Moorepark Research Report 2014

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

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Introduction

Like it or not we live in interesting times. Dairy farmers today operate in a production environment of unprecedented uncertainty but also unparalleled opportunity. For most of the last 30 years, milk output has been constrained by quotas, yet the Irish dairy sector remains one of the few indigenous sectors to have built a global footprint. Buoyed by strong international demand, the abolition of milk quotas in 2015 will finally afford dairy farmers the opportunity to expand their businesses. Notwithstanding the positive energy for expansion at farm level, there are also challenges ahead. In recent years, the financial environment of dairy farming has shifted from relatively stable and predictable annual cash flows to higher milk prices but increasingly volatile farm incomes. As an export oriented industry, the increasing integration of farming systems within interconnected global 'paddock to plate' food chains continues. We must ensure that our post quota systems meet the highest international standards of food safety and quality, while also being animal welfare friendly and environmentally sustainable. Irish dairying has an enviable reputation for sustainability; this must be enhanced post quotas. At Moorepark, much of the production systems research undertaken in recent years has focused on the continued development of resilient grass based farming systems that facilitate profitable dairy expansion in an environmentally and socially sustainable manner. Resilient businesses are technically and financially efficient, generate surplus cash, consistently achieve financial expectations and are simple to operate. Based on the triple bottom line of profitability, socially and environmentally responsible milk production, our farming systems must continue to be heavily reliant on the production of milk from grazed grass. This will require compact calving, high EBI dairy cattle and an appropriate overall farm stocking rate that is consistent with the farms grass growth capability.

Clover increases herbage yield and milk production

In 2012 a new research experiment by Teagasc Moorepark was set up on the farm at Clonakilty Agricultural College investigating the impact of tetraploid and diploid swards sown with and without clover on the productivity of spring milk production systems. Four separate grazing treatments were sown for the experiment: a tetraploid only sward, a diploid only sward, a tetraploid with clover sward and a diploid with clover sward. Four diploid cultivars (Tyrella, Aberchoice, Glenveagh and Drumbo) and four tetraploid cultivars (Aston Energy, Kintyre, Twymax and Dunluce) were chosen, and sown as monocultures with and without clover. Thirty cows were allocated to each treatment after calving. All treatments were stocked at 2.75 cows/ha and received 250 kg of nitrogen fertiliser per ha. Three distinct genotypes (Holstein-Friesian (HF), Jersey x Holstein-Friesian (JEX) and Norwegian Red x Holstein-Friesian x Jersey (3way)) are being evaluated in this study, with equal numbers of each genotype in each treatment. In 2014, the first full year of the experiment, cows grazing clover swards had greater milk and milk solids yield (5519 and 464 kg/cow) compared with cows grazing the grass only swards (4872 and 409 kg/cow). Grass ploidy had no effect on milk production. Both the clover treatments had greater annual grass DM production (17.4 t DM/ha) compared with the grass only treatments (14.9 t DM/ha). Ploidy had no effect on grass DM production. The JEX cows have produced 5.7% more milk solids (430 kg/cow) compared with the HF (407 kg/cow) and 3-way cross (407 kg/cow) cows. Herbage dry matter (DM) production has been approximately 17.6% greater on the grass clover swards compared with the grass only swards. This study will run for another four years.

Pasture Profit Index

Teagasc, in conjunction with the Department of Agriculture, Food and the Marine (DAFM), have developed a profit based index, called the Pasture Profit Index (€/ha), for perennial ryegrass cultivars in Ireland. The purpose of this index is to help grassland farmers identify the best perennial ryegrass cultivar(s) for his/her farm. The Pasture Profit Index is composed of 6-sub-indices: spring, mid-season and autumn grass DM production, grass quality (April to July, inclusive), 1st and 2nd cut silage DM production and persistency. The economic merit of a cultivar for each trait was calculated by determining the difference between the performance of each cultivar and the base value for that trait. This was then multiplied by the economic value for that trait using the Moorepark Dairy Systems Model. The economic value of an extra kg of grass DM in spring and autumn was higher than mid-season because it supported an extended grazing season. The relative emphasis on each trait was as follows: grass DM yield (49%), grass quality (10%), silage yield (16%) and persistency (25%). The performance values included in the Pasture Profit Index are based on data collected from the DAFM grass evaluation trials. Varieties are evaluated over a minimum of two separate sowings, with each sowing being harvested for two years after the sowing year. The two harvested years include: (i) a six cut system involving one spring grazing cut, followed by two silage cuts and then three grazing cuts; and (ii) an eight to ten cut system corresponding to normal commercial rotational grazing practice. Pasture Profit Index ranges from €226 to €8/ha per year for the 63 cultivars that had sufficient data available. The sub-indices provide the opportunity to select cultivars for specific purposes. For example, if selecting a cultivar for intensive grazing, the emphasis would be placed on seasonal DM yield and quality with less importance placed on the silage performance. If selecting a cultivar specifically for silage production, then greater emphasis would be placed on the performance of that cultivar within the silage sub-index. A number of successful consultation meetings have taken place with the industry stakeholders, chaired by Dr Brian Wickham. In spring 2014 a prototype of the Pasture Profit Index will be launched with a limited number of cultivars included; it is envisaged that a full list will be released in spring 2015.

Economic Breeding Index (EBI)

The fundamental characteristics of a profitable dairy cow post-quota are the same as pre-quota: high milk solids yield from grazed grass while achieving good reproductive performance, health, and longevity. This will ensure resilience to future milk price volatility. Therefore, the economic breeding index (EBI) will be as relevant post-quota as it is today. Crossbreeding with high EBI sires of alternative breeds can increase profit further. The EBI increases herd milk solids yield through a combination of: 1) direct genetic selection for milk solids; 2) achieving longer lactations through optimal reproductive performance facilitating earlier calving; and 3) reaching mature herd yield through greater cow longevity. Median calving date in Irish spring-calving dairy herds is currently 3rd March, six-week calving rate is 58%, and mean calving interval is 394 days. These statistics continue to be lower than the industry targets. Sub-optimal fertility performance is eroding farm profit in Irish herds. Therefore, it is vitally important that we continue to select high EBI bulls with a high fertility sub-index. Best estimates at present indicate that a fertility sub-index of greater than €130, in combination with good management, is required to reach industry targets. Long-term genetic gain in EBI is achievable with the use of genomic information to supplement the pedigree-based genetic evaluations. A retrospective analysis was undertaken to determine if genomic selection is more accurate than traditional pedigree analysis at predicting genetic merit. The genetic merit of bulls that entered the breeding programme between 2009 and 2012 was calculated based on pedigree, genomic proofs and current daughter performance. Daughter performance is a truer representation of bull genetic merit and was compared to what was originally predicted for those bulls on the basis of 1) traditional pedigree analysis and 2) genomic selection. Genomic selection more accurately predicted daughter milk production and fertility performance than pedigree analysis. If the genetic trend for fertility in the Irish Holstein-Friesian population persists, the heifers born in 2020 will have the same genetic merit as those born in 1989, but milk solids yield will have increased by 60% during this period. Selection on EBI, especially the fertility sub-index, must persist. The suites of traits currently being researched for inclusion in future revisions of the EBI include milk quality, feed intake, and animal health and disease. All impact profit and thus must constitute any selection index breeding for profit.

A model for energy consumption of dairy farms

The latest energy research at Moorepark is focussing on modelling the energy flows through the farm. A model was developed that simulates the energy consumption, costs and related CO_2 emissions of farm equipment on an hourly and monthly basis. The list of equipment includes milk cooling, water heating, milking machine, lighting, water pump and the winter housing facilities. The model was validated by comparing the simulated results against actual data collected from commercial dairy farms. This model is suitable for application as an advice tool for farmers to improve their energy efficiency and reduce milk production costs. The usefulness of the model was demonstrated through an electricity tariff change (i.e. from day and night rate to flat rate), which showed that total electricity costs would increase by over 30% if farmers were to use a flat rate tariff instead of a day and night tariff. This model will be used to assess the impact of managerial and technology changes on electricity consumption, associated costs and CO_2 emissions on dairy farms. Results to date indicate that pre-cooling milk with well water can reduce on-farm electricity consumption by 28%, increase overall ten year profitability by 0.8% (€3,960) and reduce annual CO_2 emissions by 4.8 tonnes on a farm with 200 cows. Investing in a solar thermal water heater can reduce on-farm electricity consumption by over 18%, saving over 3 tonnes of CO_2 per annum on a 200 cow farm. The trade-off for this fossil energy saving, however, is a reduction in farm profitability of 1.8% (€9,200) in the ten year period after investment. Ultimately, the model will lead to a set of recommendations to describe the optimal farm equipment configuration for existing dairy enterprises, new entrants and Greenfield sites to ensure low running costs and maximum profitability.

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ANIMAL RESEARCH PROGRAMME

Genetic Improvement of Animals

A novel index to rank dairy females on expected lifetime profit

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Introduction

The dairy economic breeding index (EBI) is a tool to help identify genetically elite parents of the next generation but may not be the most optimal index to rank females for culling or purchasing. Both genetic and non-genetic factors impact future performance. The objective of the present study was to develop an index to rank dairy females on expected profit for the remainder of their lifetime, taking cognisance of both additive and non-additive genetic merit, permanent environmental (including calving date and parity).

Materials and Methods

The cow own worth (COW) index was developed to rank dairy females on expected lifetime profitability from 1) expected profit in the current lactation (CL), 2) expected profit in the future lactations (FL), and 3) net replacement cost differential (NRCD).

1) $CL = \pi_{moc} + \Sigma_{t=1}^{9} PNM_t \cdot EPV_t$
2) $FL = \Sigma_{i=i^*}^{i^*+10} s_i\,(1/1+r)^{(i-i^*)+1}\,(\Sigma_{t=1}^{14} FNM_t . EPV_t + \Sigma_{j=1}^{5} P(calving) \cdot \pi_j) + \Sigma_{k=1}^{3} P(SCC) \cdot \alpha_k + D)$
3) $NRCD = (1-\rho_i) \cdot (CV - RC)$

where π is the profit differential for the current month of calving *moc* relative to February calving; PNM_t is the present net margin associated with a 1 unit change in trait *t* (milk yield, fat, protein, cull cow weight, milking speed, milking temperament, mastitis, lameness and somatic cell count (SCC)); *EPV* is the estimated performance value (sum of estimated breeding value, heterosis, recombination loss and permanent environment effect); i^* is the initial lactation number; s_i is the survival probability from parity i^* to parity *i*; *r* is the discount factor of 7%; FNM_t is the future net margin value associated with a 1 unit change in *t* (milk yield, fat, protein, cull cow weight, milking speed, milking temperament, mastitis, lameness, direct calving difficulty, maternal calving difficulty, calf mortality and progeny carcass fat, conformation and weight); *P(calving)* is the probability of calving in the j^{th} month in the following lactation (January to May), given the current *moc* and EPV decile for calving interval; π is the profit differential for each *j; P(SCC)* is the probability of the cow residing in the k^{th} SCC group in the next lactation, given the current SCC group, EPV decile for somatic cell score and parity; α_k is the profit differential for each SCC group *k; D* is the future replacements value calculated as the EBI times the cumulative discounted expressions of 0.89 (Berry et al., 2006); *RC* is the replacement cost; *CV* is the net of cull cow salvage value; ρ_i is the long term change in replacement requirements to maintain a stable herd size if 1 cow is culled at the end of parity *i*. Data from 3,156,109 spring-calving cows between the years 2010 and 2013 were used to develop transition matrices for 1) calving month, 2) survival and 3) lactation average SCC. Economic parameters for traits were taken from the Moorepark Dairy Systems Model, with a prevailing 2014 price of 34.5c/l (for CL) and future price of 29.5c/l (for FL). Individual cow EBI and COW index values were generated using information from the April 2011 national genetic evaluations for herds with ≥50 cows. Cows were categorised within herd, into 4 groups based on their value for either COW or EBI. Least squares means phenotypic production, fertility, and survival of 162,981 cows in 2,077 herds for each stratum was determined using a fixed effects linear model based on data for the 2012 calendar year.

Table 1. Least square means (se) for milk production for each quartile of animals ranked on COW or EBI.

Group	Milk (kg)		Fat (g/100g)		Protein (g/100g)	
	COW	EBI	COW	EBI	COW	EBI
1	6965	6674	4.07	4.11	3.57	3.57
	(6.17)	(6.32)	(0.003)	(0.003)	(0.001)	(0.003)
2	6695	6580	4.03	4.04	3.52	3.52
	(6.45)	(6.38)	(0.003)	(0.003)	(0.001)	(0.003)
3	6512	6530	4.01	4.00	3.49	3.49
	(6.18)	(6.27)	(0.003)	(0.003)	(0.001)	(0.003)
4	6164	6467	3.97	3.93	3.44	3.44
	(6.08)	(6.24)	(0.003)	(0.003)	(0.001)	(0.003)

Results and Discussion

Across all data, the COW index was moderately positively correlated (r=0.65) with the EBI; within herd correlations ranged between 0.08 and 0.89. The FL value had the strongest correlation (r=0.93) with COW. The CL and FL were moderately positively correlated (r=0.68) with each other. The COW index had a moderate correlation (0.24 to 0.51) with genetic merit for milk production traits. The current month of calving explained 18% of the variance in the COW and only 1% of the variance in the EBI. The top quartile of cows ranked on the COW index yielded 801 kg more milk, 39 kg more fat, 37 kg more protein (Table 1) and 76,000 cells per mL less SCC, compared to the lowest quartile. The differential in milk production and reproductive performance between divergent quartiles on COW was greater than observed between divergent quartiles on EBI. The heterosis effect for a F_1 Holstein-Jersey crossbred was €472 over the cow's lifetime.

Conclusions

Cows ranking highest on the COW index were not necessarily the females of the greatest EBI merit but, on average, calved at the most optimal period of the year, produced a greater quantity of milk solids, and were more likely to survive to the subsequent lactation.

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RMIS Project No. 6027

Genetic relationships between detailed reproductive traits with body condition score and carcass traits in dairy cows

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Introduction

Body related traits are associated with reproductive traits (Berry *et. al.*, 2014), although the underlying genetic relationship with detailed components of reproduction is unclear. Analysis of detailed reproductive traits, derived from ultrasound exanimation of the reproductive tract, can therefore provide a greater understanding of the relationship between reproductive performance and performance traits. The objective of the present study was to estimate genetic relationships between detailed reproductive traits and both body condition score and carcass traits in dairy cattle.

Materials and Methods

Resumption of cyclicity (CYCLE; n=49,587) was defined by the presence of a corpus luteum (CL) on the ovaries at the time of examination. Early ovulation (EARLY; n=1,080) was defined as resumed cyclicity within the first 15 days postpartum. Multiple ovulation (MULTI; n=42,714) was defined by > 1 CL present on the ovaries. Detected heat (HEAT; n=1,203) was defined in cows where ovulation was detected within the herd AI breeding season with an associated insemination within 5 days (HEAT=1); HEAT was coded as zero if no insemination with 5 days was recorded. Cystic structures (CYST; n=53,872) were defined by the presence of a cyst on the ovaries at the time of examination. Uterine score (UTERUS: n=48,900) was defined on a scale of 1 to 4 based on the tone of the uterine wall and fluid; a score of one was most desirable. Embryo loss (LOSS; n=43,473) was assumed to have occurred if a cow was determined pregnant at ultrasound examination but failed to calve at the in proximity to the estimated calving date based on predicted gestational age of the embryo at examination. Body condition score (BCS) was recorded by trained classifiers; only the first record per cow, undertaken within the first 305-days of first lactation was retained.

Carcass weight (WEIGHT) was measured approximately two hours after slaughter following the removal of the head, legs, thoracic and abdominal organs, internal fats, and hide. Carcass conformation (CONF) and carcass fat (FAT) grade were scored using the EUROP classification system (1=poor/little fat, 15=excellent/fat). Only carcass records from females that calved at least once were retained. Contemporary groups were defined as herd-year-season of calving for the reproductive traits, herd-year-season of assessment for BCS, and herd-year-season of slaughter for the carcass traits. Contemporary groups with less than five animals were discarded. After edits, there were 111,420 ultrasound records from 75,524 lactations on 50,354 cows and approximately 100,000 records for BCS and the carcass traits. Genetic correlations between detailed reproductive traits and the body traits were estimated using repeatability animal models in ASREML (Gilmour *et al.,* 2012). Fixed effects included in the detailed reproductive traits models included parity, stage of lactation, contemporary group, and heterosis and recombination loss coefficients of the animal. Fixed effects included in the BCS model included stage of lactation, contemporary group, and heterosis and recombination loss coefficients of the animal and for the carcass traits models included age at slaughter, contemporary group, and heterosis and recombination loss coefficients of the animal. Permanent environment effects within and across lactation were included as random effects for the detailed reproductive traits.

Results and Discussion

Heavier carcass weight and better carcass confirmation were associated with an increased likelihood of CYCLE. Similarly, better BCS was also associated with an increased likelihood of the CYCLE. This could suggest that heavier cows, in better condition are less likely to be in negative energy balance and therefore, have more energy to partition into reproductive performance. Despite the advantage of a heavier carcass weight on CYCLE, an unfavourable association with other aspects of reproductive performance existed. A heavier carcass weight was associated with a poorer UTERUS, as well as increased LOSS. No associations were detected between the remaining reproductive traits and BCS. This suggests that BCS is primarily associated with the ability to resume cyclicity possibly reflective of energy availability of reproductive performance.

Table 1. Genetic correlations (standard error) between detailed reproductive traits, carcass traits, and BCS

	CYCLE	CYSTIC	UTERUS	EARLY	MULTI	HEAT	LOSS
WEIGHT	0.19 (0.06)	0.03 (0.28)	0.16 (0.06)	0.40 (0.30)	0.11 (0.10)	0.07 (0.19)	0.27 (0.12)
CONF	0.28 (0.06)	-0.26 (0.31)	0.03 (0.09)	-0.33 (0.36)	0.11 (0.10)	-0.12 (0.10)	0.00 (0.12)
FAT	0.41 (0.08)	-0.79 (0.81)	0.28 (0.10)	0.02 (0.33)	0.07 (0.11)	-0.38 (0.21)	0.07 (0.14)
BCS	0.49 (0.08)	0.23 (0.31)	0.02 (0.11)	0.41 (0.31)	-0.06 (0.11)	0.31 (0.21)	-0.07 (0.15)

Conclusion

The strongest genetic relationship existed between the body traits and ability to resume cyclicity suggesting that cows with better energy balance postpartum had superior reproductive performance. The relationship between carcass weight and both UTERUS and LOSS indicate that heavier weights may be harmful to uterine environment and therefore, reproductive performance, regardless of the association with CYCLE.

Acknowledgments

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RMIS Project No. 6160

Genetic relationships between detailed reproductive traits and milk production in dairy cows

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Introduction

There is ample evidence to support the antagonistic genetic relationship between milk production and aggregate measures of reproductive performance. Information, however, on the association between milk production and detailed components of reproductive performance is lacking. The objective of this study was to estimate the genetic relationship between detailed reproductive traits, derived from ultrasound examinations, and milk production in Irish dairy cows.

Materials and Methods

Detailed reproductive traits were derived from the ultrasound examination of the reproductive tract. Resumption of cyclicity (CYCLE; n=49,587) was defined by two assessors as the presence of a corpus luteum (CL) on the ovaries at the time of examination. Early ovulation (EARLY; n=1,080) was defined as oestrus cyclicity resumed within the first 15 days postpartum. Multiple ovulation (MULTI; n=42,714) was defined as the presence of >1 CL on the ovaries at examination. Detected heat (HEAT; n=1,203) was defined in cows where ovulation was detected within the herd AI breeding season with an associated insemination within 5 days (HEAT=1); HEAT was coded as zero if no insemination within 5 days of detected ovulation was recorded. Cystic structures (CYST; n=53,872) were defined by the presence of a cyst(s) on the ovaries at the time of examination. Uterine score (UTERUS; n=48,900) was defined on a scale of 1 to 4 based on the tone of the uterine wall and fluid present in the uterine horn; a score of one was most desirable. Embryo loss (LOSS; n=43,473) was assumed to have occurred if a cow was determined pregnant at ultrasound examination but failed to calve in proximity to the predicted calving date determined by the predicted gestational age of the embryo at examination. Individual cow 305-day milk (MILK), fat (FAT), and protein (PROT) yield were available. Milk fat concentration (FAT%), protein concentration (PROT%), and fat to protein ratio (FPR) were calculated. Somatic cell count was normalised to somatic cell score (SCS). Contemporary groups of herd-year-season of calving were defined for each trait separately. Contemporary groups with less than five animals were discarded. After edits, there were 111,420 ultrasound records from 75,524 lactations on 50,354 cows. A random sample of contemporary groups for the milk production traits was selected resulting in a dataset with approximately 100,000 records per trait. Genetic correlations among traits were estimated using repeatability animal linear mixed models in ASREML (Gilmour *et al.*, 2009). Fixed effects included in all models were parity, heterosis and recombination loss coefficients, and contemporary group; permanent environmental effects were included as random effects. Stage of lactation was also included as a fixed effect for CYCLE, MULTI, CYST, and UTERUS.

Results and Discussion

Genetic correlations between the traits are in Table 1. Higher genetic merit for MILK, FAT, and PROT as well as FAT%, were associated with a reduced ability to resume cyclicity by the time of examination. The association between CYCLE and milk production is similar to documented association with the traditional reproductive traits calving interval and calving to first service interval (Berry *et al.*, 2014), both traits that are strongly correlated with CYCLE (Carthy *et al*, 2014). Increased genetic merit for MILK was also associated with greater genetic predisposition to multiple ovulations. Greater SCS was associated with a reduced likelihood of CYCLE, suggesting cows genetically predisposed to greater SCS, and consequently possibly infection postpartum, could be using more energy to combat the infection at the expense of reproductive performance. Furthermore, higher SCS was also associated with an increased risk of multiple ovulations and embryo loss, further demonstrating the impact of health status on reproductive performance.

Conclusion

Although, not all aspects of reproductive performance had an association with milk production, the ability to resume cyclicity postpartum, as well uterine environment, were unfavourably correlated with milk production. These results reflect the associations between milk production and traditional measures of reproductive performance.

Table 1. Genetic correlations (standard errors in parenthesis) between detailed reproductive traits and milk production

	Milk	**Fat**	**Prot**	**Prot %**	**Fat %**	**FPR**	**SCS**
Cycle	-0.25 (0.06)	-0.22 (0.06)	-0.17 (0.06)	0.06 (0.05)	0.18 (0.05)	-0.08 (0.05)	-0.32 (0.07)
Cystic	-0.05 (0.21)	-0.04 (0.22)	-0.15 (0.23)	0.17 (0.20)	-0.10 (0.20)	0.23 (0.24)	0.27 (0.25)
Uterus	-0.05 (0.08)	-0.08 (0.08)	-0.02 (0.08)	0.01 (0.07)	0.12 (0.07)	-0.08 (0.07)	-0.13 (0.09)
Early	0.13 (0.18)	0.28 (0.19)	0.32 (0.21)	0.13 (0.15)	0.17 (0.17)	0.28 (0.19)	0.05 (0.21)
Multi	0.17 (0.08)	0.02 (0.09)	0.06 (0.09)	-0.13 (0.07)	-0.20 (0.07)	0.25 (0.09)	0.25 (0.09)
Heat	-0.10 (0.12)	-0.19 (0.12)	-0.09 (0.12)	-0.12 (0.09)	-0.01 (0.09)	0.05 (0.14)	0.05 (0.14)
Loss	0.09 (0.10)	-0.13 (0.11)	0.04 (0.11)	-0.19 (0.10)	-0.04 (0.09)	0.00 (0.00)	0.35 (0.10)

Acknowledgments

OptiMIR and the Research Stimulus Fund (11/S/133)

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RMIS Project No. 6160

Regional heritability mapping to identify genomic regions associated with reproductive traits in Holstein-Friesian bulls

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Introduction

Reproductive traits are complex traits and, as such, are likely to be controlled by many genomic mutations of small effect. Thus identification of genomic regions associated with these traits requires large sample sizes and genomic markers in strong linkage disequilibrium with the mutations governing trait expression. Regional heritability mapping (RHM) estimates the variation explained by small genomic regions and is an alternative to conventional single marker regressions, in genome wide association studies (GWAS). RHM combines the effect of multiple single nucleotide polymorphisms (SNP) markers that each may explain too small a proportion of the variance to be detected by conventional GWAS. The objective of this study was to calculate regional genomic heritability for reproductive traits in Irish dairy cattle.

Material and Methods

Illumina Bovine50 beadchip genotypes were available on 3,484 Holstein-Friesian bulls. After edits, 43,304 SNPs remained. Genotype editing including the removal of SNPs on the sex chromosomes, SNPs that were monomorphic, had a minor allele frequency <1%, deviated from Hardy-Weinberg equilibrium or had a call rate <95%. Calving interval predicted transmitting ability (PTA) data were available. Breeding values for detailed reproductive traits were calculated using ASreml (Gilmore *et al.*, 2012) and included: 1) cycling at the time of examination (CYCLE), 2) multiple ovulation (MULTI), 3) cystic structures (CYST), 4) embryo loss (LOSS), and 5) uterine score (UTERUS). Deregressed breeding values (DRP) were calculated for all traits as the EBV, obtained from the traditional BLUP models, less the parent average divided by the reliability of the EBV (Garrick *et al.*, 2012). Only DRP with a reliability >10% were retained. The proportion of variance explained by all the SNPs was estimated using ASreml. RHM was calculated using the REACTA software (Cebamanos *et al.*, 2014) and a mixed model approach where the effect of the region, in this case 100 SNP regions, plus the overall genetic effect, calculated using the remaining SNPs, were added as random effects. The proportion of the total genetic variance explained was calculated as either all SNPs, or the 100 SNP regions, divided by the total variance (e.g., total SNP, regional SNP and residual variance).

Results and discussion

The proportion of genetic variation explained (standard error) by all SNPs for calving interval, CYCLE, MULTI, CYST, LOSS and UTERUS was 0.79 (0.09), 0.24 (0.09), 0.32 (0.11), 0.45 (0.07) 0.42 (0.07) and 0.35 (0.09), respectively. The RHM identified a large proportion (93%) of regions that explained <1% of the genetic variation in calving interval. One region, however, on chromosome 14 explained >7% of the variation in calving interval. The proportion of the genetic variation explained by all SNPs was lower for the detailed reproductive traits but the RHM identified more regions of the genome explaining a greater proportion of the variation (Figure 1).

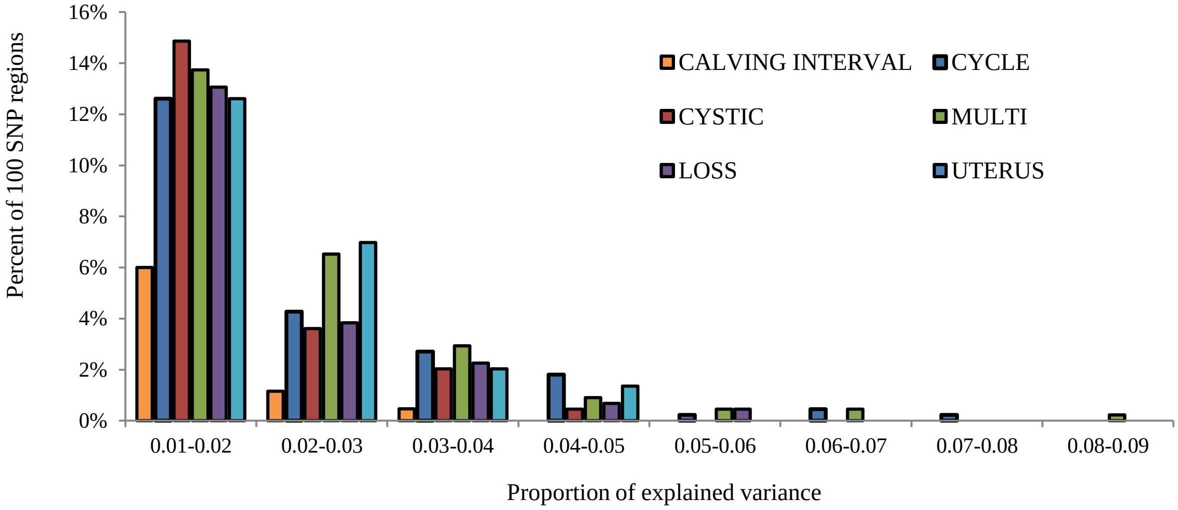

Fig. 1. The percentage of 100 SNP regions that explain greater than 1% of the variation in calving interval, CYCLE, CYST, MULTI, UTERUS, and LOSS traits.

In particular, one region on chromosome 6 (approx. midpoint 20676000 bp) explained just under 8% of the genetic variation in CYCLE. For all the detailed reproductive traits, a large proportion of the regions (i.e., between 70% and 80%) explained <1% of the genetic variation, while between 0.5% and 2% of the regions explained >5% of the genetic variation. The breeding value of calving interval is estimated using a combination of reproductive traits, including calving to first service interval and number of services, to produce a single phenotypic value. Different genomic regions may be attributed to each of the individual reproductive traits, which could explain the greater number of regions explaining a smaller proportion of the variation in calving interval compared to the detailed reproductive traits.

Conclusion

RHM identified genomic regions on chromosome 6 and 14 that could be associated with reproductive performance. This RHM method may prove to be more informative than conventional GWAS at identifying genomic regions particularly for complex traits.

Acknowledgments

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RMIS Project No. 6160

A comparison of profitability of an early and mid-season lambing flock using a bio-economic model

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Introduction

There are two main systems of lamb production in Ireland, early lambing (late December/early January) and mid-season lambing (early to mid-March); which represent 10% and 80% of the flocks in the 2013 Teagasc e-profit monitor (ePM), respectively. The objective of this study was to develop a whole farm bio-economic model to examine the effect of lambing date on profit and identify the factors which have the greatest impact on profitability.

Materials and Methods

A full farm system bio-economic model that simulates a sheep farm on a monthly basis was developed with the flock net energy (NE) demand driving the model, similar to the Moorepark Dairy Systems Model (Shalloo et al., 2004). Animal NE requirement was calculated on an individual basis according to estimated requirements for maintenance, growth, body condition score (BCS) change, pregnancy and lactation as appropriate (O'Mara, 1996). Flock feed energy requirement was expressed as requirement for grazed grass, grass silage and concentrates depending on time of year and stage of production. Livestock movements were accounted for by setting culling and mortality rates on a monthly basis. Lamb drafting was calculated depending on growth rates, with lamb price received based on the average monthly price for 2013 (http://www.bordbia.ie). Other inputs included: grass supply, land, capital, labour, veterinary and fixed costs. The outputs from the model included economic, financial and physical indicators such as flock performance, fertiliser usage and a feed budget. The model was a lowland sheep only farm, growing 8.9 tonnes of grass (DM) annually and was validated against 19 lowland mid-season flocks analysed in the 2013 ePM. The model was set to the average farm size (37 ha), flock size (362 ewes), stocking rate (9 ewes/ha) and weaning rate (1.34) for the ePM farms; economic and physical outputs were compared. The model was used to compare two scenarios; mid-season (ML) and early (EL) lambing.

Results and Discussion

The validation results showed the outputs of the model were very similar to the ePM. The model sold 0.03 less lambs/ha at an average price of €92.85/lamb compared to €91.50/lamb in the ePM. Total sales, total costs and net profit per ewe were -€2.33, -€4.15 and + €4.49, respectively, in the model compared to the ePM flocks.

When comparing ML and EL, both flocks had the same land area, scanning rate and weaning rate but different stocking rates. The early lambing flock had an extra 94 ewes joined to the ram, carried an additional 2.3 ewes/ha, and weaned an additional 126 lambs. The higher output from EL was associated with a 10% increase in silage intake, 13% increase in concentrate intake and 23% reduction in grass demand; thereby allowing more ewes to be carried on the same land area (Figure 1). The lower proportion of grazed grass in the diet of the EL flock had a substantial effect feed costs.

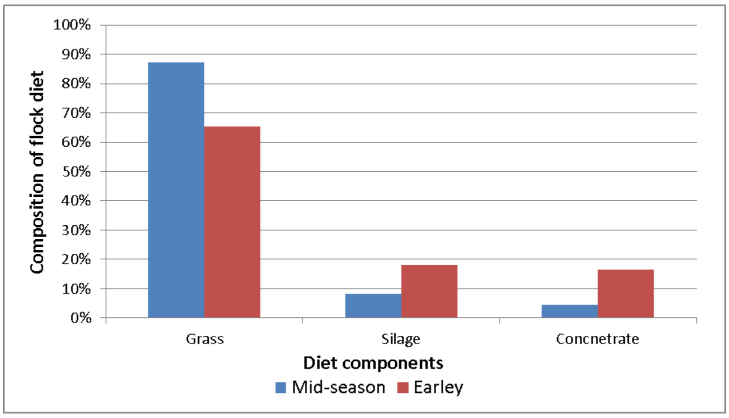

Fig. 1. Proportion of grass, silage and concentrate in the diet of early and mid-season lambing flocks

The average lamb price was €17.99 higher for EL resulting in increased lamb sales of €19,516. The differences in variable costs such as veterinary, fertiliser and silage making are highlighted in Table 1. Based on net profit (excluding labour) ML was €2,306 more profitable on a 37 ha farm. For EL to be as profitable as ML, EL would need to be an additional €4.31/lamb or a 12% reduction in the price of concentrates.

Table 1. Economic performance of ML and EL on a whole farm basis

	ML	**EL**	**Diff**
Avg. lamb price*	€92.85	€110.84	€17.99
Lamb receipts	€38,648	€58,164	€19,516
Total receipts	€44,265	€65,053	€20,788
Feed cost/ewe*	€34.05	€72.37	€38.32
Concentrates	€3,809	€18,458	€14,648
Silage making	€1,837	€5,011	€3,173
Fertiliser	€5,940	€7,571	€1,630
Vet & Medicine	€5,434	€6,228	€793
Total Variable costs	€24,910	€46,308	€21,398
Total fixed costs	€11,124	€12,601	€1,476
Net Profit*	€8,468	€6,162	-€2,306

*Average lamb price per lamb, feed costs on per ewe basis and net profit excluding owner/operator labour.

Conclusion

The validation of the model using ePM data confirmed the accuracy of the model thereby enabling the model to be used to simulate other changes to Irish sheep farm systems. Lambing season had a significant effect on the profitability of the farm; despite higher farm sales, EL was less profitable due to the increased variable cost.

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RMIS Project No. 6195

Predicted phenotypic carcass meat yield and cut yields in animals divergent in genetic merit for the Irish terminal index

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Introduction

It has been well documented (e.g., Connolly et al., 2014) that animals of superior genetic merit for carcass weight, conformation and fat score, subsequently, on average, express superior phenotypic performance for these respective traits. What is not clear is if genetic merit for these traditional terminal traits are associated with subsequent phenotypic performance for more detailed carcass attributes such as meat cut yields and, in particular, if selection on a terminal index will lead to an improvement in these carcass characteristics. The objective of the present study was to identify if animals of higher genetic merit, based on the Irish terminal index, express differences in meat yield and carcass characteristic especially the proportion of higher value carcass cuts.

Materials and Methods

Estimated breeding values (EBV) for carcass weight, carcass fat, carcass conformation, feed intake, calving difficulty, gestation length and mortality were calculated as the average of the sire and dam EBV for each respective trait based on the April 2010 national genetic evaluation. Animals were categorised as having been born in a dairy herd or in a beef herd. Contempary group was defined as herd-gender-season of slaughter; gender in the present study refers to bull, steer, or heifer. Only contempary groups with five or more records were retained. Following edits, 43,189 animals from 3,494 finishing herds remained. Animals were categorised into four terminal index groups based on individual genetic merit as: very high, high, low, and very low terminal index groups. Thresholds imposed to distinguish between terminal index groups were to achieve, as far as possible, a similar differential in mean terminal index between adjacent terminal index groups. A terminal index value center-point for the high and low index groups (i.e., middle two groups) was calculated so that the differential between the center-point of adjacent terminal index groups was equivalent. The individual animal terminal index deviation from the center-point of its respective group was calculated for use as a covariate in the statistical model; this variable describes the relative difference in terminal index value from the group terminal index center-point. The association between terminal index EBV and phenotypic performance was quantified within mixed model framework. The prediction of the carcass cut data used in the present study is described in detail by Pabiou *et al.* (2011). The dependent variables were vhvc (very high value cuts), hvc (high value cuts), mvc (medium value cuts), lvc (low value cuts), total meat yield, total bone, total bone percentage of carcass weight, and yield of vhvc and hvc as a proportion of carcass weight. Fixed effects considered in all models were terminal index grouping, dam parity, whether the animal was a singleton or a twin, gender (i.e., bull, steer, heifer), months of age at slaughter (except when the dependent variable was age a slaughter) and whether or not the animal was from a dairy-herd or a beef-herd (dairy, beef); contemporary group of herd-gender-season of slaughter was included as a random effect in all models. Terminal index was considered as either a continuous variable or as class variable with four levels.

Results and Discussion

Relative to animals in the lowest genetic merit group, animals in the highest genetic merit group had, on average, a greater yield of vhvc, hvc, mvc, lvc, and total meat yield (Table 1). Animals in the very high genetic merit group yielded, on average, 75.37 kg bone (19.50% of carcass weight) while the very low genetic merit animals yielded 73.44 kg bone (21.11% of carcass weight). The very high genetic merit animals had a greater ($P<0.001$) yield of very high value cuts as a percentage of the carcass weight at 7.91% compared to 7.58 % in the very low genetic merit animals. Carcasses from the very high genetic merit animals had a greater ($P<0.05$) percentage of high value cuts as a percentage of the carcass weight at 19.18% compared to 17.74% in the carcasses from the very low genetic merit animals. The phenotypic change in vhvc cuts (kg), hvc cuts (kg), mvc cuts (kg), lvc cuts (kg) and total meat yield (kg) per euro change in terminal index was were 0.026 kg (s.e 0.0004 kg), 0.077 kg (s.e 0.0010 kg), 0.037 kg (s.e 0.0006 kg), 0.081 kg (s.e 0.0014 kg), 0.23kg (s.e 0.0032 kg), respectively.

Table 1 Least squares phenotypic mean[1] and pooled standard error (se) for vhvc, hvc, mvc, lvc, total meat yield (total meat) and total bone (kg) for all animals

Group	vhvc	hvc	mvc	lvc	Total meat
V high	31.2^a	76.0^a	60.6^a	105.3^a	280.4^a
High	29.2^b	70.7^b	58.4^b	100.5^b	266.7^b
Low	28.3^c	67.7^c	57.0^c	97.6^c	257.9^c
V low	26.7^d	62.8^d	54.5^d	92.1^d	243.2^d
se	0.13	0..33	0.21	0.5	1.1

[1] Reference animal was a singleton animal slaughtered at 25.3 months of age (i.e., average of the dataset) from parity 5 dam

Conclusions

Animals of greater genetic merit for the terminal index had greater meat yield compared to their lower genetic merit contemporaries and this translated to more higher value cuts. This suggests that higher genetic merit animals have higher performance at producer level and at a meat industry level, thereby increasing revenue across the entire value chain.

Acknowledgements

We acknowledge ABP (Anglo Beef Processors) for financial support.

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RMIS Project No. 6195

Genetic differences in beef terminal index is reflected in phenotypic carcass weight, conformation and value differences in commercial Irish beef cattle

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Introduction

The increased demand for animal-derived protein and energy for an expanding and more affluent global human population will have to be achieved through a combination of improved animal genetic merit and management strategies. The association between genetic merit for terminal traits and subsequent performance in a large population of commercial Irish beef cattle has never been quantified. The objective of this study was to quantify the difference in carcass performance among animals differing in genetic merit for terminal traits, and in particular the current Irish terminal index. This index is composed of carcass weight, carcass conformation, carcass fat, feed intake, calving difficulty, gestation length, docility, and calf mortality.

Materials and Methods

Information on carcass conformation (scale 1 [poor] to 15 [excellent]), carcass fat (scale 1 [thin] to 15 [fat]), and carcass weight (kg) on animals slaughtered between 2010 and 2013 were available. Estimated breeding values (EBV) for all traits in the terminal index were calculated as the average of the sire and dam EBV for the respective trait based on the April 2010 national genetic evaluation which did not include phenotypic information on the animal itself. Animals were categorised as having been born in a dairy herd or in a beef herd. Contemporary group was defined as herd-gender-season of slaughter; gender in the present study refers to bull, steer, or heifer. Only contemporary groups ≥5 records were retained; 156,864 animals from 7,301 finishing herds remained. Dairy-herd and beef-herd animals were categorised separately into four terminal index groups based on individual genetic merit as: very high, high, low, and very low terminal index groups. Thresholds imposed to distinguish between terminal index groups were such to achieve, as far as possible, a similar differential in mean terminal index between adjacent terminal index groups. A terminal index value center-point for the high and low index groups (i.e., middle two groups) was calculated such that the differential between the center-point of adjacent terminal index groups was equivalent. The individual animal terminal index deviation from the center-point of its respective group was calculated for use as a covariate in the statistical model. The association between terminal index EBV and phenotypic performance was quantified within a mixed models framework. The dependent variable was age at slaughter, carcass weight, carcass conformation, carcass fat, carcass price, or carcass value. Fixed effects considered in all models were terminal index, dam parity, whether the animal was a singleton or a twin, gender (i.e., bull, steer, heifer), age (months) at slaughter (except when the dependent variable was age a slaughter), and whether or not the animal was from a dairy-herd or a beef-herd (dairy, beef); contemporary group of herd-gender-season of slaughter was included as a random effect in all models. Terminal index was considered as either a continuous variable or as class variable with four levels as previously described. An additional series of analyses replaced the independent variable, terminal index, with EBV for the phenotypic performance trait used as the dependent variable.

Results and Discussion

The regression coefficient of phenotypic carcass weight, carcass conformation, and carcass fat on their respective trait EBV was 0.92 kg (s.e 0.002 kg), 1.08 units (s.e 0.00009 units), and 0.79 units (s.e 0.00008 units), respectively. These regression coefficients are close to the expectation of unity. Relative to animals in the lowest terminal index group, animals in the highest terminal index group had, on average, heavier carcasses, superior carcass conformation, less subcutaneous fat, greater carcass value and were slaughtered younger (Table 1) with a €0.14 greater price per kg of carcass.

A greater difference in phenotypic performance existed between extreme terminal index groups in young bulls compared to extreme terminal index groups in steers or heifers. This phenomenon suggests the presence of genotype-by-environment interactions with the greatest difference expected in higher input production systems, as would likely exist in bull beef production systems. Although the interactions were statistically significant, the actual difference between genders was biologically small. Similarly, although the phenotypic difference in carcass performance among animals divergent in terminal index differed statistically by early life rearing regime (i.e., born in a dairy or beef herd), the observed interactions were generally biologically small.

Conclusions

This study clearly shows the benefits of selecting greater genetic merit animal for performance and should help instil confidence among producers in the contribution of genetic selection to improve animal performance at commercial farm level.

Table 1. Least squares phenotypic mean[1] (standard error; se) for carcass weight (Wt; kg), carcass fat (Fat; scale 1-15), carcass conformation (Con; scale 1-15), age at slaughter (age; days) and carcass value (Val; €) for animals of different terminal index groups (Group).

Group	Wt	Fat	Con	Age	Val
V high	369^a	6.14^a	8.51^a	744^a	1409^a
High	354^b	6.50^b	7.33^b	747^b	1331^b
Low	345^c	6.75^c	6.88^c	746^{ab}	1288^c
V low	330^d	6.96^d	6.30^d	750c	1222^d
se	0.33	0.02	0.33	0.83	3.2

[1] Reference animal is a singleton slaughtered at 25.3 months of age born to a parity 5 dam

^{abcd} superscripts within column are different ($P<0.05$) from each other

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RMIS Project No. 6195

Young bull genetic growth profile for carcass weight

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Introduction

Livestock mature at different rates depending on their genetic merit (Mrode and Kennedy, 1993). Therefore, animals may reach a desired carcass weight at different ages and thus the optimal age at slaughter for progeny of certain sires may differ. Random regression models may be used to model the animal-specific deviations from a given population profile across a given trajectory (Meyer, 2001). The objective of the present study was to determine growth curve parameters, using a random regression model, for carcass weight measured on young bulls across multiple beef and dairy breeds.

Materials and Methods

Carcass weight information was available on 106,139 singleton bulls from 8,327 Irish herds slaughtered in 2013. Records from bulls slaughtered <12 months or >24 months of age were discarded as were bulls with no known sire or dam. Records outside ±4 standard deviations from the mean carcass weight or age at slaughter were discarded. Dam records were restricted to parity 1 to 10, and parity was categorised as 1, 2, 3, 4, and ≥5. Only records from sires with at least 5 progeny records were retained. Two contemporary groups were defined 1) abattoir-date of slaughter, and 2) herd-year-season of slaughter; only contemporary groups with five or more records were retained. Following edits, 67,001 young bulls from 3,123 herds remained; animals were from 11,862 sires.

A sire random regression model was fitted to the carcass weight data in AsReml (Gilmour *et al.*, 2009); sire was included as a random effect with relationships among sires traced back to founder generations which were subsequently allocated to genetic groups. The random residual term was modeled as constant across age. Fixed effects included in the model were both contemporary groups of herd-year-season of slaughter and abattoir-date of slaughter, parity of the dam, as well as heterosis and recombination coefficients of the animal. Fixed and random Legendre regression polynomials were also fitted. Covariance function coefficients were estimated using the variance covariance matrix and the matrix of Legendre polynomials: $G = \Phi' K \Phi$ Where G is the variance covariance matrix for slaughter ages, Φ is the matrix of Legendre polynomial age regression coefficients, and K is the estimated variance covariance matrix of the random polynomial coefficients.

Results and Discussion

The average (standard deviation in parentheses) carcass weight and age at slaughter across all data was 366.80 (68.80) kg and 586.90 (85.60) days, respectively. A linear random polynomial regression was fitted. Animal genetic variance component functions for carcass weight followed a parabolic shape with greater variances at the very young and very old ages (Fig. 1). The genetic variance in carcass weight (standard error in parentheses) ranged from 549.05 (33.47) kg^2 to 1548.20 (83.12) kg^2 indicating that sufficient genetic variation exists for selection on this trait. The heritability (standard error in parentheses) of carcass weight was least (i.e., 0.38; se=0.01) at 520 days of age and greatest (0.64; se=0.01) at 720 days of age (Fig. 2).

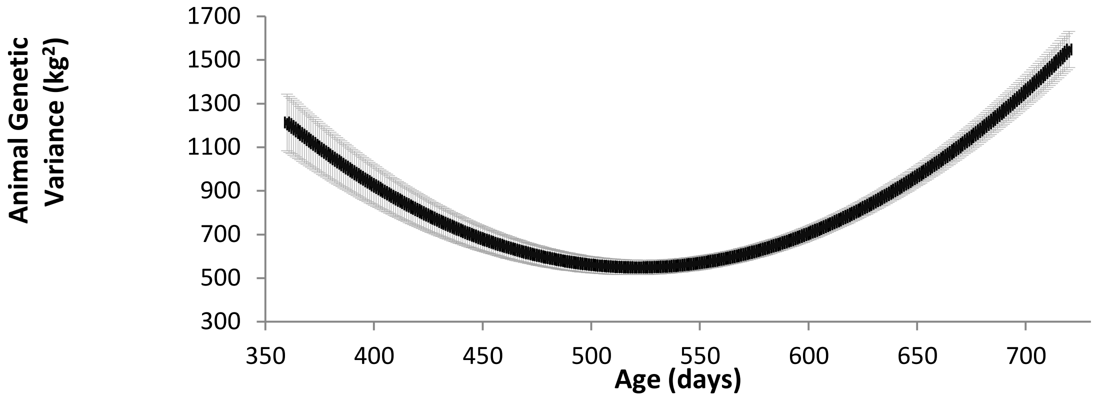

Fig. 1: Estimated animal genetic variances (•) ± one standard error (error bars) of carcass weight at each age at slaughter.

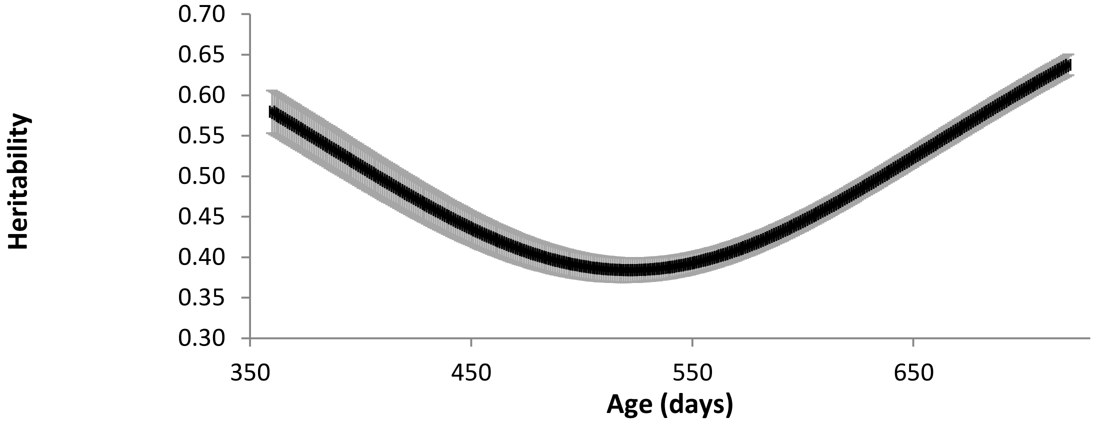

Fig. 2: Heritability estimates (•) ± one standard error (error bars) of carcass weight at each age at slaughter.

Conclusions

Random regression models using linear Legendre polynomials can be used to model the genetic variance in carcass weight across an age trajectory. Considerable genetic variation exists in the carcass weight growth curves of young bulls. Knowledge of the genetic variability in growth rate at different ages, by drawing inferences from carcass weights at slaughter could facilitate more informed selection and management decisions.

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RMIS Project No. 6195

The effect of dystocia on subsequent performance in beef cows

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Introduction

Dystocia can be defined as a calving event that required more intervention than desirable (Meijering, 1984). Dystocia is of economic importance for beef producers due to its association with calf mortality but also because of its impact on cow and calf performance post-partum. The objective of this study was to quantify the effect of calving dystocia on subsequent cow fertility, survival and calf performance in Irish beef herds.

Materials and methods

Calving dates from 972,820 cows totalling 1,389,332 calving events between the years 2010 and 2014 were available from 57,495 beef herds. Calving interval (CIV) was defined as the duration between two consecutive calvings; only calving intervals between 300 and 800 days were retained for analysis. 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. Culling, sale or slaughter data are available on all cows that are moved off farm from the Animal Identification and Movement (AIM), livestock marts and abattoirs, respectively. Cows that were sold within 50 days post-calving through livestock marts (coded SOLD), slaughtered (coded CULL) or recorded as dead (coded DEAD) were retained for analysis. A total of 130,911 weaning weight records were available to assess the effect of dystocia on calf performance. Weanlings were defined as male and female cattle aged between 6 and 12 months at the time of weighing. Only singleton weanlings weighing between 150 and 600 kg were retained. Only the first record in time per weanling was retained. 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 herd-years that recorded some level of dystocia (1 to 10%) were retained. Only calving events from parity one to five were retained. Contemporary group was defined as herd-year-season of calving; only contemporary groups with at least 5 records were retained. Following all edits 186,427 animals remained.

The effects of dystocia on subsequent cow and calf performance were determined using a mixed model (ASReml; Gilmour et al, 2012). Model effects included fixed effects of cow parity and contemporary group fixed regression of the proportion of Aberdeen Angus, Belgian Blue, Charolais, Friesian, Hereford, Holstein, Limousin, and Simmental in each cow, heterosis and recombination loss regression coefficients for each cow, dystocia (yes/no). For weaning weight gender of calf and the age of calf were also included as fixed effects. For all traits cow was included as a random effect.

Results and Discussion

The prevalence of dystocia recorded in the current study was 3.57% which is within the range previously for Irish dairy cattle (Mee et al., 2008). The average calving interval recorded in the beef population was 383 days and 83% of cows survived to a subsequent lactation. The percentage of cows that were sold, slaughtered or died within 50 days post-partum was 0.3%, 0.3% and 0.5%, respectively. The average weaning weight was 320 kg. The effects of dystocia on fertility, survival and production are summarised in Table 1.

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

Performance	Trait	*b (s.e.)*
Fertility	CIV(days)	11.26 (1.67)
Survival	SURV (%)	-0.22 (0.01)
	DEAD (%)	0.03 (0.001)
	Cull (%)	0.002 (0.001)
Production	Wean weight	-8.55 (5.30)

First parity cows were 1.05 times (95% CI = 1.03 to 1.06; P<0.001) more likely to survive to the next lactation relative to 5th parity cows. Fifth parity cows weaned calves that were on average 30 kg heavier than first parity cows. The longer calving interval associated with cows that experienced dystocia are similar to the findings by Laster et al. (1974). Cows that experienced dystocia were 1.25 times (95% CI = 1.22 to 1.27; P<0.001) less likely to survive to the next lactation. Cows that experienced dystocia were also 1.04 times (95% CI = 1.03 to 1.05; $P<0.001$) more likely to die and had a higher predicted probability of being slaughtered within 50 days post-partum. Dystocia was found to have no significant effect on the sale of beef cows in the first 50 days post-partum. Calves from cows that calved without dystocia were 8.55 kg heavier at weaning compared to their contemporaries from cows that experienced dystocia (Table 1).

Conclusions

The results in this study clearly show that calving dystocia reduces ($P<0.01$) cow fertility and survival, as well as calf performance and thereby has a knock on effect on farm profitability.

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RMIS Project No. 6195

Comparison of dairy cow breeding goals for seasonal calving production systems

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Introduction

Artificial insemination has resulted in the globalisation of germplasm. The benefit of such international trade is access to superior germplasm but also restricting the accumulation of inbreeding within a population. There is considerable trade of semen between Ireland, New Zealand, and farmers in the UK operating seasonal calving production systems. The objective of the present study was to compare the total merit indexes of Ireland (Economic Breeding Index; EBI; Berry et al., 2007), New Zealand (Breeding Worth; BW; Harris, 2006) and a spring calving index in the UK (Spring Calving Index; SCI; http://www.dairyco.org.uk/news/news-articles/august-2014/new-spring-calving-index-highlights-wide-range-of-dairy-breeds/).

Materials and Methods

Selection index theory was used to estimate the genetic correlations between the three indexes. The economic weights were those used in the calendar year 2014; a currency exchange rate of 1.26 and 0.6304 was used to convert the Sterling pound and New Zealand dollar, respectively to euro equivalents. Genetic variance components for each trait were as described on the respective country national genetic evaluation system information (http://www.interbull.slu.se); if not available, the genetic variance components were estimated from the variance of high reliability sire estimated breeding values for the respective traits. Genetic correlations among traits were those used on the Irish national genetic evaluations. Trait correlations with non-return rate (SCI) or calving in the first 42-days of the calving season (BW) were those used in the Irish national genetic evaluation for calving interval but of opposite sign. A genetic correlation of 0.9 was assumed to exist between the "same trait" in each country. The correlation matrix among all traits in all indexes was bended to be positive definite. Covariances among all traits in all three indexes were derived from the correlation matrix and the respective variances for each trait in each index.

The pairwise genetic correlation between index X and Y was calculated as:

$$r_{x,y}=\frac{\mathbf{a'_x G_{xy} a_y}}{\sqrt{\mathbf{a'_x G_x a_x \cdot a'_y G_y a_y}}}$$

where **a** is the vector of economic weight, and **G** is the genetic (co)variance matrix.

Results and Discussion

The economic weights (euros) on milk yield, fat yield and protein yield were similar between the EBI (-0.09, 1.04, and 6.64, respectively), BW (-0.06, 1.29, and 5.78, respectively), and SCI (-0.08, 1.05, and 3.67). The lower economic weight on protein yield in the UK reflects their dairy product portfolio. The genetic correlation between a sub-index of just milk, fat and protein yield among the three countries varied from 0.77 (Ireland with the UK) to 0.83 (Ireland and New Zealand); the correlation between the BW and SCI was 0.78. The genetic (co)variance and correlations among the three indexes are in Table 1. Greater variance existed for the EBI; this was largely attributable to a greater genetic variance for the three milk traits in Ireland relative to the UK or New Zealand. The genetic variance for the milk production traits included in the SCI is 66% of the genetic variance used in the national genetic evaluations in the UK. Strong genetic correlations (0.83 to 0.86) existed among all three indexes, indicating that, in the absence of strong genotype by environment interactions between the traits, all three indexes rank animals similarly. This is not surprising since the relative emphasis (i.e., calculated as the economic weight times the genetic standard deviation divided by their sum) on fertility and survival in the EBI, BW and SCI was 29%, 24% and 25%, respectively.

Conclusions

The genetic correlations between all three indexes, calculated using the approach described, were all strong. This does not however imply that bull rankings between indexes will be very similar since the covariance components among traits within and between countries may differ thereby weakening the correlation.

Table 1. Variance (€; diagonal), covariance (€; below diagonal) and correlation (above diagonal) among the EBI, SCI and BW

Index	EBI	SCI	BW
EBI	12377	0.86	0.83
SCI	5585	3394	0.84
BW	4509	2380	2356

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RMIS Project No. 6195

Comparative milk production performance of 'Elite' and 'National Average' cows based on Economic Breeding Index across a range of pasture-based systems

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Introduction

Analysis of commercial farm data (Ramsbottom *et al.*, 2012) has shown that each €1 increase in herd Economic Breeding Index (EBI) results in a €2 increase in profit per cow per lactation. The incorporation of Genomic Selection into the national breeding since 2009 has accelerated the rate of increase in EBI. The objective of this study was to evaluate the milk production performance of extremely high EBI (€249) and National Average EBI (€133) animals, across a range of seasonal pasture-based systems.

Materials and Methods

Data was available from a study comparing Holstein-Friesian cows of extremely high EBI (ELITE) with cows representative of the national average EBI (NA). Mean EBI and standard deviation (SD) for the ELITE genetic group was €249 (€26.8) with a Milk sub-index of €69 (€20.8). Mean EBI and SD for the NA genetic group was €133 (€21.0) with a Milk sub-index of €49 (€14.1). Mean predicted transmitting ability (PTA) and standard deviation (SD) for milk yield, fat yield, protein yield, fat concentration, protein concentration and somatic cell count were; +98kg (140.2), +12.5kg (4.9), +9.8kg (3.8), +17g/kg (12.1), +13g/kg (5.5) and -0.01(0.8) for the ELITE genetic group, and +166kg (142.5), +9.3kg (3.5), +8.2kg (3.2), +6g/kg (9.8), +5g/kg (4.9) and 0.00 (0.1) for the NA genetic group. The current data set spanned two years; 2013 and 2014. A total of 270 records from 186 individual cows were available for a range of milk production traits. In 2013 all cows were in parity 1, while in 2014 one third of cows were parity one and two thirds were parity two, within each genetic group. In spring each year cows were randomised across three contrasting rotational grazing feeding treatments; Control (CONTROL), Low Grass Allowance (LGA) and High Concentrate (HC), with a target post-grazing residual of 4.5-5, 3.5-4 and 4.5-5cm, respectively, as measured using the Rising Platemeter (Jenquip, Feilding, New Zealand), and a total concentrate allowance of approximately 300, 300 and 1200kg per cow per lactation, respectively. Cows were grazed as six individual management groups, with 30 ELITE and 15 NA cows allocated to each of the three feeding systems. Milk yield was recorded daily using electronic milk meters with milk constituents determined weekly from one successive p.m. and a.m. milk samples using a Milkoscan FT6000 (Foss Electric, Hillerød, Denmark). Data were analysed using the PROC GLM procedure in SAS (2011) with the following model which included the random effect of cow repeated across years: Y = μ + genetic group + cow(genetic group) + feeding treatment + parity + calving day + genetic group × feeding treatment. Year was not included in the model due to confounding with parity. The logarithm to the base ten of somatic cell count (SCC) was used to ensure normally distributed residuals, referred to as somatic cell score (SCS).

Results and Discussion

Across years, average pre-grazing sward height and standard deviation for CONTROL, LGA and HC treatments was 10.1 (1.9), 9.7 (2.3), and 9.9cm (2.1), and average post-grazing residual and standard deviation was, 5.0 (0.9), 4.1 (0.8) and 4.9cm (0.8), respectively. There was no genetic group × feeding treatment interaction observed for any of the milk production traits investigated, therefore only the main effects are presented in Table 1. The NA cows had a higher milk yield compared with the ELITE (P<0.01), whereas the ELITE had significantly higher milk fat and protein content. Consequently, ELITE produced significantly higher fat yield and similar protein yield and solids corrected milk yield per cow. Somatic cell score for the ELITE group (1.88) and NA group (1.91) did not differ significantly.

Table 1. Genetic group effect on lactation performance

	ELITE	NA	SED	Sig.
Milk yield (kg/cow)	4852	5029	124	**
Fat (g/kg)	45.1	42.3	0.23	***
Fat (kg)	218	212	2.4	*
Protein (g/kg)	36.9	35.2	0.05	***
Protein (kg)	179	178	2.2	NS
SCM (kg/cow)	4984	4958	56.5	NS
SCC (‘000 cells/ml)	132	147		NS
Milk receipts (30c/l)	1665	1631	18.8	*

SCM = Solids Corrected Milk Yield. SCC = Somatic Cell Count (raw mean) * = P <0.05, ** = P<0.01, *** = P<0.001

Milk receipt value was €34 per cow higher for the ELITE group based on a milk price of 30cent/litre (P<0.05). Concentrate supplementation averaged 295, 314 and 1038kg per cow for CONTROL, LGA and HC treatments, respectively. The mean response to concentrate supplementation was 0.74, 0.66 and 0.05kg, of milk yield, solids corrected milk yield and milk solids (fat + protein kg) per additional kilogram of concentrate offered to the HC treatment compared with the CONTROL. Similarly, the LGA treatment yielded 199kg less milk, 209kg less solids corrected milk yield and 17kg less milk solids than the CONTROL, as a consequence of grazing to almost 1cm lower.

Conclusion

Milk yield, milk fat and milk protein content, and milk receipt value differed between cows of ELITE and NA EBI. The differences, however, were in line with that predicted by their respective PTA values. Within the limits of the current study, neither response to concentrate supplementation nor response to restricted grazing differed with the two genetic groups.

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RMIS Project No. 6390

Stakeholder perspectives on including a milk quality sub-index in the Economic Breeding Index

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Introduction

Prior to 2000, the dairy cow breeding goal in Ireland was focused on milk production. Due to declining reproductive performance, traits associated with dairy cow functionality were introduced into the Economic Breeding Index (EBI). Breeding goals have since evolved to include calving, maintenance, management, health and beef sub-indexes. Included traits and their associated relative weights are evaluated periodically by the Irish Cattle Breeders' Federation (ICBF), primarily based on bio-economic models. This study investigates stakeholders' perspectives on including a specific quality sub-index in the EBI using a complimentary approach. Stakeholders for dairy cow breeding goals include milk producers, dairy processing companies, breeding companies, farm advisors, researchers, representative organisations and public bodies.

Materials and Methods

Using the Delphi technique, with two survey rounds, stakeholders were asked to (a) rate their agreement with incorporating a specific sub-index for milk quality in the EBI, (b) rate the importance they would assign to a pre-determined list of detailed milk quality traits, and (c) outline the weighting they believe should be placed on a milk quality sub-index, relative to the current existing sub-indexes within the EBI. They were also asked to give reasons for their answers. Quantitative data were analysed using descriptive statistics. Content analysis was performed on the qualitative data. Of 127 stakeholders contacted, 70% responded to round 1 and 42% to round 2.

Results and Discussion

There was general support for a proposal to include a milk quality sub-index in the EBI. At the end of the survey process, the majority (60%) of respondents agreed with the proposal, 21% disagreed and 14% neither agreed nor disagreed. The main reasons for agreeing with its inclusion were related to profit maximisation, product quality, market opportunities or improved planning. Reasons given for disagreeing with the proposal included a belief that other (non-genetic) factors have a greater impact on milk quality, lack of conviction that the incorporation of milk quality into the index would actually result in milk quality improvements. There was also a concern that such a step would impact negatively on the current breeding goal making it more complex than necessary or diluting the selection effect for other traits. This latter assertion is unfounded (Berry, 2014). Table 1 shows the importance stakeholders attributed to individual components of such a potential quality sub-index. Stakeholder opinion (indicated by median score) was that all of the identified traits were at least somewhat important, with SCC and milk composition deemed very important. Views on animal welfare were less clear; some viewed it as highly important while others viewed it as of limited importance to the quality sub-index.

Selection index theory calculations on the relative emphasis that should be placed on milk quality to halt any deterioration was in general agreement with the 6% relative emphasis proposed by stakeholders for the quality sub-index. If stakeholders' views on how the overall index should be rebalanced to facilitate incorporation of a milk quality sub-index were to be the sole input into the decision, improvements in milk quality may come at the expense of beef traits and production, as they have little desire for a reduction in weighting for calving, management or fertility. Some, but not all, would accept a slight reduction in weighting for animal health and maintenance.

Conclusion

Results from the quantitative data show a satisfactory level of stability of responses between both rounds of the Delphi study, and a good degree of agreement amongst stakeholders. Results from the qualitative data (i.e., the rationales given by respondents) show that stakeholders are able to consider a wide range of factors when evaluating traits. Some of the stakeholder concerns, which influenced evaluations, have been refuted by recent research. This study thus illustrates the suitability of the Delphi technique to engage with stakeholders, as a complement to alternative approaches, to defining breeding goals.

Table 1. Stakeholders' perceived importance of specific quality attributes within a quality sub-index

Attributes	M Rd 1	IQR Rd 1	M Rd 2	IQR Rd 2
Somatic cell count	7	6 to 7	7	6.75 - 7
Milk composition	7	6 to 7	7	6 to 7
Protein composition	6	6 to 7	6	6 to 7
Protein functionality	6	5 to 7	6	6 to 7
Consistency in milk composition across lactation	6	5 to 7	6	5 to 7
Fat composition	6	6 to 7	6	5 to 6
Sensory atributes	6	4 to 6	5	4.25 - 6
Environmental traits	5	5 to 6	5	4 to 6
Animal welfare	6	5 to 7	5	2 to 6

M=median; IQR= interquartile range; 1=not impt, 7=very impt

Acknowledgements

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RMIS Project No. 6407

Use of mid-infrared spectroscopy to predict milk technological traits in grazing Irish dairy cows

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Introduction

Rennet coagulation time (RCT), curd-firming time (k_{20}), curd firmness 30 minutes after rennet addition (a_{30}), heat coagulation time (HCT) and pH are milk quality traits of increasing interest to the Irish dairy processing sector. Nevertheless, large scale monitoring of these traits is difficult and expensive. Mid-infrared spectroscopy (MIRS) has been proposed as an innovative, rapid and inexpensive phenotyping tool (De Marchi *et al.*, 2014). The objective of the present study was to evaluate the effectiveness of MIRS to predict milk technological quality attributes of milk from Irish dairy cows.

Materials and methods

Between August 2013 and August 2014, 713 individual milk samples (50 mL) were collected weekly from 7 Irish research cow herds. Samples represented different breeds (Holstein-Friesian, Jersey, Norwegian Red and respective crosses), parities, days in milk, milking times and experimental treatments based on a grazed-grass basal diet. Within 48 hours of collection, each milk sample was analyzed for chemical composition with the MilkoScan FT6000 (Foss Electronic A/S, Hillerød, Denmark) and the relative spectrum was stored. A 10 mL milk aliquot was used to determine, using a Formagraph (Foss Electronic A/S, Hillerød, Denmark), the RCT, k_{20}, and a_{30} of each sample. Heat coagulation time was determined using an Elbanton BV (Kerkdriel, The Netherland) hot oil bath on a 3.4 g milk aliquot; milk pH was assessed with a SevenCompact^{TM} pH-meter S220 (Mettler Toledo AG, Switzerland). Six identified outlier reference values for RCT, k_{20}, a_{30} and HCT were discarded, by visual inspection of the normal distribution of each trait. The dataset was randomly divided into a calibration dataset (80% of total observations) used to develop prediction models, and a validation dataset (20% of the total observations) used to quantify model predictive ability. Prediction equations were generated using partial least square regression in SAS (SAS, 2009). Fit statistics considered were the standard error of prediction in cross and external validation (SEP_C and SEP_V, respectively), coefficient of determination in cross and external validation (R^2_C and R^2_V, respectively), ratio performance deviation (RPD), concordance correlation coefficient (CCC), and bias (i.e., average difference between the reference value and the respective predicted value) and linear regression coefficient (slope) of the reference value on the predicted values in external validation.

Results and discussion

Although previous studies (De Marchi *et al.*, 2013) have already demonstrated the predictive ability of MIRS for RCT, k_{20}, and a_{30}, to our knowledge, this is the first study attempting to predict these traits in grazing multi-breed dairy cows. De Marchi *et al.* (2013) demonstrated greater prediction accuracy in their sample population compared to the present study (R^2_C of 0.76, 0.72 and 0.70 for RCT, k_{20}, and a_{30}, respectively). The proportion of variance explained by the prediction models in external validation in the present study (Table 1) ranged from 46% (a_{30} and HCT) to 71% (pH). No prediction models had a RPD > 2, suggesting that none of the models can be used for analytic purposes. However, a CCC > 0.61 achieved for all prediction models indicates that they can be used as a screening method.

Table 1: Number of records (n) and fit statistics for the technological milk traits in cross and external validation.

	Cross Validation					External Validation						
Trait	n	SEP_C	R^2_C	RPD	CCC	n	Bias	Slope (SE)	SEP_V	R^2_V	RPD	CCC
RCT, min	450	5.64	0.61	1.59	0.76	110	-0.10	0.55 (0.05)	5.85	0.55	1.49	0.71
k_{20}, $\log_e$ min	414	0.39	0.59	1.56	0.74	109	-0.08	0.52 (0.05)	0.42	0.51	1.43	0.67
a_{30}, mm	378	11.32	0.50	1.41	0.66	89	-0.85	0.53 (0.06)	10.38	0.46	1.35	0.66
HCT, $\log_e$ min	389	0.46	0.55	1.48	0.71	103	0.04	0.47 (0.05)	0.51	0.46	1.36	0.63
pH	553	0.06	0.73	1.92	0.84	149	0.00	0.83 (0.04)	0.06	0.71	1.79	0.84

The bias of prediction for the different models was not different from zero (P > 0.05), suggesting that none of these prediction models, on average, over- or under-estimated the technological traits. The predictive ability for pH in the present study was more accurate than the only other previous study (De Marchi *et al.*, 2009) that attempted to predict pH (R^2_C 0.59 vs. 0.73). Milk HCT is a trait of great importance because all milk intended for human consumption is subjected to a heat treatment. Moreover, low HCT values have unfavourable repercussions on milk powder production (i.e. mechanical obstruction of the equipment to produce milk powder). The present study is the first that, to our knowledge, demonstrated the ability of MIRS to predict HCT, despite the subjective nature of the reference analysis.

Conclusions

Results indicate that MIRS, combined with chemometric statistical analysis, can be used as a screening method by the dairy industry to monitor and segregate milk based on technological properties.

Acknowledgements

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RMIS Project No. 6407

Mid-infrared spectroscopy to predict free amino acids in cow milk

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Introduction

Free amino acids (FAA) indicate poor quality milk, and generally are highest in concentration in the milk in early and late lactation (Davis *et al.*, 1994). Human and bovine milk have different free amino acid content and composition, in general bovine milk being lower in FAA then human (Agostoni *et al.*, 2014). Therefore, supplementation of infant formula with FAA may be of benefit in infant formula production. Mid–infrared spectroscopy (MIRS) is used worldwide to predict milk fat, protein, and lactose content (De Marchi *et al.*, 2014). The use of MIRS to predict milk quality is attractive since the MIR spectrum is available at no additional cost to routine milk recording. The aim of this study was to test the ability of MIRS to predict the concentration of FAA in milk.

Materials and Methods

Between August 2013 and August 2014, 505 morning and 225 evening milk samples were collected from 7 research farms in Ireland. Spectral data were recorded using the Foss MilkoScan FT6000 (Foss Electronic A/S, Hillerød, Denmark). Free amino acids were then quantified using a JEOL JLC-500/V amino acid analyzer (JEOL UK Ltd., Garden City, Herts., UK). All data were quality assessed; up to 22 outliers were removed and data on FAA that did not have a normal distribution were log transformed. Principal component analysis on spectra did not detect any outliers. Equations were developed to predict each FAA separately through partial least squares regression using regions of the mid-infrared spectrum as predictor variables (Proc PLS; SAS Institute Inc., Cary, NC). Accuracy of prediction equations was tested through external validation whereby 25% of data were excluded from equation calibration and used as an independent validation data set (VD). This was repeated 4 times, ensuring a different 25% of the data was used in the VD each time. Cross validation was performed on the calibration dataset. Criteria used to determine the effectiveness of MIRS predictive models were the coefficient of correlation of cross validation (r_c) and external validation (r_v), the root mean square error of cross validation (RMSEc) and external validation (RMSEv), the slope (b) between true and predicted values, the bias of prediction and the ratio performance deviation (RPD).

Results and Discussion

Milk samples analyzed were from cows that ranged from 5 to 375 days in milk and represented 4 breeds of cattle, from first to eleventh parity. To our knowledge the present study provides the first accuracy estimates of MIRS to predict FAA. Moderate prediction accuracy of FAA was observed; the strongest accuracy of prediction was obtained for glycine (r_v=0.75). The best RPD obtained was 1.38 (glycine) and the poorest was 1.14 (valine). Poorer prediction accuracy of FAA relative to other milk composition measures (e.g. protein composition) may be due to the low quantity of FAA in milk. The slope between the true and predicted values ranged from 0.92 (Aspartic Acid) to 0.76 (Valine)

Table 1: Fitting statistics* of cross- and external- validation of prediction equations.

Cross Validation					**External Validation**			
Trait (µg/ml)	n	RMSE	r_c	Bias (SE)	b(SE)	RMSE	r_v	RPD
Lysine[1]	686	0.56	0.69	-0.69 (3.30)	0.89 (0.04)	3.35	0.55	1.27
Valine[1]	646	0.57	0.60	-0.34 (1.62)	0.76 (0.04)	1.93	0.59	1.14
Glutamic Acid[1]	714	0.41	0.68	-2.07 (13.22)	0.86 (0.04)	0.46	0.59	1.20
Glycine[1]	699	0.41	0.75	-0.48 (3.54)	0.91 (0.04)	3.50	0.75	1.38
Aspartic Acid[1]	595	0.55	0.58	-0.37 (1.67)	0.92 (0.08)	1.66	0.44	1.15

RMSE=root mean square error; r=correlation between true and predicted values; b = slope; SE = standard error; RPD= Ratio Performance Deviation

[1]Traits were log transformed prior to analysis.

Conclusions

Findings from this study indicate the potential to use MIRS to routinely measure FAA rapidly and at low cost.

Acknowledgments

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RMIS Project No. 6407

Effectiveness of mid-infrared spectroscopy to predict milk colour

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Introduction

Milk colour is associated with the level of β-carotene and fat content in milk (Tian *et al.*, 2010) and may also indicate milk abnormalities (Espada *et al.*, 2002). Mid–infrared spectroscopy (MIRS) is a technique used to measure milk chemical composition and has recently been used to predict more detailed milk composition (De Marchi *et al.*, 2014). The aim of the present study was to test the ability of MIRS to predict the milk colours, white (L*), cyan (a*) and yellow (b*).

Materials and Methods

Between August 2013 and August 2014, 735 milk samples were collected from 4 breeds of cattle across 7 research farms. Spectral data were recorded using the Foss MilkoScan FT6000 (Foss Electronic A/S, Hillerød, Denmark). Milk colour was measured using a Chroma Meter CR400 (Konica Minolta Sensing Europe, Edisonbaan 14-F, Netherlands) and expressed according to the

CIE Lab (l*a*b* color space) (CIE, 1978). All data were quality assessed, subsequently 25 outliers were removed. Principal component analysis on spectra did not detect any outliers. Prediction models were developed using Partial least squares regression. External validation was performed, whereby 25% of data were excluded from equation calibration and used as an independent validation data set. This was repeated 4 times. Cross validation was performed on the calibration dataset. Criteria used to determine the effectiveness of MIRS predictive models were the coefficient of correlation of cross validation (r_c) and external validation (r_v), the root mean square error of cross validation (RMSEc) and external validation (RMSEv), the slope (b) between measured and predicted values, the bias of prediction and the ratio performance deviation (RPD). Pearson correlations between measured values for L*, a*, b* and milk fat, protein and casein were assessed.

Results and Discussion

This is the first study to predict milk colour using MIRS. Biological variability of milk samples was maximized in order to develop robust prediction models which aided the moderate prediction accuracy of the b* index (r_v = 0.72; Table 1). The r_v of 0.72 for b* indicates that this prediction model is adequate as an estimator for the yellowness of milk. However, since the RPD was < 2 the model should not be used for analytical purposes. The bias of the prediction models was not different from zero (P > 0.05). The ability of the MIRS to predict yellowness of milk may be related to the correlation between b* and milk fat and casein content, similarly L* was moderately correlated to milk casein content (Table 2). When samples from Holstein-Friesians only were used to calibrate and predict milk colour, the r_v of L* and b* were 0.61 and 0.68, respectively.

Table 1: Fitting statistics* of cross- and external- validation of prediction equations.

	Cross validation				External validation			
Trait[1]	n	RMSE	r_c	Bias(SE)	b(SE)	RMSE	r_v	RPD
L*	610	1.46	0.63	0.02(1.57)	0.88(0.05)	1.57	0.55	1.2
a*	585	0.51	0.37	-0.002(0.52)	0.81(0.11)	0.52	0.30	1.05
b*	610	1.97	0.74	-0.005(2.03)	0.96(0.04)	2.03	0.72	1.45

RMSE=root mean square error; r=correlation between true and predicted values; b = slope; SE = standard error; RPD= Ratio Performance Deviation. [1]L= white, a*= cyan, b*= yellow

Table 2: Pearson correlations[1] between the white (L*), cyan (a*) and yellow (b*) colour of milk and milk fat, protein (PRT) and Casein (CN) concentrations.

	l*	a*	b*	Fat	PRT	CN
l*	-	0.32	0.57	0.38	0.38	0.43
a*		-	-0.03^{NS}	-0.01^{NS}	-0.17	-0.21
b*			-	0.58	0.49	0.47

[1]Correlations less than 0.04 are not different (P<0.05) from zero

Conclusions

This study demonstrates that use of MIRS data provides a screening method to efficiently determine the yellowness of milk at a population level, providing a useful tool for the dairy industry and aiding in selective breeding.

Acknowledgments

This research was funded by the Research Stimulus Fund project 11/SF/311, Breed Quality.

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RMIS Project No. 6407

Imputation accuracy from high density genotypes to whole genome sequence in cattle

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Introduction

Whole genome sequencing provides the most comprehensive information of an individual's variome. The here-to-fore high cost associated with procurement of sequence data, has resulted in genome-wide association studies and genomic predictions relying on single nucleotide polymorphism (SNP) marker arrays. These marker arrays, however, rely on common variation throughout the genome and thus may be a subject of ascertainment bias. Whole genome sequence (WGS) data, however, does not suffer from ascertainment bias and contains information on rare variants which may affect phenotypic variation (Brøndum et al., 2014). Accurate genotype imputation from marker arrays to WGS could provide more information for use in genomic analyses. Therefore the objective of the study was to quantify the accuracy of imputation from the commercially available Illumina bovine high density (HD) genotype panel to WGS in a Holstein-Friesian population.

Materials and Methods

Whole genome sequence data from Run 4 (i.e. the fourth sequencing collective by the consortium) of the 1000 Bull Genomes project was available on a total of 1147 sequenced animals from 27 breeds. The average genome coverage was 11.0X and a total of 35.2 million SNP variants were identified across the genome. In total, 289 Holstein-Friesian sequences were available, of which Illumina HD genotypes were available on 73 of these. All 73 HD genotyped individuals had a call-rate >95%. SNPs of unknown position, or with a call-rate <95% were discarded as were SNPs with >2% Mendelian inconsistencies between parents offspring. Only SNPs with a minor allele frequency (MAF) of >2% were retained. The concordance between the sequence-derived genotype and the HD genotype for each locus in the 73 test animals was determined. The accuracy of imputation was determined on *Bos Taurus* autosome (BTA) 18 and 29. A total of 18,699 and 14,106 SNPs from the Illumina HD marker resided on BTA 18 and 29, respectively. Imputation was undertaken with FImpute2 (Sargolzaei *et al.*, 2014) exploiting both family-based and population-wide-based information. The 73 test animals were removed from the sequence population and using only their HD genotypes were imputed to sequence density. Imputation accuracy was evaluated using: 1) just the 215 Holstein-Friesian sequences in the reference population and 2) using the entire 1074 multi-breed sequenced individuals as the reference population. There was a total of 912,281 and 827,031 sequenced SNPs on BTA 18 and 29, respectively. Accuracy of imputation was determined as the correlation between the actual and imputed genotypes in the 73 individuals.

Results and Discussion

The mean concordance between the sequence genotype and the HD genotype was 99.09%, with a range of 98.99% to 99.21%. The majority (95.78%) of the genotype discrepancies between densities were heterozygous genotypes being called as homozygotes or vice-versa. The imputation accuracy from HD to WGS for BTA 18 and 29 was 96.79% (Table 1). This imputation accuracy was superior to the average imputation accuracy of 0.90 documented by Brøndum *et al.* (2014) in 3 main dairy breeds. The superior accuracy in the present study is likely due to a larger reference population of sequenced animals (n=1074) compared to the 369 used by Brøndum *et al.*, (2014) using Run 2 (i.e. the second sequencing collective) of the 1000 bull's genome project. Slightly greater imputation accuracy was obtained in the present study when multiple breeds were added to the Holstein-Friesian only reference population. Little improvement from the inclusion of multiple-breeds in the reference population may be due to the relatively large reference population of Holstein-Friesian animals (n=215). Imputation accuracy for low minor allele variants can be seen in Fig 1 where average accuracies were calculated in bins of 1%. The imputation accuracy for rare alleles was low, however there has been an improvement from previously reported accuracies due to the expansion of the sequence reference population since Run 2 (Brøndum *et al.*, 2014). Therefore with the continued growth of the sequence reference population an increase in accuracy for the rare alleles is expected to follow.

Table 1. Mean imputation accuracy (Acc) and mean allele concordance (Concord) between the true and imputed genotype using a single and multi- breed reference population.

	Single breed		Multi-breed	
BTA	Acc	Concord	Acc	Concord
18	96.48	98.40	96.65	98.16
29	96.87	98.37	96.92	98.55

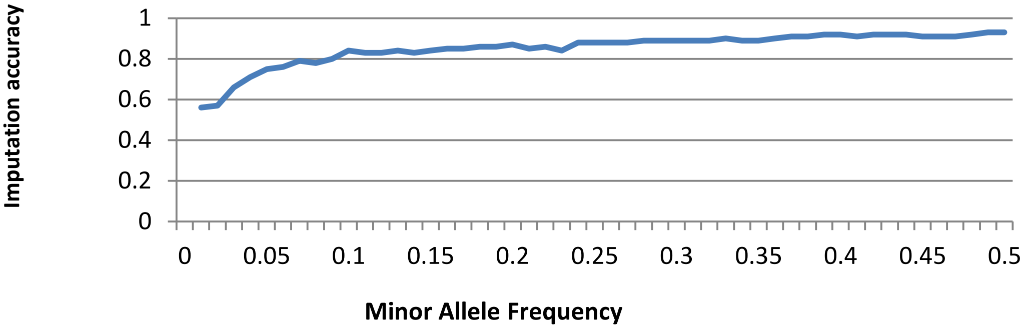

Fig 1. Imputation accuracy vs minor allele frequency

Conclusions

Accurate imputation to WGS is achievable from HD marker density data and the accuracy increased when a multi-breed reference population was used.

Acknowledgements

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RMIS Project No. 6408

Refinement of the genomic regions on chromosome 18 associated with direct calving difficulty using sequence data

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Introduction

The economic impact of calving difficulty (requirement of veterinary assistance ~€662) necessitates more in-depth analysis of its underlying genetic and genomic architecture. Several studies have identified an influential association on BTA18 associated with direct calving difficulty in the Holstein-Friesian population (Cole *et al.*, 2009; Purfield *et al.*, 2014). The objective of this study therefore was to refine the genomic associations identified on *Bos Taurus* Autosome (BTA) 18 for direct calving difficulty using sequence data.

Materials and Methods

Whole genome sequence data from Run 4 (i.e. the fourth sequencing collective by the consortium) of the 1000 Bull Genomes project was available on a total of 1147 sequenced animals from 27 breeds. In total, 289 Holstein-Friesian sequences were available, of which Illumina high density

(HD) genotypes (n=777,962) were available on 73 of the animals. The mean concordance between the sequence genotype and the HD genotype on the 73 animals with both sources of information was 99.09% (Purfield, 2014). A total of 912,281 sequence variants on BTA18 were retained for this study. High density genotypes were available on 770 Holstein-Friesian bulls. All HD genotyped individuals and single nucleotide polymorphisms (SNPs) had a call-rate >95% and only HD SNPs with a minor allele frequency of >2% were retained. Genotypes from 18,699 SNPs on BTA 18 on the Illumina HD manifest remained. Imputation was undertaken with FImpute2 as described by Purfield *et al.,* (2014) using the multi-breed sequenced reference population. Imputation accuracy was 96.65% with an allele concordance rate of 98.16%. Deregressed estimated breeding values (EBVs) and their associated reliabilities were available for all 770 HD genotyped animals. Association analysis was undertaken within a mixed model framework with allele dosage of each SNP included individually as a fixed effect in the statistical model; animal was included as a random effect with relationships among animals accounted for via the numerator relationship matrix. The dependent variable was the deregressed EBVs weighted by a function of the associated reliability. Correction for multiple testing using the Bonferroni method was applied.

Results and Discussion

Several strong associations for direct calving difficulty where detected on BTA 18 of which the 57.4-58.4 Mb interval exhibited the strongest SNP associations ($p<2.5 \text{ x } 10^{-8}$). The strongest SNP association ($p=6.3 \text{ x } 10^{-10}$;Bonferroni $p=5.7 \text{ x } 10^{-4}$) was a downstream intergenic variant located ~3Kb from the KLK14 gene. Sixteen gene/gene-products across BTA18 contained SNPs with a *p*-value $<2.5 \text{ x } 10^{-8}$; four of these SNPs were classified as missense variants. These four missense variants were distributed among three genes; two in mRNA SIGLEC12, one in the CTU1 gene, and one in the zinc finger ZNF615. The strongest missense variant association was located in CTU1 (Fig 1; $p=8.9 \text{ x } 10^{-10}$; Bonferroni $p=8.2 \text{ x } 10^{-4}$). The SIGLEC12 gene has been documented to be associated with calving difficulty in previous association studies using HD marker panels (Cole *et al.,* 2009; Purfield *et al.,* 2014). All four missense variants were classified as 'tolerated' based on SIFT (soring intolerant from tolerant) parameters, although the missense variant in CTU1 was classified as at the margin of this category (SIFT=0.06). PolyPhen scores predicted the CTU1 missense variant to result in a possibly damaging (PolyPhen=0.95) amino acid substitution of alanine to valine. The remaining three missense variants were classified as benign substitutions by PolyPhen. CTU1 has no known role in calving performance but may impact proteins with codons enriched in AAA, GAA and CAA.

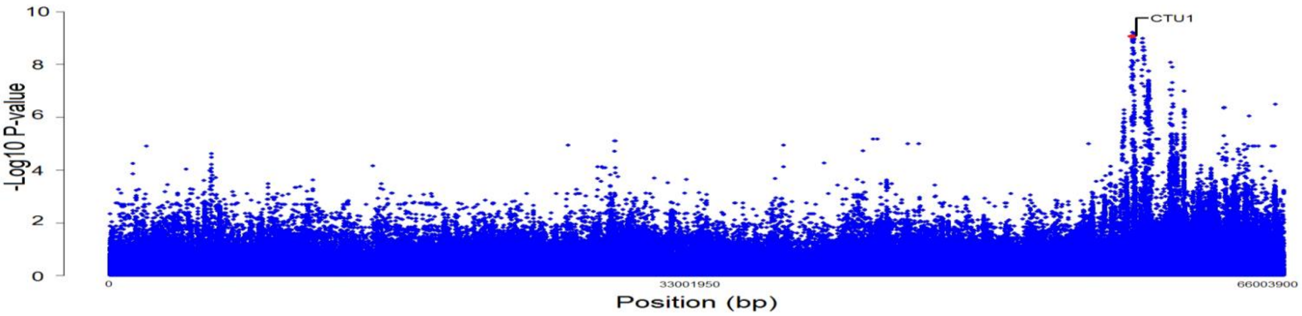

Fig. 1. Association results for direct calving difficulty on BTA 18 using imputed sequence data.

Conclusions

The use of sequence data refined the genomic associations detected previously on BTA 18 from Illumina HD genotype information. Although no definitive mutation was detected, a missense variant in CTU1 may be a contributor to the genetic variance in direct calving difficulty.

Acknowledgements

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RMIS Project No. 6408

Strong genomic associations for reproductive performance identified on chromosome 18 in Holstein-Friesian cattle

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Introduction

Calving interval (CI), defined as the number of days between two consecutive calvings, is an important measure of reproductive performance. Understanding the genomic architecture affecting CI therefore, may aid in improving our selection decisions when breeding for improved reproductive performance (Olsen et al., 2010). A haplotype on chromosome 18 has been previously associated with fertility in the Australian Holstein population; however no causative mutation was identified (Pryce et al., 2010). The objective of the present study was to refine genomic associations on Bos Taurus Autosome (BTA) 18 using sequence data and propose possible causal mutations.

Materials and Methods

Whole genome sequence data from Run 4 of the 1000 Bull Genomes project (www.1000bullsgenomes.com) was available on a total of 1,147 sequenced animals from 27 breeds. In total, 289 Holstein-Friesian sequences were available, of which Illumina high density (HD) genotypes were available on 73 of the animals. The mean concordance between the sequence genotype and the HD genotype on the 73 animals with both sources of information was 99.09%. A total of 912,281 sequence variants on BTA18 were retained for this study. High density genotypes were available on 770 Holstein-Friesian bulls. All HD genotyped individuals and single nucleotide polymorphisms (SNPs) had a call-rate >95% and only HD SNPs with a minor allele frequency of >2% were retained. Genotypes from 18,699 SNPs on BTA 18 on the Illumina HD manifest remained. Imputation was undertaken with FImpute2 as described using a multi-breed sequenced reference population. Imputation accuracy was 96.65% with an allele concordance rate of 98.16%. Deregressed estimated breeding values (EBVs) for CI and their associated reliabilities were available for all 770 HD genotyped animals (mean reliability=81.2%; range 14% to 99%). Association analyses were undertaken within a mixed model framework with allele dosage of each SNP included individually as a fixed effect in the statistical model; animal was included as a random effect with relationships among animals accounted for via the numerator relationship matrix. The dependent variable was the deregressed EBVs, weighted by a function of the associated reliability. Variant effect predictor from ensemble was used to provide SIFT (sorting intolerant from tolerant) scores for significant missense variants (www.ensembl.org/info/docs/tools/vep).

Results and Discussion

Several strong associations for calving interval were detected on BTA 18 of which the 28.23-28.31Mb interval exhibited the strongest SNP associations ($P<3.5 \times 10^{-30}$; 1.03% of the genetic variation). The strongest SNP association ($P=6.6 \times 10^{-36}$) within this region was an intergenic variant. A second strong signal of association was also detected at the 45 Mb region ($P<1.25 \times 10^{-30}$). Several possible candidate genes existed within these genomic regions including ENSBTAG00000064975, KIAA0355, GPI, PDCD2L, UBA2 and WTIP. The strongest missense variant ($P=2.97 \times 10^{-19}$) was located in the same genomic region at the 63Mb mark on BTA18 previously identified by Pryce et al. (2010). This missense variant was located within the zinc finger ZNF582, of which two neighboring genes (NLRP12 and ENSBTAG00000025288) also contained highly significant missense variants. SIFT scores for all missense variants proposed them to be 'tolerated' suggesting the amino acid substitution has no detrimental impact on the structure of these proteins.

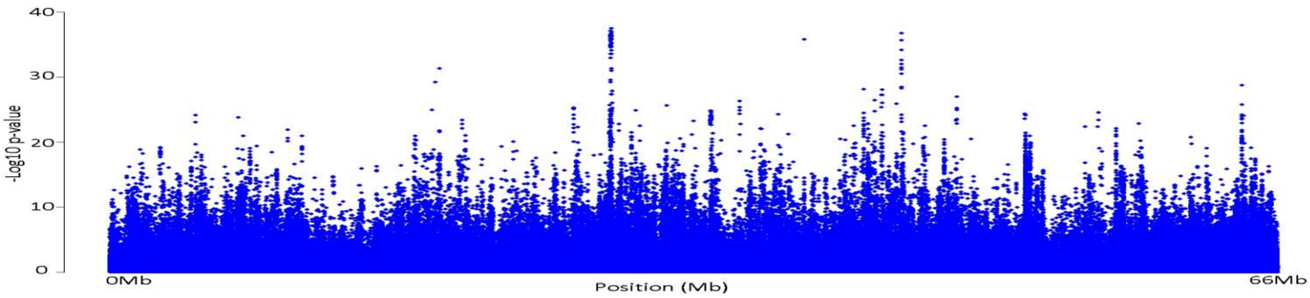

Fig. 1. Single SNP regression results on BTA 18 using imputed sequence data for calving interval in a Holstein-Friesian breed.

Conclusions

The use of sequence data confirmed the presence of statistically significant associations impacting CI on BTA 18. However, although no definitive mutation association with CI was identified; several possible candidate genes were suggested. It is hoped imputation to whole genome sequence across all chromosomes will identify strong putative associations which can be exploited to improve reproductive performance.

Acknowledgements

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RMIS Project No. 6408

Whole genome-enabled predictions of carcass merit in a multi-breed cattle population

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Introduction

Genomic-based predictions of genetic merit were launched for Irish Holstein-Friesian cattle in 2009 (Berry et al., 2009). The objective of the present study was to quantify the accuracy of prediction of genetic merit in a multi-breed cattle population using genome-wide single nucleotide polymorphism (SNP) markers.

Materials and Methods

Illumina (http://www.illumina.com) high-density genotypes (777,962 SNP) were available on 5,194 dairy and beef bulls. International dairy and beef genotypes were available on a further 54,703 individuals. All genotypes were imputed (Berry et al., 2014) to a panel density representing the commercially available Illumina Bovine50 Beadchip genotype panel (51,487 autosomal SNPs) and the Illumina High density genotype panel (i.e., 735,239 autosomal SNPs). Two national multi-trait traditional genetic evaluations for carcass weight (kg), carcass conformation (scale 1 to 15), and carcass fat (scale 1 to 15) were undertaken which included 1) all phenotypic data up to August 2014, or 2) all phenotypic day up until December 2008. The dataset of genotyped animals was divided into animal born prior to the year 2009 (i.e., calibration animals; n=28,842) and animals born after 2008 (i.e., validation animals; n=898). Estimated breeding values (EBV) for the three carcass traits were deregressed separately and a weighting factor was calculated for each trait (Garrick et al., 2013). A SNP-BLUP genomic prediction model was developed with each SNP simultaneously considered as a random effect in the statistical model with equal variance assigned per SNP. The genetic variance allocated per SNP was calculated as the total additive genetic variance divided by twice the frequency of the first allele times the frequency of the second allele summed across all loci. Only a population mean term was considered in the mixed model as a fixed effect. Each carcass trait was considered separately as the dependent variable with the associated weighting factor; only EBV for the genetic evaluation undertaken on data prior to 2009 was considered. Genomic breeding values were calculated for the 898 validation animals (with a genetic evaluation reliability of >50%) as the estimated allele effect times the individual's allele dosage summed across all loci. The correlation between the genomic prediction and the progeny based EBV from the most recent national genetic evaluation was calculated using a fixed effects model; breed was included as a fixed effect.

Results and Discussion

Mean EBV for the three carcass traits estimated from the most recent traditional national genetic evaluation compared to genomic predictions or parental average predictions based on the genetic evaluation undertaken on data prior to 2009 is in Table 1. The mean reliability of the 898 validation bulls was 70%; therefore parental average is still contributing to the most recent national EBV of these animals. Genomic predictions, on average, underestimated the progeny-based EBV which is in direct contrast to observed internationally in dairy cattle genomic predictions. The correlations between individual animal genomic predictions with progeny-based EBVs are in Table 2. Correlations were moderate (0.33) to strong (0.82) across the different scenarios investigated. Across all data, the genomic predictions were up to 82% more accurate than predictions based solely on parental average. Correlations improved by approximately two percentage units when the higher density genotypes were used.

Table 1. Mean (standard deviation) EBV for carcass weight (Cwt), Carcass fat (Cfat) and carcass conformation (Cconf) estimated based on progeny performance (Prog), genomic prediction (DGV) and parental average (PA)

Proof	Cwt	Cfat	Cconf
Prog	44.8 (19.5)	-0.35 (0.71)	2.59 (0.96)
DGV	31.9 (15.7)	-0.98 (0.57)	1.68 (0.82)
PA	25.0 (8.4)	-0.16 (0.51)	3.32 (0.95)

Table 2. Correlation between the genomic predictions and progeny-based EBV for all animals (n=898), Charolais (CH; n=430) and Limousin (LM; n=286)

Scenario	Cwt	Cfat	Cconf
All	0.73	0.82	0.73
CH	0.59	0.61	0.33
LM	0.52	0.50	0.50

Conclusions

Prediction of progeny-based EBVs is possible with the exploitation of genomic information in a SNP-BLUP framework; there is however considerable scope to improve the predictions further.

Acknowledgements

Research Stimulus Fund - MultiGS

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RMIS Project No. 6408

Inter-relationships among alternative definitions of feed efficiency in grazing lactating dairy cows across parities and lactation stages

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Introduction

International interest in feed efficiency and, in particular, energy intake and residual energy intake is increasing due to an increased global demand for animal-derived protein and energy sources. Many definitions of feed efficiency in lactating animals exist, but the correlations among these traits across lactation have not been fully elucidated. The objective of the present study was to quantify the inter-relationships between efficiency traits and energy balance (EB) across parity and stage of lactation in lactating dairy cows.

Materials and Methods

Individual cow grass dry matter intake at pasture was determined using the n-alkane technique (Mayes et al., 1986). Net energy intake (NEI) from pasture and concentrate intake was estimated up to eight times per lactation on 2,693 lactations from 1,412 Holstein-Friesian cows. A total of 8,183 individual feed intake measurements were available. Animal body condition score was recorded every two to three weeks. Lactation was divided into three lactation stages (8–90, 90–180, and ≥ 180 days in milk). Three parity classes (1, 2, and 3-5) were considered. The UFL value (French Net Energy system) of both herbage and concentrates were calculated for each intake record. Residual energy intake (REI) was defined as the residuals from least squares regression of net energy intake minus predicted energy requirements based on lactational performance (Hurley et al., 2015). Energy conversion efficiency (ECE) for each day of lactation was defined as net energy of lactation (NEL) divided by NEI. Kleiber ratio (KR) for each day of lactation was defined as NEL divided by metabolic live-weight. Energy balance (EB) was defined as the difference between energy intake and intake demand, both estimated from nutritional tables. Pearson correlations among traits within lactation stage were estimated.

Results and Discussion

Mean ECE, EB, KR and REI over the whole data set was 0.41UFL/d (SD=0.11UFL/d), 3.68UFL/d (SD=2.51UFL/d) 0.06UFL/d (SD=0.01UFL/d) and 0.00UFL/d (SD=2.17UFL/d), respectively. REI and EB had a similar trend throughout lactation (Fig. 1). Moreover, ECE declined rapidly in early lactation, while a gradual decrease occurred in mid and late lactation. Additionally, KR declined across lactation stages (Fig. 1). A strong correlation existed between EB and ECE for both parities in lactation stage one (-0.91 and -0.91), suggesting animals were most efficient in early lactation. A strong correlation existed also between EB and REI (0.88) for parity 3-5 early lactation animals; however, at the same stage in parity one a weaker correlation existed (0.70), suggesting primiparous animals were using energy for both milk production and growth. Furthermore, the correlation between KR and ECE was strong in early lactation decreasing rapidly thereafter suggesting animals were most efficient in early lactation (i.e. increased NEL for the same metabolic live-weight) (Table 1).

Conclusions

Correlations were similar in trends and magnitude between parities while variation across stage of lactation existed between the efficiency traits and energy balance.

Acknowledgements

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***Table 1**. Pearson correlations among efficiency traits and NEI across parity and days in milk (DIM).*

Parity	DIM	Trait	ECE	EB	REI
1	8-90	EB	-0.91		
		REI	-0.68	0.70	
		KR	0.52	-0.27	-0.15
	90-180	EB	-0.77		
		REI	-0.74	0.94	
		KR	0.62	-0.05	-0.03
	>180	EB	-0.64		
		REI	-0.67	0.95	
		KR	0.66	0.09	0.03
3-5	8-90	EB	-0.91		
		REI	-0.76	0.88	
		KR	0.50	-0.22	-0.12
	90-180	EB	-0.76		
		REI	-0.72	0.97	
		KR	0.60	0.002	0.05
	>180	EB	-0.67		
		REI	-0.66	0.96	
		KR	0.71	-0.03	-0.03

[1] r < |0.03| were not different from zero

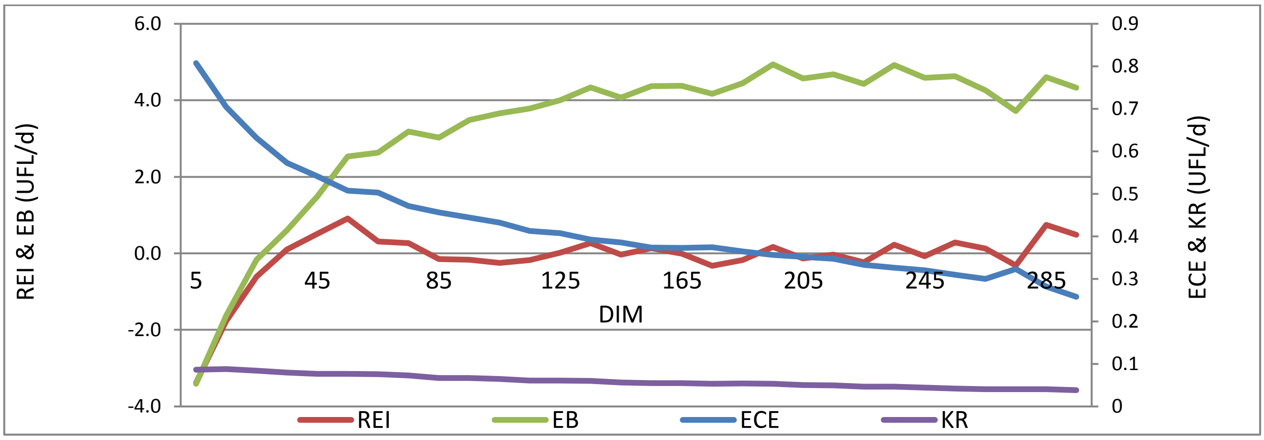

Fig. 1. Efficiency traits across lactation

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RMIS Project No. 6458

Inter-relationships among alternative definitions of feed efficiency in grazing lactating dairy cows

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Introduction

Feed efficiency in lactating animals is complex because of anabolism and catabolism of body reserves during lactation. Many alternative definitions of feed efficiency in lactating animals exist. Phenotypic correlations between these traits, however, have not been fully elucidated. Moreover, many of the proposed definitions of feed efficiency, especially the ratio traits, do not take cognisance of the contribution of body tissue mobilisation to energy kinetics. The objective of this study was to derive alternative definitions of energetic efficiencies in lactating dairy cows and quantify the inter-relationships among these alternative definitions.

Materials and Methods

In total 8,183 individual animal feed intake measurements across lactation from 2,693 lactations on 1,412 pasture-based Holstein-Friesian cows were available. Individual animal grass DMI was estimated using the n-alkane technique (Mayes *et al.*, 1986), and available on average, 6 times per lactation. Total dry matter intake (i.e., grazed grass plus concentrate) was available up to eight times per lactation. The UFL value (French Net Energy system energy value) of both herbage and concentrates consumed by each animal was calculated. Traits were classified into ratio and residual-based traits. Energy balance was determined by subtracting energy required for maintenance and lactation from intake of energy.

Residual traits

Residual energy intake (REI) and residual energy production (REP) were defined as:

$$\mathrm{REI} = \mathrm{NEI} - [\mathrm{NEL} + \textstyle\sum_{i=1}^{2} \mathrm{DIM}^{i} + \mathrm{BW}^{0.75} + \mathrm{BCS} + \mathrm{BW}^{0.75} \times \mathrm{BCS} + \Delta\mathrm{BW}^{+} + \Delta\mathrm{BW}^{-} + \Delta\mathrm{BCS}^{+} + \Delta\mathrm{BCS}^{-} + \Delta\mathrm{BW}^{+} \times \mathrm{BCS} + \Delta\mathrm{BW}^{-} \times \mathrm{BCS}]$$

$$\mathrm{REP} = \mathrm{NEL} - [\mathrm{NEI} + \textstyle\sum_{i=1}^{2} \mathrm{DIM}^{i} + \mathrm{BW}^{0.75} + \mathrm{BCS} + \mathrm{BW}^{0.75} \times \mathrm{BCS} + \Delta\mathrm{BW}^{+} + \Delta\mathrm{BW}^{-} + \Delta\mathrm{BCS}^{+} + \Delta\mathrm{BCS}^{-} + \Delta\mathrm{BW}^{+} \times \mathrm{BCS} + \Delta\mathrm{BW}^{-} \times \mathrm{BCS}]$$

where NEI is daily net energy intake, NEL is daily net energy requirements for lactation, $\sum_{i=1}^{2} \mathrm{DIM}^{i}$ is days in milk included as a continuous variable with a linear and quadratic effect, $\mathrm{BW}^{0.75}$ is metabolic live-weight, BCS is body condition score, $\Delta\mathrm{BW}^{+}$ describes animals gaining live-weight, $\Delta\mathrm{BW}^{-}$ describes animals losing live-weight, while $\Delta\mathrm{BCS}^{+}$ describes animals gaining BCS, and $\Delta\mathrm{BCS}^{-}$ describes animals losing BCS. Piece-wise regression was used to estimate the regression coefficients on BCS/BW loss and gain.

Ratio traits

Energy conversion efficiency (ECE), for each day of lactation was defined as NEL divided by NEI. Energy conversion efficiency was refined to 1) consider the energy kinetics from body weight and BCS change in both the numerator and denominator ($\mathrm{ECE}_{\mathrm{adj}}$), and 2) also consider the energy requirement for maintenance in the numerator ($\mathrm{ECE}_{\mathrm{adj2}}$):

$$\mathrm{ECE}_{\mathrm{adj}} = \frac{\mathrm{NEL} + \mathrm{b}\Delta\mathrm{BW}^{+} + \mathrm{b}\Delta\mathrm{BCS}^{+} + \mathrm{b}\Delta\mathrm{BW}^{+} \times \mathrm{BCS}}{\mathrm{NEI} + \mathrm{b}\Delta\mathrm{BW}^{-} + \mathrm{b}\Delta\mathrm{BCS}^{-} + \mathrm{b}\Delta\mathrm{BW}^{-} \times \mathrm{BCS}}$$

$$\mathrm{ECE}_{\mathrm{adj2}} = \frac{\mathrm{NEL} + \mathrm{bBW}^{0.75} + \mathrm{b}\Delta\mathrm{BW}^{+} + \mathrm{b}\Delta\mathrm{BCS}^{+} + \mathrm{b}\Delta\mathrm{BW}^{+} \times \mathrm{BCS}}{\mathrm{NEI} + \mathrm{b}\Delta\mathrm{BW}^{-} + \mathrm{b}\Delta\mathrm{BCS}^{-} + \mathrm{b}\Delta\mathrm{BW}^{-} \times \mathrm{BCS}}$$

where the b's represent the associated regression coefficients from the aforementioned REI model. Partial efficiency of milk production (PEMP) and a similar trait $\mathrm{PEMP}_{\mathrm{Nut}}$ were defined as:

$$\mathrm{PEMP} = \frac{\mathrm{NEL}}{\mathrm{NEI} - \mathrm{bBW}^{0.75}} \qquad \mathrm{PEMP}_{\mathrm{Nut}} = \frac{\mathrm{NEL}}{\mathrm{NEI} - \mathrm{NEM}}$$

where NEM is daily net energy required for maintenance calculated as (1.4 + 0.6×(live-weight/100))×1.2. The efficiency trait PEMP used the energy required for maintenance as derived from the whole population while this statistic was derived from nutritional tables for $\mathrm{PEMP}_{\mathrm{Nut}}$.

Results and Discussion

A strong correlation (0.82) existed between REI and EB, suggesting that negative REI animals (i.e., deemed more efficient animals) were also animals in more negative energy balance which is known to be unfavorably associated with reproductive performance (Butler and Smith, 1989). Nonetheless, the strong association between REI and EB was not unexpected given their mathematical similarity.

A moderately strong correlation existed between NEI with both REI (0.67) and EB (0.74). Similarly, a moderate correlation (0.56) existed between REP and NEL suggesting high REP animals, on average, produced more milk energy for a given energy intake. The strong correlation between ECE and ECE_{adj} (0.88) suggests minimal contribution of live-weight change and BCS change to the variation in ECE_{adj} in the present study. The correlation between PEMP and $PEMP_{Nut}$ was moderate (0.41) even though both traits were similarly defined.

Table 1. Pearson correlations among traits

Traits	ECE	2	3	4	5
2.ECE_{adj}	0.88				
3.PEMP	0.90	0.87			
4.$PEMP_{Nut}$	0.62	0.48	0.41		
5.$EB_{, UFL/d}$	-0.79	-0.62	-0.50	-0.58	
6.$REI_{, UFL/d}$	-0.53	-0.38	-0.23	-0.45	0.82

Conclusions

Many of the correlations between the traits differed considerably from unity implying that each trait is measuring a different aspect of efficiency.

Acknowledgements

Funding from the Research Stimulus Fund Gencost.

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RMIS Project No. 6458

Low density genotype panels for dairy and beef cattle

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Introduction

The relatively high cost of procuring a genotype is precluding the widespread uptake of genomic selection on-farm. As the cost of genotyping is a function of the number of single nucleotide polymorphisms (SNPs) to be genotyped, one option, to reduce the cost of obtaining a direct genomic value for an animal, is to use a lower density genotype panel, which can be imputed up to higher density. The objective of this study was to develop lower density genotype panels with varying number of SNPs.

Materials and Methods

Illumina Bovine50 beadchip genotypes were available on 6,369 Holstein-Friesian animals. Only autosomal SNPs with a call rate ≥95% and a minor allele frequency (MAF) >2%, that adhered to mendelian inheritance patterns, had sufficiently high genotype quality score and did not deviate from Hardy-Weinberg equilibrium were retained. SNPs that differed substantially in documented genomic location between UMD3.1 and Btau4.0 genome builds were also discarded. Following edits, 40,483 SNPs remained. Thirty of the youngest genotyped Holstein-Friesian animals (with both sire and dam genotyped) were originally selected as the dairy validation population; all paternal and maternal half-sibs to these animals, as well as animals with the same maternal grandsire (MGS) as the MGS of the original 30 animals, were also included in the validation population; the validation population consisted of 750 animals. A total of 3,103 animals with the sire, dam or MGS of the validation bulls appearing as their sire, dam or MGS were not considered further. The remaining 2,516 animals were divided into two groups: 1) 1,267 animals used to determine genomic architecture and 2) 1,249 animals used as reference animals during the imputation process. Genotype panels containing 384, 1,000, 2,000, 3,000, 6,000 or 12,000 SNPs were generated using alternative selection algorithms: 1) SNPs selected at random, 2) SNPs selected uniformly across the genome 3) SNPs selected based on a combination of MAF, genomic distance between already selected and remaining candidate SNPs, and the absolute correlation between alleles of selected and candidate SNPs (Wellmann et al., 2013), and 4) SNPs chosen based on a combination of MAF and linkage disequilibrium (LD) within blocks of the genome. Illumina 50K genotypes were also available on 1,412 Limousin and 897 Charolais animals. The youngest 148 Limousin and youngest 117 Charolais animals were selected as the validation population. For each low density panel, only the SNPs genotypes of these validation animals for the panel under investigation were retained and all remaining genotypes were masked. Imputation to the higher density panels was undertaken (for both populations separately) using either FImpute (Sargolzaei et al., 2014) or Beagle (Browning and Browning, 2009). Accuracy of imputation was determined using: 1) allele concordance rate or 2) the correlation between actual and imputed genotypes. In all instances the accuracy was calculated by including the correct genotypes of the validation groups.

Results and Discussion

Negligible difference in imputation accuracy existed between FImpute and Beagle; therefore, all subsequent results refer only to imputation using FImpute. Irrespective of SNP selection method, imputation accuracy increased at a diminishing rate in both the dairy (Fig. 1) and beef populations, as panel density increased. Regardless of SNP selection method, the variation in allele concordance rate per animal also reduced as SNP density increased. For example, with the 384 SNP panel, mean (minimum; maximum) animal allele concordance rate was 0.849 (0.730; 0.980), while with the 12,000 panel the mean allele concordance was 0.994 (0.943; 0.999). Selecting SNPs based on MAF and LD within blocks of the genome was the most accurate method of SNP selection and resulted in the greatest imputation accuracy regardless of SNP density (allele concordance rate of 0.976 with 3,000 SNPs in dairy and 0.936 in the beef). Accuracy of imputation improved further when back-pedigree with full genotypes were included in the imputation process to generate haplotypes.

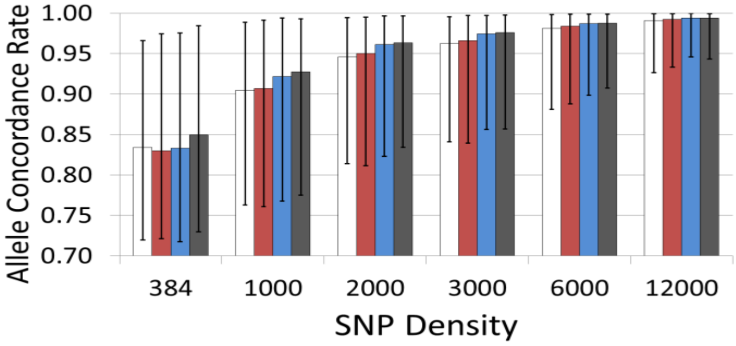

Fig. 1. Mean allele concordance rate (range represented as standard error bars) in dairy, across varying number of SNPs selected randomly (white columns), uniformly (red columns), based on genomic architecture (blue columns) or by the block method (grey columns).

Conclusion

In both the dairy and beef populations, accurate imputation is achievable with low density panels (i.e. 3000-6000 SNPs).

Acknowledgements

Funding from the FIRM research grant GENTORACE.

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RMIS Project No. 6589

Physiology of Reproduction, Growth_Lactation

The effect of type of carbohydrate supplementation during early lactation on indicators of health and fertility in pasture-based dairy cows

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Introduction

Carbohydrates are the major source of energy for rumen microorganisms and the single largest component (60-70%) of a dairy cow's diet. Carbohydrates can be divided into structural carbohydrates (SC; e.g., cellulose) and non-structural carbohydrates (NSC; e.g., starch). The aim of this experiment was to examine the effect of early postpartum supplementation with either NSC or SC on postpartum interval to first oestrus, interval to first progesterone rise, uterine health and indicators of energy reserves in lactating dairy cows.

Materials and Methods

This study was conducted on commercial herds ($n = 3$) in New Zealand between July and October 2014. All procedures and animal events had prior approval of the Ruakura Animal Ethics Committee, New Zealand. Animals were blocked by breed, age and week of calving ($n=870$), and randomly assigned to receive 4.5 kg/d of either a SC (palm kernel & soya hulls, 50:50) or a NSC (maize & barley grain, 50:50) supplement from parturition until 35 days before the planned start of mating. The SC and NSC supplements were formulated to be isoenergetic. Within each farm, all cows were managed identically after the nutritional treatments were finished. On week 4 postpartum, body condition score (BCS) was recorded on a scale of 1-10 (Roche *et al.*, 2004) and vaginal mucus scores were recorded on a scale of 0 to 5 (McDougall et al., 2007). A subset of 96 animals in each herd was selected to evaluate the interval from calving to first oestrus and first progesterone (P4) rise. Prebreeding oestrus detection was recorded by assessing tail paint removal once per week. Milk samples were taken at the am milking once per week on weeks 3, 4, 5 and 6 postpartum. Milk progesterone concentrations were determined using a competitive ELISA (Ridgeway Science, Gloucestershire, UK). Blood samples were taken on week 2 postpartum, and β-hydroxybutyrate (BHB) was measured using Freestyle Optium Blood ß-Ketone Test strips (Abbott Australasia Pty Ltd, Doncaster VIC 3108 Australia). Sub-clinical ketosis and clinical ketosis events were recorded when BHB concentrations were > 1.2 mmol/L and > 3.0 mmol/L, respectively (McArt *et al.*, 2011). Data analysis was carried out using SAS v9.3. Continuous data were analysed using mixed models (MIXED). Time dependent variables (calve to first heat and P4 rise) were analysed using survival analysis (PHREG). Binary (incidence of ketosis) and ordinal data (vaginal mucus score) were analysed using generalized mixed models (GLIMMIX). All models included the fixed effects of treatment, breed, parity, herd and their interactions, and cow was included as a random effect.

Results and Discussion

Herd had an effect ($P<0.05$) on all variables analysed and a herd by treatment interaction ($P<0.05$) was detected for BHBA concentrations on day 14 postpartum. Cows assigned to NSC treatment had lower ($P=0.004$) BHBA on week 2 postpartum compared to the cows on the SC treatment (0.58 vs. 1.29 mmol/L; 95% CI: 0.42-0.78 and 0.82-2.02 mmol/L, respectively). The incidence of both subclinical (14.5% vs. 42.3% of cows; $P < 0.001$) and clinical ketosis (0.7% vs. 4.9% of cows; $P < 0.03$) was reduced by the NSC supplement compared with the SC supplement. There was no effect of treatment on BCS (4.27 vs. 4.18; $P = 0.18$) or reproductive tract health status (mean score 1.42 vs. 1.41; $P = 0.7$) on week 4 postpartum. Neither the interval from calving to first progesterone rise (28.9 vs. 31.0 days; $P = 0.50$) nor first observed oestrus (32.7 vs. 33.5 days; $P =0.70$) were affected by treatment.

Conclusions

Feeding lactating dairy cows a NSC supplement immediately postpartum reduced circulating BHBA concentrations and the incidence of subclinical and clinical ketosis at 2 weeks post-partum compared with feeding a SC supplement. The type of carbohydrate supplement had no effect, however, on BCS, uterine health status, and postpartum resumption of cyclicity. It remains to be determined if the type of carbohydrate supplement had a significant effect on pregnancy establishment.

Acknowledgements

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RMIS Project No. 6406

The use of in vitro assessments to predict bull fertility

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Introduction

Currently, the only reliable method to assess a bull's fertility is to perform hundreds of test inseminations in the field (Oliveira *et al.*, 2013). This takes time, is costly, and a bull's fertility can vary over time. The aim of this study was to use a multi-pronged *in vitro* approach to correlate field fertility of two cohorts of bulls whose semen was used in the field as non-sorted (NS) frozen semen or sex-sorted (SS) frozen semen.

Material and Methods

Experiment 1: The aim of this experiment was to correlate *in vitro* sperm functional parameters to pregnancy rates using bulls of varying fertility. NS frozen semen, at 20 x 10^6 sperm per dose (n=6 bulls), and X-SS frozen semen, at 2.1 x 10^6 sperm per dose (n=6 bulls), was donated from two Irish artificial insemination centres. The phenotypic pregnancy rates for the NS bulls ranged from 35 to 69% (Year 2014), and from 28 to 58% for the SS bulls (Year 2013), based on a minimum of 200 inseminations. In total, 3 straws from each of 3 ejaculates of each bull were assessed for each *in vitro* parameter. Motility, thermal stress tolerance, and morphology were assessed using microscopy based techniques. Viability, hypo osmotic swelling test, mitochondrial membrane potential and acrosome integrity in the live population were assessed using flow cytometry. The fertilising ability of the sperm was assessed using *in vitro* fertilisation (IVF).

Experiment 2: The aim of this experiment was to correlate seminal plasma (SP) composition to pregnancy rates of bulls of varying fertility, whose semen was used as either NS or SS frozen semen (same bulls as Experiment 1). In order to isolate SP, ejaculates (n=3 per bull) were centrifuged at 2000 *g* for 10 min at 4 ^{o}C, snap frozen in liquid nitrogen and stored at -80 ^{o}C. SP was subsequently analysed for amino acid and fatty acid composition using gas chromatography mass spectrometry (GC-MS). *In vitro* data for both cohorts of bulls, NS and SS, were examined for normality, and correlated with phenotypic pregnancy rates of the corresponding bulls using SPSS software (version 22.0, IBM, Chicago, IL).

Table 1: Correlations between *in vitro* sperm functional parameters and pregnancy rate (Experiment 1)

Parameter	Non Sorted Bulls				Sex Sorted Bulls			
	Mean (%)	±SEM (%)	Correlation Coefficient R	p-value	Mean (%)	±SEM (%)	Correlation Coefficient R	p-value
Pregnancy Rate	54.2	1.75			47.8	1.33		
Motility	58.9	1.31	-0.32	0.54	55.3	3.43	0.84	0.04
Motility Post Stress	30.8	3.34	-0.69	0.13	12.8	2.35	-0.41	0.41
Normal Cells	85.1	1.25	0.64	0.18	89.3	0.76	0.3	0.60
Viable	50.6	4.85	-0.10	0.86	81.3	1.28	0.80	0.05
Cleaved	73.5	2.69	0.04	0.95	68.2	2.81	0.64	0.17
Day 6 Blastocysts	15.0	1.02	0.43	0.39	6.6	0.92	0.76	0.08
Total Blastocysts	36.2	1.77	0.43	0.75	17.2	1.36	0.76	0.24

Results and Discussion

Experiment 1: In the NS cohort of bulls there was no correlation between any of the sperm functional parameters assessed and pregnancy rates (Table 1). However, within the SS cohort of bulls motility was correlated to pregnancy rates (R = 0.84; P<0.05). Also, within the SS cohort both viability and Day 6 blastocyst rate both approached significance in their correlation with pregnancy rate (R = 0.80 and 0.76; P=0.05 and 0.08, respectively). These results support the theory that the sex sorting process alters the sperm population and *in vitro* assessments may be more useful in predicting fertility than with NS semen.

Experiment 2: In the NS cohort of bulls Isoleucine and Tricosylic acid (C23:0) were correlated with pregnancy rate (R=0.80 and 0.74, respectively, P<0.05). Within the SS cohort of bulls both Glutamic acid and Arachidic acid (C20:0) correlated to pregnancy rate (R=0.84 and 0.82, respectively; P<0.05). Furthermore, both Aminoisobutyric acid and Elaidic acid (C18:1n9t) approached significance in their correlation with pregnancy rates (R=-0.78 and -0.74; P=0.07 and 0.09, respectively). SP composition may have a greater effect on SS sperm than on NS sperm which may be due to prolonged exposure of sperm to SP prior to sex-sorting.

Conclusion

While sperm functional i*n vitro* assessments are of limited use in predicting the fertility of bulls whose semen is used as NS frozen, they are more useful when semen is used as SS semen. Analysis of SP composition may also be useful in determining which bulls are best suited to undergo sex-sorting.

Acknowledgements

We gratefully acknowledge support from the Department of Agriculture, Food and the Marine under the Research Stimulus Fund (Project 11/S/116).

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RMIS Project No. 6448

Examination of the effects of acute or chronic pasture restriction on indicators of cow fertility and metabolic health status

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Introduction

Grass is the primary feed in Irish dairy production systems. The likely increase in stocking rates on many farms during the next decade due to milk quota abolition expansion will result in a greater demand for grass, especially in spring. Annual variation in pasture growth rate has a major effect on farm covers and grass availability. The aim of this study was to determine the effect of imposing different durations and severity of pasture restriction on indicators of metabolic health and reproductive status in early lactation dairy cows.

Materials and Methods

Ninety six cows were enrolled on a study at the Teagasc Moorepark Research Farm, Co. Cork in March 2014. Cows were blocked by calving date, breed, parity, milk yield, body weight and body condition score, and randomly assigned to one of four daily herbage allowances (DHA) for either two or six weeks (12 cows per treatment). The DHA were 60, 80, 100 and 120% of intake capacity (calculated using equation of Faverdin et al. (2011)). No concentrate was fed during the experimental period (24 March to 5 May 2014). The cows were managed as individual treatment groups during the experimental period and as one group thereafter. Blood sampling took place weekly from two weeks before the treatments began until 5 weeks after treatment termination. All blood samples were collected after the morning milking into 10 ml lithium heparin vacutainer tubes (Becton Dickinson, Plymouth, United Kingdom), centrifuged at 1500 x g for 15 minutes and the plasma stored in aliquots at -20 °C until analysis. All plasma samples were analysed for glucose, non-esterified fatty acids (NEFA) and β-hydroxybutyrate (β-HBA). Milk samples were collected 3 times per week for milk progesterone (P4) analysis from calving until pregnancy diagnosis. Milk P4 was determined using a competitive ELISA (Ridgeway Science, Gloucestershire, UK). The interval to commencement of luteal activity (CLA) was calculated. Data were analysed using SAS v9.3. All data were analysed using the mixed models procedure of SAS with repeated measures, where appropriate.

Table1. Effect of pasture restriction and duration of restriction on mean metabolite values during the experimental period

	DHA_Duration									
Metabolite	60_2	60_6	80_2	80_6	100_2	100_6	120_2	120_6	S.E.M	DHA*dur
Glucose (mmol/l)	3.27^{a}	3.01^{b}	3.53^{c}	3.07^{bd}	3.38^{ac}	3.22^{ad}	3.34^{ac}	3.29^{a}	0.08	**
β-HBA (mmol/l)	0.63^{a}	1.10^{d}	0.41^{a}	1.02^{d}	0.65^{a}	0.71^{a}	0.79^{ad}	0.75^{a}	0.12	**
NEFA (mmol/l)	0.53^{a}	0.69^{ac}	0.56^{a}	0.84^{b}	0.70^{bc}	0.61^{a}	0.63^{ac}	0.57^{a}	0.05	***

The model contained fixed effects of DHA, duration, experimental week, parity and their interactions. Block was included as a random effect. The mean metabolite concentrations in the pre-experimental samples were used as a covariate.

Results and Discussion

The metabolic data are summarised in Table 1. Significant interactions between DHA and duration were detected for glucose, β-HBA and NEFA (all $P<0.01$). In general, the most nutritionally restricted groups (60x6 and 80x6) had the lowest circulating glucose concentrations and the greatest circulating NEFA and β-HBA concentrations.

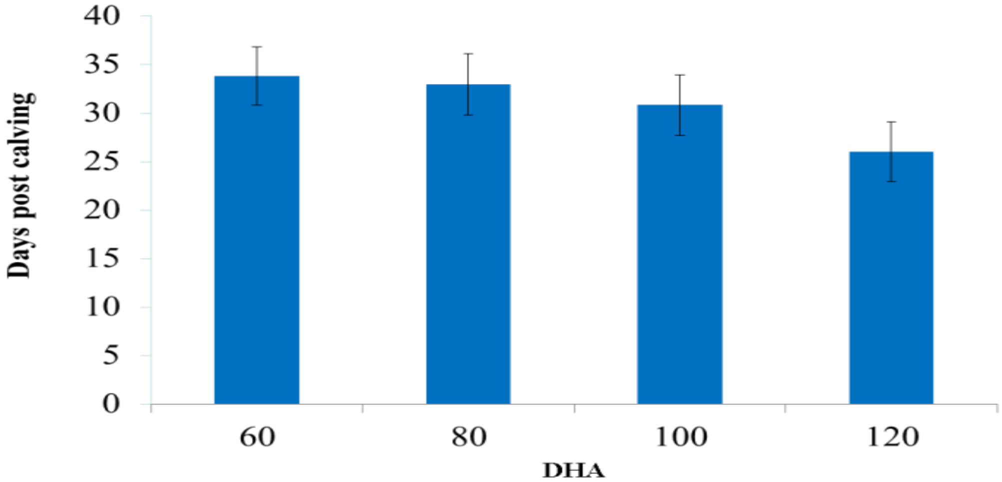

Figure 1 Main effect of daily herbage allowance on the commencement of luteal activity.

There was no overall effect of DHA on CLA (P=0.28), but CLA tended to be longer in the cows assigned to the 60 % DHA compared to 120 % DHA (P=0.06; Fig.1). There were no significant interactions of DHA and duration for CLA.

Conclusions

This study replicated the potential grass supply shortages that can be encountered on dairy farms in Ireland throughout the spring. From these initial results, short periods (up to 2 weeks) of restricted pasture do not have a marked effect on metabolic status and resumption of cyclicity. This study needs to be repeated in order to validate these initial findings.

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RMIS Project No. 6387

Comparison of IGER behaviour recorder and a commercially available activity meter for measuring grazing duration

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Introduction

Grazing duration is one of the main factors influencing grass intake, along with grass intake per bite and rate of biting (O'Connell *et al.*, 2000). Current methods of measuring grazing behaviour, for example, the IGER (Institute of Grassland and Environmental Research) behaviour recorder, record for a limited period of time. As a technology, it is antiquated, laborious and prone to breakages, and realistically is only suited to recording under a controlled research environment. Activity meters, used primarily for health and fertility monitoring in dairy cows, have recently begun to incorporate behavioural traits, enabling continuous monitoring of behaviour which could be of enormous benefit, assuming they provide accurate information. The hypothesis of this experiment was that the activity meter provides similar information on grazing duration to that generated by the IGER behaviour recorder for lactating dairy cows, thereby providing an acceptable alternative but with multiple uses.

Materials and Methods

One hundred first and second lactation Holstein-Friesian cows were used in this experiment between 26 August and the 30 September 2014 at the Teagasc, Dairygold research farm, Kilworth, Co. Cork. Grazing time was recorded using IGER behaviour recorders which have been validated to measure grazing behaviour (Rutter *et al.*, 1997). IGER recorders (n=15) were attached to sub-groups of cows after morning milking between 07:15 and 09:00 hours. In total, 100 records were attained over 14 separate days. Recorders were detached the following morning having completed a 24-hour recording. The time when recorders were fitted and removed from the cows was recorded. Individual files were downloaded using the "Graze" analysis software (Rutter, 2000). If the record was unusable, the animals were fitted with an IGER recorder for a second 24 hour period. All cows were fitted with 'MooMonitor+' activity meters (Dairymaster, Causeway, Co. Kerry). Total grazing time data from the MooMonitor+ was obtained for all animals on all days during the trial period from the Dairymaster database. The MooMonitor+ data were summarised into 15 minute intervals; only data corresponding to the 24-hour period coinciding with when the IGER behaviour recorders were also fitted were retained. Cows were offered fresh grass in 24-hour allocations during the trial period. One hundred usable IGER records were collected. Total 24-hour grazing duration determined by the IGER grazing recorder was linearly regressed on the MooMonitor+ grazing duration to determine the association between each method; no intercept was fitted in the model. A fixed effects linear model was used to quantify the association between parity, day measurement period (for each sub-group) and IGER recorder number on the IGER recorded grazing duration. Two-way interactions between the MooMonitor+ measure of grazing duration and the main fixed effects were considered in the model to determine if the association between the MooMonitor+-determined grazing duration and IGER-determined grazing duration differed by any of the main effects.

Results and Discussion

Mean 24-hour grazing duration was 543 (±6.39 SEM; Standard Error of the Mean) minutes for IGER recorders and 540 (±5.9 SEM) minutes for MooMonitor+ devices. A correlation of r=0.72 existed between the IGER-determined grazing duration and MooMonitor+-determined grazing duration. The regression coefficient of IGER grazing duration on MooMonitor+ grazing duration was 1.003 (±0.008 Standard Error) which was not different from the expectation of unity should the measured differences in grazing duration between the two devices be equivalent. Neither parity nor calendar day was associated with the difference in grazing duration estimated by the two devices. Estimated grazing duration between both devices, however, differed (P=0.01) by IGER recorder. The association between the MooMonitor+-determined grazing duration and the IGER-determined grazing duration did not differ by parity or day of the year but did differ (P<0.001) by IGER recorder. The regression coefficient of the IGER-determined grazing duration on the MooMonitor+-determined grazing duration varied from 0.87 to 1.1. Neither parity nor IGER recorder number were associated with IGER-determined grazing duration. The IGER-determined grazing time declined (P=0.03) across the 11 weeks of the trial from 587 minutes per cow on 26 August to 493 minutes per cow on 30 September. This may be explained by decreasing daily sunlight hours from 14.0 hours on 26 August to 11.0 hours on 30 September.

Conclusions

Although the IGER recorders are generally considered the "gold standard" to measure grazing behaviour in dairy cows they are not without their limitations The MooMonitor+ offers potential for data collection on a greater scale. The results from this study, albeit from a limited dataset, indicate good concordance between 24-hour grazing duration estimated from the IGER recorders and MooMonitor+ recorders.

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RMIS Project No. 6511

Animal Health and Well Being

An investigation of the association between calf hygiene practices and calf morbidity and mortality on Irish dairy farms

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Introduction

As calves are born agammaglobulinaemic they are extremely susceptible to disease, particularly prior to the development of active immunity at approximately 6 weeks of age (Chase *et al.*, 2008). Good hygiene practice is important in preventing the spread of infectious diseases such as cryptosporidium in young dairy calves (Gulliksen *et al.*, 2009). Illness in pre-weaned calves has both immediate and prolonged negative effects on growth rate and performance (Lorenz *et al.*, 2011). The methods used and frequency of cleaning pens and feeding equipment on dairy farms in Ireland has not previously been investigated. The objective of this survey was to investigate the hygiene of calf housing and feeding equipment, and their associations with calf morbidity and mortality on Irish dairy farms.

Materials and Methods

A survey was conducted using a study population (n=320) selected from the Irish Cattle Breeding Federation (ICBF) HerdPlus members. Selection was random and was balanced for herd size and geographical location. The survey consisted of four sections: 1) cow management, 2) calving management, 3) colostrum management and 4) calf management. Questions from section 4 are described in the current paper. These questions included frequency and method used to clean calf pens e.g. clean out with water. Additional questions on calf feeding equipment hygiene were also included such as how equipment was cleaned e.g. hot water or cold water. The most common age and causes of pre-weaned calf morbidity was also investigated. Questions were predominantly close-ended, and were structured to obtain concise and accurate information, while also ensuring ease-of-use. Surveys were distributed via post between 11 July and 15 August 2013. Responses were entered onto the online survey tool *SurveyMonkey.com* prior to downloading and collation in Excel (Microsoft, 2010). The main cause of calf illnesses, obtained from survey responses, were described as scour only, pneumonia only, navel ill only or a combination of 2 or more of these illnesses. With permission from respondents and the ICBF, data of calf births and deaths were obtained from the ICBF database to obtain mortality rates. Data editing and analysis was conducted using SAS v9.3. A univariate chi-square analysis was conducted to investigate the associations between frequency of cleaning calving pens, calf rearing pens and calf feeding equipment × method of cleaning these pens × cause of illnesses × age at which calves fell ill. Mortality was investigated as a continuous variable using the MIXED procedure of SAS (2011) and difference of LSM was calculated in the model.

Results and Discussion

The survey response rate was 85% (*n*=271). More than 95% of respondents cleaned calf pens at some point in the year. Almost 20% of surveyed farms cleaned pens infrequently (≤once/month) while 30% cleaned just between calving seasons. Infrequent cleaning of pens and other calf equipment can lead to a build-up of bacteria and ammonia in the pen, which can result in cryptosporidium or other infections (Gulliksen *et al.*, 2009). The overall model association between mortality and all hygiene practices was not significant (P=0.08), however there were some univariate associations: respondents that cleaned monthly had lower mortality than those who did not clean pens at all (P<0.05), further supporting the evidence of the importance to have a hygienic environment for dairy calves (Gulliksen *et al.*, 2009). Respondents that cleaned pens between calves (21% of respondents) and between seasons only (29%) were more likely to both wash and use disinfectant while cleaning pens than clean out only (without washing or using disinfectant). However, infrequent cleaning may counteract this as pathogen build-up is associated with increased mortality rates (Svensson *et al.*, 2006). In the current study respondents with a regular cleaning schedule were less likely to identify one main morbidity issue on their farm (e.g. scour) than respondents cleaning between calf groups/between seasons only (P<0.01). Respondents that cleaned pens between calf groups only (21% of respondents) or between seasons only (29%), were more likely to have an issue with navel infections compared to calves housed in pens that were cleaned regularly (<once/month). This demonstrates that, similar to Svensson *et al.* (2006), regular cleaning reduces the incidence of persistent problems such as scour and pneumonia. The overall most common age of illness was 2 to 7 weeks old (85% of all farms). Method used to clean feeding equipment was associated with age of calf illness (P<0.01). Of respondents that washed equipment with water (hot and cold) only (69%) had calves frequently falling ill at many different ages (approximately 80% falling ill at 2 to 7 weeks) compared to those that used detergent (approximately 60% falling ill aged 2 to 4 weeks). Thoroughly cleaning equipment minimises disease spread by minimising cross-contamination between calves (Svensson *et al.*, 2006).

Conclusion

This study indicates that thorough and frequent cleaning of housing and feeding equipment is important for the control of calf morbidity and mortality on Irish dairy farms. Regular cleaning of calf pens appears to be associated with lower incidences of persistent illnesses and lower mortality rates. Detergent should be used to minimise cross contamination between calf pens and thus, reduce disease risk.

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RMIS Project No. 6009

Effect of bacteria level in colostrum on dairy heifer serum IgG concentration and pre-weaning growth rate

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Introduction

Colostrum with an immunoglobulin G (IgG) content of >50g/L is defined as good quality and has sufficient IgG for essential immune protection in neonatal calves. Adequate passive transfer (APT) of IgG occurs in calves when serum has an IgG content ≥10g/L (Godden, 2008). Colostrum is not only vital for neonatal health but can also affect average daily weight gain (ADWG) (Godden, 2008). Approximately 90% of Irish dairy farmers store colostrum (Cummins *et al.*, 2014a). Storage >4°C results in an increased total bacterial count (TBC) (Cummins *et al.*, 2014b) that may compromise APT (Godden, 2008). Currently 100,000 colony forming units (CFU/ml) is the maximum total bacterial level advised in colostrum (Godden, 2008). However, the direct effect of bacteria level in colostrum on APT and ADWG is uncertain. The aim of this experiment was to investigate the effect of colostrum stored at varying temperatures to induce a difference in bacteria levels on the rate of passive transfer of IgG and ADWG from birth to weaning of dairy heifer calves.

Materials and Methods

Colostrum was collected immediately post-partum from individual Holstein-Friesian (HF) cows, tested for IgG concentration using a colostrometer (to block for quality), and assigned to 1 of 5 treatments to create colostrum of varying bacteria levels: 1) pasteurised, 2) fed when freshly collected, 3) stored at 4°C for ≥48 hours (reflects fridge storage), 4) stored at 13°C ≥48 hours, and

5) stored at 22°C ≥48 hours. Seventy-five HF and HF×Jersey (JEX) heifer calves were removed from their dam and assigned to a treatment immediately post-partum at Teagasc Moorepark Research Farm, Co. Cork, from 3 Feb. to 25 Mar. 2014. Treatment assignment was conducted using a randomised block design accounting for breed, birth date, and birth weight (BW). All calves were fed 8.5% of their BW in colostrum via stomach tube within 2 hours. A sample of colostrum corresponding to each calf was stored for subsequent testing of IgG concentration using Radial Immunodiffusion (RID Triple J Farms, WA, USA) and TBC, using serial dilution (Cummins *et al.*, 2014b). Calf blood samples were collected at 0 (control) and 24 hours of age and analysed for IgG concentration via RID. Calves were weighed weekly and weaned at 90kg (HF) or 85kg (JEX). Data was checked for normality and the MIXED procedure in SAS (v9.3, 2011) was used to examine the effect of treatment on serum IgG concentration and ADWG to weaning.

Results and Discussion

Pasteurised colostrum had an expectedly low TBC (<9,000 CFU/ml), TBC of fresh colostrum was 68,000 CFU/ml; below the recommended level of 100,000 CFU/ml (Godden, 2008). Colostrum stored at 4°C had a high bacterial load (>2 million CFU/ml), currently not recommended for feeding; Colostrum stored at 13°C and 22°C had significantly higher TBC's (>92 and >1000 million CFU/ml, respectively). These results are similar to values observed in previous studies (Cummins *et al.*, 2014b). When tested via RID, the minimum colostrum IgG concentration was 62g/L (colostrum stored at 22°C). The overall average colostrum IgG concentration across all treatments was 97g/L. Calf serum samples at zero hours contained no IgG whereas there was a wide range in 24 hour serum IgG concentrations across all treatments: from 10.3 to 63g/L. Despite all calves achieving APT, there was a significant effect of treatment on serum IgG concentration. Serum IgG of calves from the pasteurised, fresh, and stored at 4°C treatments were not significantly different, however these treatments were significantly higher than colostrum with the higher TBC (13°C and 22°C storage) (Fig. 1). Although colostrum stored at 4°C had high bacterial levels, the rate of passive transfer was not different to colostrum with bacteria levels below 100,000CFU/ml. This suggests that it may be acceptable to feed colostrum with bacteria levels higher than the maximum previously advised by Godden (2008). There was no significant difference in ADWG between treatments (Fig. 2).

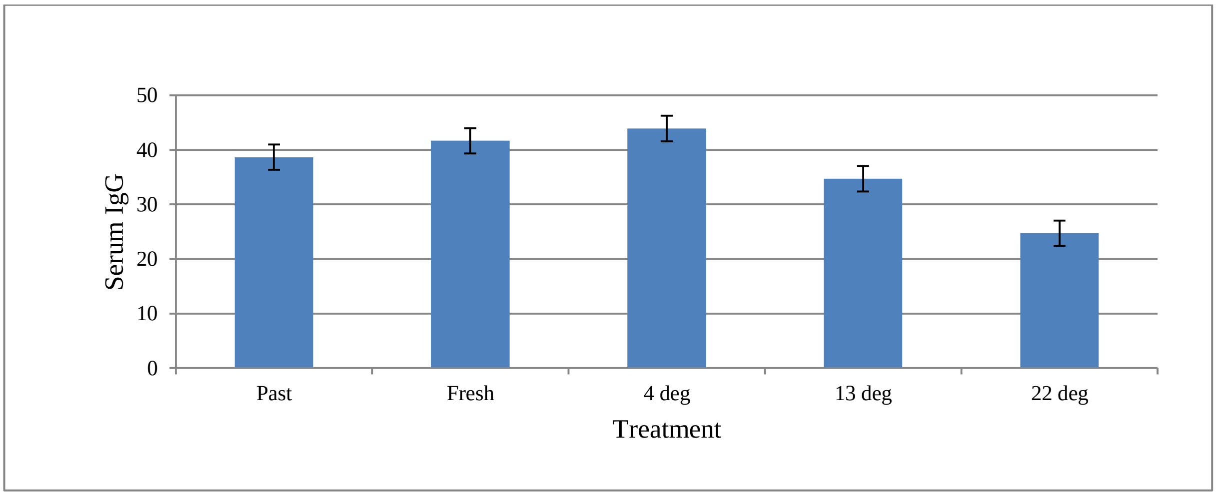

Fig. 1. Comparison of calf serum IgG concentrations at 24 hours when calves were offered colostrum with varying bacteria levels

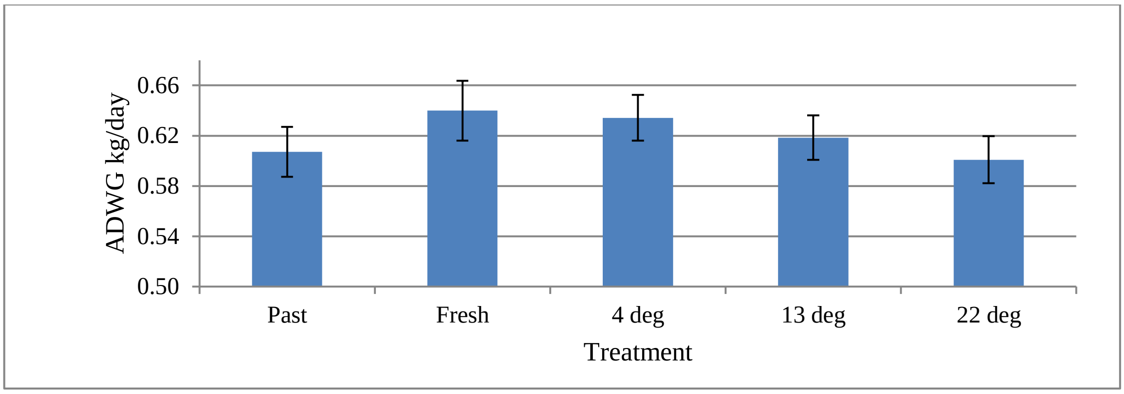

Fig. 2. Comparison of pre-weaned calf ADWG between colostrum with varying bacteria levels

Conclusions

Colostrum with high levels of bacteria had a negative effect on IgG absorption in the pre-weaned dairy calf. Colostrum should be stored ≤4°C to minimise bacterial growth and improve subsequent passive transfer of immunoglobulins.

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RMIS Project No. 6009

Preliminary investigation of production losses associated with MAP ELISA positive status

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Introduction

Johne's disease (JD) is caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP) with young calves most susceptible to infection. Clinical signs include weight loss and chronic diarrhoea manifesting between 2-5 years of age. JD is invariably fatal once clinical signs occur. Infection can remain latent in infected animals for many years without showing clinical signs, making diagnosis difficult. Faecal culture is regarded as the gold standard reference test for MAP. Enzyme linked immunosorbent assay (ELISA) testing of sera, however, is often the method of choice for herd-based diagnosis, despite poor diagnostic sensitivity and specificity, due to speed and relatively low cost compared to culture methods (Manning and Collins, 2001). Animal Health Ireland's (AHI) JD pilot programme utilises ELISA tests as an integral part of the scheme. An Irish study estimated costs of over €7000 per year on an infected 100 cow dairy herd (Mee *et al.*, 2008). Many international studies investigating the economic impact of JD have been conducted, with reported losses a result of decreased milk yield and sub-optimal fertility (Hasonova *et al.*, 2006). The aim of this study was to replicate AHI's testing regime on a subset of Irish dairy farms and investigate production losses associated with testing JD ELISA positive.

Material and Methods

Between 2010 and 2014, a total of 7318 dairy cows, over two years of age, from 28 farms, were sampled for MAP. Herd sized ranged from 70 to 300 cows. Over 14000 samples were collected in total, 15% of which were milk samples, the remainder blood. Due to routine annual on-farm culling a proportion of cows were only sampled on a single occasion. Serum and milk samples were tested using a commercial ISO17025 accredited laboratory using the IDvet MAP Antibody Test Kit. Samples were considered positive if an S/P ratio of ≥ 70 was recorded on blood or ≥ 15 on milk. Production data for each farm were downloaded from the Irish Cattle Breeding Federation (ICBF) database. Parameters examined included milk yield (MY), average annual lifetime milk yield (LMY), milk fat and protein (%), somatic cell count (SCC) and calving interval (CI). Only calving intervals of greater than 250 and less than 500 days were retained for analysis. Production data were not available for 961 animals; these consisted of breeding bulls and suckler cows. ELISA test results for each cow were matched to production parameters for each year of testing. All data was checked for normality using ladder of powers histograms in Stata version 12. Following the transformation of SCC all data met the assumption of normality. Multilevel mixed models were used to analyse the association between MAP ELISA status and production data. All models accounted for repeated measures in the cases of cows with multiple results. Random effects included cows nested within herd. Fixed effects included breed (Friesian, Jersey, Norwegian red, other), parity (1year to >10years), herd size (more or less than 150 cows) and EBI (coded 1-4 representing quartiles). The significance level was set at P=<0.05.

Results and Discussion

Of the 6357 cows included in the analysis, 9.8% tested positive on at least one occasion and 431 tested positive on more than one occasion. Statistical analysis revealed no statistically significant association between testing MAP ELISA positive and MY, milk solids, CI, and SCC, although a tendency did exist for a lower milk yield in ELISA positive cows (Table 1). The LMY, however, was not significantly associated with MAP status. These results are in agreement with a previous Irish study conducted in 2004 (Hoogendam *et al.*, 2009), and with a number of international studies (Hasonova *et al.*, 2006).

Table 1: Differences in production parameters between JD positive and negative

Parameter	Difference positive *vs.* negative	Standard error	*P* value
Milk Yield (Kg)	-65.7	33.98	0.053
LMY	11.44	10.75	0.287
CI	-0.33	1.38	0.807
SCC (‘000 cells/ml)	8.96	10.29	0.384
Protein %	-0.008	0.009	0.354
Fat%	-0.1	0.16	0.533

It should be noted that clinical cases were not examined in this study or by Hoogendam *et al.* (2009), which is a weakness of both studies. Further investigation is required to include larger datasets and culture positive individuals. As a number of international studies however, have identified losses utilising ELISA tests only (Hasonova *et al.*, 2006), it may be the case, that on-farm losses due to the presence of MAP on Irish farms are minimal.

Conclusion

No statistically significant associations were identified between cow production parameters and MAP ELISA status.

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RMIS Project No. 6325

Paratuberculosis in cattle: epidemiology, economic impact and control strategies

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Introduction

Paratuberculosis (Johne's disease; JD) is a disease characterized by chronic, contagious, progressive granulomatous enteritis caused by Mycobacterium avium ssp. paratuberculosis (MAP). The disease primarily affects ruminants but it has also been reported in other animals (Office International des Epizooties [OIE], 2014). Paratuberculosis in ruminants is a chronic, debilitating condition causing inflammation and malfunction of the intestinal tract leading to diarrhoea, submandibular oedema, weight loss despite normal appetite, malnutrition, anaemia, emaciation, lethargy, and eventually death. Most affected animals become infected during the first six months of life and show clinical signs between two and six years of age. This review covers some aspects of the epidemiology, economics and control of paratuberculosis including challenges related to disease detection, estimations of the prevalence and economic effects of the disease and the implementation of control programs.

Diagnostics and MAP prevalence

The diagnostic tests more commonly used are faecal culture, serum-ELISA and milk-ELISA. In general, the sensitivity of the current diagnostic tools is low and therefore new tests such as PCR are being developed. The apparent prevalence of MAP will partly depend on the diagnostic strategy used. Test sensitivity and specificity can vary but in general, the sensitivity of culture seems to be superior to that of ELISA. As an example, Smith et al. (2009) found a prevalence varying from 0 to 4.9% when using ELISA and a prevalence of 0 to 13.6% when using faecal culture. Moreover, cross-reactivity to diverse Mycobacterium is possible and can interfere with the correct identification of MAP infected animals (false positives). False negative and false positive results represent a challenge for the correct identification of MAP infected animals and for disease control. MAP prevalence in cattle herds depends on a number of factors such as the clinical history and herd management. The animal-level prevalence of paratuberculosis found in a study conducted in Ireland was 2.7% for dairy herds and 3.1% for beef herds (Good et al., 2009), which is similar to that found in Spain (3%) (Dieguez et al., 2007) and in the United States (3.8%) (Lombard et al., 2005). Reported apparent herd-level prevalence of paratuberculosis varies widely across countries e.g. for dairy cattle: 15% in Spain (Dieguez et al., 2007), 31.5% in Ireland (Good et al., 2009) and 85% in Denmark (Nielsen, 2007) and for beef cattle: 7% in Belgium (Boelaert et al., 2000), 17.9 % in Ireland (Good et al., 2009) and 40% in USA (Thorne and Hardin, 1997). However, comparable estimates of prevalence are difficult to obtain (Nielsen and Toft, 2009) as they depend on factors such as sampling strategy and diagnostic methods used (Muskens et al., 2000).

Epidemiology

MAP bacteria can survive in a variety of environments (e.g. hot, cold, dry and acidic conditions), in soil up to 47 months (Caldow et al., 2001) and in water environments for longer than in soil. Infected cattle can excrete MAP in faeces, in milk and colostrum. In fact, MAP has been detected in raw milk and in pasteurized milk (Grant et al., 2002; Ellingson et al., 2005). The faecal-oral route is considered the primary route of MAP infection. Epidemiological studies have identified several main risk factors: age, herd size, introduction of new animals, herd depopulation (restocking) and risk factors associated with increased exposure of calves to contaminated faecal matter (Muskens et al., 2003; Hirst et al., 2004; Groenendaal, 2005; Mee and Richardson, 2008; Sayers and Cook, 2009; Barrett et al., 2011).

Economic impact

Paratuberculosis may cause substantial economic losses to the cattle industry. The net economic impact of paratuberculosis in the US dairy industry has been estimated to vary from US$ 200 to US$ 1500 million annually (Jones, 1989; Ott et al., 1999). Economic losses are mainly related to increased premature culling, replacement costs, decreased milk yield, reduced feed conversion efficiency, fertility problems, reduced slaughter values and increased susceptibility to other diseases or conditions (Chi et al., 2002; Rideout et al., 2003; Villarino and Jordan, 2005; Barrett et al., 2006; Bhattarai et al., 2013). The economic impact of MAP infection in cattle will depend on the number of animals showing clinical signs or in the subclinical stage of the disease. The impact on business profitability when there are clinical cases can be substantial but the impact due to subclinical cases seems less clear (Lombard, 2011). Other factors may also have an influence such as production system, herd size, herd management and geographical area. Therefore, the economic impact of the disease can vary widely. In the Republic of Ireland, information based on data from one case study over a ten year period indicated that the annual average gross margin in this herd decreased between €130 and €155 per cow during the study period (AHI, 2012). Barrett et al. (2006) reported significant reductions in net profit margin of between €168 and €253 per cow in an Irish herd affected with paratuberculosis. Significant reductions in milk production parameters have been linked to animals testing MAP positive by faecal culture or with ELISA (Chi et al., 2002; Barrett et al., 2006; Gonda et al., 2007; Raizman et al., 2009; Smith et al., 2009).

Control strategies

Worldwide countries such as the UK, the Netherlands, Denmark, USA, Canada and Australia among others are implementing paratuberculosis control programs. For example, the U.S. Voluntary Bovine Johne's Disease Control Program (VBJDCP) provides participant producers with guidelines for the control of Johne's disease and classifies herds based on risk assessment (Carter, 2012). The combination of control strategies (e.g. farm management practices such as providing better housing for calves, separating calves from the cows and providing more hygienic water supplies) with diagnostic testing has been strongly recommended (Groenendaal and Galligan 2003; Flynn *et al.*, 2005; Dorshorst *et al.*, 2006; Weber, 2006; Kudahl *et al.*, 2011). Several studies suggest that test-and-cull strategies alone are not cost-effective (Weber, 2006; Kudahl *et al.*, 2008; Bennett *et al.*, 2010).

Conclusions

Paratuberculosis is considered an important disease of cattle although the impact of the disease can be variable. The main challenge identified for the control of paratuberculosis in cattle seems to be the low sensitivity of current diagnostic tests for the correct detection and classification of animals. Improving biosecurity is highly recommended for the control of paratuberculosis and to reduce the risk of introduction and/or spread of other infectious diseases.

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RMIS Project No. 6416

Immuno-inflammatory bio-marker analysis in stillborn calves – a novel construct

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Introduction

The unexplained stillbirth is a diagnostic challenge. The fetal inflammatory response syndrome (FIRS) is considered an important risk factor for human perinatal mortality. Little is known about the immuno-inflammatory response in stillborn calves. The objective of this study was to compare immuno-inflammatory biomarkers in stillborn calves diagnosed with intrauterine infection, traumotocia and unexplained cases.

Materials and Methods

The 84 calves were selected from a necropsy database of stillborn calves from Irish dairy farms using the inclusion criteria: full-term ($\geq$260 days gestation), dead within one hour of birth and did not consume colostrum. Three mutually exclusive diagnostic groups were compared: intrauterine infection (INF; n=21), 2. traumotocia (TRAUM; n=22), 3. unexplained death (UNEXPL; n=41).

Results and Discussion

The concentrations of serum amyloid A (SAA ug/ml; ELISA-Tridelta Ltd.), haptoglobin (Hp mg/L; microplate guaiacol method) and immunoglobulins G_1 and M (IgG_1 and M mg/L; ELISA, Bethyl) were determined in plasma samples collected at necropsy. The mean (sd) concentrations of all biomarkers were numerically higher in the INF [SAA 24.7 (31.1), Hp 105.2 (397.9), IgG_1 100 (231.2), IgM 280.4 (521.1)] compared to the TRAUM [SAA 11.9 (11), Hp 13.3 (29.8), IgG_1 66.1 (152.2), IgM 81.5 (189.6)] and UNEXPL groups [SAA 10.7 (19.5), Hp 16.3 (41), IgG_1 67.1 (137.3), IgM 134.2 (315.1)] and tended to be significantly so for SAA (P=0.06). Values did not differ between the TRAUM and UNEXPL groups.

Conclusion

These results demonstrate upregulation of the immuno-inflammatory response in stillborn calves exposed to intrauterine infection. This is the first reported detection of an elevated acute phase protein response in stillborn calves.

RMIS Project No. 6493

Sero-surveillance of Schmallenberg virus in Irish dairy herds using individual blood and bulk milk samples

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Introduction

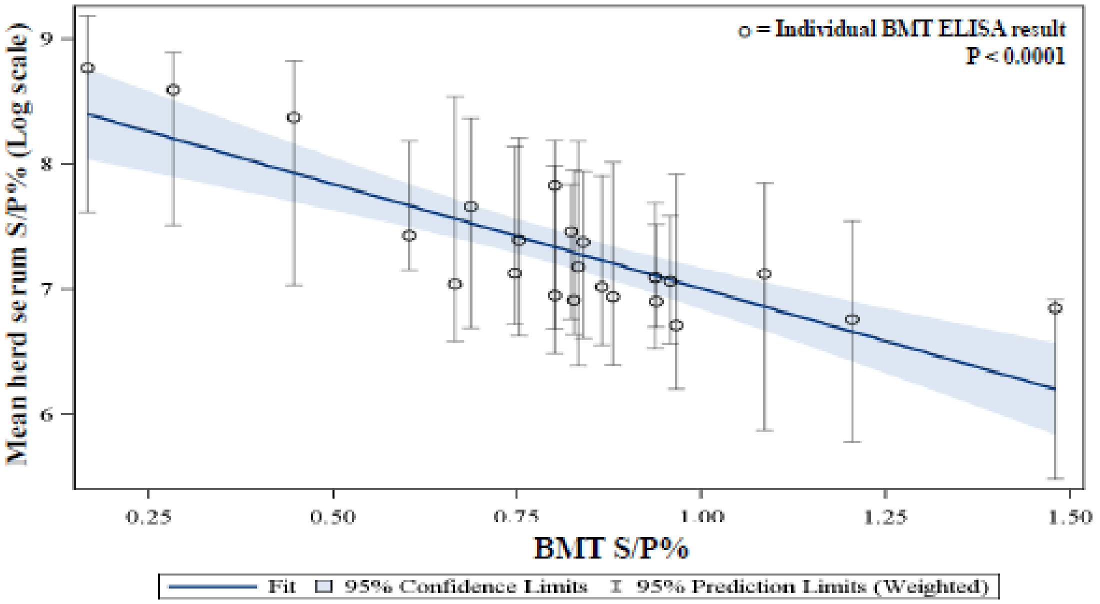
Schmallenberg virus is a recently discovered Orthobunyavirus which has been implicated in milk drop syndrome in dairy cattle and congenital defects in neonatal ruminants across Europe. Schmallenberg virus (SBV) is seroendemic in many regions in Europe including Ireland (Collins *et al.*, 2014). However, the within-herd and between-herd SBV seroprevalence in these regions is sparsely documented and largely unknown. The objectives of this work were to determine the SBV seroprevalence in a seroendemic region and to determine the relationships between blood and bulk milk ELISA results for SBV.

Materials and Methods

A total of 5,527 individual animal blood samples (73% cows, 27% replacement heifers) were collected from 26 Munster dairy herds (range 58 to 444 lactating cows/herd) between March 14th and April 5th 2014. Blood samples and BMT samples were analysed for SBV-specific antibodies using a competitive ELISA (ID screen® Schmallenberg virus Competition Multi-species, ID Vet) and indirect ELISA (ID screen® Schmallenberg virus Milk indirect, ID Vet), respectively. As the serological data were skewed, these were log (natural) transformed and then regressed on BMT results [for both sample/positive (S/P) and optical density (OD) values in each case]. Herds with similar BMT ELISA results were compared to determine whether the distributions of individual cow serology results could produce similar BMT results. To do this, the empirical cumulative distribution function curves for the individual animal serology results in herds with similar BMT results were compared using the Kolmogorov-Smirnov (KS) test.

Results and Discussion

Animal-level sero-prevalence was 61%. Sero-negative animals (38%) were predominantly replacement heifers (97%). Within-herd seroprevalence ranged widely (8.3% to 98%) in the 26 herds suggesting individual herds have different levels of risk of new infection. Twenty four herds were BMT-ELISA positive (herd seroprevalence ranged between 29.9% and 100% in lactating cows) and two herds were BMT-ELISA negative (seroprevalence 10.5% and 15.8% in lactating cows). A large population of sero-negative animals, principally less than 2 years old, were identified suggesting they were not exposed to SBV during 2013 and could be at risk of SBV infection in the 2014 and future vector-active seasons if virus recirculation occurs. Mean herd serum and BMT ELISA results were significantly correlated; R^2 OD serum-BMT = 0.72, S/P serum-BMT = 0.69, both $P<0.0001$ (Fig.1). Approximately 70% of the variance in the BMT values could be explained by their relationship with the serology values. The remainder could be due to the accuracy of BMT sampling and the test characteristics of the ELISA. In comparing herd A and herd B which had almost identical positive BMT ELISA OD values, the cumulative distribution function curves of the serum values differed significantly ($P<0.0001$) (Fig.1). Thus, a positive BMT value can come from a small number of highly seropositive cows or a large number of moderately seropositive cows.



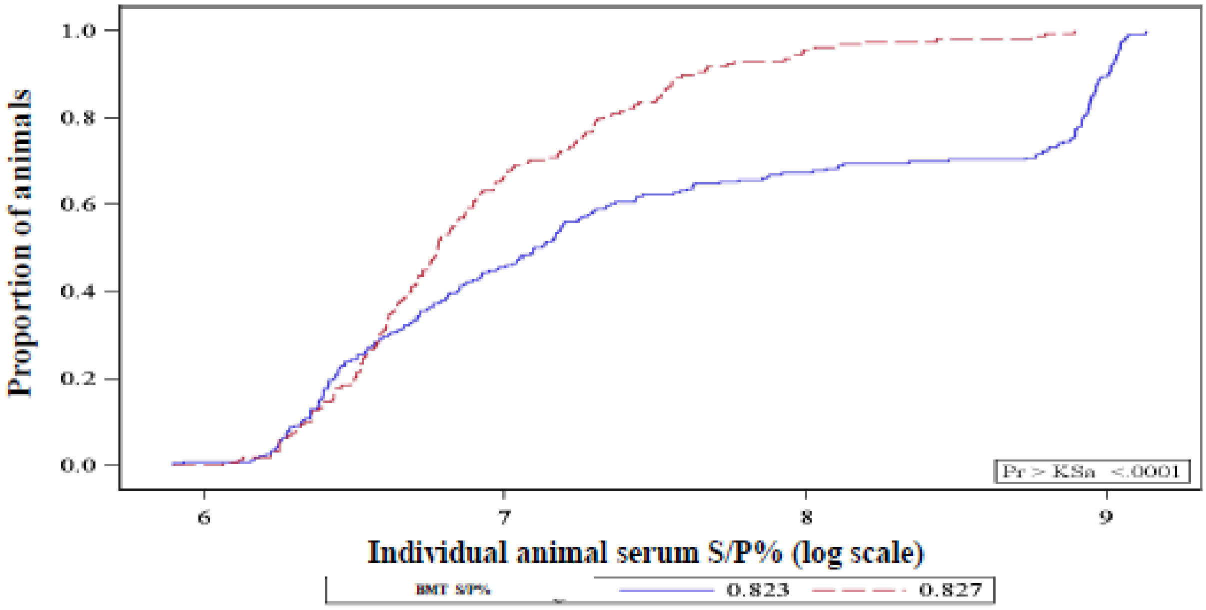


Fig. 1. Relationship between herd mean serology and BMT (upper panel) and between individual animal serology and BMT results (lower panel)

Conclusions

The moderate-high correlations between herd serum and BMT-ELISA results suggest BMT-ELISA results are moderately predictive of within herd SBV seroprevalence. Herds with similar BMT results can have a wide variation in individual animal serology results. Furthermore, herds with negative BMT ELISA results can have seropositive animals. Herds with similar BMT results can have a wide variation in individual animal serology results. This may have implications in estimating the risk of new Schmallenberg virus infections in herds classified as exposed using BMT-ELISA.

Acknowledgements

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RMIS Project No. 6520

Social network analysis of cattle positive for Johne's disease by faecal culture, from submissions to Cork Regional Veterinary Laboratory

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Introduction

Disease transmission occurs in two levels of organisation: within farm and between farms. Networks can be used to represent the patterns of connectivity of populations, and therefore describe aspects of disease transmission. Social network analysis (SNA) has recently been used in veterinary epidemiology as a valuable tool for describing epidemics with an underlying contact network structure. It provides a tool for analysis and illustration of the relationships between the movements of animals and the transmission of a contagious pathogen associated with those movements. The objective of this study is to describe the network of confirmed Johne's disease (JD) positive animals by linking their movements through different premises throughout their productive life. This will identify those nodes (premises) more likely to facilitate the spread of infection thus increasing our understanding of the potential herd-to-herd transmission of the disease.

Materials and Methods

The networks were constructed by linking a dataset of historical laboratory records of JD culture positive animals (n=179) with the Animal Identification and Movement System database. A movement event (n=327) was defined as the transportation of one or more animals from an identified premise (i.e., herd) of origin to an identified premise (i.e., herd, factory, knackery) of destination. Due to the pathogenesis of JD, a passing movement through a mart from premise A to B was represented as A to B. Movements to a factory or knackery are not included in this summary. The dataset was exported to Pajek32 v4.01a for analysis (De Nooy *et al.*, 2005). The data, organised in an adjacency matrix, consisted of a collection of nodes (premises) and an array of arcs (directed movements) linking the nodes. The nodes were categorised (attributes) as in Fig. 1 and the adjacency matrix graphed, by the Kamada-Kawai projection algorithm available in Pajek, in an arbitrary space for visual assessment. The out-degree centrality of each node, structural attribute which represents its importance within the network and its potential to disease spread (Fig. 2), was calculated by counting the outgoing number of arcs to other nodes in the network.

Results and Discussion

Out of 217 nodes, 118 were classified as 'JD positive' and 99 as 'unknown JD' status (Fig. 1). Twenty nodes (i.e., 9%) had an out-degree ≥2. The maximum geodesic distance was 6. Out of the 179 animals moved during the 13 year observation period and excluding movements to marts, factories or knackeries, 47% moved once, 36% moved twice, 9% moved three times and 8% four to six times. The network was fragmented in 84 components ranging from 1 to 12 nodes; 26 were single nodes, the rest (58) were formed by two or more connected nodes. Twenty one of the components (i.e., 25%) had two to five JD positive herds linked by movements of positive JD animals.

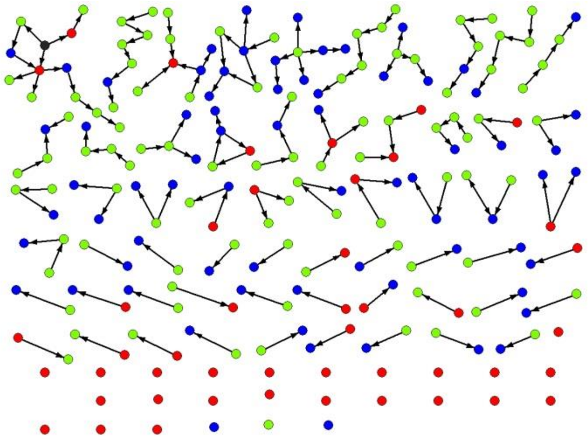

Fig. 1. Network of JD positive animals. Nodes (shaded circles) represent premises and arrows movements (Red: herd with at least one JD positive homebred animal; Blue: herd with at least a positive animal born outside the farm and unknown homebred positive animals; Green: unknown JD status; Black: imported animals).

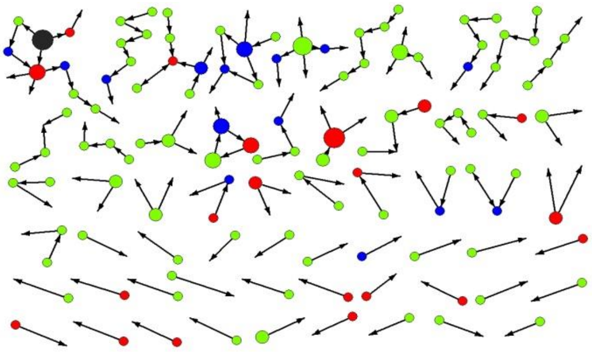

Fig. 2. Out-degree centrality: relative node size, determined by node out-degree, illustrating their importance to disease spread. Nodes coded as in Fig. 1.

Conclusions

This study addresses the relationship between animal movements and disease detection. It identifies those premises more likely to facilitate the spread of JD via animal movements in and out. This node identification can reduce the effort required to control JD and provide an evidence-based approach to the development of risk-based surveillance activities and disease prevention programs.

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RMIS Project No. 6520

Preliminary study of prevalence of rumen fluke in Irish sheep flocks

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Introduction

Paramphistomosis are cosmopolitan trematodes in ruminants produced by different species of the Paramphistomidae family, which can cause important gastrointestinal diseases, decreased production and even death. Their life cycle is indirect and involves freshwater snails as intermediate hosts. In the ruminant host, juvenile parasites first locate in the small intestine causing more damage than the adult worms. Eventually, the parasites migrate upwards to the reticulum and rumen where they mature and produce eggs. Paramphistomosis is highly prevalent in tropical and subtropical countries where it causes high morbidity, nevertheless in Europe, it was considered practically inoffensive for many years. However, in recent years the number of reports of clinical paramphistomosis in both sheep and cattle has increased in Great Britain and Ireland. Rumen fluke is now being recognised as a clinical entity in Irish livestock and multiple mortalities have been reported on individual farms (AHI, 2011), although data on their clinical impact and true prevalence is lacking. Bearing all the above in mind, the aim of this study was to investigate the prevalence of *Paramphistomum* spp. in Irish flocks, which will allow reliable epidemiological model.

Materials and Methods

A total of 254 commercial sheep farmers volunteered to partake in this study. It was ensured that participating farms represented an adequate geographical spread of republic of Republic of Ireland. Each farmer submitted 20 faecal catch samples for 20 ewes between October and November 2014. Standardised sampling kits were provided containing 20 sampling bottles, a pair of gloves, instruction leaflet, sample submission form and a pre-paid pre-addressed envelope for sample submission to the School of Veterinary Medicine laboratory (UCD) for faecal egg counting. Farmers were requested to take fresh samples and post them immediately. For each batch of 20 samples, two composite samples of 30g were prepared using 3g of faeces from each pot. From each composite, 5g of faeces were pooled and homogenised with water and passed first through a coarse mesh sieve and then a finer, 250 µm mesh sieve. The filtrate was allowed to stand for 5 minutes to sediment and the supernatant was removed by aspiration. Sedimentation was repeated 1-2 times as required. The supernatant was removed and sediment was stained with two drops of 1% methylene blue. Eggs were counted on a stereomicroscope as outlined by Taylor *et al*. (2007). Faecal egg counts (FEC) are reported as eggs per gram (epg). Prevalence was reported based on percentage of herds recording positive results against total flock numbers tested in each of seven regions of the Republic of Ireland. To compare the distribution of paramphistome burdens in different farms, flocks were classified into one of the following categories; zero epg + (<20epg), ++ (20–50 epg) and +++ (>50 epg faeces).

Results and Discussion

This is the first study to determine the prevalence of *Paramphistomum* spp. in Irish flocks; the results revealed that 201 out of the 254 farms (79%) were positive for rumen fluke. This prevalence is meaningfully higher than those established by other authors in Spain, France or Italy (Diaz *et al*., 2007). However, this analysis coincides with recent reports of an apparent increase in the incidence of paramphistomosis in Ireland.

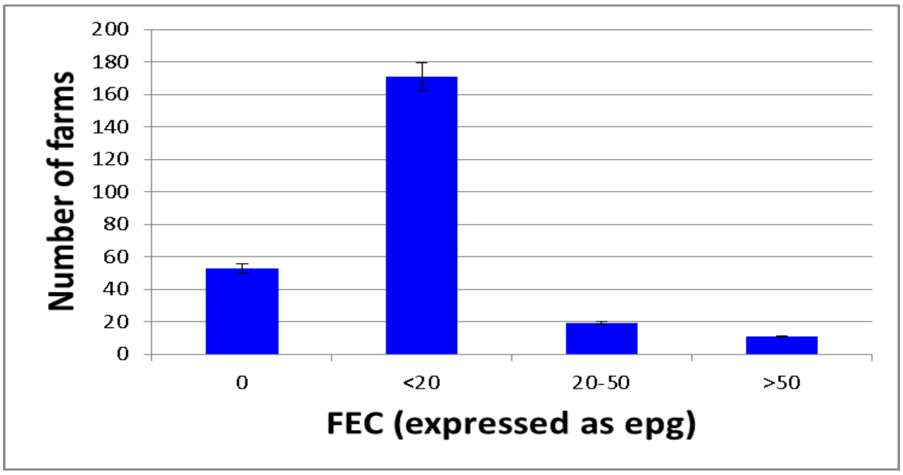

Fig 1. Number of farms with differing FEC status

The prevalence in different regions ranged between 68% in the South-West to 100% in the Mid-West. The transmission of *Paramphistomum* spp. depends on the distribution of the intermediate host snails. This distribution, as well as the development and survival of the larval stages of the parasite are determined by climatic and other environmental conditions, which may vary considerably among different regions.

Conclusions

This study is the first approach to gain knowledge of the prevalence of rumen fluke in Irish flocks. The high proportion of infected farms found here highlights the need to develop sustainable parasite control programmes. Further studies are required to generate a comprehensive epidemiological model of paramphistomosis and to investigate the production and economic outcomes of rumen fluke infestations.

Acknowledgements

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RMIS Project No. 6605

Prevalence of *Fasciola hepatica* in Irish sheep flocks in 2014: Preliminary results

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Introduction

Fasciola hepatica is one of the most important helminth parasites of sheep in temperate climatic zones. The presence of the intermediate host (*Galba truncatula*) in these areas determines the presence of the trematode. The importance of this parasite in sheep relates to the fact that it can cause a per-acute syndrome which is fatal as a result of haemorrhage and liver damage. This results in significant economic losses in fluke-infested flocks and it has been estimated that *F. hepatica* results in annuals losses of €90 million across Irish livestock (AHI, 2010). Temperature and moisture are the most important factors for *F. hepatica* development. It must take place in a wet environment with temperatures higher than 10°C (Borgsteede, 2011). The Irish climate, therefore, provides ideal environmental conditions for *F. hepatica* development at certain times of the year. The objective of the current study was to determine the national prevalence of *F. hepatica* in Irish flocks as these data are not currently available.

Material and methods

A total of 254 commercial sheep farmers volunteered to partake in this study. It was ensured that participating farms represented an adequate geographical spread according to the Census of Agriculture 2010 (COA - CSO). Each farmer submitted 20 faecal catch samples for 20 ewes between October and November 2014. Samples were sent to the School of Veterinary Medicine, UCD laboratory for faecal egg counting. Farmers were requested to take fresh samples and post immediately. For each batch of 20 samples, two composite samples of 30 g were prepared using 3g of faeces from each pot. From each composite, 5g of faeces were pooled and homogenised with water and passed first through a coarse mesh sieve and then a finer, 250 µm mesh sieve. The filtrate was allowed to stand for 5 min to sediment and the supernatant was removed by aspiration. Sedimentation was repeated 1-2 times as required. The supernatant was removed and sediment was stained with two drops 1% methylene blue. Eggs were counted on a stereomicroscope as outlined by Taylor *et al.* (2007). Faecal egg counts (FEC) are reported as eggs per gram. Prevalence was calculated for seven different regions of Ireland based on the COA - CSO and the number of farmers with varying FEC values determined.

Results and discussion

Of the 254 flocks analysed, *F. hepatica* eggs were detected in 48% of herds. The prevalence varied in different regions from 40% (West & Mid-West) to 59% (South-West) (Table 1) which may have been expected to vary to a greater extent between wetter western regions and other parts of the country. No eggs were detected on 115 farms with a minority of farms recording greater than 2 eggs per gram (epg) (Fig. 1) which again may have been expected to be greater, based on the time of year.

Table 1. Prevalence of *F. hepatica* FEC positive flocks in different regions of Ireland.

Region	*n*	Prevalence
Border	61	54%
Midland	20	48%
West	61	40%
Mid-East & Dublin	24	56%
Mid-West	7	40%
South-East	25	41%
South-West	22	59%

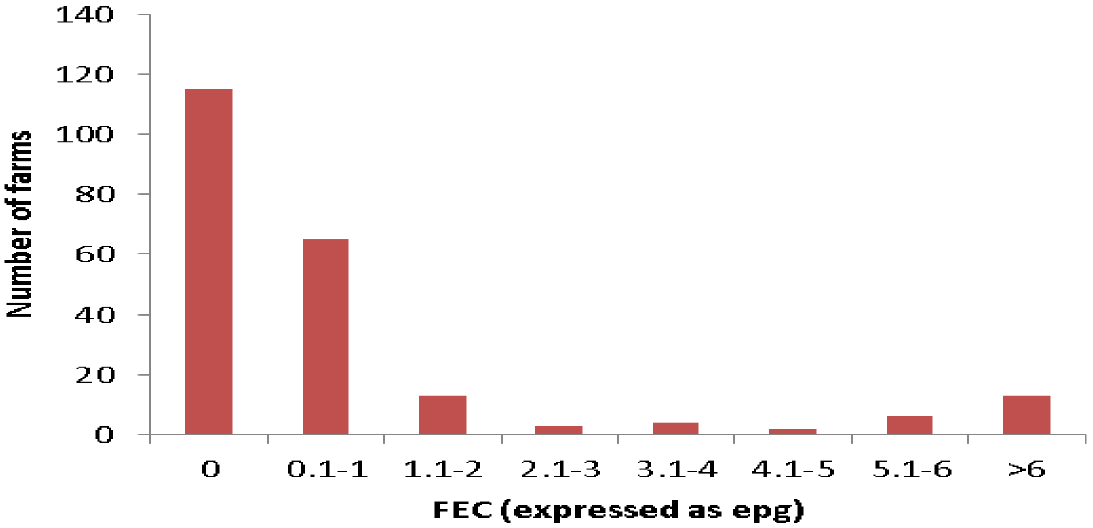

Fig. 1: Number of farms with differing FEC status.

It should be noted, however, that in cattle experimentally infected with *F. hepatica* in Scotland no liver fluke eggs were detected during FEC in early or late stages of fluke infection. That study also highlighted that ELISA (enzyme immunoassay) generated superior fluke detection levels than FEC. With this in mind, FEC may not be the most sensitive method of determining liver fluke status in Irish livestock and prevalences may indeed be higher than the levels detected in the current study. FECs were used in this study for practical reasons.

Conclusion

Mature *F. hepatica* are present in an unacceptably high number of sheep flocks and dosing regimens should be examined and reviewed to ensure their appropriateness and effectiveness.

Acknowledgements

This study is an output from DAFM RSF funding.

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RMIS Project No. 6605

Efficacy of vaccination on the incidence of subclinical mastitis in primiparous Irish dairy cows

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Introduction

Somatic cell count (SCC) is used as an indicator of udder health and is used to detect mastitis. Subclinical mastitis is determined to have occurred when the udder and milk appear normal but an increase in SCC is detected. It is generally accepted that primiparous cows free from mastitis should have an SCC of <100,000 cells/ml. The vaccine used (Startvac, Hipra Spain) is commercially available and contains inactivated strains of *Escherichia coli* and *Staphylococcus aureus*. One of the aims of vaccination with this product is to reduce the incidence of subclinical mastitis caused by *S. aureus* in lactating cows. The objective of this study was to investigate if vaccination affected subclinical mastitis incidence in primiparous cows. Results will help ascertain if the vaccine could be an effective mastitis management tool to assist the prevention of mastitis in primiparous cows on Irish dairy farms.

Materials and Methods

The study was conducted on 210 pregnant heifers of various breeds (n=7) Holstein-Friesian, Jersey, Norwegian Red, Jersey-Holstein, Norwegian Red–Holstein, Ayrshire-Jersey-Norwegian Red and Norwegian Red-Holstein-Jersey, from four spring-calving dairy herds in southern Ireland. All animals were located within experimental herds at the time of data collection. On-going experiments included 1) differences in stocking rate, 2) differences in feed allowance and 3) clover inclusion in the diet. Some heifers were mixed with cows prior to vaccination. For the purposes of this study, heifers were randomly assigned (within on-going experiment) to one of two treatments: 1) heifers were vaccinated (V; n=106) or 2) heifers were not vaccinated (C; n=104). The vaccination protocol comprises a three injection immunisation programme given according to the expected calving date. The initial two injections were given 45 days and 10 days (+/- 3 days) respectively before parturition and the third injection was administered 52 days (+/- 3 days) post-calving. All injections were given intramuscularly.

Weekly measurements of individual composite SCC from calving (approximately February) until 30th September were quantified using CombiFoss™. For analysis, SCC was normalised to somatic cell score (SCS) using the transformation: SCS = log10 (SCC*1000). Variables examined in the analysis included: mean SCS (MeanSCS), maximum SCS (MaxSCS), minimum SCS (MinSCS) recorded across heifer lactation, and number of weekly SCC records >100,000 cells/ml expressed as a percentage of the total number of weekly records for each heifer (SCS100). Lactation was divided into three periods; Weeks 1 to 12 (LS1), 13 to 24 (LS2) and 25 to 36 (LS3) and these variables were examined. The effect of vaccination status on the variables listed was investigated using multilevel linear models in SAS 9.3 (SAS, Cary, NC. 2011). Fixed effects included in the models were breed, farm × experimental code, status prior to vaccination (i.e. mixed with cows or not), and vaccination status. Heterosis and recombination were included as continuous effects. Least squares means for vaccination status were extracted.

Results and Discussion

All results are presented as SCC back-transformed from SCS. The variables MeanSCS, MaxSCS, MinSCS and SCS100 did not differ significantly between V and C as shown in Table 1.

Table 1. Effect of vaccine status on mean, max, and min SCC across lactation and SCS100

Trait	V	C	P-value
Mean SCC	51,286	48,978	0.87
Max SCC	251,189	309,030	0.64
Min SCC	6,918	6,918	0.98
SCS100	64.74	63.54	0.79

It might be expected that the level of antibodies produced in response to the vaccine could decline as lactation progressed. Accordingly, it was sought to determine if the vaccine was as effective after secondary and tertiary immunisations. It was found that vaccination did not alter SCC significantly at any stage of lactation (Table 2).

Table 2. Effect of vaccine status on mean SCC at different stages of lactation

Trait	V	C	P-value
LS1	50652	50223	0.84
LS2	49625	47973	0.39
LS3	50839	48239	0.23

No effect on subclinical mastitis could be found in this study. The results may be influenced by the potential herd immunity provided by vaccinated animals to control animals in the same herd (indirect vaccine effect; Halloran *et al.*, 1991). One might expect the effect of vaccine to be diluted in a population consisting of both vaccinated and unvaccinated animals. It may also be the case that on farms such as these where SCC is generally low (data not shown), vaccination does not further lower SCC significantly.

Conclusions

This study failed to find a positive effect of vaccination when used as a mastitis management control tool in assisting the prevention of mastitis in primiparous cows on Irish dairy farms. Excellent management, hygiene and adherence to stringent mastitis control measures remain paramount in reducing mastitis.

Acknowledgements

This study was supported by Dairy Levy Funding.

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RMIS Project No. 6621

Animal Facilities, labour, Automation & Energy Efficiency

Water required for grass growth on Irish dairy farms

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Introduction

Water resources can be divided up into green and blue water. Rain-fed crop production consumes green water which is defined as water stored in the soil from precipitation. Irrigated crop production consumes blue water which refers to the water stored in rivers, lakes and aquifers. Irish milk production is largely a rain-fed pasture based system and is the 10th largest dairy exporter in the world (DAFM, 2012). As a consequence of exporting dairy products there is also an export of 'embedded' water. Irish agriculture does not suffer water shortages due to the nature of Ireland's temperate climate. On global scales water availability is limited, increased knowledge on sustainability indexes or a reduction of water consumption in production will improve the market potential of Irish dairy exports. Water consumed through forage production makes up 94% of the water footprint of milk production (Mekonnen *et al.*, 2012). As demand for water resources increases due to increased food production, population growth and climate change it is important to quantify the volumes of water that are embedded in dairy products in order to ensure sustainable production. The objective of this study was to quantify the green water resources that are embedded in Irish milk production.

Material and Methods

Data collected included, climatic data, soil type, imported concentrate and forages, herd size and milk production from 24 specialised Irish dairy farms from May 2012 to April 2013. Milk production data were sourced from the Irish Cattle Breeding Federation records. Rainfall data were sourced from Met Eireann meteorological stations nearest to each farm. Annual grass and silage utilisation on each farm was modelled with the Grass Calculator (Teagasc, 2011) using the difference between the net energy in units of feed for lactation (UFL), between external supplements (concentrates and forages) and the net energy demands of farm stock (O'Mara, 1996). It was assumed that 1 UFL equates to 1 kg dry matter of grass. It was assumed that 85% of the grass grown was utilised. The volume of water required for grass growth was computed using grass yield data, soil site specific data and climate data using the method described by De Boer *et al.* (2013).

Results and Discussion

Average milk production per farm was 516,463 litres. The milk output on the study farms was greater than the national average farms for 2012. The study farms therefore, represent larger than average dairy farms, indicative of future farm sizes, a result of farm expansion prior to the milk quota abolition in 2015. The average volume of water required for the growth of grass was 286,082m^3/farm/year (range 117,860 – 435,583m^3). The average volume of water available through rainfall occurring on the farms was 751,514m^3/farm/year (348,106 – 1,177,576 m^3).

Table 2. Summary of 24 study farms compared to national average farm description.

	Min.	Mean	Max	Nat. Avg.
Farm Area (Ha)	32	69	108	57
Milk Yield (000's L)[a]	259	516	883	316
Grass grown (T)[b]	222	550	834	627
Rainfall (m^3/Farm)[c]	348,106	751,514	1,177,567	622,440
GWR[d] (m^3/Farm)	117,860	286,082	435,583	311,429

[a] 000's litres; [b] Tonnes: [c] cubic meters rainfall over farm area; [d] Grass water requirement for growth.

The water required for grass growth consumed on average 38% of the rainfall occurring on the farms. This green water when exported in the form of dairy products could be considered as a national water loss; referring to the fact that water used for producing dairy products which are then exported is not available for domestic or industrial purposes. Green water cannot be easily re-allocated to other uses besides natural vegetation or alternative rain-fed crops, hence the use of green water in milk production takes advantage of this readily available resource. O the dairy products exported in 2012, 38% were to international markets including South-East Asia and the Middle East (DAFM, 2012). These areas are already water stressed. By importing water embedded in agricultural commodities they can 'save' water by outsourcing milk production to a water rich country.

Conclusions

The rain-fed pasture based milk production systems in this study used 38% of available green water. The utilisation of green water which is plentiful in Ireland and available at low opportunity cost to produce milk demonstrates the sustainability of milk production in Ireland.

Acknowledgements

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RMIS Project No. 6590

Effect of omitting pre-milking teat preparation on bacterial levels in bulk tank milk

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Introduction

Bulk tank total bacterial count (TBC) is a general reflection of the hygienic condition of the farm environment, the cow and the milking equipment. Likewise the presence of thermoduric bacteria in milk is used as an indicator of parlour hygiene. The European Union currently impose a regulatory limit of <100,000 cfu/ml for TBC with no limit for thermoduric bacteria. However, some milk processors in Ireland have implemented more stringent TBC (<30,000 cfu/ml) and thermoduric (<500 cfu/ml) regulations on milk producers. Similarly, for somatic cell count (SCC) there are a number of incentives at the processor level to achieve a target <200,000 cells/ml, which is 50% of the EU regulatory limit (400,000 cells/ml). In Ireland, it is a common practice on seasonal farms to omit teat preparation entirely prior to cluster application (Kelly *et al.*, 2009). This may have implications for bacterial levels in milk and new infection rates. The objective of this experiment was to investigate the effect of omitting teat preparation prior to milking on bacterial levels in milk.

Materials and Methods

Eighty Holstein-Friesian dairy cows were assigned to two pre-milking teat preparation treatments over a complete lactation: (i) washing of teats with warm running water, drawing of foremilk, application of an iodine-based disinfectant (0.5%) followed by drying using individual paper towels per cow; (ii) no teat preparation. Monthly individual cow measurements included: individual quarter SCC and teat swabs for the presence of *Bacillus cereus.* On four occasions individual quarter milk samples were taken and analysed for SCC and presence of bacteria. On seven monthly occasions, all milk produced over a 24h period (2 milkings) from each treatment group was diverted into two separate milk tanks. Milk in each tank was sampled and analysed for TBC, thermoduric counts, presence of *B. cereus* and sulphite-reducing *Clostridia spores* (SRC). Clinical cases of mastitis were recorded. The analysis of the data was using with linear models (SAS, 2011) with log transformation as appropriate.

Results and discussion

Average milk TBC over the season tended to be higher (3,152 cfu/ml) when teat preparation was omitted compared with milk TBC when teats were prepared (1,678 cfu/ml; P=0.10). TBC of all milk was significantly lower in June (1,167 cfu/ml) compared with August (4,406 cfu/ml) and October (4,299 cfu/ml; P<0.05). However, the thermoduric count in bulk tank milk was higher when teat preparation was omitted (P<0.01). This result is in agreement with a previous study in which it was reported that teat preparation reduced thermoduric counts in bulk milk (Magnusson *et al.,* 2006). The thermoduric counts reported in this study were well within the limits considered satisfactory for good quality milk. The *B. cereus* and SRC in bulk milk samples did not differ between treatments. However, teats not prepared had significantly higher colony counts of *B. cereus* present on teat skin particularly during late lactation (P<0.001). Contact of teats with soil is the main route of *B. cereus* contamination of bulk tank milk during the grazing season. Therefore, higher numbers would be expected on teat skin where teat preparation was omitted. Individual quarter SCC tended to be higher for un-prepared teats (159,000 cells/ml) compared to prepared teats (133,000 cells/ml; P<0.09). A similar trend was observed for bulk tank milk SCC with the unprepared teats tending to have a higher SCC (156,000 cells/ml) compared to prepared teats (102,000 cells/ml; P<0.09). The number of clinical cases, sub-clinical cases and latent infections did not differ between treatments. On farms with a higher herd SCC and with inadequate equipment cleaning protocols, omitting teat preparation may have a significant effect on SCC and TBC.

Table 1. Bacteriological milk measurements from cows with prepared and unprepared teats prior to milking

	No teat prep	Teat prep	Sig. Treat	Sig. date
^{a}TBC (cfu/ml)	3,152	1,678	0.10	**
^{a}Thermoduric (cfu/ml)	11	5	**	*
^{a}SCC (cells/ml)	156,000	102,000	0.09	NS
^{a}SRC (cfu/ml)	NS	NS	NS	NS
^{b}*B. cereus* (cfu/ml) swab	50	5	***	***
^{b}SCC (cells/ml)	159,000	133,000	0.09	NS

***P<0.05, a=bulk tank, b=individual quarter

Conclusion

The results of this study indicate that in a grazing situation, where a high level of equipment hygiene is implemented, the omission of pre-milking teat preparation has a minimal effect on milk quality as the levels observed for both teat preparation treatments were low. However, the numerically higher TBC, and significantly higher thermoduric count observed from un-prepared teats may have implications when milk is stored for a number of days on farm. Different results could be expected if teat preparation was omitted during the indoor housing period when environmental conditions would be more challenging.

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RMIS Project No. 6237

The effect of storage duration and temperature on the total bacterial count of bulk tank milk

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Introduction

EU guidelines state that milk can be stored on dairy farms at 6°C when collection is not carried out daily (Annex A, Directive 92/46). Typically milk is stored at 4°C for 48 hours (as per processors guidelines) on dairy farms prior to collection. Milk collection intervals are often extended on farm at the beginning and end of the year when milk production is minimal. Extending the storage period may have implications for milk quality. Previous studies have shown that bacterial counts increase in stored milk (Leitner *et al.*, 2008). However, these experiments were laboratory based and failed to investigate the changes in microbiological quality when fresh milk is added to stored milk which is a daily occurrence on dairy farms. Additionally, these studies investigated storage temperatures that exceed current regulatory thresholds. Therefore, performing an on-farm storage experiment at relevant temperatures is desirable to study the effect of storage conditions on the microbial quality of bulk tank milk. The objective of this study was to look at the effect of storage temperature (2°C, 4°C or 6°C) and duration (0 to 96 hours) on the total bacterial count (TBC) of raw bulk tank milk.

Materials and Methods

Three identical bulk tanks were installed at the Moorepark dairy research farm. Equal volumes of milk were pumped into each tank at each milking for four days (n=8 milking's) each week, for two 6-week periods (August-November, 2014). Milk was cooled to 14.5°C prior to entering each tank using three single stage plate coolers. Each bulk tank was set at a different temperature (2°C, 4°C or 6°C) at the beginning of each week. An in-line drip sample was taken at each milking to measure the quality of the milk entering the tanks. Duplicate milk samples were collected aseptically from each tank every 24 hours before morning milking and analysed for TBC. The initial sampling was conducted after morning milking. Milk samples were stored at 4°C until analysis. All samples were tested on the day of collection for TBC using Petrifilm (3M) in accordance with the procedure outlined by Wehr and Frank (2004) and incubated at 32°C for 48 hours. Daily means for total bacterial counts were log transformed for normality and analysed as repeated measurements using the Mixed procedure of SAS software (version 9.3, 2011). Class effects included in the model were week (1 to 12), time (0, 24, 48, 72 and 96 hours), tank (n=3) and temperature (2°C, 4°C or 6°C). The interaction between temperature and day was also tested. Treatment means were compared using the Tukey test at 5% error probability.

Results and Discussion

The TBC entering the bulk tanks ranged from 1,050 CFU/mL to 17,000 CFU/mL and the mean TBC count was 3,376 CFU/mL. Total bacteria counts were greater ($P<0.001$) when milk was stored at 6°C (9,269 CFU/mL) compared to either 2°C (3,147 CFU/mL) or 4°C (3,526CFU/mL). There was no difference ($P>0.05$) in TBC when milk was stored at either 2°C or 4°C. Total bacteria counts were also affected ($P<0.001$) by storage duration whereby the TBC increased as storage duration increased from 0 hours (2,793 CFU/mL) to 96 hours (10,297 CFU/mL). An interaction ($P< 0.001$) was observed between day and temperature for TBC (Fig 1). As the storage temperature and storage duration increased the TBC of bulk tank milk increased; this is in agreement with other studies (Muir *et al.* 1978). Statistically significant interactions between temperature and time were observed for 6°C at 72 and 96 hours with no differences observed for 2°C and 4°C.

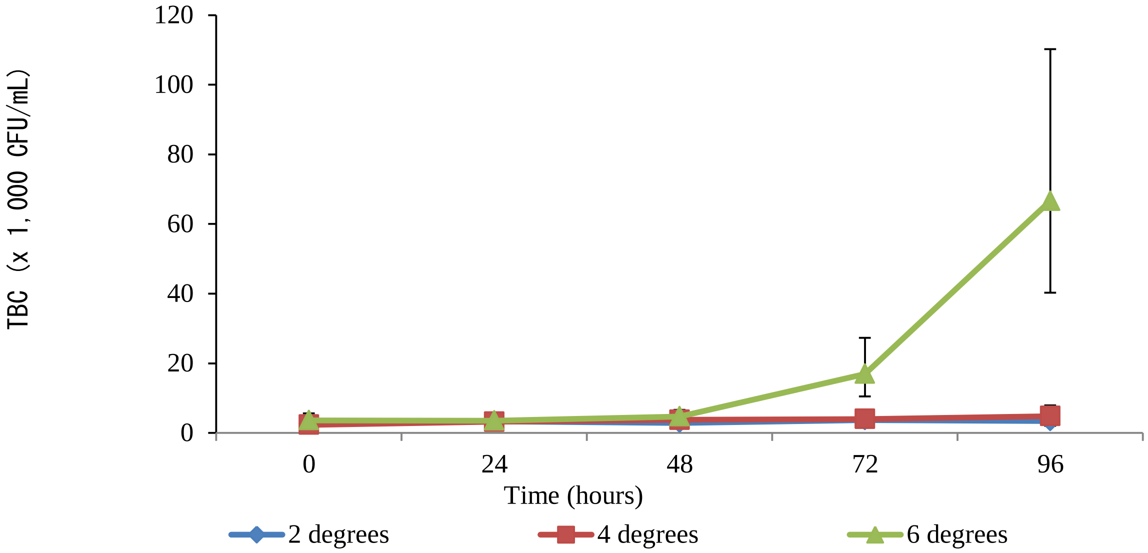

Fig. 1. Effect of storage time and temperature on the total bacterial count of bulk tank milk.

Conclusions

When the initial TBC count of milk entering the tank was low the TBC of milk stored for up to 48 hours remained low regardless of the storage temperature applied. Compared to milk cooled at 4°C, cooling milk to 2°C, did not reduce the bulk tank TBC as the TBC of milk stored at both temperatures remained the same up to 96 hours. The TBC of milk stored at 6°C increased rapidly after 48 hours. Therefore, storing milk at 6°C for more than 48 hours is not recommended. Achieving low TBC after 72 and 96 hours of storage is critically dependent on the initial bacterial count of the milk entering the tank. In this study the bacterial count of the milk entering the tank was low. Therefore, any recommendations to farmers should highlight the importance of the initial bacterial count of the milk.

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RMIS Project No. 6237

Strategies to improve cow traffic and milk yield in late lactation for an automated milking system integrated with grazing

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Introduction

The successful integration of an automatic milking system (AMS) with grazing is reliant upon voluntary movement of cows around the farm system and achieving an even distribution of milkings over 24 hours. Lyons *et al.* (2013) compared the use of supplementary feed pre- and post-milking in a grazing system and observed a reduced voluntary return time of cows from the paddock with pre-milking supplementation. Reduced pre-milking waiting time enhances animal welfare and was achieved by providing concentrate at the milking unit in a voluntary robotic rotary system (Scott *et al.*, 2014). The current study assessed the effects of milking permission and concentrate supplementation in late lactation on milk yield and cow traffic.

Material and Methods

The AMS was located on a farm divided into 3 grazing sections; A, B and C. Cows moved voluntarily to and from the paddock, passing through the milking yard, between the grazing sections. The herd had access to new pasture from 00:00 in A, 08:00 in B and 16:00 in C. The dairy featured one Fullwood Merlin 225 AMS unit (Fullwood Ltd., Kanturk, Co. Cork, Ireland). Sixty five cows were randomly allotted to four groups and balanced for breed, lactation, days in milk, previous milk yield and milking frequency. There were 2 concentrate levels (3kg, 0.84kg) and 2 milking permissions (3.2, 1.8 times per day). During 11 weeks (18/08/14 to 02/11/14) the groups consisted of high concentrate with high milking permission (HCHP) and low milking permission (HCLP) and low concentrate with high milking permission (LCHP) and low milking permission (LCLP). The statistical model used was a repeated measures ANOVA in SAS (PROC MIXED) and Tukey's post-hoc analysis. The fixed effects were week, breed, days in milk, previous yield per cow per day and milking permission, while the random effects included cow traffic and milk production.

Results and Discussion

For the dependent variables of milk production (milk yield per visit and per day) and cow traffic (milking frequency, milking interval per visit, milking duration per day and waiting time per visit) the interaction between milking permission and concentrate level was not significant. The effects of milking permission and concentrate level were significant for each dependent variable. Cows on the high and low milking permission had a milking frequency of 1.9 and 1.3 per day, respectively. Cows on HC and LC had an allowance of 3 and 0.84 kg per day, respectively. Cows with lower milking permission (HCLP and LCLP) compared to cows with a higher milking permission (HCHP and LCHP) had a significantly lower milking frequency ($p < 0.0001$), longer milking interval per visit ($p < 0.0001$), higher milk yield per visit ($p < 0.0001$) lower milk yield per day (p 0.002), shorter milking duration per day ($p < 0.0001$) and less time waiting to be milked per day ($p=0.003$). Cows with the lower concentrate level (LCHP and LCLP) compared to cows with the higher concentrate level (HCHP and HCLP) had a significantly lower milking frequency ($p=0.022$), longer milking interval per visit ($p < 0.012$), higher milk yield per visit ($p < 0.008$), lower milk yield per day ($p < 0.0001$) and a shorter milking duration per day ($p=0.001$). Decreasing milking permission had a positive impact on cow traffic as cows spent significantly less time waiting to be milked. This effect was not observed by increasing concentrate supplementation, instead an increase milk yield per visit and per day was achieved.

Conclusions

Reducing milking frequency reduced time spent waiting to be milked which may increase opportunities for AMS access and reduce time spent standing on hard surfaces enhancing cow welfare. It is possible to achieve a milk yield response to concentrate supplementation in the latter stages of lactation with correct AMS settings.

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Table 1. Effect of milking permission and concentrate supplementation on milk yield (MY kg), milking frequency (MF), milking interval (MI hrs), milking duration (MD min) and waiting time (WT hrs) per day (d) and per visit (v). Least square means and standard error (S.E.) are represented.

	Milking Permission/Day				
	1.8		3.2		*p* value
	Mean	S.E.	Mean	S.E.	
MY/d	15.0	0.17	15.7	0.17	0.002
MY/v	11.1	0.17	8.1	0.18	<.0001
MF/d	1.3	0.02	1.9	0.02	<.0001
MI/v	16.6	0.27	11.6	0.29	<.0001
MD/d	8.6	0.13	10.5	0.13	<.0001
WT/d	1.6	0.13	2.1	0.14	0.003
	Concentrate (kg)				
	0.84		3		*p* value
	Mean	S.E.	Mean	S.E.	
MY/d	14.5	0.17	16.2	0.18	<.0001
MY/v	9.3	0.17	10.0	0.17	0.008
MF/d	1.6	0.02	1.7	0.02	0.022
MI/v	14.6	0.28	13.6	0.28	0.012
MD/d	9.2	0.13	9.9	0.13	0.001
WT/d	2.0	0.14	1.7	0.14	0.230

RMIS Project No. 6337

The effect of reducing milking frequency in mid lactation on milk production and cow traffic in an automatic milking system integrated with grazing

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Introduction

Milking frequency is one of the key performance indicators within an automated milking system (AMS). It has been demonstrated that integration of automatic milking with a pasture based system reduces milking frequency (Garcia and Fulkerson, 2005). Lyons *et al.* (2013) showed that milking frequency at pasture can be improved by increasing the number of fresh allocations of grass each day. However, when an AMS unit is saturated with cows, reducing daily milking frequency may allow the system to accommodate more cows. Jago *et al.* (2006) proposed that the capacity of an AMS unit milking over a 24 hour period could be increased to 112 cows with a milking interval of 18 hours. The objective of this study was to establish the effect of reducing milking frequency on milk production and cow traffic in mid lactation.

Materials and Methods

The farm system comprised of a milking platform and a dairy containing one Fullwood Merlin 225 AMS unit (Fullwood Ltd., Kanturk, Co. Cork, Ireland). The milking platform was divided into 3 grazing sections (A, B and C) of approximately 8 ha each, which were then further subdivided into paddocks of 0.5 ha. Cows had access to fresh pasture at 00:00am, 08:00am and 16:00pm, in A, B and C, respectively. Cows moved voluntary between each of the 3 sections over the 24 hour period.

A herd of 68 primiparous and multiparous cows of mixed breed (Holstein Friesian, Jersey, Jersey x Friesian and Norwegian Red) were randomly assigned into two groups that were balanced for breed, parity, days in milk, previous 25 days milk yield and milking frequency. Milking permission of 2 and 3 times per day were assigned to group 1 and 2, respectively. Cows adjusted to this treatment over a 10 day period, which was followed by a data collection period of 12 weeks between the 12th of May 2014 and 3rd of August 2014. During the experimental period cows were offered on average 17.3 kg dry matter (DM) grass and 0.8 kg concentrate. Cows received a fresh allocation of grass in each grazing block each day. Allocations were of equal sizes in each block. Milk production data were obtained from the AMS unit. Cows were identified with a time stamp at three independent areas; a separation gate pre milking, at the AMS unit itself and at a separation gate post milking. Cow traffic data were collected from each of these. Data were analysed using repeated measures analysis (PROC MIXED) in SAS. The fixed effects were week, breed, days in milk, previous yield per cow per day and milking permission, while the random effects included cow traffic (including milking frequency) and milk production.

Table 1. Mean milking frequency, milk yield and cow traffic performance for each group

	Group1	SD	Group 2	SD	P Value
Milking Frequency/day	1.4	0.014	1.8	0.017	<0.0001
Milk Yield/visit (kg)	12.8	1.21	10.3	1.00	0.1629
Milk Yield/day (kg)	18.4	1.45	18.6	1.55	0.1694
Milking Interval (h:min)	15:16:44	2:09:19	12:44:50	1:25:30	<0.0001
Return Time/visit (h:min)	06:42:42	00:49:13	07:03:46	00:56:59	0.1711
Return Time/day (h:min)	17:13:03	01:30:38	17:30:41	1:25:59	0.4268
Wait Time/visit (h:min)	01:27:21	00:25:43	01:18:50	00:23:19	0.3007
Wait Time/Day (h:min)	01:55:42	00:34:27	02:11:54	00:39:45	0.028

Results and Discussion

Although cows were allowed milking permission of 2 and 3 times per day, milking frequencies of 1.4 and 1.8, were achieved for groups 1 and 2, respectively. This was due to the voluntary nature of the system, whereby cows must present themselves for milking. The difference observed in milking frequencies was significant (P<0.0001). Milking interval is influenced by milking frequency, thus a significant difference in milking interval was also observed between group 1 (15:16:44) (h:min:sec) and group 2 (12:44:50). However, milk yield/cow/day was not significantly affected by milking frequency (Table 1). Although group 2 had permission to milk up to 3 times per day, this did not affect the return time of the cows to the AMS unit, per visit or per day. However, while waiting time/visit was similar for both groups, waiting time/day was significantly longer for cows with a milking frequency of 1.8. This reduced waiting time/day associated with the lower milking frequency would have positive implications for a herd as it would allow for additional time available for grazing.

Conclusions

The results indicate that milking frequency can be reduced in an AMS integrated with grazing, without any negative effect on milk production or cow traffic in mid lactation.

Acknowledgements

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RMIS Project No. 6337

Calibration of an automated grass measurement tool to enhance the precision of grass measurement in pasture based farming systems

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Introduction

Irish and European pasture-based systems of farming rely upon precise grass measurement and allocation to (a) achieve optimal economic return, as grazed grass is the cheapest feed source, and (b) to maintain the regrowth of high quality grass in each subsequent grazing. An Irish study has shown that profit per hectare is increased by €160 for each additional tonne of grass utilized per hectare within dairy systems (Dillon, 2011). On farms implementing an intensive grazing system, grass management is usually carried out by subjective visual measurement and intuitive decision-making. To add objectivity to this process an automated grass measurement tool has been developed, which will increase the precision of grass measurement and allocation for pasture based systems of farming. The aim of this study was to calibrate this tool to ensure the precision of grass height measurement and thus allow it to represent a decision support tool (DST) which farmers could use in the future.

Materials and Methods

The calibration of the new automated grass measurement tool (the 'Grasshopper') for height measurement was conducted at Teagasc Moorepark research farm between September and November 2014. The Grasshopper (True north technologies, Shannon, Co. Clare) may be described as a sensor that emits micro-sonic waves and measures distance (height) by recording the time taken for the micro-waves to travel to and reflect from a surface. The manual Jenquip rising plate meter (New Zealand) is considered the gold standard in grassland measurement. Thus, the Grasshopper module was attached to the shaft of a Jenquip plate meter. This allowed the micro-waves to be emitted from the Grasshopper and reflected from the plate of the Jenquip. This subsequently allowed simultaneous Grasshopper (automatic, digital) and Jenquip (manual) readings for each measurement point simultaneously. Thirty two PVC pipes cut to exact heights ranging between 2.5 cm and 18 cm increasing in increments of 0.5 cm were obtained. The height of each pipe was measured on 150 occasions by the Grasshopper and by the Jenquip with its own plate and mechanical measurement. A Pearson's correlation was obtained using the PROC CORR procedure in SAS to assess the relationship between the actual pipe heights and pipe height measurements recorded by both the Grasshopper and by the Jenquip.

Results and Discussion

The 150 measures recorded by both the Grasshopper and the Jenquip at each pipe height were averaged. When the pipe height measurements recorded by the Grasshopper were compared to the actual pipe heights a Pearson correlation (R) of 0.999 was obtained (Fig.1). When the pipe height measurements recorded by the Jenquip were compared to the actual pipe heights a Pearson correlation (R) of 0.998 was obtained (Fig. 2).

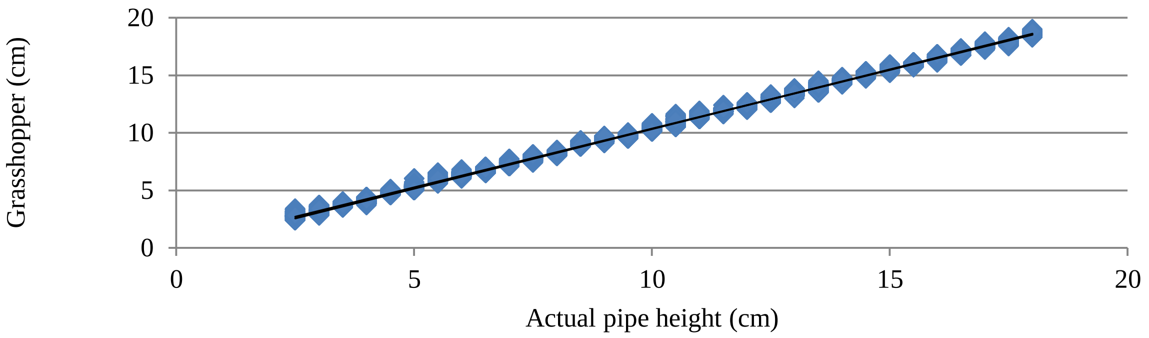

Fig. 1. Relationship between actual pipe heights and pipe heights measured by the Grasshopper (150 measures taken at each of 32 pipe heights)

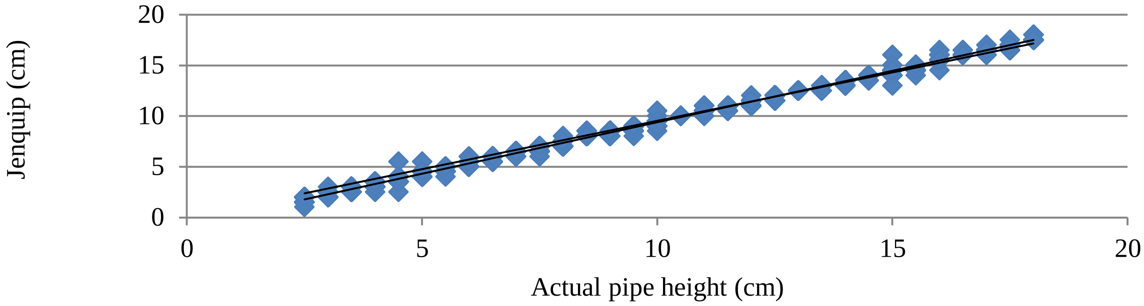

Fig. 2. Relationship between actual pipe heights and pipe heights measured by the Jenquip (150 measures taken at each of 32 pipe heights)

The average standard deviation and average coefficient of variation for the differences between the actual pipe height and pipe height measured by both the Grasshopper and Jenquip tools, averaged over the 32 pipe heights are shown in Table 1. These descriptive statistics were similar, therefore the precision of the Grasshopper was similar to that of the Jenquip for pipe height measurement. The Grasshopper has been shown to be capable of precise height measurements in this study. Future studies will be carried out to assess its precision in grass dry matter yield prediction

Table 1. Difference between actual and measured (by Grasshopper and Jenquip) pipe heights

	Difference from actual pipe height (cm)	Standard Deviation (cm)	Coefficient of Variation
Grasshopper	0.37	0.16	0.02
Jenquip	-0.61	0.18	0.03

Conclusions

An automated grass height measurement tool has been developed which has similar accuracy to that of the Jenquip rising plate meter in height measurement.

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RMIS Project No. 6338

The effect of pasture allowance offered for different durations of time on the dry matter intake of early lactation dairy cows

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Introduction

Grazed grass is the cheapest source of feed for dairy cows in Ireland (Finneran *et al.*, 2010). The 50% increase in milk production proposed in Food Harvest 2020 will be achieved by an earlier spring calving date, higher stocking rates and increased milk yield per cow. This greater demand for grass, especially in spring, will result in greater nutritional deficits as grass supply at this time can be extremely variable (Ganche *et al.*, 2013). The objective of this experiment was to determine the dry matter intake (DMI) of early lactation grazing dairy cows allocated to one of four pasture allowances (PA) for either two or six weeks, and to establish if restricting DMI in early lactation would affect DMI in later lactation.

Materials and Methods

This study took place at Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork from 25 March to 27 November 2014. Ninety-six early lactation dairy cows (41 primiparous and 55 multiparous) were blocked by (mean ± s.d.) calving date (February 17 ± 15.5 d), breed, parity (2.4 ± 1.61), pre-experimental milk yield (22.6 ± 4.20 kg), body weight (BW) (469 ± 68.2 kg) and body condition score (BCS) (3.09 ± 0.193). From within block cows were randomly allocated to one of eight treatments in a randomised complete block design with a 4 × 2 factorial arrangement. The cows were offered one of four PA (60, 80, 100 and 120% of intake capacity) for either two or six weeks. The cows in the 100% PA treatment were offered to 100% of their intake capacity and all other treatments were calculated from this (if 100% = 18 kg DM/cow/day then 80% = 14.4 kg DM/cow/day). The 100% PA was calculated according to the intake capacity equation of Faverdin *et al.* (2011) and was dependent on age, parity, days in milk, BW, BCS and potential milk yield. Pasture allowance was calculated using pre-grazing herbage mass (>3.5 cm), which was measured by cutting two strips (1.2 m × 10 m) per paddock and per treatment area twice weekly, with an Etesia mower. Pre- and post-grazing sward heights were measured daily using a rising plate meter. Cows assigned to the 2-week treatment were allocated a PA of 100% of intake capacity once the 2-weeks had elapsed; all 6-week cows were offered a 100% PA following 6-weeks. The cows were offered fresh grass after each milking during the experimental period and on a 24-hour basis during the carryover period. The treatment groups did not re-graze their respective treatment areas until the first 6 weeks of the experiment had finished. Grass DMI was estimated during weeks 2, 6 and 13 using the n-alkane technique (Mayes *et al.*, 1986; Dillon and Stakelum, 1989). The data were analysed using covariate analysis and mixed models in SAS v9.3, with terms in the model for allowance, duration, the interaction between allowance and duration, and the appropriate pre-experimental covariate.

Results and Discussion

During week 2, there was no significant effect of duration on DMI. Dry matter intake was similar between the 100% and 120% allowances but their DMI was significantly greater than the 60% and 80% allowances, which were also significantly different to each other. During week 6, there was a significant interaction between PA and duration ($P<0.01$). Cows assigned to the 2-week treatments had similar DMI. Dry matter intake was significantly higher for the 120x6 treatment compared to the 100x6 and 80x6 treatments, which did not differ from each other, and in turn, were significantly higher than the 60x6 treatment. Compared to the 100% cows, the 120% cows likely had a greater ability to select pasture which was higher in digestibility and energy value, and lower in fill units, enabling a greater DMI. Although the 120x6 cows had a 20% higher PA compared to the 100x6 treatment they only had a 9% higher DMI which may result in poorer sward utilisation and have consequences for grass quality in subsequent rotations. The post-grazing sward height of the

120x6 treatment during weeks 3 to 6 was 4.3 cm compared to 3.8 cm for cows allocated 100% of IC. During week 13, there was no significant effect of treatment on DMI (15.1 kg DM/cow).

Conclusions

As expected the quantity of pasture offered to dairy cows in early lactation significantly affected their DMI. Restricting DMI in early lactation did not however significantly affect DMI in later lactation.

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Table 1. Effect of pasture allowance offered for different time durations on early lactation dairy cow dry matter intake

	60x2	60x6	80x2	80x6	100x2	100x6	120x2	120x6	SED	PA	D	PA*D
Wk2	10.6	10.3	11.6	11.4	13.4	13.2	13.9	14.2	0.58	***	NS	NS
Wk6	14.2^{ad}	10.7^{b}	14.1^{ad}	12.3^{c}	13.4^{ac}	13.3^{ac}	13.8^{ad}	14.6^{d}	0.60	***	***	***
Wk13	15.2	14.6	16.1	15.4	14.6	14.8	14.5	15.8	0.67	NS	NS	NS

PA=pasture allowance, D=duration, PA*D=pasture allowance*duration, Wk=week, ***=P<0.001, NS=not significant

RMIS Project No. 6517

The duration of time for which varying pasture allowances are imposed effects milk solids production in early lactation

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Introduction

There is little over winter grass growth in Ireland (Hurtado-Uria *et al.*, 2013). This may result in limited early spring feed supply in intensive grazing systems. In the post-quota era increased herd sizes and stocking rates on farms may further deplete the availability of grass in spring. The objective of this experiment was to investigate if different pasture allowances (PA) offered to early lactation grazing dairy cows for varying time durations influenced milk solids yield (MSY).

Materials and Methods

Ninety-six dairy cows (41 primiparous and 55 multiparous) were assigned to a randomised complete block design experiment with a 4×2 factorial arrangement of treatments from 25 March to 27 November, 2014. Only data from the first 10 weeks of the experiment are presented. Cows were blocked on calving date (17 February, s.d. 15.5 d), breed, lactation number (2.4, s.d. 1.61) pre-experimental milk yield (22.6, s.d. 4.20 kg/d), bodyweight (BW; 469, s.d. 68.2 kg) and body condition score (BCS; 3.09, s.d. 0.193). Cows were randomly assigned from within block to one of four PA (60%, 80%, 100% or 120% of estimated intake capacity; IC) for either 2 or 6 weeks. Once the 2- and 6-week time durations had elapsed, the treatments were offered 100% of estimated IC. Intake capacity was calculated using the equation of Faverdin *et al.* (2011) based on age, parity, days in milk, BW, BCS and potential milk yield. The eight treatments grazed independently for the first 2 weeks of the experiment. Then the four 2-week treatments were amalgamated into one grazing group; the four 6-week treatments continued to graze independently until all treatments were amalgamated at the end of 6 weeks. Fresh grass was offered twice daily during weeks 1 to 6 of the experiment and once daily for the remainder of the experiment. Herbage mass (HM; >3.5 cm) was measured twice weekly by cutting 6 strips (120m^2 in total) per treatment grazing area. Treatment groups grazed adjacent to each other to ensure similar HM was offered. Milk yield was recorded daily and milk composition was measured weekly. Data were analysed using covariate analysis and mixed models in SAS v9.3. Terms for parity, breed, PA, duration and the interaction of PA and duration were included. Pre-experimental values were used as covariates in the model.

Results and Discussion

The mean PA for the 60, 80, 100 and 120% treatments for weeks 1 and 2 were 8.1, 10.7, 13.4 and 16.0 kg DM/cow/day, respectively ($P<0.001$). This resulted in post-grazing heights (PGH) of 2.6, 3.1, 3.7 and 4.2 cm, respectively ($P<0.001$). The mean PA during weeks 3 to 6 were 8.7, 11.6, 14.4, 17.5 and 14.3 kg DM/cow/day for the 60, 80, 100 and 120% 6-week treatments and the 2-week treatment; PGH were 2.8, 3.3, 3.9, 4.3 and 3.8 cm, respectively. During weeks 1 to 2 the 60% cows had a lower ($P<0.001$; 1.60 kg/day) MSY than the 100% (1.76 kg/day) and 120% (1.91 kg/day) cows. The 80% (1.68 kg/day) treatment was not different to the 60% treatment but it was lower than the 100 and 120% treatments, which also differed significantly. There was an interaction between PA and duration for MSY during weeks 3-6 ($P<0.01$) and weeks 7-10 ($P<0.01$; Table 1). Average MSY during weeks 3 to 6 was similar for the four 2-week treatments indicating no carryover effect. There was a difference among the four 6-week treatments. The 60x6 and 80x6 were similar but lower than the 100x6 which, in turn, was lower than the 120x6 treatment. During weeks 7 to 10 no differences were observed in MSY between the four 2-week treatments. There was a difference among the four 6-week treatments. The 60x6 was lower than the 100x6 and 120x6 treatments but was similar to the 80x6 treatment. The 80x6 and 100x6 treatments were similar; the 100x6 treatment was also similar to the 120x6 treatment, indicating differences in PA imposed for a 6-week period affected subsequent production. This carryover effect was not observed when treatments were applied for 2 weeks. There was a significant PA × duration interaction on cumulative 10-week MSY. The four 2-week treatments were similar (116 kg/cow), but offering cows 60% of IC for 6 weeks resulted in a lower cumulative 10-week MSY compared to the 100x6 treatment which, in turn, was lower than the 120x6 treatment.

Table 1. Milk solids yield of early lactation dairy cows offered 1 of 4 pasture allowances for either a 2 or 6-week period

	60*x2$^{\#}$	80x2	100x2	120x2	60x6	80x6	100x6	120x6	SED	PA	D	PAxD
Wk3-6 (kg/day)	1.67^{ad}	1.73^{d}	1.70^{d}	1.78^{cd}	1.43^{b}	1.52^{ab}	1.76^{d}	1.93^{c}	0.083	0.001	0.174	0.004
Wk7-10 (kg/day)	1.59^{ac}	1.59^{ac}	1.50^{ab}	1.51^{abc}	1.36^{b}	1.49^{ab}	1.58^{ac}	1.72^{c}	0.080	0.149	0.849	0.002
Wk1-10 (kg)	114^{ad}	117^{ad}	115^{ad}	119^{cd}	101^{b}	107^{ab}	118^{d}	129^{c}	5.4	0.001	0.397	0.01

*PA, as % of intake capacity; $^{\#}$ D, weeks; PA = Pasture allowance; D = Duration; SED = standard error of the difference

Conclusion

The results of this study suggest that MSY recovers immediately after short term (i.e. 2-week) changes in PA however imposing varying PA for a 6-week period can affect cumulative early lactation MSY. Other variables such as cow BW and BCS will be considered in order to obtain a complete picture of the residual effects of altering PA in early lactation.

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RMIS Project No. 6517

Effect of feed allowance at pasture on behaviour and locomotory ability of dairy cows

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Introduction

Pasture based systems are most efficient when herbage utilisation is maximised so that feed costs remain low (Finneran *et al.*, 2010). Thus for Irish dairy farms to remain competitive after the abolition of milk quota, it is imperative that herbage remain the primary nutrition for the cow. However, grass growth in Ireland can be extremely low and variable in spring, which could result in nutritional deficits for the cow, and a challenge to her welfare through increased risk of health disorders. Lying behaviour is often used as a welfare indicator for cows, and the daily pattern varies with daily herbage allowance (DHA) e.g. cows stand for longer once allocated fresh feed when fed a low DHA (O'Driscoll *et al.*, 2010). A low feed allowance can also affect locomotory ability, as the digital cushion in the hoof becomes thinner, which increases the risk of hoof horn disorders (Bicalho *et al.*, 2009). This study aimed to establish how a low DHA in early lactation affects dairy cow lying behaviour and locomotory ability.

Materials and Methods

The study was carried out from March - May 2014 at Teagasc Moorepark Research Centre as part of a project investigating the effect of DHA in early lactation on dairy cow production. Ninety six dairy cows were blocked according to breed (Holstein-Friesian, n=52; Jersey × Friesian, n = 38; Norwegian Red, n = 6), parity (2.40 ± 1.61), calving date (17 Feb 14, ± 16d) and BCS (3.09 ± 0.19) into 12 groups of 8 cows, then randomly assigned to one of 8 treatments in a 2 × 4 factorial arrangement: 2 × treatment durations (2wk or 6wk), and 4 × DHA (60%, 80% 100% or 120% of intake capacity). Daily herbage allowance increased as the experiment progressed in line with increasing intake capacity. Lying behaviour was recorded from all cows on the 6wk treatments using dataloggers (Tinytag Plus, Re-Ed volt, Gemini Dataloggers (UK) Ltd., Chichester, UK), attached to the right hind leg. Behaviour of 16 cows was recorded each day (4 per DHA allowance) until cows had 7 × 24h recorded. Stand/lie was recorded every 30 sec, then the data filtered, and total time lying, no. lying bouts per day, and lying bout duration calculated. Five aspects of locomotion were scored from 1 (normal) to 5 (anomalous: spine arch, tracking, head bob, ab/adduction and speed) prior to the start of the experiment and thereafter every 16 ± 3 d until after treatments concluded. Scoring of dermatitis and heel erosion of the hoof (from 1 (normal) to 5 (anomalous)) was validated, and carried out in the milking parlour at the start of the trial and thereafter every 19 ± 5 d until the end of the trial. Data from the 2wk and 6wk treatments were analysed separately using the Mixed and Glimmix procedures of SAS, accounting for repeated measures. Daily herbage allowance, recording day, and their interaction, breed, lactation number and calving date were used in the models, as well as initial data as covariates.

Results and Discussion

There was no effect of DHA on overall lying time. In all treatments time spent lying approached 9h per day which is within the normal range for cows at pasture. However, there tended to be an effect of treatment on lying bout duration ($P = 0.1$). Cows on the 120% treatment had shorter lying bouts than all others ($P = 0.05$), whereas cows on the 60% treatment had fewer lying bouts than all others ($P < 0.05$; Fig. 1). Longer, but fewer, lying bouts could have arisen because cows were less motivated to stand and feed once herbage was depleted. Moreover, cows on the lower feed allowance treatments took longer to lie following afternoon milking ($P < 0.01$). There was no effect of feed allowance in either the 2wk or 6wk treatments on locomotion score. However in the 2wk treatments, 60% cows tended to have worse locomotion than 100% and 120%, and were more likely than cows in all other treatments to have a tracking score greater than 1 ($P < 0.05$). Spine arch score was less likely to be greater than 1 in the 120% treatment than in any other ($P = 0.01$). In the 6wk treatments, cows on the 60% treatment were more likely, and on the 120% less likely, than cows in the other treatments to have a spine arch score greater than 1 ($P < 0.05$, $P = 0.1$, respectively). There were no effects of DHA in either duration on hoof scores, thus differences in locomotory ability are probably driven by hoof disorders other than heel erosion or dermatitis.

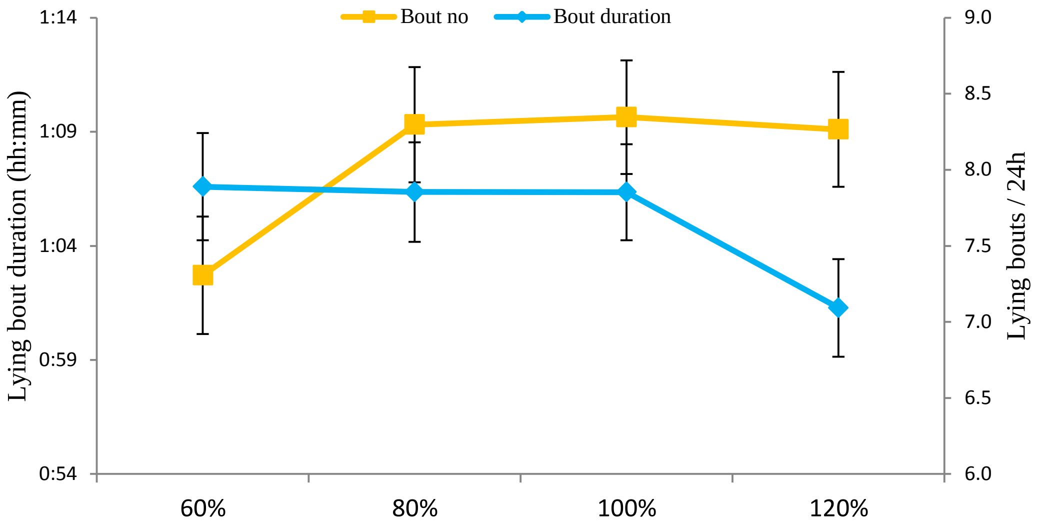

Fig. 1. Lying bout duration and no. lying bouts across DHA allowances

Conclusions

Changes to the pattern of lying behaviour in low DHA cows may be due to depleted feed supply, and could be indicative of hunger. Furthermore, low DHA cows had impaired locomotion, but dermatitis and heel erosion scores similar to other treatments. Further work is planned to investigate hoof health, and indications of hunger, in more detail.

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RMIS Project No. 6517

Grass Breeding

Evaluation of dry matter yield of ryegrass varieties on Irish grassland farms

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Introduction

The development of a comprehensive national grassland database such as PastureBase Ireland (PBI) (http://www.pasturebase.teagasc.ie) has the potential to considerably increase grassland-related understanding. Generating phenotypic DM yield data for individual varieties on commercial farms provides valuable information on individual variety performance across a range of different environments (e.g., soil type) and management systems. Routine on-farm evaluation of large numbers of grass varieties is prohibitively expensive and the internationally followed practice is to use small scale replicated field-plot trials under fixed protocols. The development of an on-farm DM yield phenotyping strategy would facilitate the quantification of variety DM yield across a much wider range of environmental conditions and management practices than can be achieved with traditional plot evaluation trials. Long-term experiments such as that described by Wilkins and Humphreys, (2003), are necessary to evaluate varieties for persistence and stress tolerance. However, the on-farm trials are unlikely to achieve the same precision as in plot trials. The objective of the present study was to quantify the differences in DM yield for a number of recommended list grasses when assessed on Irish dairy farms and to relate this to their yield when assessed in simulated grazing plot studies within the Department of Agriculture, Food and the Marine recommended list (RL) evaluation scheme.

Materials and Methods

The on-farm variety evaluation involved the establishment of monocultures of several varieties on 44 different dairy farms . The varieties, sown at 34.5 kg/ha per paddock, were AberChoice (diploid 'D'), AberGain (tetraploid 'T'), Astonenergy (T), Drumbo (D), Kintyre (T), Twymax (T) and Tyrella (D). Tyrella was established on each of the 44 dairy farms as a control variety. Varieties were sown in either 2011 or 2012. Dry matter production was determined on 228 paddocks from 1 Jan. 2013 until 10 Dec. 2013. Grazing and silage yields (assessed prior to grazing or at the conservation harvest date) were measured seperately and where necessary combined to generate total DM yield. Least squares means for the different varities were estimated using mixed models. Paddock nested within farm was included as a random effect with a compound symmetry covariance structure assumed among paddocks within farm. The dependent variable was total paddock yield (kg DM/ha). Fixed effects considered in the mixed model were sowing rate, number of years since reseeding, and the variety. An additional analysis replaced the variety (class effect) with the continuous fixed effect of DM yield from the plot studies of the RL evaluation; the regression coefficient from this analysis is the expected change in paddock DM yield (on-farm) per unit change in DM yield from the RL plots.

Results and Discussion

The range in DM yield between the highest and lowest yielding variety on-farm was 1.6 t DM/ha. For the on-farm trials, the Least squares means DM production (t DM/ha) per variety were AberChoice (12.7; se=0.878), AberGain (T) (13.6; se=0.858), Astonenergy (T) (11.97; se=0.540), Drumbo (12.4; se= 0.894), Kintyre (T) (13.5; se=0.590), Twymax (T) (12.6; se=0.742) and Tyrella (12.2; se=0.412). The overall conversion factor between the farm generated yields and the RL plots simulated grazing yields was an increase of +0.64 t on-farm per tonne yielded from the plots. Despite these overall mean differences in yield no significant yield differences were recorded between varieties on-farm. Due to the high level of between-farm variability and what is currently the first year of a longer term study, it was concluded that the relatively low sample size currently available is likely to have generated type II errors. Over time with increased farm measurements and an increase in cumulative years data it is expected that this will be overcome and with increased precision, it will be possible to better determine if these varieties perform significantly differently between farms and compared to plot based evaluations.

Conclusion

On-farm grass variety evaluation is potentially an alternative means of a determining the true agronomic potential of ryegrass varieties. The current network of on-farm grass growth monitoring through the PBI national grassland database, is becoming an important means of knowledge transfer on grassland performance potential to ruminant farmers in Ireland. However, this study has quantified the initial levels of variability encountered by farmer-generated yield data and the need for very large data sets to screen out the inherent variability. The continuation of this study will determine at what level of data collection that varietal differences in performance can be isolated from the background noise. By making assessments across a wide range in such factors as topography, fertilizer use, stock management and farm specific micro-climates, it will be possible to determine how robust and relevant the variety performance ranking from limited plot evaluation trials are to the spectrum of farms that rely on this information to optimise grass performance.

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RMIS Project No. 6410

Dairy cow milk production and herbage production in high stocking rate grass-based systems from fertilised grass clover swards

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Introduction

White clover (WC; *Trifolium repens L.*) is the most important forage legume in temperate regions (Frame and Newbould, 1986). Milk production benefits from mixed PRG WC swards compared to perennial ryegrass (*Lolium perenne* L.; PRG) swards have been observed, particularly in the second part of the grazing season (Riberio Filho *et al.*, 2003). High nitrogen (N) fertiliser application can reduce sward WC content since PRG responds to N more efficiently than WC and can result in PRG domination in a mixed sward over time (Ledgard and Steele, 1992). The objective of this study was to compare herbage and milk production from a PRG only sward receiving 250 kg N/ha and PRG/WC swards receiving 150 or 250 kg N/ha in an intensive grazing system.

Materials and Methods

A farm systems experiment was established at Teagasc, AGRIC, Moorepark, Fermoy, Co. Cork. The experiment compared milk production from a PRG sward receiving 250 kg N/ha/yr (Gr250) and PRG/WC swards receiving 250 kg N/ha/yr (Cl250) or 150 kg N/ha/yr (Cl150) in an intensively grazed system over two grazing seasons, 2013 and 2014. Spring calving Holstein-Friesian dairy cows were blocked on calving date, pre-experimental milk yield and parity, and randomly allocated to one of the three treatments ($n = 14$ in 2013 and $n = 19$ in 2014). As this was a farm systems experiment, either 250 kg or 150 kg N/ha was applied to the whole farm, depending on treatment. The same quantity of N was applied to the silage and grazing areas. Fertiliser N application was similar on all treatments until April, after which N was reduced on the Cl150 for the remainder of the year. Treatments were stocked on a whole farm basis at 2.74 LU/ha. Herbage was allocated daily to achieve a target post-grazing sward height of 4 cm. Pre-grazing herbage mass (>4 cm; HM) was determined twice weekly using an Etesia mower. Sward WC content was estimated twice weekly as described by Egan *et al.* (2013). Milk yield was measured daily and milk solids (MS) yield weekly. Data were analysed using a mixed model in SAS with terms for treatment, time (week or rotation), year and the associated interactions. Fixed terms were year, treatment and week or rotation, and random terms were cow and paddock.

Results and Discussion

Herbage production was similar ($P>0.05$) across treatments within year (Table 1). There was a treatment × week interaction ($p<0.01$) effect on WC content. Sward WC content was similar until early July on both WC treatments. From July to the end of the year WC content was greater on Cl150 than Cl250. This increase in Cl150 WC content coincided with the reduction in N fertiliser application to Cl150, similar to the effect reported by Ledgard and Steele (1992). Year had an effect ($p<0.001$) on clover content; it was greater in 2014 (0.27 g/kg DM) than in 2013 (0.23 g/kg) DM. This result is in contrast to Ledgard *et al.* (1995), who found a decrease in WC content from year 1 to year 3 with the application of N fertiliser. The Gr250 treatment had lower ($p<0.001$) MS production than the Cl150 and Cl250 treatments (Table 1). From mid-June to the end of the lactation, milk production was greater on Cl250 and Cl150 compared to Gr250; similar to Riberio Filho *et al*. (2003) and Egan *et al*. (2013).

Table 1. Daily and cumulative milk production and cumulative herbage production on grass only swards receiving 250 kg N/ha (Gr250) and grass clover swards receiving 150 kg N/ha and 250 kg N/ha (Cl150 and Cl250, respectively) and average sward clover content on Cl150 and Cl250.

	Cl150	Cl250	Gr250	S.E.[1]	TRT	Year	Wk.	TRT[2]×Wk.	TRT×Yr
Milk yield (kg/cow/d)	21.13	22.05	20.62	0.44	***	NS	***	*	NS
Milk solids (kg/cow/d)	1.69	1.70	1.58	0.03	***	NS	***	NS	NS
Milk fat (g/kg)	4.58	4.47	4.43	0.26	NS	NS	***	*	NS
Milk protein (g/kg)	3.61	3.58	3.62	0.05	NS	NS	***	NS	NS
Cumulative milk solids (kg/cow)	485	489	454	2.85	***	NS	***	NS	NS
Cumulative herbage production (kg DM/ha)	14355	14317	14233	434	NS	***	-	-	-
Clover content (g/kg DM)	0.27	0.24	-	0.02	NS	***	***	**	NS

[1]S.E. = Standard Error; [2]TRT = Treatment, Wk. = Week

Conclusions

Sward white clover content had a positive effect on dairy cow milk production in both production years. White clover content increased from year 1 to year 2 despite high N fertiliser application.

Acknowledgements

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RMIS Project No. 6120

Nitrogen fixation in grazed grass-white clover plots: effect of N fertiliser application rate

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Introduction

There is interest in the inclusion of white clover (Trifolium repens L.; clover) in grazed grass swards as a low cost and sustainable alternative N source. The main benefit of clover in grass-based swards is related to its ability to supply N through biological nitrogen fixation (BNF). Low growth rates of clover during spring can compromise overall annual herbage production, although N fertilizer application can overcome this disadvantage. However, sward clover content (dry matter (DM) basis) and BNF can be supressed by N fertiliser application (Andrews et al., 2007). The objective of this experiment was to identify an appropriate N fertilisation rate to maximise herbage production and BNF without compromising clover content in grass-clover swards.

Materials and Methods

A series of grazing plots (8 m × 8 m) were established at Moorepark Dairygold Research Farm, Fermoy, Co. Cork in 2009. The experiment had a 2 × 5 factorial arrangement of treatments with three replicates, in a split-plot design, and measurements were made from 2010 to 2013, but only data from 2012, when BNF estimation were undertaken, are presented. Treatments were two swards as the main plots: grass only (GO) and grass-clover (GC), and five fertiliser N rates: 0, 60, 120, 196, 240 kg N/ha/year as the subplots. Dairy cows rotationally grazed the swards 10 times in 2012. Target post-grazing sward height was 4 cm. Pre-grazing herbage mass in each plot was estimated by cutting a strip with an Etesia lawn mower (Etesia UK. Ltd., Warwick, UK). Harvested herbage was weighed, and sub samples removed to determine herbage DM content. Sward clover content was estimated by removing a herbage sample (approx. 70 g) and separating it into grass and clover components. Two microplots (1 m × 1 m) were marked within each GC plot and 1 kg N/ha as ammonium sulphate (98 atom% ^{15}N enrichment) was applied in Nov. 2011 to estimate BNF as described by Unkovich et al. (2008). Data were analysed using Proc Mixed (SAS, 2005) with treatment (2 × 5) and the interactions as fixed effects and the sward type × replicate interaction as a random factor. The daily BNF model also included grazing rotation as a repeated measure.

Results and Discussion

Although GC treatments produced 2 t DM/ha more than the GO swards, there was no significant effect of sward type or the sward type × N fertiliser rate interaction on herbage DM production ($p=0.13$ for both). Herbage DM production was affected ($p<0.001$; Table 1) by N fertiliser rate; plots receiving between 120 and 240 kg N/ha produced more herbage than plots receiving 60 and 0 kg N/ha (15.8 and 13.4 t DM/ha; $p<0.05$), but no other significant differences in herbage production were observed. The N fertilizer rate affected ($p<0.001$) sward clover content and BNF; every additional 10 kg N/ha reduced sward clover content by 0.6% and BNF by 5 kg. Clover content reduction was low (especially for the plots receiving 60 and 120 kg N/ha) compared to previous reports (e.g. Andrews et al., 2007), but absolute BNF values are similar to those reported for GC swards under grazing conditions (Carlsson and Huss-Danell, 2003). It is possible that the frequent and tight grazing used in this experiment reduced the N fertiliser effect on clover content. The daily BNF was only estimated from the fifth grazing (mid-June) onwards, when the ^{15}N applied was stabilized. The daily BNF increased rapidly from May until September, but decreased in October (Fig. 1). Increasing N rate reduced daily BNF with greater effects during autumn ($p<0.001$, Fig 1.).

Table 1. Effect of sward type and N fertiliser rate on herbage production (t DM/ha), clover content (DM%) and biological N fixation (BNF; kg/ha).

	N fertiliser (kg N/ha)						p *values*	
	0	60	120	196	240	SEM	Sward	N
Grass only	11.5	12.4	14.9	14.8	16.0	0.88	0.13	<0.001
Grass-clover	15.1	14.9	16.5	15.8	17.2			
% clover	28.1	21.8	18.6	14.6	12.8	1.75		<0.001
Clover BNF	142	103	74	34	25	10.7		<0.001

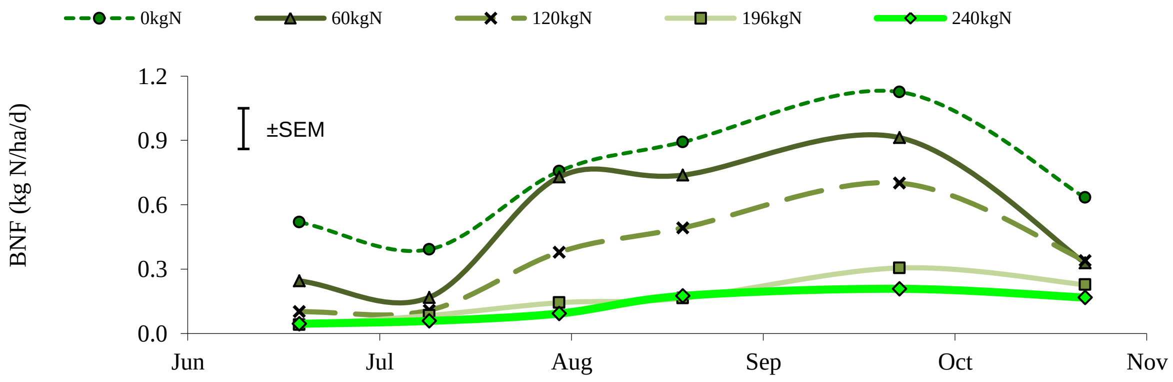

Fig. 1. Effect of N fertiliser rate and grazing rotation on clover biological nitrogen fixation (BNF) rate.

Conclusions

Clover inclusion in grass swards did not result in an increase in herbage production in 2012, regardless of N fertiliser application rate. Increasing N application rate reduced sward clover content and biological N fixation, but the reduction was less severe up to 120 kg N/ha.

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RMIS Project No. 6120

The effect of tetraploid and diploid swards sown with and without white clover on milk production

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Introduction

The utilisation of increased quantities of grazed grass on farms will provide the basis of sustainable dairy cow systems that will help Ireland to achieve the 50% milk production increase targeted in the Food Harvest-2020 report (DAFM, 2011) Recent research has indicated that dairy cows grazing tetraploid grass monocultures produced more milk than those grazing diploid monocultures (Wims *et al.*, 2013). Research has also shown the benefit of white clover (WC) over perennial ryegrass swards for milk production, particularly in the second half of lactation (Riberio Filho *et al.*, 2003; Harris *et al.*, 1998). Therefore, the objective of this study was to evaluate the effect of tetraploid and diploid grass cultivars with and without white clover inclusion on the productivity of spring-calving milk production systems.

Materials and Methods

A farm system experiment to investigate the impact of grass ploidy and clover content on milk production was established in Clonakilty Agricultural College, Co. Cork in 2012. The experimental design was a randomized complete block with a factorial arrangement of treatments, i.e. two grass ploidies (tetraploid and diploid) × two clover treatments (clover and non-clover), resulting in four treatments (tetraploid only; (T), diploid only (D), tetraploid + clover (TC) and diploid + clover swards (DC)). There were 30 cows per treatment group and all treatments were stocked at 2.75 cows/ha and received 250 kg nitrogen per hectare. Each treatment had a separate farmlet of twenty paddocks. One hundred and twenty dairy cows comprising of three breeds (Holstein-Friesian (HF), HF × Jersey (J) and HF × J × Norwegian Red) were assigned to one of the four treatments, in February 2014, based on breed, calving date, parity, and pre-experimental milk yield. Herbage allowance (HA) and herbage removed were measured using the method of Delaby and Peyraud (1996).

Individual milk yields (kg) were recorded at each milking. Milk composition was measured weekly from a consecutive AM and PM milking. Milk production data were analysed using General Linear Models (PROC GLM) in SAS (SAS, 2006). Terms included in the model were ploidy, clover content, parity, breed and their interactions. Calving day of year was included as a covariate.

Results and Discussion

There was no interaction between perennial ryegrass ploidy and clover for any of the variables presented. There was a tendency (P=0.056) for diploid treatments (D and DC) to have greater daily HA (16.3 kg dry matter (DM)/cow) compared with the tetraploid treatments (T and TC; 15.1 kg DM/cow). Clover inclusion did not affect HA (16.1 kg DM/cow for T and D vs. 15.4 kg DM/cow for TC and DC). Milk production results for 2014 are presented in Table 1. Ploidy did not affect any of the milk production variables. Clover inclusion had an effect (P<.0001) on both daily and cumulative milk and milk solids yields per cow. Cows grazing both TC and DC had greater daily milk and milk solids yields/cow than cows grazing T and D. This resulted in TC and DC having greater cumulative milk and milk solids yields/cow compared with T and D. Clover inclusion did not affect milk fat content, increased milk lactose content (P<0.01) and tended to increase milk protein content (P=0.052).

Table 1: Effect of perennial ryegrass ploidy and white clover inclusion on milk production

	Tetraploid	Diploid	Tetraploid + Clover	Diploid + Clover	S.E.	Ploidy	Clover	P × C
Milk yield (kg/cow/day)	17.7	17.5	20.0	20.0	0.28	0.765	<.0001	0.881
Milk solids (kg/cow/day)	1.50	1.46	1.68	1.67	0.025	0.418	<.0001	0.495
Fat (g/kg)	47.4	47.0	46.5	46.8	0.73	0.935	0.457	0.725
Protein (g/kg)	37.3	36.5	37.5	37.5	0.30	0.158	0.052	0.117
Lactose (g/kg)	47.6	47.4	47.9	48.2	0.14	0.582	0.002	0.178
Cumulative milk yield (kg/cow)	4895	4848	5532	5506	63.7	0.708	<.0001	0.914
Cumulative milk solids (kg/cow)	414	403	464	463	5.5	0.407	<.0001	0.520

Conclusion

Perennial ryegrass ploidy did not significantly affect animal performance. There was a positive effect of white clover on milk production regardless of ploidy. The results indicate that inclusion of white clover in grass-based swards is an effective strategy to increase animal performance in spring milk productions systems however; further research is required to see if these results are repeatable and dependable.

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RMIS Project No. 6130

The effect of perennial ryegrass ploidy on sward clover proportion in a mixed sward across an entire grazing season; two years after sowing

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Introduction

White clover (*Trifolium repens* L.) is widely considered to be the most common and important forage legume grown in temperature regions worldwide (Dewhurst *et al.*, 2009), contributing to animal performance, increased quality of consumed herbage, and increased soil fertility via nitrogen fixation. It is generally grown with a companion grass in Ireland, commonly perennial ryegrass, *Lolium perenne* L. (Black *et al.*, 2009). Previous studies have indicated that clover can contribute to herbage yield and quality but that this is highly dependent on the grass cultivar used, grazing management and nitrogen (N) fertiliser input (Chapman *et al.*, 1996). Little research work has been undertaken to investigate the effect of grass ploidy on sward clover content during an entire grazing season. The objective of this study was to monitor the change in clover proportion of both diploid and tetraploid swards across an entire grazing season.

Materials and Methods

A farm systems experiment was established in Clonakilty Agricultural College in 2012, to examine the effect of ploidy on sward characteristics sown with and without white clover. The experimental design was a 2 x 2 factorial arrangement of treatments, consisting of two ploidies (tetraploid, diploid) and two sub-treatments (non-clover, clover). Four tetraploid (AstonEnergy, Kintyre, Twymax and Dunluce) and four diploid (Tyrella, AberChoice, Drumbo and Glenveagh) cultivars were sown as monocultures in 2012 (37 kg/ha, and 30 kg/ha; respectively) with and without clover (sown at 5 kg/ha). Each cultivar was sown five times across the 20 experimental blocks, creating four individual farmlets of each treatment, each containing 20 paddocks. Each treatment received 250 kg nitrogen/ha. 2014 encompasses the second year of measurements. The proportion of clover in the sward was determined prior to grazing from April to November. A grass sample was taken at random using a quadrat (25 x 25 cm). The plant material within the quadrat was harvested above 4 cm using a Gardena (Accu 60, Gardena International GmbH, Ulm, Germany) hand shears. This material was mixed to give a representative 70 g subsample from each paddock that was separated into grass and clover components, and dried at 90^0C for 24 hours to estimate dry matter content of treatments and clover proportion in each treatment. Clover data were analysed using Mixed Models in SAS (SAS, 2011). Terms included in the model were ploidy, month and their interactions.

Results and Discussion

There was no difference in sward clover proportion between tetraploid and diploid swards ($P > 0.05$). Average clover proportion for the tetraploid and diploid swards during the measurement period was 0.38 and 0.41, respectively. There was no interaction between ploidy and month for clover proportion ($P > 0.05$). Month had an effect on clover proportion ($P < 0.001$). The clover proportion in the swards was highest in July, August and September for both treatments (Figure 1); reflective of higher soil temperatures, conditions more conducive to clover accumulation and the natural pattern of clover growth. The results from this study are not consistent with the review of Stewart and Hayes (2011) as ploidy had no effect on clover proportion. Stewart and Hayes (2011) stated that more open, patchy tetraploid swards allow for the establishment and spread of clover plants to a greater extent than in diploid swards. Tozer *et al.* (2014) reported no effect of ploidy on sward clover proportion in pastures of three age classes; ‘young’, ‘medium’, and ‘old’, which is consistent with the results of the current study with a ‘young’ (two years after sowing) sward.

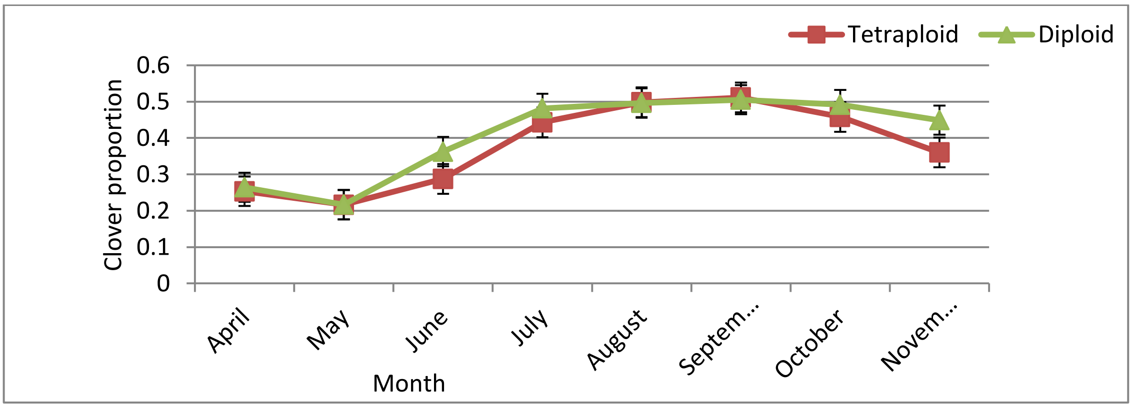

Fig. 1. Clover proportion (expressed by mean values; standard error represented by error bars) of diploid and tetraploid swards

Conclusion

This study found no effect of grass ploidy on sward clover proportion. Month had a significant effect on sward clover proportion, as expected, due to the natural pattern of clover growth. However, these are initial results from a long term study and the swards need to be monitored for a number of years to fully investigate the effect of ploidy on sward clover proportion.

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RMIS Project No. 6130

Modelling the economic consequences of increasing stocking rate and supplementation levels

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Introduction

The end of milk quotas in 2015 will give an opportunity to dairy farmers to expand their dairy enterprises unhindered for the first time since 1984. Models can help to determine the most profitable on farm strategy around the expansion process. The objective of this study was to combine three different models to evaluate the optimum expansion pathway at farm level by comparing different stocking rates and concentrate supplementation strategies.

Materials and Methods

Three different stocking rates (SR) were modelled; 1.9 cow/ha (1.9), which was simulated with a post grazing height of 5.2 cm and a nitrogen fertilisation level of 160kg/ha; SR of 2.2 cow/ha (2.2), with a post grazing height of 4.5 cm and a nitrogen fertilisation level of 200 kg/ha; SR of 2.5 cow/ha (2.5), with a post grazing height of 3.8cm and a nitrogen fertilisation level of 250 kg/ha. Across the three stocking rates three levels of concentrate supplementation were evaluated (0.5 t; 1.0 t and 1.5 t/cow/lactation) resulting in a total of 9 scenarios. Each scenario was simulated across 10 different years of meteorological data from 2004 to 2013. Three different models were combined to complete the simulation; the Moorepark Grass Growth Model (MGGM) (Paillette *et al.*, submitted) which is a dynamic model of daily grass growth.

Table 1: Effect of the different scenario on the total farm profit in euros depending on the different milk price (MP) and concentrate prices (CP)

Stocking Rate	LSR			MSR			HSR		
Concentrate	500	1000	1500	500	1000	1500	500	1000	1500
MP 29.5 c/l CP 250 c/kg	18010	13145	3914	21339	16176	5756	23698	18567	6775
MP 24.5 c/l CP 250 c/kg	-3747	-9477	-19310	-3269	-9523	-20680	-3614	-10109	-22807
MP 34.5 c/l CP 250 c/kg	39768	35767	27137	45947	41874	32192	51010	47244	36358
MP 29.5 c/l CP 350 c/kg	12866	3752	-10848	15412	5337	-11266	17018	6344	-12591
MP 29.5 c/l CP 150 c/kg	23014	22283	18272	27104	26719	22313	30196	30457	25613

The simulated grass growth was incorporated within the Pasture Based Herd Dynamic Milk model (PBHDM) (Ruelle *et al.*, submitted), which is a dynamic, stochastic agent based model of a dairy farm which simulates on a daily basis the individual intake, milk production and body condition score of animals. The PBHDM model generated information around levels of feed consumed, milk yields and body condition score. This data was then incorporated in the Moorepark Dairy Systems Model (MDSM) (Shalloo *et al.*, 2004) which is a stochastic budgetary simulation model of a dairy farm. The MDSM was then used to simulate the effect of the 9 scenarios across the ten years of meteorological information. Three different milk prices (24.5, 29.5 and 34.5 c/l) and concentrate prices (150, 250 and 350 c/kg) were included in the analysis

Results

An increase in SR resulted in a decrease in the milk production per cow (average through all levels of concentrate of 6,038, 5,942 and 5,686 kg of milk per lactation for the 1.9, 2.2 and 2.5 scenarios respectively) while resulting in an increase in milk production per hectare (average through all levels of concentrate of 11,472, 13,073 and 14,216 kg of milk/ha for the 1.9, 2.2 and 2.5 respectively). The response to concentrate supplementation increased with stocking rate and reduced with increasing levels of supplementation. The economic benefits on farm of the different scenarios evaluated are presented in Table 1. Overall, the increase of concentrate led to a decrease of the farm profit except when concentrate costs were low at a high SR. Within the SR increases modelled there was an increase in profitability when stocking rate was increased.

Discussion

As stocking rate and level of concentrate feed increased there is an increase in the vulnerability of the business to variation in input and output prices. However this study has shown that the system that results in the highest profitability is the HSR at 0.5 T of concentrate across most milk and concentrates price scenarios. The increase in benefit with an increase of SR is true within the ranges of SR modelled, however, further investigation needs to be completed to predict the impact of higher SR.

Conclusion

Within the range of SR modeled with a cow type that could be described as a typical Irish cow, an increase of SR lead to an increase in profit. Overall the increase of concentrate supplementation was not beneficial and lead to a decrease in overall profit.

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RMIS Project No. 6334

Grass Feed Value

Effect of autumn closing date on dry matter intake and *in vivo* dry matter digestibility of spring grass

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Introduction

Growth of perennial ryegrass is seasonal (Brereton, 1995), with daily growth during the summer reaching 100 kg DM/ha and over the winter period only sometimes exceeding 3 kg DM/ha (O'Donovan *et al.*, 2002). In order to ensure adequate provision of grass for early spring grazing, it is essential that grass is accumulated by closing swards the previous autumn. Delaying the closing date (CD) in autumn reduces pre- grazing herbage mass (PGHM) but increases *in vitro* dry matter digestibility (DMD) and leaf content of the sward (Hennessey *et al.*, 2006). The objective of this experiment was to evaluate the effect of three CD in autumn on grass PGHM, dry matter intake (DMI) and *in vivo* DMD in sheep the following spring.

Materials and Methods

The experiment was run in spring 2014 as a 3×2 incomplete Latin Square design with three treatments, swards which had different CDs: early - 1 October (E), mid - 15 October (M), late - 1 November 2013 (L) and two periods (P1 (Early): 25 Feb to 9 Mar, P2 (Late): 19 Mar to 30 Mar). Each period was 11 d consisting of 5 d adaptation and 6 d measurement. Twelve Texel wether sheep were blocked by body weight into 4 blocks and were randomly assigned from within block to treatment, giving four sheep per treatment per period. The sheep were housed in individual stalls that allowed for the measurement of DMI and the total collection of faeces for each individual sheep. Fresh herbage was cut once daily each morning using a motorised Etesia (Etesia UK Ltd., Warwick, UK). Sheep were fed at 110% of *ad libitum* intake, split into a.m. and p.m. feeds. Feed refusals were collected every morning. During the measurement phase a representative sample of the grass offered and faeces voided were collected from each sheep daily. The average DMI and DMD over the 6 d measurement phase was calculated for each sheep. The PGHM was measured using a Gardena hand shears (Accu 60, Gardena International GmbH, Ulm, Germany) and a 0.25 m^2 quadrant on days 1, 4, 7 and 10 of each period. On day 8 of each period a 40 g sample of each sward was separated into leaf, pseudostem, true stem and dead proportions above a 4 cm stubble height. All swards received 35 kg of inorganic nitrogen fertiliser on 23 January 2014. Data were analysed using PROC MIXED in SAS (2002). Treatment, period and the interaction between treatment and period were included as fixed effects. Sheep was included as a random effect.

Results and Discussion

There was a tendency for an interaction between period and CD for PGHM (Table 1). This was due to an increase in PGHM for E and M swards, but a slight decrease for L swards, from P1 to P2. There was a tendency for L and M swards to have a greater DMI than E swards. There was an interaction between CD and period for DMD. In P1, there was no significant difference in DMD between the three CD swards. In P2, the M sward had a higher DMD than the E sward, and the L sward was intermediate. Closing date had an effect on sward morphology. The L and M swards had a significantly greater leaf proportion than E swards. Pseudostem and dead proportion were significantly greater in E than in L and M swards. In summary, due to the greater proportion of dead and lower leaf proportion in the E sward, DMD was lower and DMI tended to be lower. The mid CD had no effect on DMI or DMD compared to the late CD, but had a higher PGHM available in spring, which is desirable.

Table 1. Effect of closing date on pre-grazing herbage mass >4 cm (PGHM), grass dry matter intake (DMI), dry matter digestibility (DMD) and leaf, pseudostem, true stem and dead proportions of the sward (>4 cm) the following spring

	Period 1 (Early; 25Feb-9Mar)			Period 2 (Late; 19Mar-30Mar)						
Treatment	Early	Mid	Late	Early	Mid	Late	SEM	CD	Per	CD × Per
Days closed	156	142	125	177	163	146				
PGHM (kg DM/ha)	2364	1647	1070	2977	2263	831	225.4	**	*	†
DMI (kg/d)	0.96	1.20	1.13	1.43	1.52	1.50	0.102	†	***	ns
DMD (g/kg)	800^{ab}	802^{a}	805^{a}	769^{b}	814^{a}	796^{ab}	9.2	*	†	*
Leaf (%)	57.7	74.8	74.4	56.1	67.0	69.9	3.19	*	†	ns
Pseudostem (%)	18.6	14.7	15.6	24.7	21.2	20.4	1.63	**	ns	ns
True stem (%)	0	0	0	2.6	1.1	0	0.73	ns	†	ns
Dead (%)	23.7	10.5	10.0	16.6	10.7	9.7	2.98	*	ns	ns

Early=1st Oct, Mid=15th Oct, Late=1st Nov; $^{a-b}$ means with a different superscript within a row are significantly different; † P <0.10, * P<0.05, **P<0.01, ***P<0.001, ns not significant

Conclusion

Early closed swards in this study had PGHM that would be considered very high for early spring. If early closed (October) swards are available for grazing in spring they should be grazed first (Feb) as if grazing occurs later (late March) the DMD of early closed swards is reduced compared to later closed swards.

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RMIS Project No. 6194

Comparison of *in vivo* dry matter digestibility of cows and sheep offered grass differing in pre-grazing herbage mass

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Introduction

Grass dry matter digestibility (DMD) is a key variable that affects system output and animal performance. Changes in grass DMD can affect animal performance due to effects on grass intake and utilisable energy content. Garry *et al.* (2013) found a significant effect of pre-grazing herbage mass (PGHM) on *in vivo* DMD in sheep. It is unclear as to how this relates to lactating dairy cows. The objective of this study was to compare grass DMD, from swards differing in PGHM, when offered to dairy cows and sheep concurrently.

Materials and Method

Eight wether sheep and eight spring-calving lactating dairy cows were used to determine the *in vivo* DMD of two treatments, namely two different PGHM (1700 kg DM/ha – low mass (LM) and 4000 kg DM/ha – high mass (HM)). A Latin square design experiment (2 (treatments) × 2 (periods)) was repeated twice (time stage 1 (TS1): Apr-May 2014, TS2: Jul-Aug 2014). Each TS had two periods of 12 days: a six day adaptation phase and a six day measurement phase (MP). The sheep and cows were housed in individual stalls to allow for individual feeding and for total faecal collection. Sheep were blocked on body weight, while cows were blocked on body weight, body condition score, milk yield and milk solids yield. Animals were assigned from within block to LM or HM for period 1 of each TS. Fresh grass was cut once daily each morning using a Pottinger mower and silage wagon (Pottinger M. GmbH, Grieskirchen, Germany). Sheep and cows were offered grass *ad libitum* (110% of DMI) in a split feed morning and evening, and grass DMI was recorded daily. Pre-grazing herbage mass was measured using a Gardena hand shears (Accu 60, Gardena Int. GmbH, Ulm, Germany) and a 0.25 m^2 quadrant twice weekly during each period. During the MP, a representative sample of the grass offered to, and faeces voided by, each sheep and cow was collected daily. The daily grass and faeces samples were dried and then bulked to give one sample of each per PGHM per MP for each species. Dry matter digestibility was calculated as (kg DM ingested – kg DM output in faeces) / kg DM ingested. The DMD data were analysed using PROC MIXED in SAS (2002). Treatment, period within TS, TS, species and the interactions between TS, species and treatment were included as fixed effects. Animal was included as a random effect.

Results and Discussion

No significant interactions between species, TS and PGHM were found for DMD (Table 1). This was an important finding as it indicated that the species effect on DMD was consistent across the different times of the year evaluated, and across different PGHM. There was a tendency (P=0.09) for sheep to have greater DMD than dairy cows. Average sheep DMD was 752 g/kg compared to average cow DMD of 739 g/kg. Previous research suggests that cattle and sheep digest ryegrass equally at both *ad libitum* and maintenance feeding levels (Prigge *et al.*, 1984). There was an effect of PGHM on DMD as LM swards had greater DMD than HM swards (P<0.01). The TS also had an effect on DMD with greater DMD in TS1 than in TS2 (P<0.001). Garry *et al.* (2013) found similar effects of TS and PGHM on DMD when evaluated with sheep alone. They measured lower DMD in HM and TS2 swards due to increased proportion of true stem compared to LM and TS1 swards respectively.

Table 1. The effect of PGHM on grass dry matter digestibility (DMD) in wether sheep and spring-calving lactating dairy cows in Apr-May and Jul-Aug

	PGHM	Species	DMD (g/kg)
TS1 Apr-May	High	Sheep	756
		Cow	745
	Low	Sheep	783
		Cow	774
TS2 Jul-Aug	High	Sheep	730
		Cow	697
	Low	Sheep	740
		Cow	739
P value	SEM		15.0
	PGHM		**
	TS		***
	Species		†
	PGHM*TS		ns
	PGHM*Species		ns
	TS*Species		ns
	PGHM*TS*Species		ns

PGHM = pre-grazing herbage mass, TS = time stage, † P <0.10, **P<0.01, ***P<0.001, ns not significant

Conclusions

It can be concluded that the effect of animal species on grass DMD was consistent across the different times of the year evaluated, and across different PGHM. There was a tendency for sheep to have a higher DMD than cows.

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RMIS Project No. 6194

Labour input on Irish dairy farms

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Introduction

Dairy farming is the most profitable farm enterprise in Ireland with the majority of milk produced using grass-based seasonal-calving systems (Horan *et al*., 2004). The EU milk quota system will end in 2015 and it is that milk output is targeted to increase by 50 per cent by 2020 (DAFM, 2010). It is expected that average herd size will increase with an associated implication of increased labour demand on farms. Consequently, there will be a need for Irish dairy farmers to address their level of labour efficiency before considering herd expansion. Labour efficiency on dairy farms must be optimised from two perspectives: family labour input needs to be sustainable, while at the same time, the labour demand which exceeds family input must be minimised to maintain lower hired labour costs. Thus, the aim of this study was to quantify the annual labour input on Irish dairy farms and to establish seasonal patterns of labour utilisation over a two-year period across a range of herd sizes.

Materials and Methods

During 2012 and 2013, a small survey study was performed on spring-calving dairy farms with dairy as the sole enterprise (n=94). The farms were selected based on their previous participation in monthly farm discussion groups coordinated by Teagasc. Herd sizes ranged from 19 to 320 cows. The farms were subdivided into four groups based on herd size as follows: Herd 1=19-55 cows (n=11), Herd 2=56-110 cows (n=59), Herd 3=111-250 cows (n=20), and Herd 4=251+ cows (n=4). The labour input data and management practices were reported retrospectively by the main farm operator on a once off occasion through a paper questionnaire. The farms were subdivided into categories to be representative of traditional farms, expanding farms and very large farms. The data were then summarised using the PROC MIXED procedure of SAS and Tukey's test. Natural log transformation was used when data was not normally distributed.

Results and Discussion

The average farm labour input across herd sizes was 5,362 h/year with the farmer working 57% of those hours and all other forms of labour input representing 43% of the hours (spouse=3%, family=12%, and employees=28%) (Table 1). Total number of hours worked increased as herd size increased, while the hours input by the farmer did not change (P=0.29) across herd size categories. Employee input was higher (P<0.001) on larger farms as well as labour efficiency (P<0.001), with the highest labour input per cow per year (89h/c/yr) being observed with the lowest herd size (Herd Size 1) and the lowest labour requirement per cow was observed in the larger herd size 4 (28h/cow/yr). This was similar to trends seen in other studies (O'Brien *et al*., 2005; Bewley *et al*., 2001). When the most efficient farms were identified across herd sizes, it was noted that these farms implemented a number of labour saving techniques such as utilising contractors to perform various tasks on farm. Total labour input may appear lower on these farms due to allocation of certain tasks to contractors. The labour input of the main operator followed a seasonal profile with maximum and minimum labour inputs observed in the spring and winter respectively (Figure 1). Actual labour input exceeded the farmer desired level (57 hours per week) for two seasons of the year. Given that the majority of dairy farms follow a spring-calving season to utilise optimal grass growth for their grazing herds, it was expected that the highest labour demand would be recorded in the springtime. In autumn the demand for labour decreased until a sharp decline in the winter season when cows were dried off.

Table 1. Average yearly dairy labour input (hours) and dairy labour efficiency (h/cow/yr) across different herd sizes

Herd Size	Total (h)	Farmer (h)	Family (h)	Employees (h)	h/cow /yr
1	3891	3154	576	22	89
2	4255	3206	594	310	55
3	5403	3118	984	1106	35
4	7900	2745	492	4626	28
all	5362	3056	662	1516	38

1=19-55 cows, 2=56-110 cows, 3=111-250 cows, and 4=251+ cows

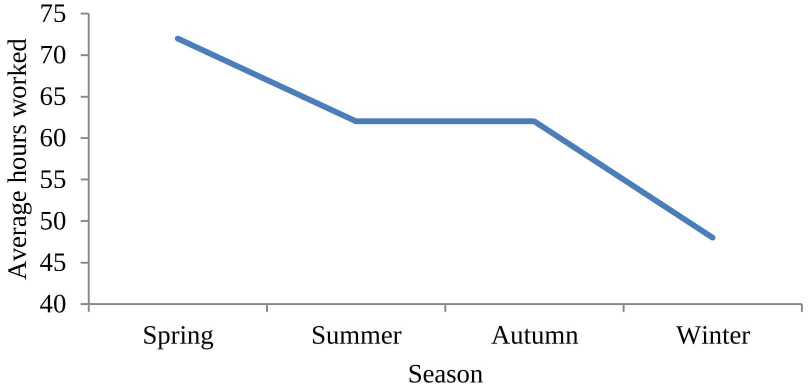

Fig. 1. Seasonal variation in weekly labour input of main operator on Irish dairy farms

Conclusions

In conclusion, there was a distinct seasonal pattern to the hours worked with the highest labour input in the spring and lowest in the winter. Labour efficiency was improved and hired labour input increased as herd size grew larger. Contractors were utilised more frequently for certain farm tasks on the more efficient dairy farms.

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Relating the carbon footprint of milk from Irish dairy farms to economic performance

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Introduction

The Irish dairy sector is a key source of national greenhouse gas (GHG) emissions (~10%), which are projected to increase (O’Brien *et al.*, 2014). Ireland has agreed to reduce emissions from the non-emissions trading sector (includes dairy production) by 20% relative to 2005 levels by 2020 (European Council, 2009). Several strategies are available to mitigate GHG emissions, but producing milk with low GHG emissions per unit of milk or carbon footprint (CF) of milk does not necessarily imply that this is economically viable. Thus, the goal of this study was to evaluate the relationship between the CF of milk production and farm economic performance in terms of profitability and labour income.

Materials and Method

The national farm survey (NFS) database (Hennessy *et al.*, 2013) was used to assess economic performance and the CF of Irish milk. The NFS primarily collects financial data from a nationally representative sample of dairy farms and was used in this study to estimate pre-tax profit margin and labour income on a gross and net basis. Thus, gross margin was estimated as the difference between gross output and variable costs. Net margin was calculated by subtracting overhead costs from gross margin. Gross or net farm margin was expressed per unit of labour (paid and unpaid) to assess labour income. One labour unit was defined as at least 1800 hours worked per year by a person over 18 years. To simulate GHG emissions the NFS was expanded to collect technical farm data on for instance farm feeding practices (Table 1). The survey was then carried out on 256 dairy farms in 2012. In total, sufficient data was collected on 221 farms to estimate GHG emissions.

Table 3. Key technical data used to simulate carbon footprint of milk for the bottom, mean and top third of 221 Irish dairy farms ranked in terms of gross profit/ha.

Item	Bottom	Mean	Top
Farm area, ha	36	35	34
Culled cows, %	19	17	15
Stocking rate, cows/ha	1.59	1.89	2.24
Milk yield, t/cow	4.5	5.2	5.8
Milk yield, t/ha	7.3	9.8	13.0
Fat, %	3.90	3.94	3.97
Protein, %	3.37	3.40	3.43
Concentrate, kg DM/cow	929	898	929
Grazing days	221	239	249
Purchased fuel, l/ha	114	110	113

The NFS data was applied with the GHG model of O'Brien *et al.* (2014), which was independently certified to comply with the British standard (BSI, 2011) for life cycle assessment (LCA). Thus, the model calculated annual on and off-farm GHG emissions from imported inputs (e.g. electricity) up to the point until milk was sold from the farm in CO_2-equivalent (CO_2-eq). Annual GHG emissions computed using LCA was allocated to milk based on the economic value of dairy farm products and expressed per kg of fat and protein corrected milk (FPCM). PROC REG and PLS of SAS was used to evaluate relationships between economic performance and farm factors that influenced significant ($P < 0.05$) associations.

Results and Discussion

The mean CF of milk was 1.19 kg of CO_2-eq/kg of FPCM (range 0.60-2.18 kg of CO_2-eq/kg of FPCM). The CF of the top third of farms in terms of gross margin/ha was 7% lower than the mean and 15% lower than the bottom third. Financial performance measures were inversely correlated to CF of milk (Table 2). Partial least square (PLS) regression analysis ranked the length of the grazing season, concentrate feeding/cow, milk yield/ha and milk yield/cow as the most important measures in explaining the association between financial and environmental performance.

Extending the grazing season and increasing milk yield/ha or per cow had a mitigating influence on CF of milk and improved economic performance. However, increasing concentrate feeding had a negative effect on profit and income. Thus, to improve the CF of milk and economic performance grass-based dairy farms should aim to increase milk output from grazed grass.

Table 2. Correlations[1] between economic performance, carbon footprint of milk (CF), concentrate feeding/cow (CO), the length of the grazing season (GS), milk yield/cow (MY/C) and milk yield/ha (MY/ha).

Measure[2]	CF	CO	GS	MY/C	MY/ha
CF	N/A	0.07	-0.34	-0.43	-0.36
GM/litre	-0.43	-0.43	0.41	0.28	0.20
GM/ha	-0.39	-0.31	0.34	0.51	0.78
GI/labour unit	-0.26	-0.25	0.29	0.44	0.45
NM/litre	-0.45	-0.38	0.42	0.29	0.22
NM/ha	-0.38	-0.36	0.40	0.40	0.52
NI/labour unit	-0.35	-0.21	0.40	0.37	0.36

[1] All correlations < 0.10 were significant ($P < 0.05$); [2] GM = Gross margin GI = Gross income NM = Net margin NI = Net income

Conclusion

This study indicates that the goals of improving economic performance and reducing CF of milk are not contradictory. Thus, grass-based dairy farmers can implement “win-win” strategies to mitigate the CF of milk and increase profitability.

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RMIS Project No. 6409

The effect of allocation method on the carbon footprint of milk and dairy derived beef

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Introduction

It is predicted that the global population will increase to over 9 billion by 2050 leading to an increase in demand for animal products (FAO, 2009). With this in mind, increased production from livestock might well be associated with increasing environmental impact, particularly in relation to the earth’s climate. Therefore, reducing greenhouse gas (GHG) emission per unit of milk and beef (carbon footprint, CF) is becoming a priority. A major problem estimating the CF of food is the allocation of emissions between multiple outputs (such as milk and meat). The aim of this study was to evaluate the effect of different allocation methods on the CF of milk and meat.

Materials and Method

Dairy farm technical data was obtained from the NFS 2012 (Hennessey *et al.*, 2013), in which farms were categorised based on their gross margin/ha. These data were applied using the GHG model of O`Brien *et al.* (2014), in order to determine the CF of milk and meat. The model used the life cycle analysis (LCA) method and was developed in accordance with the PAS 2050 British standard for LCA (BSI, 2011). The LCA method was applied to quantify GHG emissions from all on and off-farm sources associated with agriculture up to the farm gate. Thus, the approach included upstream emissions from manufactured inputs e.g. fertiliser. The model originally allocated GHG between milk and meat based on their economic value, but to test the effect of allocation method on CF the model was adapted. The following methods were added:, physical causality, protein content, energy content, emergy content, mass of liveweight (LW), and mass of carcass weight (CW). System expansion was also used.

Table 4. The effect of method of allocating GHG emissions in CO_2-equivalents (eq) between milk and meat on the carbon footprint of both products for the bottom third, mean and top third of Irish dairy farms in terms of gross margin/ha.

Allocation method	GHG allocated to milk			Carbon footprint of milk ($kg\ CO_2$-eq/kg FPCM)			Carbon footprint of meat ($kg\ CO_2$-eq/kg LW)		
	Bottom	Average	Top	Bottom	Average	Top	Bottom	Average	Top
Mass CW	98%	99%	99%	1.59	1.40	1.29	1.59	1.40	1.29
Mass LW	97%	97%	98%	1.57	1.38	1.27	1.57	1.27	1.27
Emergy	94%	95%	96%	1.52	1.35	1.25	3.01	5.35	4.94
Protein content	91%	93%	94%	1.48	1.32	1.22	8.44	7.52	7.04
Energy content	91%	93%	94%	1.47	1.31	1.22	8.76	7.83	7.26
Economic	83%	86%	88%	1.35	1.22	1.14	8.11	7.47	7.05
Physical causality	80%	84%	86%	1.29	1.19	1.13	9.77	8.58	7.86
System expansion	62%	64%	66%	1.01	0.90	0.86	13.05	12.57	12.21

Results and Discussion

Table 1 illustrates the effect of different allocation methods on the CF in CO_2 equivalents for both milk and meat. The results highlight, that the percentage of GHG emissions allocated to milk varied from 62%-99%. As a result, there was a wide range in the CF of fat and protein corrected milk (FPCM) for each farm group (Table 1). System expansion had an allocation factor range for FPCM from 62–66% with a resultant CF range of 12.21–13.05 kg CO_2-eq/kg CW, which was the greatest resulting CF for meat. Economic allocation, the preferred approach to allocation by PAS 2050 after system expansion, had an allocation factor range from 83–88% (FPCM) with a resulting CF range of 7.05–8.11 kg CO_2-eq/kg LW. It can also be said that economic allocation is also in keeping with option two of ISO (2006) that the relationships referred to here should be causal in nature. However, when adopting economic allocation, the accuracy of the results, are subject to price fluctuations. Mass of LW allocation has an allocation factor range from 97–98% with a resulting CF range of 1.27–1.57 kg CO_2-eq/kg LW, which was the lowest for meat.

Conclusions

Milk or meat CF results are not comparable when different allocation methods are used. Thus, a uniform approach needs to be agreed.

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RMIS Project No. 6409

Effect of stocking rate and animal genotype on milk production performance in spring calving dairy cows

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Introduction

The biological and financial efficiency of grass-based milk production is uniquely dependent on achieving a balance between the competing objectives of generous feeding to achieve high production per animal and restricted feeding to achieve increased grass utilisation per hectare. The imminent removal of milk quotas provides significant opportunity for Irish dairy farmers to increase milk production and increasing stocking rate (SR) is recognised as one avenue to increased productivity post quotas (McCarthy *et al.*, 2011). Previous studies have indicated that higher SRs are associated with increased grazing severity and a reduction in daily herbage allowance and dry matter intake per animal (McCarthy *et al.*, 2014). Consequently, foremost among the choices facing Irish dairy farmers is the selection of a dairy cow with the capability for high milk productivity within integrated higher SR and increasingly feed restricted grass-based production systems post quotas. In this regard, previous studies have highlighted beneficial effects of smaller crossbred dairy cattle in both production and health traits (Prendiville *et al.*, 2011). The objective of this experiment was to investigate the existence of potential interactions of SR and animal genotype (B) on milk production in spring calving grass-based dairy systems.

Materials and Methods

Two hundred and seventy eight dairy cows (68 Holstein-Friesian (HF) cows and 71 Holstein-Friesian x Jersey crossbred (JX) in both 2013 and 2014, respectively) were randomly assigned, within breed and across parity, to one of three stocking rate treatments based on achieving a similar body weight per hectare (BW/ha) for each B. The three SRs were; low (LSR; 1,200 kg BW/ha), medium (MSR; 1,400 kg BW/ha) and high (HSR; 1,600 kg BW/ha). Milk yield was recorded daily and milk constituents weekly. Body weight and body condition score (BCS) were measured fortnightly. 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 LSR, MSR and HSR, respectively. Least square means for each SR and B group were estimated using mixed models. The dependent variables of interest included milk and fat plus protein (milk solids; MS) yield per cow and per hectare. Fixed effects in the model included production year, calving date, SR, B and parity. Cow was included as a random effect.

Table 1. Effect of stocking rate (kg bodyweight/ha) and animal genotype (B) on milk production.

Stocking rate (SR)	Low		Medium		High			P-Value	
Animal genotype (B)	HF	JX	HF	JX	HF	JX	SEM[1]	SR	B
Post-grazing height (mm)	44.5	45.0	38.9	39.2	35.1	35.3	0.07	0.001	
Herbage allowance (kg DM/cow/day)	18.5	18.1	14.1	13.3	13.0	12.2	0.49	0.001	0.1
Cumulative production									
Milk yield (kg/cow)	5,441	5,052	5,293	4,866	5,020	4,734	101.1	0.01	0.001
(kg/ha)	13,013	12,727	15,432	14,848	16,564	16,138	301.7	0.001	0.1
MS[2] (kg/cow)	446	454	435	438	410	424	7.3	0.001	
(kg/ha)	1,067	1,145	1,269	1,338	1,354	1,445	22.0	0.001	0.001

SEM[1] = Standard error mean,–MS[2] = Milk solids (fat plus protein)

Results and Discussion

Stocking rate and breed had significant effects on grazing characteristics and milk production, while there was no significant SR × B interaction (Table 1). Based on a greater daily herbage allowance, LSR achieved the greatest daily and cumulative milk and MS yields per cow whereas HSR was least. In contrast, HSR achieved the greatest milk and MS yields per hectare, whereas LSR was least. At similar live weight/ha, the HF cows produced greater milk yields per cow at each SR compared to JX. In contrast and based on a lower daily herbage allowance, JX produced greater MS yields per ha at each SR. The absence of an SR × B interaction indicates that at similar BW per hectare, the milk production response to a change in SR was similar for HF and JX animals.

Conclusions

The results of this study are consistent with previous studies (Coffey *et al.*, 2014) and indicate that MS production per hectare will be maximised by the selection of JX crossbred dairy cattle and higher SR grazing systems on Irish dairy farms post quotas.

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