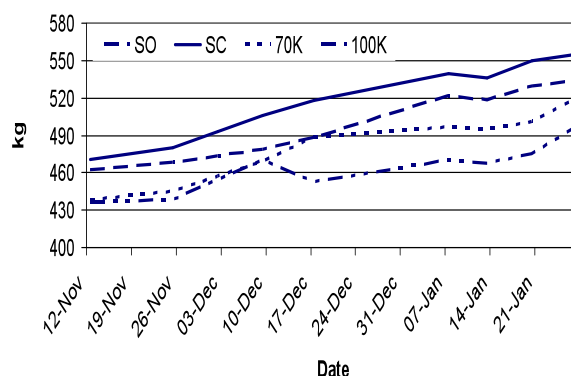


Figure 1. Profile of heifer weight during the winter feeding period

Conclusions

This study has shown that high levels of weight gain were achieved over the winter period by the SC and 70K heifers. Cumulative milk yield and milk solids yield were similar between all treatments. This study suggests that forage crops can be used as a viable alternative to grass silage based feeding treatments over the winter feeding period.

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RMIS Project Number 5892

The effect of a seasonal versus a non-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 low-cost grass-based systems of milk production. Although this has benefits at farm level in terms of a low cost source of feed (grazed grass) it creates 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 non-seasonal supply profile (50% spring:50% autumn) on overall industry profitability (farmers and processors).

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 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. Both models were run simultaneously, with the outputs of one model feeding into the other model as an input 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 50% of the herd calving in each period. This calving pattern lowered the peak compared to the seasonal supply, with proportionately more milk produced at the shoulders of the season, effectively flattening the milk supply profile. These supply profiles were fed into both the farm and processing models to determine the impact on profitability.

Results

Using the national milk pool of 5,189.9 million litres and based on average product market values (2008-2010) the non-seasonal supply profile was more profitable for the processing sector. Based on a 40 hectare

farm the seasonal supply profile was more profitable for the farm sector. At industry level the seasonal milk supply profile resulted in higher net industry returns than the non-seasonal supply profile.

Table 1. Processing sector, farm sector and net industry returns for both supply profiles			
Supply profile	<i>Seasonal</i>	<i>Non seasonal</i>	<i>Differential</i>
Processors 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; the difference in costs at farm level outweighed the increased milk price at processor level with the less seasonal milk supply profile. Maintaining seasonal milk production, while investing in additional processing facilities is more profitable for the Irish dairy industry. Optimising the product portfolio subject to market demands, processing capacities and market returns will help ensure a sustainable Irish dairy industry.

RMIS Project Number 5794

Nitrogen use efficiency on commercial dairy farms

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Introduction

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

Materials and Methods

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

Results and Discussion

The mean stocking rate was equivalent to 183 kg ha⁻¹ (s.d. 31.6) of organic N. The results of N balances indicated N surpluses on all the twenty-one farms. There was high variability between farms in terms of N surpluses and N use efficiencies mainly due to variable N imports in fertilizer N (range: 97-297 kg N ha⁻¹) and purchased feeds (range: 6.4-82.2 kg N ha⁻¹) resulting in variable N exports in milk (range: 35.7-88.1 kg N ha⁻¹). Therefore, the farm-gate N surpluses (kg N ha⁻¹) ranged from 73 to 285 with a mean of 196 (s.d. 62.6). Nitrogen use efficiency ranged from 16% to 43% with a mean of 28% (s.d. 5.71). Overall, NUE (R² = 0.58; P < 0.001; s.e. 0.017) decreased with increased N surpluses (Fig.1). In comparison with earlier studies conducted in the mid 1990's (Mounsey *et al.*, 1998) and between 2003 and 2006 (Treacy *et al.*, 2008),

stocking density in the present study was lower; 183 kg N ha⁻¹ compared with 219 kg N ha⁻¹ in the mid 1990's and 202 kg N ha⁻¹ between 2003 and 2006.

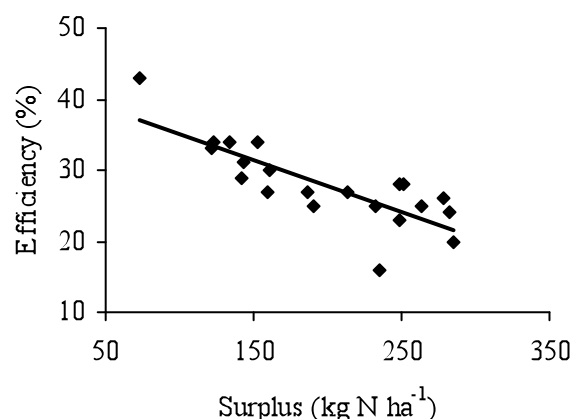


Figure 1. Relationship between N use efficiencies (Y) and N surpluses (X) on 21 dairy farms in 2010 ($R^2 = 0.58$; $P < 0.001$; s.e. 0.017)

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

Conclusions

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

Acknowledgements

The authors acknowledge financial support from the ERDF Interreg IVB Dairyman project and the Teagasc Walsh Fellowship Scheme.

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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

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

Materials and Methods

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

Results and Discussion

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

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

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

Conclusions

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

Acknowledgements

We acknowledge the financial support of the Irish Dairy Levy trust for this research project.

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RMIS Project Number 6015

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

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Introduction

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

Materials and Methods

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

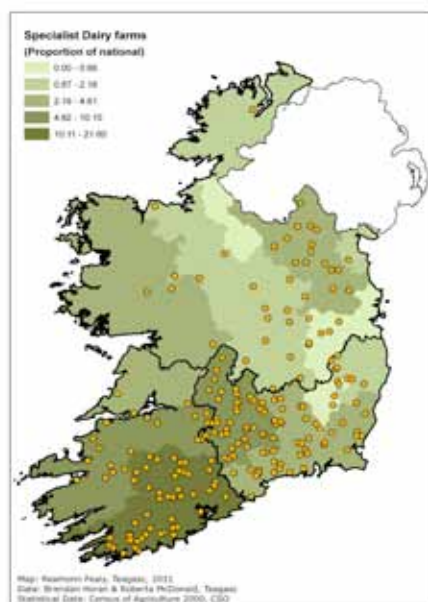


Figure 1. Regional distribution of new entrant dairy farms overlapping the distribution of existing specialised dairy farms

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

Results and Discussion

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

There was no significant effect of region, dairy experience or education on the expectations and intentions of new entrants. Younger and specialised dairy entrants have fewer owned resources, an increased reliance on additional borrowing and substantial expectations for the productive capacity of their potential farm businesses, when compared to older entrants or those with alternative income sources (Table 1). The

average age of new farmers is 36 years with 81% of all new entrants located in the south of Ireland. As a result quota abolition is likely to result in an increased regional bias of milk production in Ireland

Table 2 A summary analysis of the expectations of new entrants to the Irish dairy industry (2009-2011)		
	Average	s.e
Total Land (ha)	58.08	
Cow numbers	70.2	1.55
Stocking Rate (LU/ha)	1.74	0.039
Milk solids/ha (kg MS/ha)	655	17.6
SFP received (€)	18,576	1128.4
Capital Borrowed (€)	88,165	5651.3
<i>Total Expenditure</i> (€)	188,681	8417.1
Expected profit per litre (€)	0.05	0.007
Exp. profit per hectare (€)	422	50.7

Conclusions

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

Acknowledgements

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

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RMIS Project Number 6090

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

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Introduction

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

Materials and Methods

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

Greenhouse gas emissions were calculated using a dairy farm GHG model (O'Brien et al., 2011). The model estimates the main GHG emissions: carbon dioxide (CO₂), nitrous oxide (N₂O), and methane (CH₄). The GHG model operates in combination with the Moorepark Dairy System Model (MDSM, Shalloo et al., 2004). The MDSM defines key parameters (e.g. animal feed budgets) required for the GHG model to estimate emissions. The GHG model quantified emissions using the IPCC and LCA methods. The IPCC method only

considers GHG from on-farm sources. In contrast, the LCA approach quantifies emissions from all processes associated with dairy production up to the point milk is sold from the farm. Thus, the approach includes emissions from the manufacture of purchased inputs e.g. fuel. Greenhouse gas emissions were estimated in terms of their 100-year global warming potentials (CO₂-eq), which on a weight basis relative to CO₂ was set to a factor of 21 for 1 kg of CH₄ and 310 for 1 kg of N₂O (IPCC, 1996). The main output of the GHG model for both methods was a static account of dairy systems annual GHG emissions, which were expressed, per kg of milk solids (MS). Besides producing milk, dairy farms also produce meat. Thus, GHG emissions were allocated between these products using a physical allocation approach developed by the IDF (2010), where impacts were related to the cow's use of feed to produce milk and meat. Allocation of GHG emissions was also necessary for some concentrate by-products e.g. distillers grain. For these inputs, emissions were allocated based on their relative economic value because a physical relationship could not be established.

Results and Discussion

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

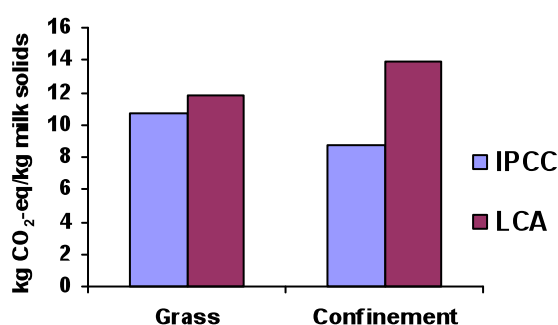


Fig. 2. Greenhouse gas emission of a grass and a confinement dairy system calculated using the Intergovernmental Panel on Climate Change (IPCC) and Life Cycle Assessment (LCA) methods.

Conclusion

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

Acknowledgements

This study was funded by DAFF (RSF-07-517)

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