

Agricultural Research Forum 2015

9th & 10th March

Incorporating the Annual Research Meeting of the

Irish Grassland and Animal Production Association

(41st Annual Research Meeting)

Irish Tillage and Land Use Society

(23rd Annual Research Meeting)

Soil Science Society of Ireland

(38th Annual Research Meeting)

Irish Agricultural Economics Society

(15th Annual Research Meeting)

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Summary of Papers

Presented at the

Agricultural Research Forum 2015

Incorporating the

Irish Grassland and Animal Production Association

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Irish Tillage and Land Use Society

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Held at Tullamore Court Hotel

Monday and Tuesday, 9th & 10th March 2015.

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Programme Agricultural Research Forum 2015

Monday 9th March 2015	<i>Arrival & Tea/Coffee</i>	
	Room D.E. Williams III	Room D.E. Williams II
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11:00-13:15	Session 5A Systems / Knowledge Transfer/ Milk Technology Chairperson: Dr Padraig French	Session 5B Animal Health & Welfare II Chairperson: Dr Laura Boyle
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Monday 9th March 2015

Session 1A: Fertilisers / Soils / Environment

Venue D.E. Williams III

Chair Dr David Wall

Teagasc, Johnstown Castle Environmental Research Centre, Co. Wexford

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Chair Dr Riona Sayers

Teagasc, AGRIC, Moorepark, Fermoy, Co. Cork

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Chair Dr Owen Fenton

Teagasc, Johnstown Castle Environmental Research Centre, Co. Wexford

Session 2A: Soils

Venue D.E. Williams III

Chair Dr Owen Fenton

Teagasc, Johnstown Castle Environmental Research Centre, Co. Wexford

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14:00 “The Irish Soil Information System”, Dr Rachel Creamer

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Chair Dr Owen Fenton

Teagasc, Johnstown Castle Environmental Research Centre, Co. Wexford

Session 2B: Grassland

Venue D.E. Williams II

Chair Dr Deirdre Hennessy

Teagasc, AGRIC, Moorepark, Fermoy, Co. Cork

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Monday 9th March 2015

Session 3A: Livestock Systems

Venue D.E. Williams III

Chair Dr Paul Crosson

Teagasc, AGRIC, Grange, Dunsany, Co. Meath

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Monday 9th March 2015

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Venue D.E. Williams II

Chair Dr Noirin McHugh

Teagasc, AGRIC, Moorepark, Fermoy, Co. Cork

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Tuesday 10th March 2015

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Venue D.E. Williams III

Chair Dr Padraig O'Kiely

Teagasc, AGRIC, Grange, Dunsany, Co. Meath

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Tuesday 10th March 2015

Session 4B: Reproduction - Cattle

Venue D.E. Williams II

Chair Dr Sean Fair

Faculty of Science and Engineering, University of Limerick, Limerick

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Tuesday 10th March 2015

Session 5A: Systems / Knowledge Transfer/ Milk Technology

Venue D.E. Williams III

Chair Dr Padraig French

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Tuesday 10th March 2015

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Chair Dr Laura Boyle

Teagasc, AGRIC, Moorepark, Fermoy, Co. Cork

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Chair Dr Michael O'Donovan
Teagasc, AGRIC, Moorepark, Fermoy, Co. Cork

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Tuesday 10th March 2015

Session 6B: Animal Breeding / Molecular Biology

Venue D.E. Williams II

Chair Dr Paul Cormican

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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 suppressed 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% ¹⁵N 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 ¹⁵N 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

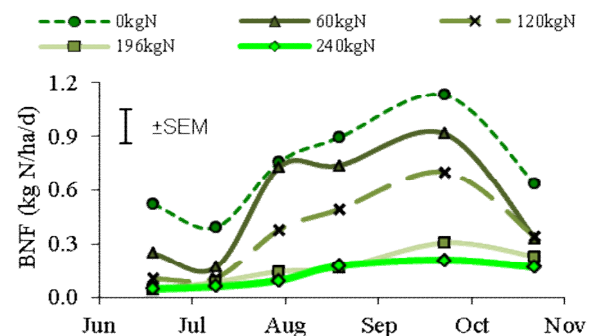


Fig. 1. Effect of N fertiliser rate and grazing rotation on clover biological nitrogen fixation (BNF) rate.

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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Comparing fertiliser nitrogen alternatives to calcium ammonium nitrate: the impact on nitrogen uptake and fertiliser recovery in grassland

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Introduction

Substituting calcium ammonium nitrate (CAN) with urea-based nitrogen (N) fertiliser limits the soil residence period of nitrate, the major substrate for nitrous oxide (N₂O) loss via denitrification. Approximately 12% of Ireland's national emission of greenhouse gases is N₂O. Fertiliser N selection offers a potential opportunity to maintain N input rates but mitigate N₂O losses. Urea is susceptible to ammonia (NH₃) volatilisation but this risk can be managed using a urease inhibitor. The aim of this study was to evaluate the effects of switching from CAN to urea, or urea with the urease inhibitor N- (n-butyl) thiophosphoric triamide (n-BTPT) and/or the nitrification inhibitor dicyandiamide (DCD) on N uptake and apparent N fertiliser recovery (AFR).

Materials and Methods

This is a two year experiment that commenced in March 2013 at three permanent pasture sites; poorly drained (Hillsborough), moderately drained (Johnstown), well drained (Moorepark). The experiment was a randomised complete block design with 5 replicates. The treatments were CAN, urea, urea with the urease inhibitor n-BTPT, urea with the nitrification inhibitor DCD and urea with both the urease inhibitor n-BTPT and the nitrification inhibitor DCD, all at 200 kg N ha⁻¹ yr⁻¹, and a zero N control. The DCD was incorporated into the fertiliser granule at manufacture at a rate of 10% DCD on a urea-N weight basis and the n-BTPT was coated onto the exterior of the granule at a rate of 500 ppm n-BTPT on a urea weight basis. The fertiliser treatments were surface broadcast by hand to the experimental plots. The annual fertiliser N rate was applied in five equal splits. Grass yield and N uptake were measured at the end of each fertiliser application cycle. A generalised linear mixed modelling approach was used to analyse the data using the PROC GLIMMIX procedure of SAS 9.3 (SAS, 2011). The sources of variation in the model were fertiliser N formulation and site. Mean comparisons were by F-protected L.S.D. test. Block was treated as a random effect.

Table 1. Statistical analysis of grass N uptake and apparent fertiliser recovery (AFR) showing overall significance levels using Type III Tests of fixed effects

Effects	Grass N uptake	AFR
Formulation	P<0.001	P<0.001
Site	P<0.001	P<0.001
Formulation X Site	P<0.01	P=0.28

Table 2. Grass N uptake at three sites in 2013 at 200 kg N ha⁻¹. Treatments with different letters are different according to F-protected LSD test (P<0.05), pooled SEM = 9.34.

Fertiliser formulation	Moorepark N uptake (kg N ha ⁻¹)	Johnstown N uptake (kg N ha ⁻¹)	Hillsborough N uptake (kg N ha ⁻¹)
Control	184 d	189 b	107 c
CAN	357 ab	313 a	202 ab
Urea	339 bc	295 a	208 a
Urea + n-BTPT	374 a	318 a	217 a
Urea + DCD	325 c	294 a	185 b
Urea + n-BTPT + DCD	332 bc	296 a	214 a

Table 3. Mean AFR for three sites in 2013 at 200 kg N ha⁻¹. Treatments with different letters are different according to F-protected LSD test (P<0.05), pooled SEM = 3.2.

Fertiliser formulation	AFR%
CAN	65 ab
Urea	60 bc
Urea+n-BTPT	71 a
Urea+DCD	54 c
Urea+n-BTPT+DCD	60 bc

Results and Discussion

Statistical analysis of grass N uptake (Table 1) shows a significant formulation x site interaction, consequently the data are presented for each individual site (Table 2). No significant difference in N uptake between CAN and the urea based formulations was detected at any of the sites. Urea DCD had significantly lower N uptake than urea n-BTPT at two sites. Statistical analysis of AFR (Table 1) showed no formulation x site interaction (P=0.2799), the mean of the AFR for the three sites is presented in Table 3. No significant difference in AFR between CAN and the urea based formulations was detected apart from urea DCD which had significantly lower AFR than CAN. Urea n-BTPT had significantly higher AFR than the three other urea based treatments. Switching fertiliser from CAN to any of the urea based formulations had no significant impact on N uptake. However, the choice of urea formulation could result in reduced N recovery relative to CAN. Apparent fertiliser recovery for urea n-BTPT compares favourably with CAN.

Conclusion

Urea-based N fertiliser with or without inhibitors were viable alternatives to CAN in terms of N uptake. However, in terms of AFR, urea with DCD performance was significantly lower than CAN.

Acknowledgements

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Evaluating the effect of fertiliser nitrogen type on grain yield in spring malting barley

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Introduction

The dominant nitrogen (N) fertiliser used on arable crops in Ireland is calcium ammonium nitrate (CAN). CAN contains 50% nitrate and 50% ammonium. Ammonium rapidly converts to nitrate in the soil. While readily available to plants, nitrate can be lost to the environment by leaching and denitrification representing an economic loss. There is potential for urea to be used to reduce these N losses. However N can be lost from urea through ammonia volatilisation. Inhibitor technologies, which are additives that slow the loss of N, can be used to reduce these N losses (Watson *et al.*, 2009). The urease inhibitor n-butyl thiophosphoric triamide (n-BTPT) slows urea hydrolysis and reduces ammonia volatilisation. The nitrification inhibitor dicyandiamide (DCD) slows the conversion of ammonium to nitrate and potentially reduces leaching and denitrification losses. Reducing these losses retains N in the soil for plant uptake representing a potential economic benefit to farmers. The objective of this study was to assess the effect of supplying crop N as CAN, Urea and Urea with inhibitors on spring barley grain yield.

Materials and Methods

Two sites with contrasting drainage characteristics and cropping history were used, a free-draining long term arable and a moderately-draining short-term arable site. The experiment was conducted in 2013 and 2014 using the spring barley cultivar “Sebastian” (sown in mid-April). The experimental design was a randomised complete block, with five replicates. The fertiliser treatments were CAN, Urea, Urea+n-BTPT, Urea+DCD, Urea+n-BTPT+DCD at 150 kg N ha⁻¹ and a control. Fertiliser was applied in two application timings 30 kg N ha⁻¹ at sowing (Mid-April) and 120 kg N ha⁻¹ during early tillering (Mid-May). The crops from both sites were harvested in August and grain yield and quality was determined. A generalised linear mixed model was used to analyse the data using the PROC GLIMMIX procedure of SAS 9.3. The sources of variation in the model were fertiliser N type, site and year. Block was treated as a random effect. Mean comparisons were by F-protected L.S.D. test.

Results and Discussion

The three way interaction of fertiliser N type x site x year was significant ($P < 0.01$). Grain yield from the unfertilised control plots was significantly higher at the short-term arable site ($P < 0.01$) with a yield of 6.5 t ha⁻¹ compared with 3.5 t ha⁻¹ at the long-term site for 2013. This difference is associated with organic manure application history at the short-term site. All N fertiliser treatments gave significantly higher grain yields than the control at all sites and years. Fertiliser N type did

not significantly affect grain yield (Fig. 1). CAN and urea based treatments produced similar yields which was unexpected as we know that urea is susceptible to N loss via volatilisation.

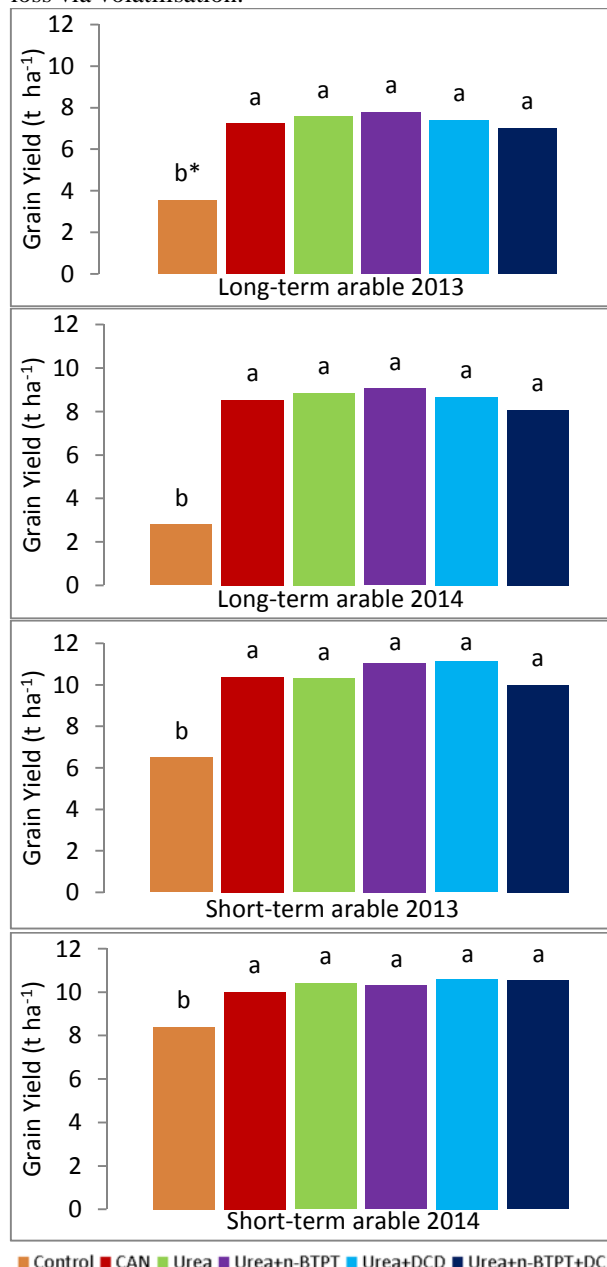


Fig. 1. Grain yield for both sites for 2013 and 2014

*Different letters (within graphs) represent significant difference between treatments at $P < 0.05$ by LSD test

Conclusions

CAN and urea produced comparable grain yield in these trials. However, losses of N from urea can occur through volatilisation, therefore the inclusion of a urease inhibitor may be important to mitigate these losses. Further understanding of ammonia losses from urea are needed to give assurance that urea will consistently maintain yields compared with CAN.

Acknowledgements

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Development of a phosphorus critical source area index using high resolution digital elevation models

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Introduction

Critical source areas (CSAs) of phosphorus (P) losses to surface waters are high risk areas where large P sources coincide with high transport potential via surface runoff. P Index (PI) tools are used to identify CSAs at the field scale by estimating the risk of P loss using P source and transport factors. Transport factors typically include distance-to-stream as a proxy for runoff risk. However, as topography is a dominant factor controlling runoff-generating-areas and pathways, topographic indices provide stronger correlations and may be more appropriate transport factors within PIs (Marjerison *et al.*, 2011). Furthermore, erosion factors typically use field scale estimates of slope length and steepness in the Universal Soil Loss Equation (USLE) which ignores sub-field topographic variability. The objectives of this study were (i) to develop a PI that accounted for the role of topography when estimating P transport potential, and (ii) to identify CSAs at the sub-field scale.

Materials and Methods

A PI was developed using seven source, mobilisation and transport factor datasets in four agricultural catchments within the Teagasc Agricultural Catchments Programme (Table 1). Three topographically based transport factors utilised 2 m resolution digital elevation models (DEMs) derived from Light Detection and Ranging (LiDAR); runoff risk derived from the Topographic Wetness Index (TWI), hydrological connectivity derived from the Network Index (NI) by Lane *et al.* (2004), and erosion risk derived from the Unit Stream Power Erosion Deposition (USPED) model by Mitsova *et al.* (1996). USPED integrates USLE factors but replaces slope length and steepness with DEM-derived upslope contributing area.

Table 1. PI source/transport factors and datasets

Factor type	Factor	Topographic index/model used	Dataset	Year
Source	Soil test P	-	Field samples	2013
Mobilisation	Water soluble P	-	Field samples	2011
Transport	Runoff risk	TWI	2 m DEM	2011
Transport	Hydrological connectivity	NI	2 m DEM	2011
Transport	Erosion risk	USPED	2 m DEM	2011
Transport	Soil drainage class	-	USLE data	2013
Transport	Sub-surface artificial drainage	-	Soil type	2011
Transport			Fieldwork maps	2013

A PI soil drainage class factor accounted for runoff potential from different soil types, and presence of subsurface artificial drainage increased subsurface P loss risk. For all factors, values were categorised and assigned relative risk scores (ranking P loss potential) in ArcGIS, and datasets rasterised at 2 m cell resolution. The sum of the product of weighted source, mobilisation and transport factors for each runoff and erosion pathway was used to calculate total risk scores.

Results and Discussion

The new topographically based PI mapped in-field risk variability and hence sub-field scale CSAs (Fig. 1). Furthermore, P loss pathways were also indicated. This could significantly improve the targeting of mitigation measures such as at agri-environmental schemes and riparian buffers at critical downslope locations.

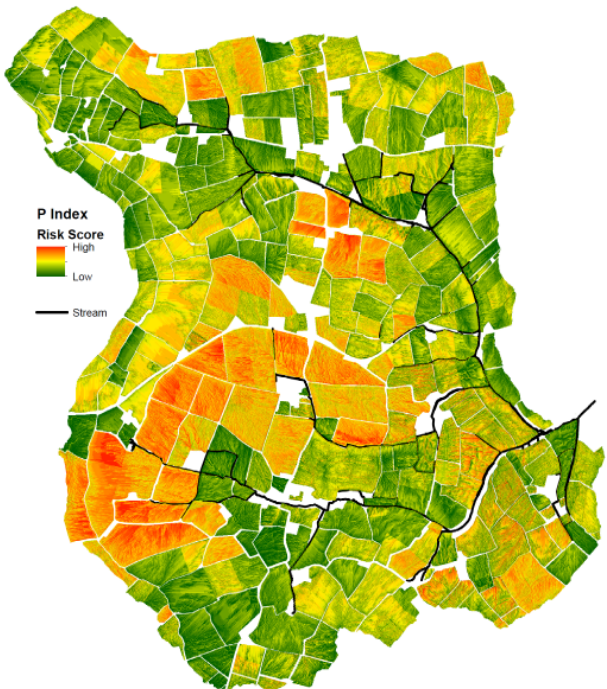


Fig. 1. PI risk map identifying CSAs (in red)

Conclusions

The use of topographic transport factors within PIs using LiDAR DEMs allows topographic control on hydrology and P losses to be considered, and sub-field CSAs to be identified. Catchment and sub-catchment scale validation of PI risk scores and components will be undertaken using measured water quality data at catchment outlets and snapshot sites.

Acknowledgements

We thank the Department of Agriculture, Food and the Marine and the Teagasc Walsh Fellowship Scheme for funding, and Dr Faruk Djodjic from SLU, Uppsala, Sweden for USPED training.

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Maintenance P applications for sustainable silage grass production in Northern Ireland

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Introduction

According to RB209 8th Edition (DEFRA, 2010), phosphorus (P) applied to cut grassland at the target soil P index is simply a maintenance dressing designed to replace that removed in silage crops. However, it is important to note that DEFRA recommendations are based on field trials conducted in England and Wales between 1970 and 1988, where maximum yields of swards rarely exceeded 12 t DM ha⁻¹ yr⁻¹. Not only are the results of these trials out of date, since modern higher yielding varieties of perennial ryegrass are now available, but the cutting interval was only 4-6 weeks, i.e. appreciably shorter than the 6-8 week cutting interval for silage crops in Northern Ireland (NI). The objective of this study was to evaluate the maintenance P requirement of 3-cut silage crops in NI using data from locally conducted field experiments, and to test its suitability, province-wide, for sustaining soil P status.

Materials and Methods

Dry matter (DM) yield and P offtake data were available for 4 field experiments at Hillsborough, three (W₁, W₂ & B) on clay loam soils and one (F) on a sandy clay loam, and all at soil Olsen-P index 3. The experiments had fully randomised block designs and tested sward responses to multiple rates of N, when basal dressings of P, potassium and sulphur were applied in accordance with RB209 recommendations, except on site F where no P was applied. They were conducted in different years (F:2001, B:2007, W₁:2010 & W₂:2011) and on ryegrass swards of different ages (W₁:1 yr, W₂:2 yrs, B:3 yrs & F:10 yrs). Quadratic relationships were fitted to DM yield (or P offtake) versus N rate responses. Information on P management (i.e., manure P plus fertilizer P inputs per annum) and on soil Olsen-P status were available for 10 silage fields on 8 dairy farms from four counties in NI (with grass growing conditions representative of most of NI), initially at the target soil P index of 2⁺ (21-25 mg Olsen-P l⁻¹), which had been managed continuously for 3 cuts of silage over 3 or 4 years. Out of > 300 silage fields only 10 were found suitable for this exercise, since others within the required Olsen-P (target) index 2⁺ range, had either been ploughed and reseeded during the monitoring period, or else had had varying numbers of cuts taken per year. Soil P levels in each of the 10 fields at the end of the monitoring periods, were used to evaluate average annual changes in soil Olsen-P. The latter changes were then regressed on the difference between average annual rates of P applied to each field and the RB209 P recommendation for 3 cuts of silage.

Results and Discussion

As shown in Fig. 1a, DM yields peaked at between 14 and 17 t DM ha⁻¹; with highest yields for youngest swards (W₁ & W₂). However, regardless of sward age, P offtakes peaked at between 40 and 48 kg P ha⁻¹ i.e. some 5 to 13 kg P ha⁻¹ more than the P offtake assumed in

RB209 (35 kg P ha⁻¹) for 3 cuts of silage. If swards are removing more P than will be replaced according to the recommendations, then adhering to the latter will gradually deplete soil P reserves and undermine the sustainability of silage grass production. To test this hypothesis, 10 silage fields (from across NI), initially at soil P index 2⁺, and managed continuously for 3 cuts of silage for 3 or 4 years but with varying P inputs, were re-soil tested to see what changes had occurred in soil P.

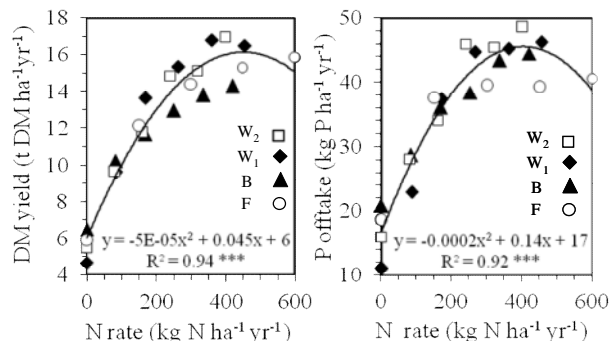


Fig. 1. (a) Annual DM yield by swards versus N application rate, and (b) annual P offtakes versus N application rate, with fitted quadratic curves

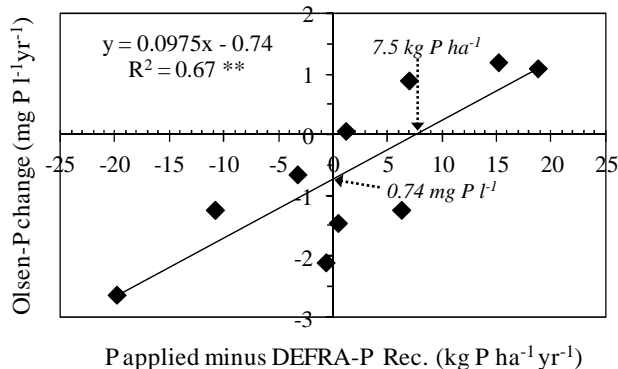


Fig. 2. Average annual change in Olsen-P in silage fields managed continuously for 3-cuts of silage versus the difference between P applied and P recommended

As shown in Fig. 2, adhering to P recommendations (i.e. zero on the abscissa) for 3-cut silage crops on soils at the target P index of 2⁺, resulted in an annual 0.74 mg P l⁻¹ decline in soil Olsen-P, whereas Olsen-P was maintained at 'steady-state', i.e., neither increasing nor decreasing with time, when 7.5 kg P ha⁻¹ yr⁻¹ more than the RB209 recommendation was applied. It would appear therefore that 3-cut silage swards in NI are removing more than the maintenance P requirement allowed in RB209. It is worth noting, that the Republic of Ireland allows 40 kg P ha⁻¹ as a maintenance P dressing for 3 cuts of silage (Coulter and Lalor, 2008), which is 5 kg P ha⁻¹ greater than that allowed in RB209.

Conclusion

Our results indicate that RB209 P recommendations for 3 cut-silage crops should be increased by about 7.5 kg P ha⁻¹ yr⁻¹ to fully allow for the P removed in silage crops and to prevent unsustainable declines in soil Olsen-P.

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Phosphorus loss from groundwater driven agricultural river catchments

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Introduction

Mitigating diffuse phosphorus (P) delivery to rivers, lakes and estuaries in the agricultural landscape is important for ecological quality management. In order to plan this management, it is useful to identify and quantify dominating P transfer pathways and their variation in the landscape and in time. While P is anticipated to mainly be transferred to rivers episodically via quick surface pathways, there have been studies showing that leaching may elevate the concentrations of dissolved P in groundwater and P loss in rivers may originate from groundwater (Holman *et al.*, 2008; Mellander *et al.*, 2012). The aim of this study was to quantify P transfer pathways *via* groundwater in two Irish groundwater driven catchments (*ca.* 10 km²) with intensively managed land.

Materials and Methods

One catchment (Grassland) is located in Co. Cork and uses 88.5% of its land for dairy production. The soils are mostly well-drained brown earths overlying sandstone and mudstone. The other catchment (Arable) is located in Co. Wexford and uses 54% of its land for continuous crop production. The soils are mostly well drained brown earths overlying slate and silt-stone. An end-of-catchment estimation of total P [TP] and total reactive P [TRP] transfer pathways, divided into *quick-flow* (surface runoff and drain-flow), *interflow* (lateral flow in unsaturated zone), *slow-flow* elevated during the event (shallow groundwater) and *slow-flow* as baseflow (deep groundwater), was made using Loadograph Recession Analysis (Mellander *et al.*, 2012) on five years of high frequency data of river discharge (Q) and P concentration. The method was validated with dissolved reactive P (DRP) concentrations in groundwater from four years of monthly sampling.

Results and Discussion

Total P loads leaving the catchments were low although the Grassland catchment had close to three times higher annual P loss than the Arable catchment (0.661 kg ha⁻¹ yr⁻¹ and 0.228 kg ha⁻¹ yr⁻¹). This was largely a signal of rainfall-to-discharge and the form of P correlated to the runoff coefficient in a similar manner for both catchments. The spatial five-year average DRP concentrations in the groundwater were similarly low in the two catchments (0.019 mg l⁻¹ and 0.016 mg l⁻¹ respectively). However, in the groundwater of the Grassland catchment DRP concentration was heterogeneous, with some zones in the landscape (near-stream and upslope shallow groundwater) where concentrations of 0.035 mg TRP l⁻¹ were exceeded throughout the monitored period. This is expected in

grasslands due to more preferential flow paths and heterogeneous organic nutrient loading than arable land where preferential flow paths are less occurring (Kramers *et al.*, 2012). There was a substantial proportion of P loss *via* groundwater. In the Grassland catchment 83% of the discharge was generated by groundwater *via* *slow-flow* pathways (Table 1) and transferred 59% of TRP (39% of particulate P (PP)). The *quick-flow* pathways generated 13% of the discharge and transferred 35% of TRP (56% of PP). Remaining loss was from *interflow* (6%). In the Arable catchment 64% of the discharge was generated by groundwater and transferred 50% of TRP (16% of PP). The *quick-flow* pathways generated 32% of the discharge and transferred 42% of TRP (83% of PP). Remaining flux was from *interflow* (8%). Elevated P in groundwater contributed to P loss and highlighted the implications for nutrient management in terms of transfer pathways and longer lag times between fertilizer application and delivery to the stream. In the Grassland catchment there was also a potential for elevated P loss from incidental P *via* surface runoff from near-stream fields in summer events, while in the Arable catchment drain-flow contributed substantially with TRP loss *via* *quick-flow* in winter events.

Table 1. Average proportion (%) of water flow (Q) and total reactive phosphorus (TRP) transfer pathways for the closed periods (15th October – 12th January) 2010-2014.

	Grassland		Arable	
	Q	TRP	Q	TRP
Quick-flow	13	35	32	42
Interflow	4	6	4	8
Slow-flow (elevated)	21	15	13	9
Slow-flow (base)	62	44	51	41

Conclusions

Phosphorus loss *via* *slow-flow* pathways in groundwater needs to be considered when reviewing mitigating strategies in intensively managed groundwater fed catchments. In the two catchments presented here, 50 and 59% of the reactive P was lost *via* shallow and deep groundwater. Such P loss could be minimised by identifying groundwater Critical Source Areas targeted for mitigation of P leaching.

Acknowledgements

This study was part of the Agricultural Catchments Programme, funded by the Department of Agriculture, Food and the Marine. We thank catchment farmers for participation and access to land.

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CO₂ emissions from temperate grassland under elevated soil temperature

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Introduction

In the past century the average Earth surface temperature increased by 0.6°C, and it is predicted to rise 1.5-4.5°C with a doubling atmospheric CO₂ concentration (IPCC, 2013). Climatic warming could potentially stimulate nutrient mineralisation and lengthen the growing season, which would increase plant growth and carbon sequestration. However, it could also accelerate the biospheric metabolism, resulting in a greater release of CO₂ to the atmosphere (Luo *et al.*, 2001). Therefore the goal of this study was to examine the effect of ecosystem warming on ecosystem respiration and net ecosystem exchange of CO₂.

Material and Methods

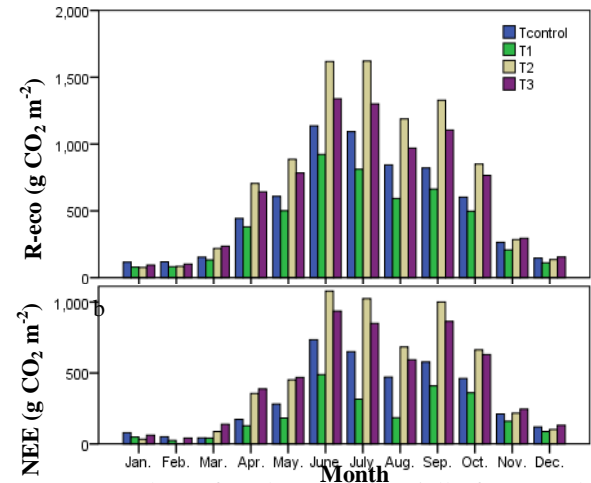
A permanent temperate mixed grassland site of 100 m² on a stagno-fluvic gleysol soil in Giessen, Germany was divided into 16 plots. Each plot was assigned to one of four treatments (+1°C (T₁), +2°C (T₂), +3°C (T₃) above ambient and a control (T_{control})) according to a Latin square design (each treatment once in each row and column). Ceramic infrared heaters at different heights were used to control the temperature increase. Heating started on January 24, 2008. Between March 2013 and February 2014 frequent CO₂ flux measurements were taken using a LI-COR 8150 multiplexer with LICOR LI-8100A Analyser Control Unit (LI-COR biosciences, Lincoln, Nebraska). Both clear and dark chambers were used for the measurements to quantify net ecosystem exchange (NEE) and ecosystem respiration (R-eco). Each month, except for May and January, a measurement campaign, with hourly measurements, was held. The clear chambers were only used in March, April, July and October. In total 32889 valid (R²≥.9) R-eco and 2793 valid NEE measurements were taken. All measurements taken within one hour were considered to be part of the same sequence; in total 2164 sequences were measured. SPSS v22 (R-eco and regression) and SAS v9.4 (NEE) were used for statistical analyses. Average ecosystem respirations per treatment per sequence were compared using repeated measures ANOVA. NEE measurements were compared using a GLIMMIX Procedure (Schabenberger, 2005). Daily NEE and R-eco were modelled according to equation 1 and 2, using half hourly temperature and radiation data and daily soil moisture data. Parameters β₁-β₃ were optimised using parameters for R-eco based on R-eco measurements in months with NEE measurements (R²=.90) to minimise the error induced by an error in the R-eco estimate.

$$R\text{-eco} = \alpha_1 \cdot e^{\frac{308.56}{temp-\alpha_2}} \cdot e^{\frac{(soil\ moisture-\alpha_3)^2}{\alpha_4^2}} \quad (1)$$

$$NEE = R\text{-eco} - \beta_1 \cdot radiation \cdot e^{\frac{(temp-\beta_2)^2}{\beta_3^2}} \quad (2)$$

Results and Discussion

Ecosystem respiration was significantly different under the 4 different treatments (p<0.001). Overall T₁ was lowest while T₂ and T₃ were the highest. Similar patterns were observed for each month. NEE was also significantly different under the four treatments (p<0.001). Again T₂ and T₃ had the highest fluxes. However, more significant differences were found during night-time than during daytime. This suggests that during daytime, increased photosynthetic uptake can generally offset the increased respiration. However respiration is increased 24h a day, and the increased photosynthesis during daytime is not enough to counteract this. Soil temperature, soil moisture and R-eco were correlated. Non-linear regression analyses of R-eco according to equation 1 gave an average R² of .79 (stdev .018). Regression analyses of NEE according to equation 2 gave an average R² of .65 (stdev .090). Fig. 1 shows modelled R-eco and NEE for the different treatments. From this figure it becomes clear that an increase in soil temperature of 2 or 3°C leads to consistently higher R-eco and NEE. A positive NEE



means a net loss of Carbon. So especially for T₂ and T₃ more carbon is lost from the system.

Fig. 1. Monthly modelled R-eco (a) and NEE (b).

Conclusions

A soil temperature increase of 2°C was found to lead to an increase in ecosystem respiration and NEE. This suggests that shifting the proportion of photosynthesis and respiration might lead to an increase in C sink potential in the coming years, but may ultimately result in a lower C sink potential in grasslands with the continuing onset of climate change.

Acknowledgements

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The effect of mole drainage on background N₂O emissions from an unfertilised clay-loam soil

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Introduction

Nitrous oxide (N₂O) is a potent greenhouse gas (GHG) with N₂O flux from soils is primarily produced by microorganisms present in the soil, through multiple processes which are affected by factors such as soil contents of nitrate, moisture, carbon, oxygen and soil temperature. On the present site, the longevity of mole versus gravel-mole drains was demonstrated to be two to three years (Tuohy *et al* 2014). A number of previous studies have shown that modification of the soil physical factors such as increased water filled pore space (WFPS) potentially increase the soil nitrogen (N) fluxes (Bhandral *et al.*, 2007). The aim of the current study was to investigate the effect of mole drainage on N₂O emissions from grassland systems, shortly after installation and after three years.

Materials and Methods

The study site (6.5 ha) comprised clay loam textured soils (>40% clay) with slope of 1.4% and mean perched water table at 1 m below ground level (BGL). A collector drain was excavated 2 m BGL intercepting perched groundwater along the lower axis of the site. The remaining three sides were hydrologically isolated using a ditch 1 m deep and filled with aggregate (100 to 50 mm). The experimental area was divided in four blocks (60 m x 100 m). Each block was sub-divided into four main plots (15 m x 100 m). Each main plot contained two sub-plots (2 x 10 m) near the highest point of the plot (deep WT) and in the lower point of the plot (shallow WT). Each sub-plot was un-grazing and un-fertilized in order to assess the impact of drainage treatments on background N₂O emissions. The four treatments (four replicates) were allocated to the main plots in a randomized complete block design and the sub-plots (WT depth) were a split plot on the main plots. The four treatments were (C) control/un-drained, (WM) mole drainage installed in January 2011, (SM) mole drainage installed in July 2011 and (GM) gravel mole drainage installed in July 2011. N₂O was sampled using the static chamber technique in each sub-plot and analysed by gas chromatography. N₂O emissions were measured on C and WM between June and November 2011 and on all treatments between January and June 2014. Mean daily N₂O emissions were analysed using ANOVA with drainage treatment and WT depth as factors in the model.

Results and Discussion

All drainage treatments controlled water table height post-installation, with the volume differential disappearing after three years. Drainage had little effect

on either water-filled pore space or N₂O emissions, either directly after installation or at the end of their effective lifetime (Table 1, Fig. 1).

Table 1: Percentage WFPS for control and drained treatments

	C	WM	SM	GM	SEM	P value
2011	87.74	81.11	-	-	0.34	***
2014	74.21	67.95	67.44	65.81	0.18	***

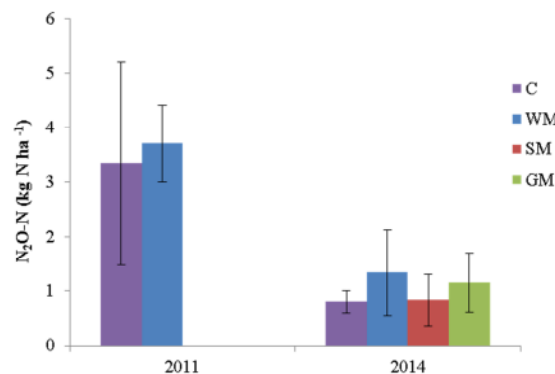


Fig. 1. Cumulative N₂O emissions, over a six month sampling period. Bars indicate the standard error of each mean. Treatments C: control/un-drained, WM: mole of January, SM: mole of July and GM: gravel moles of July.

Cumulative N₂O emissions were 7.06 ± 2.58 kg N₂O-N/ha during the sampling period in 2011 and 4.15 ± 2.02 kg N₂O-N/ha in 2014. Higher emissions in 2011 can be partly attributed to rainfall and higher water-filled pore space (Table 1). Monthly N₂O emissions were positively correlated with the average water-filled pore space between January and June 2014 ($y = 59.15 + 1.43x$, $R^2=0.35$). Hence, N₂O emissions were controlled by water-filled pore space in the top 10 cm of soil, which, in turn were driven by climatic factors such as daily precipitation rather than water table management. For drainage to affect the entire soil profile, moles would need to be coupled with deep collector drains. In such a scenario, the WFPS would be influenced by drainage and thus alter gaseous emissions from the system.

Conclusions

Background N₂O emissions from an unfertilised, heavy wet grassland were high but unaffected by mole and gravel mole drainage. Precipitation was the main driver for emissions as it influenced soil oxic conditions.

Acknowledgements

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The effect of inorganic fertiliser nitrogen application rate and fertiliser type on the yield of forage maize grown under plastic film in a single year and site

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Introduction

Nitrogen (N) is lost from cropping systems by a number of pathways and a single solution to this N loss is unlikely (Binder *et al.*, 2000). One possible solution is synchronisation of nutrient supply with crop demand, reducing opportunities for loss. Maize typically increases nitrogen uptake during the middle of the vegetative growth period. Thus, applying a second application at growth stages V6-V8, approximately 58 days post sowing, may be a strategy of supplying N to meet the demand of the crop. It is thought that $\geq 80\%$ of forage maize in Ireland is sown under plastic film (DAFM, 2014). Lynch (2014) found that there was no additional yield or quality benefits due to a second application of granular N to forage maize grown under plastic film. This is because incomplete film deterioration prevented fertiliser reaching targeted plants compared to when the fertiliser was applied directly to the seedbed. There has been relatively little research on the effect of application rate and fertiliser type of inorganic N for forage maize production. Therefore the aim was to determine the effects of application rate and fertiliser type of N for a second application on production of forage maize.

Material and Methods

The experiment was conducted at UCD Lyons Research Farm, during 2014 on a medium-heavy clay loam soil. The preceding crops were perennial ryegrass and white clover ley (2011-2012) and winter wheat (2013) indicating the soil is index 3 for N according to available guidelines (Coulter and Lalor, 2008). A 4x2 factorial arrangement of treatments with three replicate blocks was used to investigate four annual inorganic N rates (0, 50, 100 and 150 kg N/ha) of which 50% was applied at planting (Urea 460 g N/kg) and 50% at growth stages V6-V8. Maize hybrid P7905 was planted on the 28th April at a seeding rate of 102,200 seeds/ha and sown under degradable plastic film (Samco Yellow 28 pin holed, 7 μ m thick) using the Samco 3-in-1 system (Samco 2200 film laying machine). Individual plots (3.5 m x 20 m) contained four rows of plants. Two fertilizer types were used for the second N application; granular (CAN; 270 g N/kg) and foliar liquid (N16; 160 g N/kg). At the timing of the second application of fertiliser, 94% of all film was degraded. On the 21st October, 5 m lengths of the two centre rows of each plot were harvested and fresh weight yield recorded. A sub sample of chopped whole plant was retained for dry matter (DM) determination. In addition a sub-sample of entire plants was retained for grain weight determination. Data were analysed using a model that

accounted for N rate (separated into linear and quadratic components), N type, N rate x N type, and block.

Results and Discussion

There was no effect of fertiliser type on whole crop yield ($P > 0.05$; SEM 0.83) or grain yield ($P > 0.05$; SEM 0.53) nor was there a N rate x N fertiliser type interaction. There was a tendency towards a linear increase ($P=0.1$; SEM 0.63) in whole crop yield as N application increased, however there was no significant effect on grain yield ($P > 0.05$; SEM 0.42) (Fig 1). A previous study by Ma *et al.*, (2004) found similarly little difference between foliar N or with the equivalent N applied to the soil. The supply of nitrogen to the plant may have been sufficient from the soil N pool to result in no whole crop yield response to N application type.

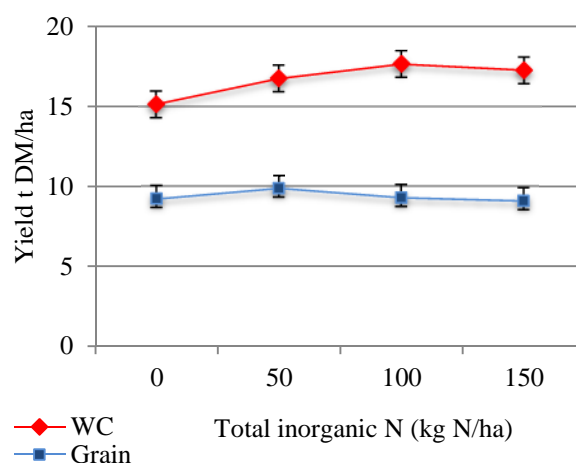


Fig. 1. The least square means of the effect of total inorganic N on whole crop and grain yields (t DM/ha). Error bars represent standard error.

Conclusions

Granular and foliar N as sources of inorganic N for a second application of N resulted in similar whole crop and grain yields. However, there was a tendency towards increased forage maize yield as the rate of N applied at the second application increased. This work was carried out in a single year and site and the study is continuing.

Acknowledgements

Teagasc Walsh Fellowship scheme and The Agricultural Trust.

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Assessing the environmental risks associated with newly revised P application limits for farmland in NI

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Introduction

As an outcome of the review of the 2011-2014 Nitrates Action Programme (NAP) for Northern Ireland (NI), it was agreed that the current target soil P index of 2 for grassland (16-25 mg Olsen-P l⁻¹) be split into a new 2⁺ target range (21-25 mg P l⁻¹) and a 2⁻ 'P-building' range (16-20 mg P l⁻¹), and proportionately higher rates of P applied to grassland in the 2⁻ range to counter P deficiency problems mid-season (Bailey *et al.*, 2014). Under the 2011-2014 NAP, farmers in NI can only apply chemical fertilizer P to land to make up a crop P requirement unmet through the application of organic manures. But under the accompanying Phosphorus Regulations NI (2006), they have to assume that manure P is 100% crop available, which it is not. Consequently, in situations where soil P status is low (index 0 & 1) farmers may not be able to apply sufficient available (chemical & manure) P to meet crop requirements. The availabilities of P in manures were therefore reduced in the 2015-2019 NAP to 50% for liquid manures and 60% for solid manures when applied to farmland of low P status, in keeping with DEFRA (2010). Before the new P recommendations for index 2⁻ grassland or the changes to manure P availabilities could be adopted, their effect on P-loading of land had to be assessed, and the results of the assessment are reported in this paper.

Materials and Methods

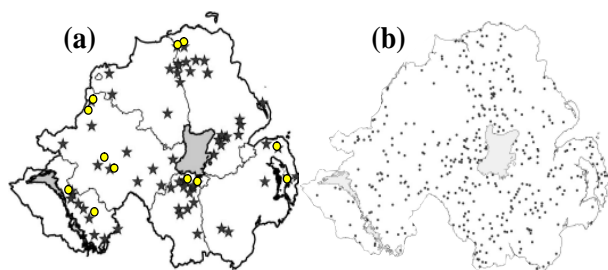


Fig. 1. Locations of grassland fields and/or farms that were soil sampled in 3 separate soil monitoring surveys

Representative soil P index data for lowland farmed grassland in NI were available for 330 silage fields on 67 dairy farms in 2006 (Fig 1a - black stars), 574 silage and grazing fields on 12 dairy farms in 2009 (Fig 1a - yellow circles), 500 grassland fields on 500 farms (> 170 kg organic N ha⁻¹) between 2005 and 2009 (Fig 1b), and from soil samples collected independently by farmers from 889 grassland fields across NI in 2012 (locations unknown), to help estimate the proportions of total farmed grassland (788,000 ha) within different soil P index ranges. Soil P data for 852 arable fields in 2012 were also available to estimate the proportions of the arable area (50,100 ha) within different soil P index ranges. Using this soil P index breakdown information, together with census data on land areas occupied by different crops, and their P requirements as provided by DEFRA (2010), it was possible to estimate the total 'available' P needed to satisfy the needs of arable and

grassland crops in different P index ranges including the new 2⁻ range for grassland. The total amount of manure P available for application to crops was estimated from the numbers of different livestock on NI farms and their associated P excretion rates (DEFRA 2010). The P excreted by grazing animals was ignored as the DEFRA recommendations already allow for this recycled P. Chemical P available for application was also known.

Results and Discussion

Table 1. Percentages of fields in soil P index ranges in separate surveys of arable and grassland fields in NI

Soil P index	Arable	Grassland fields sampled in surveys				
	852 (%)	330	574	500	889	Total
0	2	2	3	2	5	3
1	12	13	10	7	17	13
2 ⁻	30	16	9	10	17	13
2 ⁺		14	12	12	17	14
3	40	38	44	36	32	37
>3	16	17	22	33	12	20

Table 2. Phosphorus requirements of arable and grassland crops in NI and the manure and chemical P resources available to meet these requirements in 2014

Land type [†] (P index)	Total P Req. (t)	Organic Manure			
		Type	Tot P (t)	Avail. (%)	Avail P (t)
A (0/1)	315	Poultry	525	60	315
A (2/3)	511	Poultry	511	100	511
G (2 [§] /3)	5,214	Cattle	5,214	100	5,214
G (0/1)	4051	Poultry	104	60	62
		Pig	595	50	297
		Cattle	2,606	50	1,303
Totals	10,091		9,555		7,702
Chemical P supplied					2,794
Total Available P supplied					10,496
Total available P minus Total P requirement					405

[†] A = Arable and G = grassland; [§] P index 2⁻ and 2⁺

Soil P index breakdown information representative of arable and grassland areas in NI are given in Table 1. For grassland, the relevant breakdown was that totalled over all 4 surveys and given in the final column. As shown in Table 2, the estimated total P requirement of NI farmland is 10.09 kt P yr⁻¹, 8 kt of which can be met by the 'available' P in organic manures and the remainder by the chemical P imported into NI each year. No additional P-loading to farmland is therefore anticipated as a result of changes to the target P index and manure-P availabilities, and hence no additional threat to water quality is expected. Indeed, there appears to be scope for reducing chemical P inputs by 405 t yr⁻¹.

Conclusion

The extra P loading to farmland as a result of changes to the target soil P index and manure-P availability, will effectively be zero, and should not pose any additional threat to water quality. Indeed applying manures to meet the available P requirements of crops on low-P soils, by encouraging better manure distribution on farms, may in fact reduce P-loading to land already enriched with P.

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Assessing the effectiveness of manure export as a strategy for reducing the P loading of grassland soils

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Introduction

It is estimated that almost 50% of farmed grassland soils in Northern Ireland (NI) are above soil P index 2⁺ (21–25 mg Olsen-P l⁻¹) the agronomic optimum. There is a significant body of research demonstrating a strong relationship between soil P concentration and P loss to water, with soils above index 2 posing a significant risk to water quality (Watson *et al.*, 2007). While farmers are currently prohibited from applying chemical P fertiliser to soils above P index 2, this restriction does not apply to organic manures. Consequently, depending on stocking rate, it is possible that Olsen P concentrations in high P index soils may continue to increase regardless of restrictions on chemical P usage. Strategies are needed therefore to sustainably reduce the concentration of P in these high P index soils, and hence the potential for P export to water, without negatively impacting on soil fertility or grass production. The objective of this study was to assess the effectiveness of exporting manure off farms as a strategy for reducing the P status of highly P-enriched grassland (i.e. soil P index 3, 4 or 5), and to investigate the implications, if any, for grass production.

Materials and Methods

The field selected for the study was a 1.65 ha grass silage field at Hillsborough, with a clay loam top soil overlying Silurian shale parent material. Soil samples were collected (0–75mm depth) from the field in February of each year and analysed for Olsen-P and extractable K. At the start of the 6-year study in 1997 the field had a soil P index of 5 (81 mg Olsen-P l⁻¹) and a soil K index of 4 (425 mg K l⁻¹). Fertiliser N was applied annually at 300 kg N ha⁻¹ (no P or K applied) in 3 split applications for 3 cuts of silage in accordance with MAFF (2000) recommendations. Each year the sward was mowed three times, wilted, and the wilted grass subsequently removed in silage wagons. Dry matter (DM) yields per cut were estimated using tare weights for each wagon-load of grass and the DM contents of the grass. Grass samples from each wagon-load were oven-dried at 80°C to determine their DM content, then milled and chemically analysed for mineral elements. Diagnosis and Recommendation Integrated System (DRIS) indices, which provide a very reliable measure of herbage N, P, K and S sufficiency statuses, were calculated for all swards (Bailey *et al.*, 1997). Phosphorus and K offtakes over the 6 year period were estimated from the DM yield and mineral data.

Results and Discussion

Over the 6 years of the study, approximately 235 kg P ha⁻¹ and 1,640 kg K ha⁻¹ were removed from the land in silage crops causing significant declines in soil P and K (Fig 1). In the case of soil P, the decline was fairly steady, i.e. by about 10 mg Olsen-P l⁻¹ yr⁻¹, from 81 mg P l⁻¹ (index 5) in February 1997 to 33 mg P l⁻¹ (index 3) in February 2002, but failed to reach the target index 2⁺

range (21–26 mg P l⁻¹). At least 2 more years of zero-manure P inputs would be required to achieve this goal. Significantly, herbage DRIS P indices at all cuts, including at the close of each season (at 3rd cut), remained optimal, i.e. greater than 5, throughout the 6 year period (Fig 2), and confirmed that grass production had not been curtailed by P deficiency during this time.

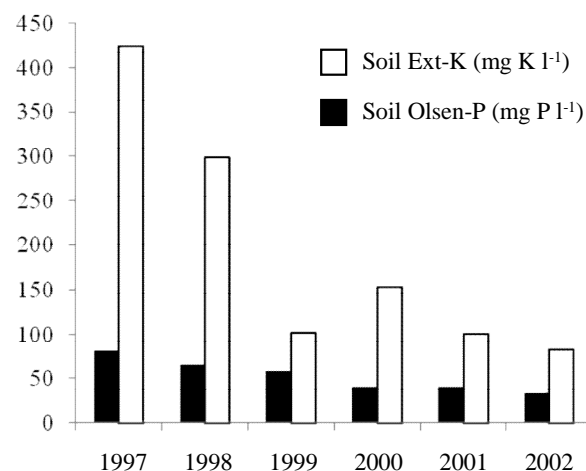


Fig. 1. Soil Olsen-P and K concentrations in February of each year between 1997 and 2002

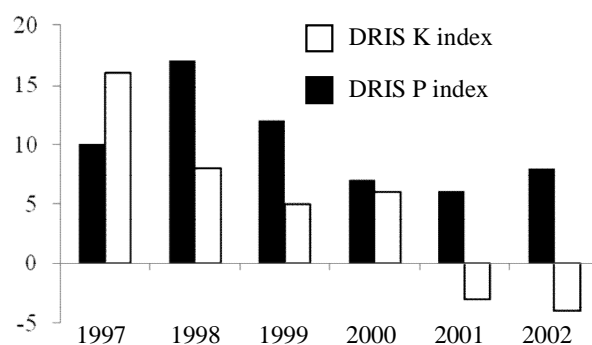


Fig. 2. Herbage DRIS P and K indices at 3rd cut each year between 1997 and 2002

Soil K, however, declined rapidly from 425 mg K l⁻¹ to 100 mg K l⁻¹ (K index 1) within just 3 years, and as a result, after 2000, DM production at 3rd cut (and 2nd cut) was limited by K deficiency, as shown by the negative herbage DRIS K indices (Fig 2). Indeed annual DM production declined from 13.3 t ha⁻¹ in 1999, to 11.2 t ha⁻¹ in 2002; i.e. a 16% reduction due to K deficiency.

Conclusion

Exporting manure rather than recycling it to P-enriched grassland under cutting management is probably the quickest and most effective strategy for lowering the soil P status of this grassland. However, the strategy has a downside in that it may cause an undersupply of K to grassland, leading to suboptimal soil K status and impaired grass production, unless expensive fertiliser K is purchased to replace the K exported in manure.

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Suspended sediment fluxes in five intensive agricultural river catchments

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Introduction

Soil erosion and sediment loss from land can decrease the chemical and ecological quality of freshwater resources. Prediction of soil erosion risk from agricultural land is, however, complicated by physical catchment characteristics such as topography, soil erodibility, connectivity and climate. Assessment of sediment loss magnitudes in relation to a range of agricultural settings is an important step to improve understanding of critical transfer periods and develop evidence-based and cost-effective management strategies. The aim of this study was to quantify the amount of sediment exported from five river catchments with different agricultural land uses over multiple years of analysis. A secondary aim was to investigate trends between catchments in relation to physical and land use characteristics to produce a conceptual model of sediment loss in Irish agricultural catchments.

Materials and Methods

Sediment data were collected in five (3–11 km²) intensive agricultural river catchments in Ireland referred to here as Grassland A (GA), Grassland B (GB), Grassland (GC), Arable A (AA) and Arable B (AB). All catchments have agricultural utilisable land areas of >90%. Physical and land use characteristics are summarised in Table 1. High-resolution suspended sediment concentration data (SSC - using a calibrated turbidity proxy) and discharge data were measured at the catchment outlet and combined to estimate suspended sediment yield (SSY – t km⁻² yr⁻¹). Three hydrological data years were analysed at GA and GC (2010–2013); four years data were available at GB, AA and AB (2009–2013). Average annual SSY estimates used data from 2010–2013 in all five catchments.

Table 1. Characteristics of five study catchments

	Size (km ²)	Median slope (°)	Dominant soil drainage class	Land use (% of utilised area)
GA	7.9	4	Well	95% grassland 5% arable
GB	11.5	3	Poor	85% grassland 15% arable
GC	3.3	6	Moderate	94% grassland 6% arable
AA	11.2	3	Well	42% grassland 58% arable
AB	9.4	3	Poor	60% grassland 40% arable

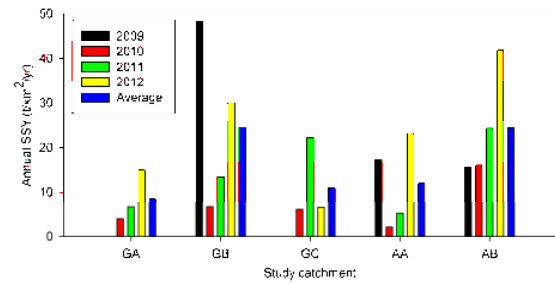


Fig. 1. Annual SSY at five study catchments

Results and Discussion

Average annual SSYs were highest in poorly drained catchments: GB and AB, than those with well drained soils: GA and AA (Fig. 1). The AB catchment, with 25% more arable land than GB had a third higher average SSY despite similar soil drainage characteristics. Catchments which combine poorly-drained soils (where low infiltration capacities readily establish overland flow during rainfall events) and land use dominated by row crops (with extended periods of bare ground through the tillage cycle) are at greatest risk of field-scale soil erosion. Inter-annual variability of annual SSY within catchments was significant; GA 50–188%, GB 28–120%, GC 50–183%, AA 17–142%, AB 67–175%, showing that during a single year, relatively high sediment yields may also feature in grassland catchments. These SSY results combined with catchment characteristics (Table 1) show that sediment loss risk can be generalised based on soil drainage class and land use, this concept is summarised in Fig. 2.

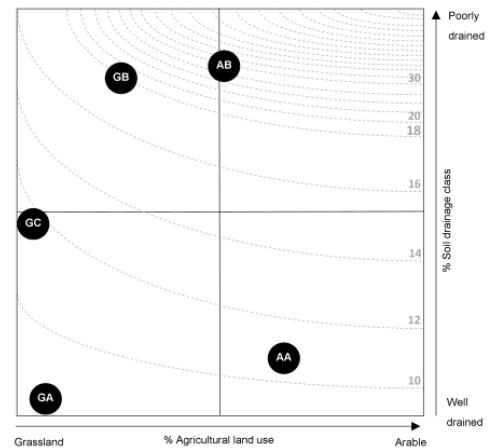


Fig. 2. Conceptual model of SSY (contours; t km⁻² yr⁻¹) according to land use and soil drainage characteristics

Conclusions

Sediment losses from five intensive agricultural catchments with a range of land uses showed that poor soil drainage increased SSY, and, within a particular soil drainage class, SSY was greater where the percentage of arable land use was larger. Effective soil erosion and sediment management should address catchment specific characteristics.

Acknowledgements

This study was funded by the Walsh Fellowship Programme and the Agricultural Catchments Programme (funded by the Department of Agriculture, Food and Marine). We acknowledge support from the farmers and landowners of the study catchments.

Kinetics of anaerobic co-digestion of pig manure and food waste

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Introduction

There is a growing demand for technologies which can reduce greenhouse gas (GHG) emissions from agriculture. There is also a demand for alternatives to landfilling of domestic organic waste. Anaerobic co-digestion of pig manure (PM) and food waste (FW) has the potential to address these demands by providing a means to generate renewable energy which can offset GHG emissions from the agricultural sector and by providing a new disposal route for organic wastes. This study aimed to assess the specific methane yields (SMY) and digestion kinetics associated with co-digested pig manure (PM) and food waste (FW) in a batch anaerobic digestion assay.

Materials and Methods

Pig manure was obtained from the underground slatted tanks of the finishing unit of a local pig farm. Food waste was collected from the brown bins of six different student residences immediately prior to the establishment of the assays. Batch digestion was performed in triplicate on PM and FW alone, while a 50:50 mix of both (mixed in terms of volatile solids (VS) content) was performed with 6 replicates. Each reactor comprised a 500 ml conical flask with a butyl-rubber stopper with two ports; one for liquid sampling and the other for biogas sampling. Biogas was collected in 1 L gas sampling bags. Biogas volume was measured routinely via a water displacement method, while biogas composition was determined by gas chromatography. A two-sample t-test was used to compare mono-digestions to co-digestion. Kinetics were analysed via a modified Gompertz model defined as

$$M(t) = M_m \exp \left\{ -\exp \left[\frac{R_m}{M_m} \lambda (t+1) \right] \right\}$$

where $M(t)$ is the cumulative methane yield (CMY) at time t (mL); M_m is the methane production potential (mL); R_m is the maximum methane production rate (mL/d); λ is the lag phase (d); t is the duration of the assay (d); and e is the $\exp(1) = 2.7183$. Due to the observed lag phase, PM was not included in the kinetic analysis.

Results and Discussion

As illustrated by Fig. 1, mono-digestion of PM resulted in a delay in methane generation from day 0 to day 35. This was due to high ammonium concentrations temporarily inhibiting methanogenic activity. The PM tended to generate a higher SMY (399 ± 29 ml CH_4/gVS) than FW (369 ± 6 ml CH_4/gVS), however, the difference was not significant (p value 0.225). The SMY of the PM and FW mix was significantly higher than SMYs of the mono-digestions (p value of 0.001), with an output of 448 ± 22 ml CH_4/gVS . Mixing FW and PM increased

the SMY by 12% and 20%, respectively, compared to mono-digestion of either PM or FW alone.

It should be noted that the SMY measured for the PM used in this study was higher than the SMYs measured for Irish PM in previous studies (Xie *et al.*, 2011). However, the PM analysed in previous studies was taken from overground open storage tanks, rather than from under the slatted units, as was the case in this study. This illustrates the potential role that manure collection may play in the productivity of AD systems treating PM.

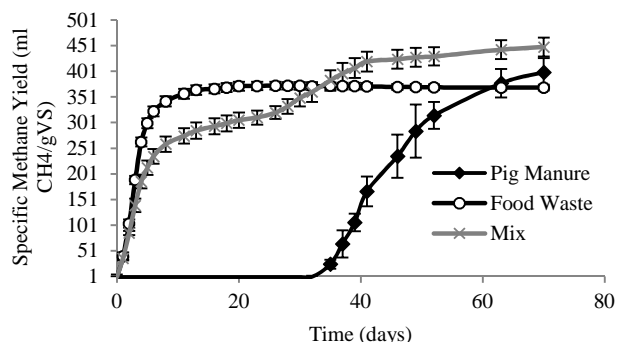


Fig. 1. SMY emission profiles of the substrates assessed.

As shown in Table 1, kinetic analysis illustrated that the Gompertz model fits the digestion of FW (0.99) better than that of the PM and FW mix (0.90). This was due to the distinct bimodal emission profile of the mix, where FW appeared to be rapidly converted to CH_4 between day 0 and 10, and PM appeared to be converted to CH_4 from day 26 to 41. While it was not possible to apply the model to the PM emission profile, it is important to note the long (38 days) effective emission period. The model indicates that FW had a higher maximum daily methane yield and lower lag time than the mixed substrate.

Table 1. Kinetic analysis of digestions via Gompertz model

Sample	Theoretical SMY (ml CH_4/gVS)	Max. daily yield (ml/gVS)	Lag time (days)	r^2
FW	360.8	79	1.4	0.99
Mix	432.9	13.6	4	0.90

Conclusions

Co-digesting PM and FW has the potential to significantly increase methane yields. While kinetic analysis indicates that mono-digestion of food waste may generate more methane per unit time in continuous operation, in practice such digestion is difficult to keep stable. The addition of PM has been shown to stabilize such digestions, in addition to increasing SMY, as shown in this study.

Acknowledgements

Funding for this study was provided by Science Foundation Ireland (Ref: 12/IP/1519).

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Evaluation of environmental compliance of on-farm, fluidised bed combustion of poultry litter

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Introduction

Disposal of poultry litter (PL) poses significant risks to the environment while simultaneously offering potential as a low carbon biomass fuel for combustion. Combustion of PL, in both fluidised bed combustors (FBC) and grate fired furnaces, has been shown to be viable in large scale operations such as BMC Moerdijk (31 MW_e) in the Netherlands where PL is transported to these utilities where it is used for electricity generation. Recently, Billen *et al.* (2014) conducted a life cycle analysis of the combustion of PL for electricity generation versus its land spreading, and found that land spreading actually results in greater emissions of NH₃, N₂O and NO_x, and that the overall total impact is lower for combustion. Large scale PL combustion in the EU needs to comply with the Industrial Emissions Directive while on-farm combustion of PL falls under the remit of the Animal By-Products Regulation which allows its use as a fuel in combustion units $\leq 5\text{MW}_{\text{th}}$ subject to the utilisation of the generated thermal energy. The purpose of this work was to evaluate the feasibility of small-scale combustion of PL in an 0.5 MW_{th} FBC, and to establish the emissions profile of the unit and test the compliance against a recent update to the emission limit values (ELVs) for sulphur dioxide (SO₂), nitrogen oxides (as NO₂) and particulate matter (PM) of 50, 200 and 10 mg Nm⁻³ respectively.

Materials and methods

Experiments were undertaken using a 0.5 MW_{th} atmospheric bubbling FBC burning 100 % PL in its as-received state at a feed rate of $209 \pm 10 \text{ kg h}^{-1}$. A schematic of the unit is shown in Fig. 1. Emissions monitoring was conducted once steady state conditions had been achieved and flue gas emission monitoring was undertaken over 12 h and was repeated three times over three consecutive batches to capture any variation arising from changes in feedstock or bird management. Monitoring was conducted in compliance with the UK Environment Agency's Monitoring Certification Scheme (MCERTS).

Results and Discussion

Table 1 provides the results of the emission monitoring together with the applicable limits and those set for waste incineration under the industrial emissions directive.

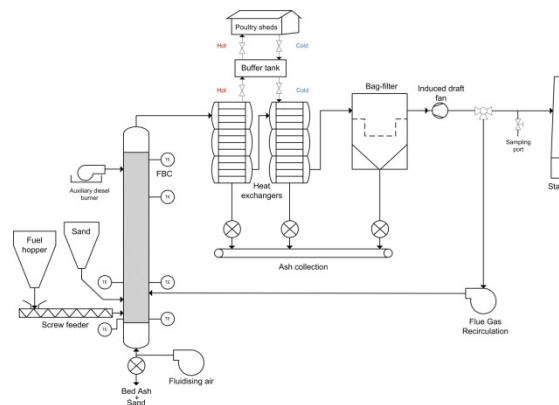


Fig. 1. Schematic of 0.5 MW_{th} atmospheric bubbling FBC

Average particulate matter (PM) was below the ELV. Emissions of heavy metals were well within the limits indicating efficient dust collection, the majority of heavy metals (Co, Cu, Cr, Mn, Ni and V) remain associated with the coarse ash collected from the heat exchangers. The more volatile elements (As, Pb and Mo) were found to bind with the finer ash collected in the baghouse filter.

Table 1: Flue emissions tested according to BS845-1

Parameter mg m ⁻³	Average	Limit 1	IED 2	MER kg year ⁻¹ *
PM	5.0	10	10	354
PM ₁₀	2.59	-	-	183
PM _{2.5}	2.19	-	-	155
HCl	2.08	-	10	147
Cd & Tl	<0.002	-	0.05	0.14
Heavy Metals	0.072	-	0.5	5.07
Hg	0.0004	-	0.05	3.07E-02
PCDD/Fs (I-TEQ ³)	0.0617	-	0.1	4.37E-03
SO ₂	14.2	50	50	1005
HF	0.09	-	1	8.14
TOC	4.7	-	10	335
NO _x	141	200	200	9952
CO	9.1	-	50	646
CO ₂ % v/v	7.0	-	-	973
O ₂ % v/v	12.8	-	-	-

Conclusions

The use of small scale FBC combustion of PL demonstrates met all the relevant legislative ELVs.

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Ammonia concentrations in ambient air, a monitoring campaign from June 2013 to July 2014

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Introduction

Ammonia (NH₃) is a gaseous reduced-nitrogen form, released mostly from animal urine and feces, and nitrogen fertilizers, depending on husbandry and nutrient-management practices. NH₃ is a potential pollutant: reduced-nitrogen deposition will probably not cause ecosystem effects below a critical load of about 10 kg/(ha year). A European critical level for direct plant impacts is 8 µg m⁻³, though this may be set too high (Cape *et al.*, 2009). Preliminary results (Doyle and Cummins, 2014) emphasised the agricultural origins, with expected distribution around Ireland. This paper shows results from a full year of monitoring. The primary objective of this study is to measure ambient atmospheric ammonia air concentrations across Ireland for one year which will improve the understanding of its spatial and temporal variability, informing the design of a continuous nation-wide monitoring network.

Materials and Methods

Atmospheric ammonia concentrations were monitored from June 2013 to July 2014, following a similar survey in 1999 (deKluizenaar and Farrell, 2000). Willems-badge passive samplers were exposed in triplicate, at 25 volunteer-operated stations, away from significant ammonia point-sources. Ammonia is collected on an absorbent acid layer within the sampler. Samplers were exposed continuously, at 1.2 m height, and replaced on a two-week cycle, and one four-week period in December 2013. Ammonia amounts, determined from each passive sampler by spectrophotometric analysis, are converted to air concentrations (µg m⁻³) based on diffusion physics across a still-air gap between a filter and the sorbent. Concentration measurements from each station are accepted where triplicate values are available and the coefficient of variation is below 25 percent. Laboratory and travel blanks are used as controls.

Results and Discussion

Large and consistent spatial variation across Ireland is observed, with distinct and separate trends of increasing ammonia concentration towards the northeast midlands and the southeast.

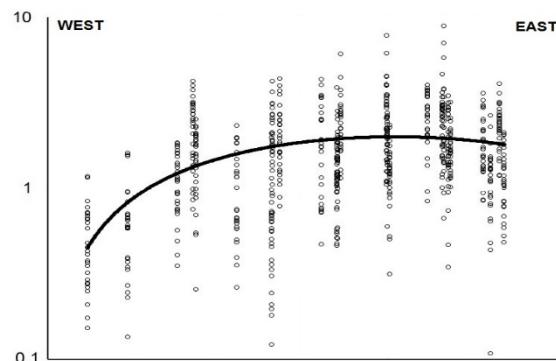


Fig. 1. NH₃ concentrations (µg m⁻³, on a log scale) grouped by site, plotted from west to east.

The lowest annual mean concentration, 0.48 µg m⁻³, was at Mace Head, Co. Galway, and the highest, 2.96 µg m⁻³, at Leiter, Co Cavan. Two sites in suburban Dublin show ammonia levels lower than the rural background, however elevated concentrations recorded at the Dublin city center station suggest an urban source. Also, a single high-elevation site in the Slieve Bloom mountains may under-represent the surrounding agricultural lowland.

Table 1. Summary statistics, complete data set (µg m⁻³)

Mean	St. Dev.	Median	Minimum	Maximum	Range
1.72	0.70	1.76	0.068	10.5	10.4

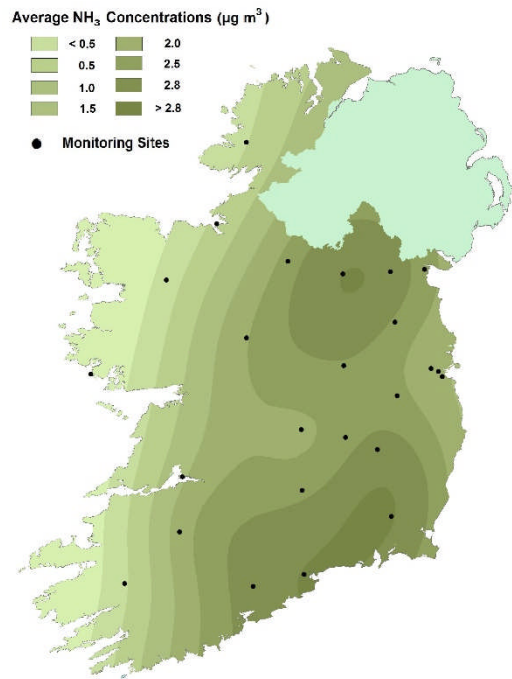


Fig. 2. Mean NH₃ concentrations (µg m⁻³) for June 2013 to July 2014 obtained by kriging.

Conclusions

One year of monitoring shows a distinct trend of increasing ambient ammonia concentrations towards the north east midlands and towards the south east. Mean levels from all sites are below the current 8µg NH₃ m⁻³ ceiling, though some exceedences do occur, even away from point sources. In order to operate a national network with a similar density to the Northern Ireland ammonia network, a minimum of 14 stations are required. The location of sites for optimum coverage becomes a priority when network density is reduced.

Acknowledgements

We acknowledge the EPA STRIVE Programme for funding; collaboration with Trent University, Canada; and the network volunteers. www.ucd.ie/ammonia

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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.

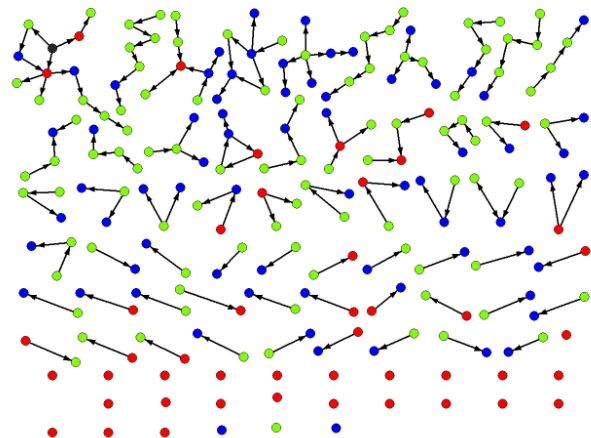


Fig. 1. Network of JD positive animals. Nodes (shaded circles) represent premises and arrows movements (Red: herd with at least one JD positive homebred animal; Blue: herd with at least a positive animal born outside the farm and unknown homebred positive animals; Green: unknown JD status; Black: imported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

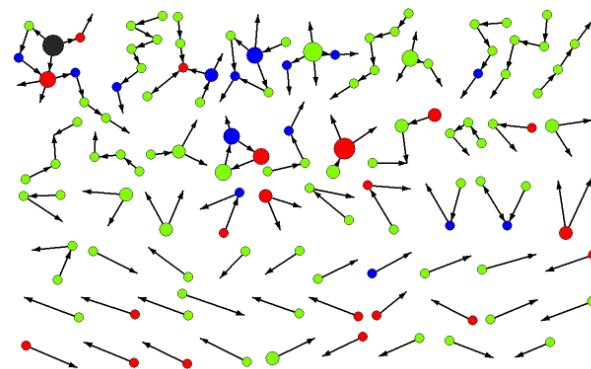


Fig. 2. Out-degree centrality: relative node size, determined by node out-degree, illustrating their importance to disease spread. Nodes coded as in Fig. 1.

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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Comparison of laboratory tests for the diagnosis of bovine paratuberculosis

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Introduction

Johne's disease is a chronic infectious disease of ruminants caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP). This granulomatous enteritis is characterised by a long incubation period with clinical signs typically appearing several years after infection. Diagnosis of MAP infection is difficult. The current study compares serum ELISA, faecal culture and faecal PCR for ability to identify infected animals. Faecal culture was considered the reference method.

Materials and Methods

As part of the DAFM funded ICONMAP research project, ten MAP infected herds were identified and blood and faecal samples were collected from animals aged >20 months. Serum was tested for MAP antibodies using the Idexx Paratuberculosis Screening ELISA kit (Idexx Laboratories, Riverside House, Windsor Berkshire, UK). Positive and suspect samples were re-tested using the Idexx verification ELISA kit and S/P values of 55% or greater were considered to be positive. Faecal samples were stored frozen at -20°C. The Cornell double incubation decontamination method was used to decontaminate the samples and they were cultured using the Trek ParaJem ESP II system (Liquid Culture). Smears for Ziehl-Neelsen staining were prepared from culture fluid and mycobacteria identified as MAP using mycobactin dependency and F57 PCR. Direct PCR was performed on faecal samples using the TaqVet *M. paratuberculosis* Advanced kit (Laboratoire Service International, 69380 Lissieu, France). Two grams of faeces underwent an initial preparation step. The pellet obtained was heat treated and then disrupted using a MagNa lyser (Roche Burgess Hill RH15 9RY, England). After the addition of lysis solution, DNA was extracted using the QIAamp DNA mini kit (Qiagen, Manchester M15 6SH, England). PCR was performed using the Stratagene Mx3005 and samples were considered to be MAP positive where Ct values were ≤ 45 . The MXPro software was used to generate the Ct value.

Results and discussion

There were 1650 cattle sampled and culture and ELISA testing is complete. To date 1045 animals have been tested in direct PCR. Faecal culture identified 204 cattle as infected. Serum ELISA identified 16.8% of infected animals as positive and is significantly less sensitive than culture ($P < 0.001$, Table 1).

Table 1. Comparison of Liquid Culture with ELISA

	ELISA Positive	ELISA Negative	Total
Culture Positive	34	168	202
Culture Negative	18	1404	1422

Direct PCR classed 20% of infected animals as negative and is significantly less sensitive than culture ($P = .002$, Table 2). In culture a single organism has the ability to replicate over the 42 day incubation period, while in PCR the efficiency of DNA extraction is critical.

Table 2. Comparison of Liquid Culture with Direct PCR

	PCR positive	PCR negative	Total
Culture positive	136	34	170
Culture negative	353	522	875

Direct PCR offers advantages over culture in terms of throughput and time to obtain a result but a complicating factor in evaluating its usefulness is the finding that one third of culture negative animals were PCR positive. The liquid culture reference method of this study is widely used in diagnostic laboratories but can only identify animals which are shedding MAP above a threshold level in their faeces. Culture and PCR tests may be detecting different populations of infected animals, but it is more probable that in infected herds, MAP cells can be passively ingested and MAP DNA then extracted from the faeces of uninfected cattle resulting in a positive PCR test (Kralik *et al.*, 2014). Follow up sampling over the coming years will establish the true status of these animals.

Conclusions

Testing of this initial sample set from infected herds indicates that serology may not be sufficiently sensitive for use in known infected herds and that the true status of the PCR positive, culture negative animals needs to be ascertained.

Acknowledgements

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Effects of major genes and genetic diseases on performance of Holstein Friesian dairy cattle

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Introduction

A custom genotyping chip, the International Dairy and Beef (IDB), was developed in 2012 by Teagasc in collaboration with the ICBF and Weatherbys to service the current and future requirements of the cattle industry (Mullen *et al.*, 2013). The IDB and IDBv2 (second version released in March 2014) provide the ability to: 1) verify parentage (SNPs to SNPs or SNPs to Microsatellites); 2) improve imputation accuracy to higher density SNP panels; 3) genotype polymorphisms of research interest and; 4) screen for lethal recessives, genetic diseases and mutations with major effects. The objective of this study was to estimate the effects of lethal recessives, genetic diseases and major genes on production traits in dairy cows screened using the IDB to date.

Materials and Methods

The major gene/genetic disease content of the IDBv2 has been updated to include 137 tests (7 disease haplotypes, 96 Mendelian disorders, and 34 mutations with large effect) of which 65 have been validated to date (McClure *et al.*, 2015). Genotypes and phenotypes were obtained from the Irish Cattle and Breeding Federation (ICBF). A total of 3310 Holstein-Friesian (HF) cows with call rates $\geq 90\%$ were available for analysis. Only SNP with call rates $\geq 90\%$ were retained for analysis. In total 20 production related traits were selected encompassing milk yield and composition, fertility, calving, health and carcass traits. Phenotypes (expressed as PTA's) were deregressed and parental contributions removed following Garrick *et al.* (2009). The association between the SNP and performance were individually quantified using mixed models (EMMAX, Kang *et al.* (2010) accounting for relationships between animals using a genomic relationship matrix. Bonferroni adjustment for multiple testing was also undertaken within gene.

Results and Discussion

For the purposes of this paper, summary data on the validated mutations (n=65) are presented and all associations are nominal unless stated otherwise. The A2 β -casein variant has received much interest in recent years with milk containing high levels of A2 β -casein linked to improved human health. No associations ($P>0.1$) were observed between the A2 β -casein mutation and any of the traits examined in the current study suggesting that selection for this variant would not penalise genetic improvement efforts. K-casein which improves cheese production was associated (variant 13104) with increased milk protein yield (0.96 kg, s.e. 0.43, $P<0.05$). There was no evidence a DNA variant responsible for polledness in cattle (INDEL 202) was negatively associated with any of the traits examined

($P>0.10$). Citrullinaemia, a lethal recessive disorder affecting the urea cycle, was as expected associated with increased calf mortality ($P<0.05$). Complex Vertebral Malformation (CVM) was associated with increased milk production (69.6 kg, s.e. 33.5, $P<0.05$) and increased calving interval (17.3 days, s.e. 5.59, $P<0.01$) as previously reported (Ghanem *et al.*, 2008). SNP associated with Weaver disease (a progressive degenerative myeloencephalopathy) were also associated with increased milk traits (14 kg protein, s.e.6.38, $P<0.05$) as previously reported by Georges *et al.*, (1993). Five mutations in the STAT gene family (STAT3 and 5) which affect milk composition and embryo survival were associated with both milk traits (yield and fat composition) and increased calf mortality rates (2.2 %, s.e.0.95, $P<0.05$). In addition, two of these mutations (STAT3 19069 and 25402) were also associated with carcass conformation ($P<0.05$). DGAT1 and F279Y were, as previously reported, strongly associated (adj. $P<0.001$) with milk traits (Table 1).

Table 1. Known mutations affecting milk traits in dairy cattle

Gene	MAF	Trait ^a	Effect (s.e)	P value	%
DGAT (K232A)	0.42	Fat (%)	0.15 (0.007)	$<10^{-20}$	12.8
		Milk (kg)	-127 (11.5)	$<10^{-20}$	3.6
		Protein (kg)	-2.4 (0.34)	$<10^{-10}$	1.6
GHR (F279Y)	0.08	Fat (%)	-0.05 (0.01)	$<10^{-6}$	0.5
		Milk (kg)	76.9 (19.9)	$<10^{-5}$	0.5
ABCG2 (Y581S)	<0.01	Fat (%)	-0.12(0.05)	0.02	0.2

^aFat: milk fat percentage; Milk: milk yield (kg); Protein: milk protein yield (kg); %: % phenotypic variance.

Conclusions

This initial analysis has identified novel and validated previous associations between putative causative mutations and production traits in Holstein Friesian cattle. Increasing the frequency of mutations of interest to industry such as A2 β -casein, Kappa casein or the polled variants for example showed no evidence of significant negative effects on the other production traits examined in this study. As additional genotypes become available reanalysis using larger sample sizes will result in more accurate estimations of effects. The incorporation of causative mutations onto the IDB provides the opportunity for integration into the national genomic selection program.

Acknowledgements

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The impact of infection with Schmallenberg virus on weaning rate in Irish sheep flocks

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Introduction

Schmallenberg virus (SBV) infection emerged and spread rapidly across Northern Europe in 2011 (Hoffmann *et al.*, 2012). In Ireland, targeted sampling of congenitally malformed bovine and ovine foetuses with PCR testing of foetal brain for the presence of SBV commenced in 2012 with the first confirmed case identified in October 2012. Subsequent PCR detections and serosurveys clearly showed widespread exposure of flocks and herds in the South and East of the country by the end of 2012. However, the effects on enterprise performance could not be assessed, as generally only one case was submitted from each herd / flock and there was no accessible production database. A contemporaneous serological survey of cattle in December 2012 showed high levels of sero-conversion in the same regions. The objective of this study was to quantify the impact of SBV infection on the productivity and profitability of Irish sheep flocks, based on data collected from Irish sheep farmers.

Material and Methods

A questionnaire on productivity and management practices in sheep flocks was developed and distributed among sheep farmers to gather relevant production data for 2012/2013. Data collected included flock number, county, livestock enterprises, the presence of marshy pasture, breeding practices, fertility indices and parasite control policies. Valid responses from 267 sheep farmers were received. Mean weaning rate was chosen as a robust index of productivity. Univariate and multivariate negative binomial regression modelling was carried out on the data using Stata SE 12 (Statacorp, USA).

Results and Discussion

Flocks with a laboratory confirmed diagnosis of SBV had a 10% reduction in weaning rate. Sheep type (lowland versus mountain), the weaning rate in the previous season and barren ewe rate were also found to be statistically significant in the multivariate analysis. The 10% reduction in weaning rates consequent on incursion of Schmallenberg virus into Ireland in 2012 is a justifiable concern for sheep farmers. Several other factors relating to management and breeding were also found to significantly affect weaning rate. As there was no pre-existing production database in existence, the data had to be collected by questionnaire. In a broader context, this study shows the potential value of interrogating production data in conjunction with an animal disease database to estimate the economic impact of an emerging disease.

Table 1. Negative binomial regression model for weaning rate among 267 sheep flocks in Ireland

Independent variables	IRR*	P> z
Constant	0.720	0.000
Group 3: SBV free, exposed county	1.004	0.811
Group 2: Suspected SBV	0.985	0.681
Group 1: Confirmed SBV	0.895	0.000
Sheep type (referent: lowland)		
Mountain	0.916	0.015
Lowland and mountain	0.947	0.009
Pedigree and mix of the above	1.005	0.837
2013 ewe barren rate	0.393	0.000
Weaning rate 2012	1.645	0.000

Conclusions

Weaning rates in flocks with a confirmed diagnosis of SBV were approximately 10% lower than those of flocks in known negative areas. While the value of production data in informing management decisions at farm level is well-accepted, this present study also clearly shows the potential value of production databases in assessing the economic impact of a novel disease entity on a national basis. Such assessments will inform risk managers so that they can quantify the costs and likely benefits of any intervention.

Acknowledgements

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Prevalence and risk factors for limb and claw lesions and lameness in replacement and pregnant gilts on Irish farms

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Introduction

Sow longevity is a key component of an efficient and profitable pig farming enterprise. However, the culling rate of Irish sows is increasing at a rate of between 0.7% and 1% p.a. (currently 50% - Teagasc advisory service database [PigSys] 2013). Lameness is a major reason for culling with younger animals being particularly susceptible (Boyle *et al.*, 1998). The prevalence and risk factors for lameness in Irish gilts are not known but other studies show that housing system and flooring are important risk factors (KilBride *et al.*, 2009). The aims of this study were to determine the prevalence and risk factors for limb and claw lesions and lameness in gilts in Irish herds.

Material and Methods

A sample size of 59 farms was determined for this cross-sectional survey based on an expected overall prevalence of limb and foot lesions of 95%, a population of 297 integrated (i.e. 'farrow to finish') pig farms, a 95% confidence interval and a precision of 5% (Win Episcopes 2.0). A total of 68 pig farms were selected from PigSys and visited between March 2011 and December 2012. All had >100 sows and a single production site. As this work was conducted prior to the implementation of Directive 2001/88/EC the sample included farms with stall housing for pregnant gilts. On each farm 1 pen of replacement gilts and 1 pen or 10 individual stalls of pregnant gilts were examined. Pens and individual stalls were randomly selected, using a random number generator, and every gilt in each selected pen was examined if there were ≤ 10 gilts per pen and 10 gilts were randomly selected and examined if there were >10 gilts in a pen. All 4 limbs were examined for: scratches, wounds, swellings, abscesses, calluses and bursitis. Capped hock was only scored in the hind limbs. All limb lesions were defined and scored from 0 to 3 on the basis of area affected as per Kilbride *et al.*, (2009). Claw lesions (overgrown, broken and fully amputated dew claws and toes) were scored as present or absent. Locomotory ability was scored from 0 to 5 (Main *et al.*, 2000). A gilt was considered lame if it received a score of ≥2. Pen or stall materials and dimensions were recorded and a questionnaire including information on management practices, feeding routines and genetics was answered by the farmer. Data were stored in Microsoft Access 2003. The prevalence of each limb and claw lesion for each group was calculated using the maximum severity score and presence/absence of each lesion per gilt. Data were analysed using MlwiN 2.27. A 2 (stalled only) or 3 (pens only) level mixed effect logistic regression model was used to determine risk factors.

Results and Discussion

Five hundred and eighteen replacement gilts and 525 pregnant gilts were inspected. All the former were in groups (median=10, Inter Quartile Range 8-13) while 335 of the pregnant gilts were in 48 pens and 190 were in stalls. Several limb lesions were highly prevalent (Table 1) and there were high levels of lameness with 38.9% of replacement gilts and 41.1% of pregnant gilts receiving scores ≥2. These findings reflect the high levels of culling for lameness in the early parities. Claw lesions were lowly prevalent, likely due to underestimation, as gilts with severely damaged claws are usually moved to hospital pens or culled.

Table 1. Prevalence (%) of limb and claw lesions in replacement and pregnant gilts on 68 farms

Lesion	Gilt stage	
	Replacement	Pregnant
Scratches	78.1	62.7
Wounds	34.7	28.8
Abscesses	0.19	0.20
Swellings	30.3	20.2
Calluses	100.0	99.8
Bursitis	25.0	19.3
Capped hock	11.6	12.7
Overgrowth dew/toe	3.1/1.7	5.6/15.5
Broken dew/toe	0.6/0.2	3.5/1.4

There was little variation between farms in terms of flooring with 91.4% of replacement and 99.2% of pregnant gilts being housed on partially or fully slatted flooring without bedding. This explains why no risk factors for lameness or claw/limb lesions associated with flooring were identified. No risk factors were identified for lameness in replacement gilts. There were higher odds of lameness in pregnant gilts in group (48.1%) compared with stall (30.4%) housing (OR 3.66, CI 1.23-3.66). There was an increased risk of limb swellings in replacement gilts that were separated from the finishers at weights of >90kg compared with those separated at <50 kg (OR 3.1, CI 1.6-7.7). There was a reduced risk of overgrown toes (OR 0.29, CI 0.14-0.61) in pregnant gilts housed in groups compared with individual stalls.

Conclusions

There are high levels of limb lesions and lameness in both replacement and pregnant gilts in Irish production systems likely related to the widespread use of slatted flooring (KilBride *et al.*, 2009). This helps explain the high culling rate in Irish sow herds. Preferential treatment of replacement gilts at an earlier stage in their development could help to improve limb health. There is a higher risk of lameness in group systems compared to stalls. These findings have serious implications for the longevity and efficiency of the Irish national sow herd given the ban on stall housing since 2013 and the operation of group systems without bedding which is protective against lameness (KilBride *et al.*, 2009).

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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.

Acknowledgements

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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.

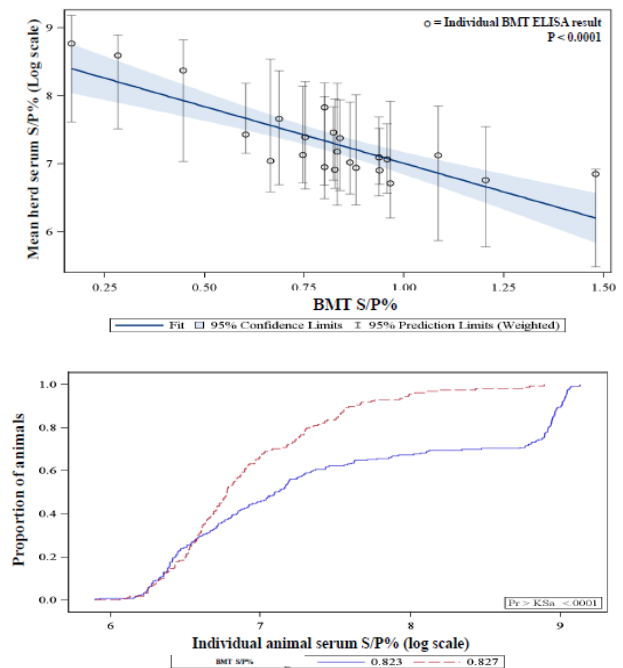


Fig. 1. Relationship between herd mean serology and BMT (upper panel) and between individual animal serology and BMT results (lower panel)

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.

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Prevalence and distribution of exposure to Schmallenberg virus in Irish cattle during November 2012 to November 2013

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Introduction

The first case of SBV was confirmed in a malformed bovine foetus calf in Ireland in October 2012 (Bradshaw *et al.*, 2012). Serological data from the countries most severely affected by SBV have indicated rapid and high levels of seroconversion, while serological data from regions further away from the centre of the epidemic have shown less complete seroconversion (Gache *et al.*, 2013). As Ireland was on the margins of the epidemic in Europe it was uncertain as to how the disease would spread, although given the spread of SBV in several European countries, it was anticipated that SBV would spread north-west wards during the 2013 vector season. The objectives of this study were to determine the level of exposure among the Irish cattle population initially at the end of 2012 and to document the spread of SBV in Ireland over the course of the 2013 vector season.

Material and Methods

Samples of brain or external foetal fluids from cases of abortion or stillbirth submitted to the Dept. of Agriculture's virology division. These cases which had suspect lesions such as hydrancephaly or arthrogryposis were tested using a RT-PCR detecting an 88bp fragment of the S3-segment of the SBV genome (Hoffman *et al.*, 2012). Three national serosurveys were conducted to estimate SBV exposure in Irish cattle, using sera collected between November 2012 and November 2013, as part of the national brucellosis eradication programme. At the first, second and third SBV serological surveys, samples were collected from 3,192 cattle from 529 herds, 3,101 samples from 517 herds, and 3,204 samples from 534 herds, respectively. Sera were screened using a commercially available SBV Antibody Kit (Idexx Laboratories). Data were managed and analysed using Microsoft Excel (Microsoft Corporation, Redmond, WA, USA) and ArcGIS 9.1 (ESRI, Redlands, CA, USA).

Results and Discussion

Between October 2012 and May 10th 2013, SBV was confirmed by RT-PCR in brain tissues from 49 malformed bovine fetuses in Ireland. These herds were geographically distributed in the south, south east and east of the country. The overall herd level prevalences in the three surveys varied from 51% to 53%, and the overall animal level prevalence was also consistent over the course of the three surveys, ranging from 32.2% to 35.8%, both prevalence rates were remarkably consistent, with the greatest rates of seroconversion in the south, south east and east. Herd

level seroprevalence within counties ranged from 0% to 100%, with the counties in the south and southeast having the highest seroprevalence (>50%), the midlands a moderate seroprevalence (10-50%) while the northern and northwestern counties had a low seroprevalence (0-10%). The areas with the greatest SBV seroprevalence coincided with the area where SBV was detected by PCR in brain tissue of malformed bovine fetuses. Unlike several other European countries the spread of SBV was curtailed during the second vector season, as evidenced by this study and the fact that there has been no confirmed (PCR positive) case of SBV in Ireland since May 10th 2013. Given the inactivity of the virus since 2012, it is likely that the younger age cohort in herds where SBV was previously endemic are now immunologically naïve, and would be susceptible if the virus were to be re-introduced to Ireland. Likewise, substantial proportions of animals on the margins of affected areas remain immunologically naïve to SBV, and susceptible to infection if the virus was re-introduced to the country.

Conclusions

This study has clearly shown that exposure to SBV was confined to the south and south east of Ireland. However, it should be noted that the lack of widespread circulation of SBV in 2013 does not provide an assurance that Ireland is free of the virus.

Acknowledgements

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Clinical investigation of arthritis and mastitis associated with *Mycoplasma bovis* in Irish dairy herds in 2013 and 2014

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Introduction

Mycoplasma (M) bovis is a bacterial cause of respiratory disease, arthritis and mastitis in cattle. It occurs worldwide, including in Irish cattle. During the last 20 years, respiratory disease has been the most common clinical presentation of *M bovis* in Irish cattle. Cases of arthritis have also occurred sporadically, predominantly in calves, young cattle or housed beef fattening cattle, either as a sequel to respiratory disease or occasionally as a primary clinical presentation of *M bovis* infection. The carpus, hock and fetlock joints were most frequently affected. Until 2013, arthritis caused by *M bovis* was rarely diagnosed in Irish dairy cows. Mycoplasmal mastitis has been diagnosed in a limited number of Irish dairy herds prior to 2013. In 2013 and 2014, a different pattern of occurrence of clinical disease was observed in cows in a number of Irish dairy herds, involving arthritis and/or mastitis cases, associated with *M bovis*. The aim of this study was to describe the clinical pattern observed, diagnosis and control measures applied.

Materials and methods

Clinical cases of either lameness and/or mastitis were initially investigated by private veterinary practitioners on behalf of the herd-owners. Samples of aseptically collected joint fluid or milk samples were submitted to the Department of Agriculture, Food and the Marine (DAFM), Regional Veterinary Laboratories and referred to the Central Veterinary Research Laboratory and were subjected to microaerophilic culture on mycoplasma broth and agar plates and to polymerase chain reaction for *M bovis* (Sachse *et al.*, 2010). A questionnaire was circulated to the herd-owners requesting information about the number of cows similarly affected, time affected, their response to treatment and their outcome. Several of the herds were visited by personnel from DAFM Laboratories.

Results and Discussion

The herds affected were all seasonal spring-calving dairy herds, ranging in size up to 200 dairy cows. During the first four months of the years 2013 and 2014, multiple cases of swollen joints and lameness, affecting predominantly dairy cows, were observed in 13 dairy herds. Several dairy cows developed similar clinical signs of lameness and reduced flexibility and swelling of one or more joints, within a limited period of time from three to seven weeks of the occurrence of

the first clinical case in each herd. Most cows were affected in one limb and apparently in one joint only. The severity of lameness varied between cases. The metacarpo-phalangeal joint (fetlock of forelimb) was the most frequently affected joint, but the carpus, hock and metatarso-phalangeal joint were also affected in other cases. *Mycoplasma bovis* arthritis was diagnosed by isolation of mycoplasma colonies on selective culture media and by polymerase chain reaction, from samples of joint fluid from one or more cows in 12 of those herds and from milk samples from cows in the remaining one of those 13 herds. Cases of *M bovis* mastitis were diagnosed, mostly in cows that were not affected by lameness, in 5 of those 13 herds. Mycoplasmal mastitis was diagnosed in cows in 4 further dairy herds for which no cases of arthritis were reported during 2013 and 2014. Mycoplasmal arthritis occurred as a primary clinical presentation in most of the affected cows. No clinical signs of respiratory disease were reported in the majority of the affected cows. In some herds *M bovis* was also isolated from cases of arthritis or respiratory disease in calves. The extent of mycoplasmal mastitis in the affected herds was determined by testing of milk samples. Cows detected were segregated and milked last. When implemented this was followed by a cessation of occurrence of new cases of mycoplasmal mastitis.

Conclusions

Mycoplasma bovis arthritis and mastitis were diagnosed in adult dairy cows in Ireland in a series of herd outbreaks affecting 17 dairy herds in the years 2013 and 2014. Control programs were devised and applied in order to contain the extent of clinical arthritis and eliminate the mycoplasmal mastitis from affected herds.

Acknowledgements

The input of staff of the Central Veterinary Research Laboratory and Regional Veterinary Laboratories is appreciated. The pro-active involvement of veterinary practitioners and herd-owners contributed greatly to this work.

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Does a reduction in the number of anthelmintic treatments administered to lamb preweaning incur a production penalty?

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Introduction

Nematodirus battus is a gastrointestinal parasite that can seriously challenge spring-born lambs preweaning. This challenge can be controlled by taking advantage of the fact that *N. battus* has a year-long life cycle with transmission being mainly from one lamb crop to the next. If this cycle cannot be broken by alternation of the grazing area in successive years or by avoiding use of area grazed by lambs from mid April to late May in the previous year (Good *et al.*, 2001), anthelmintic treatment is the only practicable method of effective control. In this scenario, dosing March-born lambs at 3 week intervals in April and May was advised (Kearney *et al.*, 1984). In Teagasc flocks at Athenry lambs are routinely dosed at 5, 10 and 14 weeks of age. In the context of the need for measures to delay the development of anthelmintic resistance, such as reducing the number of anthelmintic treatments, the present study was undertaken to evaluate the effect that omission of one treatment from the routine treatment schedule (5, 10 and 14 weeks) would have on lamb growth to weaning. Previous work indicated a clear decline in the number of *N. battus* eggs in faeces by 14 weeks of age (Good *et al.*, 2006). Because lambs in this study were grazing unsafe pasture, and given that majority of lambs are born in March, omission of the treatment at 5 weeks of age was considered high risk; thus treatment at 10 weeks of age was the only choice for omission of an anthelmintic dose preweaning.

Materials and Methods

Twin-reared lambs, managed as a group, were used. The lambs used were born in late March to early April and received anthelmintic treatment at 5 weeks of age. At 10 weeks of age lambs were randomly assigned, within twin pairs, to treatment (\pm anthelmintic) and returned to the same pasture. All lambs were weighed at 5, 10 and 14 weeks of age. In year 1 (2009) lambs were purebred Belclare ($n=50$) while in year 2 (2010) lambs were either Belclare ($n=34$) or Cambridge ($n=30$). In year 2, faecal egg counts were on a flock basis at 10 weeks and on individual lambs at 14 weeks of age using the FECPAK system and McMaster methods (ANON 1986), respectively. Faecal egg counts for *Nematodirus* spp. (FEC_{NEM}), *Strongyloides papillosus* (FEC_{SPAP}) and 'other trichostrongyles' (FEC_{OT}) were recorded separately. FEC data (at 14 weeks) were analysed using Proc MIXED of SAS®. The model used had fixed effects for treatment (\pm anthelmintic), breed and treatment \times breed interaction with dam as a random term. Prior to analysis, the FEC data were log transformed ($\ln(x+25)$). Live weight at 14 weeks was also analysed using the MIXED procedure of SAS. The model included dam as random and treatment, sex and breed \times year as fixed effects with live weight at 10 weeks as a covariate.

Results and Discussion

Lambs that were dosed at 10 weeks were 0.5 (s.e 0.23) kg heavier at 14 weeks than their siblings that remained undosed ($P = 0.03$); male lambs were heavier than females ($+0.6$ kg; $P = 0.02$). While year-by-breed differences were highly significant ($P < 0.001$) there was no evidence for any interaction between these effects and treatment. FEC_{SPAP} were negligible (data not shown). The mean FEC_{NEM} and FEC_{OT} for lambs in 2010 at 10 weeks of age were 330 and 120 epg, respectively; clearly lambs had been exposed to *N. battus* challenge. Results for FEC measurements at 14 weeks of age are in Table 1. Undosed lambs had higher FEC_{NEM} at 14 weeks of age, which, given normal weather conditions, would have implications for the next season's lamb crop. There was no evidence of a breed or breed \times treatment interaction effects for either FEC variable.

Table 1. Geometric mean (95% confidence interval) FEC (epg) for lambs at 14 weeks of age – data for 2010

	Treatment at 10 weeks of age		P-value
	Dosed	Undosed	
FEC_{OT}	187 (112-301)	331 (207-522)	NS
FEC_{NEM}	6 (0-21)	73 (40-121)	< 0.001

Conclusions

Dosing at 10 weeks is required to control effects of gastrointestinal challenge on performance. Moreover, the higher count for *N. battus* eggs in faeces from the animals left undosed at 10 weeks of age has negative implications for lamb performance on the same pasture in the following grazing season. Further study would be required to evaluate this establish the magnitude of any such effect.

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Effect of gestation feed intake on survival traits of piglets

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Introduction

Maternal nutrition during gestation can influence foetal development, and thus piglet vitality and survival. One of the most important indicators of survival is piglet birth weight. However, high birth weights could have a negative effect on piglet vitality, due to the risk of prolonged farrowing or increased birth intervals. These are associated with increased blood lactate levels as a result of hypoxia (van Dijk *et al.*, 2005). Ability to thermoregulate is also a critical measure of vitality. Thus rectal temperature and time to reach the udder are predictive of piglet vitality and survivability, as suckling improves thermoregulation (Baxter *et al.*, 2008). The objective of the research undertaken was to determine the effect of increasing maternal feed intake at targeted windows throughout gestation on traits related to piglet vitality.

Material and methods

The experiment was performed at Teagasc Moorepark Research Centre in January 2005, using 51 sows, as a sub-experiment of a much larger study (McNamara *et al.*, 2011). Sows were dry fed ad-libitum from weaning to service. From day (d) 0 to d25 of gestation, all sows were fed 30MJ DE/day. At d25, sows were weighed and back fat measurements taken, then randomly assigned to one of 4 dietary treatments (T): Control (CON: 30MJ DE/day gestation diet; n = 9 sows), EARLY (as control, but 47MJ DE/day from d25 - d50; n = 17 sows), MID (as control, but 47MJ DE/day from d50 - d80; n = 15 sows) and LATE (as control, but 45MJ DE/d from d80 - d112; n = 10 sows). At farrowing the following measures were taken: number of piglets born alive (BA) and dead (BD), birth weight (BW), temperature at birth and 1 hour (h) later, farrowing duration, and time to reach the udder. Colostrum intake was estimated as weight at 24h minus BW, and piglet live weights recorded on d7, d14 and d28. T was considered a fixed effect, piglet within sow, and day as repeated effects (Proc Mixed, SAS V9.3) Number, BA and BW were included as covariates where appropriate.

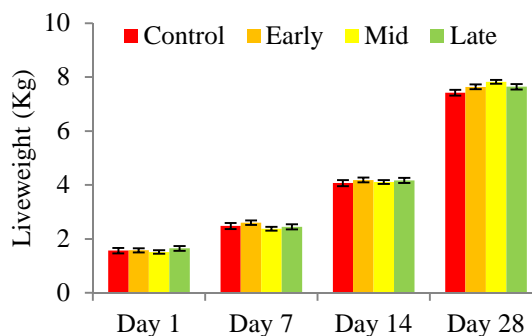


Fig. 1. Piglet liveweights between 1 and 28 d post-partum

Results and discussion

T had an effect on BW, with MID sows tending to have heavier piglets than CON and LATE ($P \leq 0.10$). There was also an interaction between T and d for liveweight ($P < 0.05$; Fig 1.). CON piglets were lightest by d28 and MID were heaviest. When considering only d28 there was an effect of T on liveweight ($P < 0.05$), in agreement with McNamara *et al.* (2011) who found that supplementation between d50-80 resulted in heavier weaning weights than CON. As well as greater piglet BW, MID sows also tended to have the longest farrowing duration (Table 1). Although not significant, there were large numerical differences in BD between treatments. Similarly McNamara *et al.* (2011) found that sows supplemented in early and mid-gestation had greater numbers BD than control sows. Piglets from MID sows had the highest temperature at birth, indicating better thermoregulatory ability compared with smaller litter mates, at greater risk of hypothermia (Baxter *et al.*, 2008). However piglets from EARLY sows consumed most colostrum, and were numerically heavier up to d14 possibly indicating enhanced postnatal growth.

Conclusion

Increasing feed allowance between d50-80 of gestation improved more indicators of piglet vitality than the other treatments as well as birth and weaning weights.

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Table 1. Effect of timing of increased nutrition during gestation on indicators of piglet survival (mean \pm SE)

Measures	Control	Early	Mid	Late	P-value
Born alive	11.0 \pm 1.2	11.1 \pm 0.8	11.1 \pm 0.9	10.7 \pm 1.1	NS
Born dead	0.9 \pm 0.4	0.5 \pm 0.3	1.3 \pm 0.3	1.3 \pm 0.4	NS
Birth weight (Kg)	1.35 \pm 0.08 ^a	1.54 \pm 0.06 ^{a,b}	1.56 \pm 0.05 ^b	1.36 \pm 0.07 ^a	0.03
Birth temp ($^{\circ}$ C)	37.2 \pm 0.3 ^{a,b}	37.1 \pm 0.2 ^a	37.7 \pm 0.2 ^b	37.1 \pm 0.3 ^{a,b}	0.09
1 Hour temp ($^{\circ}$ C)	37.8 \pm 0.3	38.0 \pm 0.2	37.9 \pm 0.2	38.2 \pm 0.3	NS
Farrowing duration (h)	2.23 \pm 0.90 ^{a,b}	3.82 \pm 0.64 ^{a,b}	4.31 \pm 0.67 ^a	1.83 \pm 0.78 ^b	0.07
Time to udder (h)	1.09 \pm 0.14	0.87 \pm 0.10	0.90 \pm 0.09	-	NS
Colostrum consumed (g)	38.5 \pm 25.7 ^{a,b}	77.4 \pm 19.9 ^a	16.8 \pm 16.9 ^{a,b}	31.2 \pm 22.3 ^b	NS

^{a,b} indicates differences within rows at $0.05 < P \leq 0.1$

Variation between farms in tail lesion scores of slaughter pigs

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Introduction

Tail biting is a behavioural abnormality which leads to tail injuries in pigs. Much of the focus is on severe outbreaks of tail biting which producers believe is a sporadic problem (Devitt *et al.*, 2014). Indeed, severe tail lesions which are often the only tail damage recorded during ante and post mortem inspection, occur at a low level (i.e. 0.7 and 1.0%, Harley *et al.*, 2012; 2014). However these authors also showed that 7.8 - 25.3% of carcasses have mild to moderate tail damage. This suggests that high levels of tail directed behaviour (i.e. chewing not necessarily severe biting) by pigs is a more widespread chronic problem. Such behaviour may also be a precursor to more severe outbreaks. The aim of this study was to identify variation between farms in levels of mild to moderate tail damage as the first step in identifying farm based risk factors for tail biting.

Material and Methods

Two observers scored herd, sex, and tail lesion scores (0 – 5) of pig carcasses at two factories (A and B) during June – July 2014. Tails were scored as 0 – no evidence of tail biting; score 1 – healed or mild lesions; score 2 – evidence of chewing or puncture wounds, but no evidence of swelling; score 3 – evidence of chewing or puncture wounds with swelling and signs of possible infection; score 4 – partial loss of the tail; score 5 – total loss of the tail (adapted Kritas & Morrison, 2007). Scores were collapsed into 3 levels: none/mild (score 0 + 1), moderate (score 2 + 3), and severe (score 4 + 5) and the prevalence and range of each was determined. Batch size was obtained from the factory and retrospectively categorized into small, medium and large batches on the basis of quartiles. Effects of factory, batch size and sex were analysed using generalised estimated equation models with farm as random effect (SAS V9.3 PROC GLIMMIX).

Results and discussion

In total, 13,133 carcasses were inspected from 61 farms. Moderate and severe tail lesions were present in 27.3% and 1.0% of the pigs, respectively. Males had a higher odds of moderate (OR = 1.5, 95%CI 1.38 – 1.63) and severe tail lesions (OR = 3.9, 95%CI 2.49 – 6.15) than females. Herd level prevalence ($P < 0.001$) for severe tail lesions ranged from 0 – 9.7% and for moderate tail lesions this was 4.0 – 66.8% (Fig. 1). All farms had pigs with moderate lesions and in 42% of the farms the prevalence was above average (27.6%). Severe tail lesions were recorded in 47% of the farms but only 26% of the farms had above average levels of severe tail lesions (0.9%). This shows that moderate tail lesions are much more common than severe tail lesions. Nevertheless, it should be taken into account that severe cases are often euthanized on farm and hence the prevalence on the slaughterline could be an

underestimation. Pigs in factory B had significantly lower odds for moderate (OR = 0.2, 95%CI 0.16 – 0.26) than in factory A which is in agreement with Harley *et al.* (2012). No differences were found for severe tail lesions, probably due to the lower occurrence of severe scores. The effect of factory could have been confounded by farm characteristics as typically more pigs from larger batches were supplied to factory B. Pigs from larger batches had a lower odds for severe tail lesions (OR = 0.5, 95%CI 0.21 – 1.16, $P < 0.05$) than pigs from small batches. Different management procedures in these farms could make them more equipped to deal with tail biting.

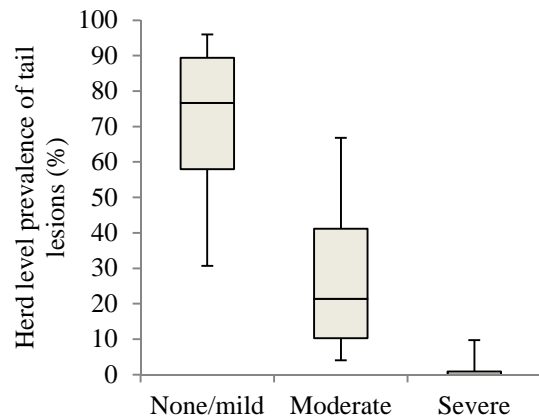


Fig. 1. Range of herd level prevalence of none/mild, moderate and severe tail lesion outcomes

Conclusions

Tail lesions are common in Irish slaughter pigs. While these are mostly moderate in severity our results prove that tail biting is present in some form on all pig farms. The multi-factorial nature of the tail biting problem is emphasized by the large variation between farms in the different severity outcomes for tail lesions. Most of the variation occurred in none/mild and moderate tail lesion categories showing that there is room for improvement in different farms. This emphasizes the potential of incorporating different degrees of severity of tail lesions in the meat inspection process as a welfare diagnostic tool. Future work should focus on identifying risk factors for moderate tail lesions and possible relationships with farm performance parameters.

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Grasslands carbon sequestration potential

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Introduction

Soil organic matter (SOM) is important in agricultural systems; it supplies nutrients, enhances soil structure and water infiltration, reduces risk of erosion and soil crusting, and improves root development. Soils are the second largest carbon (C) pool after the oceans. Through mineralisation, soil organic carbon (SOC) is lost to the atmosphere as CO₂, contributing to the greenhouse gas effect. Therefore, the capture and storage of soil organic matter not only affects soil quality, but aids mitigation of climate change. Soils are made up of a variety of building blocks, known as aggregates. Aggregates are found in a range of sizes: a) very recalcitrant silt and clay-sized aggregates (<53 µm), b) microaggregates (53-250 µm) in which occluded organic matter is protected from microbial breakdown, c) macroaggregates (250-2000 µm) containing microaggregates held together by particulate organic matter (POM), and d) large macroaggregates (>2000 µm), which consists of groups of macroaggregates and sand held together by POM (Six et al., 1998). The type of aggregates present in a soil is thought to be important in terms of C stability. SOM contained inside aggregates is not easily available to microorganisms (Bronick and Lal, 2005), thus avoiding mineralisation, and consequently CO₂ emissions. Understanding the key mechanisms for soil aggregation and therefore the potential SOC storage capacity of soils is vital for long term mitigation of climate change. The objective of the current research is to determine the national baseline of SOC fractions associated with grassland soils in Ireland, the sequestration potential and long-term stability according to soil type.

Materials and methods

Forty grassland sites were selected, in conjunction with the Irish Soil Information System project, according to their soil type; Typical Brown Earths (TBE), Humic Brown Earths (HBE), Stagnic Brown Earths (HBE), Stagnic Luvisols (SLU), Typical Luvisols (TLu), Typical Lithosols (TLi), Typical Surface-water Gleys (TSWG) and Humic Groundwater Gleys (HGG), to provide a spectrum of soil properties from a representative range of Irish soil types. 1 kg of soil was collected from all horizons to 1 m depth at each site and stored at 4°C. A 300 g subsample of the 1 kg soil was passed through an 8 mm sieve, dried at 40 °C and stored at room temperature. The wet sieving method described by Six et al. (1998) was used to fractionate samples into large macroaggregates (>2000 µm), macroaggregates (250-2000 µm), free microaggregates (53-250 µm) and silt & clay (<53 µm). Briefly, 80 g of the air dried subsample was immersed in distilled water on top of a 2000 µm sieve for five minutes. The sieve was then agitated for 3 minutes at a rate of 33 movements per minute. Large macroaggregates were collected from the sieve. The same procedure was repeated with a 250 µm

sieve for macroaggregates, and 53 µm sieve to separate microaggregates from silt and clay. All fractions were dried at 50 °C, weighed and analysed for C and nitrogen (N) with a LECO Truspec CN Analyser.

Results and Discussion

Comparing the first horizon of the above named soil types, no differences were found in terms of C content in each aggregate size. Figure 1 shows data for all horizons illustrating the percentage of total C contained in each aggregate size. It can be observed that soil types of a related nature follow similar trends. Brown Earth soils contain more C in their macroaggregates, while there is a higher percentage of C in microaggregates for the two Luvisols, followed by the Typical Surface Water Gley. The same trend can be observed in the <53 µm fraction. Luvisols are, according to the Irish Soil Classification Key, soils with clay enriched subsoil. This aligned with the results presented by Power and Prasad (1997), who found that OM content was two to four times greater in clayey soils than in sandy soils. Due to its colloidal nature, clay has a large surface area, which attenuates SOM (Rice, 2002). Different soil types have, if depth is considered, different SOC sequestration potential, as OM occluded in <250 µm aggregates is stored and stabilised for the long term due to its slow turnover (Six et al., 1998).

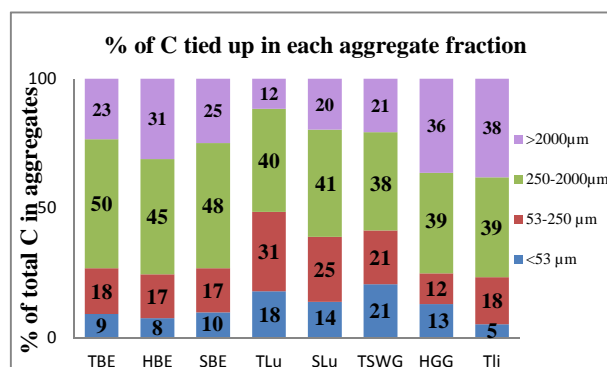


Fig. 1. Total C % present in each aggregate fraction.

Conclusions

The C sequestration potential was greatest with the microaggregate and silt&clay fractions. These were most prevalent in lower horizons of Luvisols and Surface-water Gleys. In general, accounting for C stocks and modelling, total OC is only analysed to the first 30 cm. This research showed that analysis of horizons deeper than 30 cm and SOM fractionation is needed in order to capture the real C storage potential.

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Deriving bulk density from Pedotransfer functions to calculate accurate soil organic carbon stocks

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Introduction

Soil organic carbon (SOC) plays a major role in the global carbon budget and can act as a source or a sink of atmospheric carbon, thereby influencing the course of climate change. However the estimate of the SOC pool depends upon suitable data in terms of organic carbon content and soil bulk density and on the methods used to upscale point data to comprehensive spatial estimates. Whereas information on SOC in relation to soil type can be found in national soil survey databases (Hollis *et al.*, 2006; Batjes, 2005), bulk density is often poorly documented. Bulk density (D_b) measurements are commonly missing from databases due to sampling constraints, such as difficulties when samples are taken (too stony the soil) or cost of sampling, as this is a labour intensive field method. Pedotransfer functions (PTF) based on easily measured soil attributes, such as organic carbon and clay content, show strong potential to replace D_b measurements when their direct measurement is not feasible. However, bulk density has been found to vary with depth (Leonavičiūtė, 2000) and soil group (Manrique and Jones, 1991) and the use of generic pedotransfer functions, can result in large errors in the calculation of SOC stocks. The aim of the work was to test and select the best of 10 published PTFs, using data from the recent Irish Soil Information System project with 430 measured D_b across different genetic soil horizons, to facilitate accurate calculation of SOC stock at 1 m depth.

Materials and Methods

In 2014 Teagasc released a new national soil map and associated database (Irish Soil Information System). This database has data of 563 pits from the soil survey of An Foras Talúntais and 246 pits described over the last 2.5 yrs. Data on measured D_b , texture and C content was available for 471 horizons. Of the total dataset, 432 samples were utilised to select and recalibrate PTFs from the literature for each horizon designation (Ap, Ap1, Ap2, Apg, Ah, O, E, AB, Bw, Bg, Bs, Bt, Btg, BC, C and Cg) and 39 samples were used for the validation. Since for both datasets the same sampling and analysis methods were used, validation can be considered to be internal. Pedotransfer functions (PTF) were applied to each horizon using equations derived from the literature, following key papers in this subject. For mineral soils eight were applied: Manrique and Jones (1991); Bernoux *et al.* (1998); Leonavičiūtė (2000) (x4); Kaur *et al.* (2002) (x2). For organic soils four PTF were applied from the literature: Jeffrey (1970); Manrique and Jones (1991); Tamminen and Starr (1994). Profiles were split by horizon and the average measured bulk density for each horizon type was calculated (D_{bM}). This was then compared to the predicted D_b and the most appropriate PTF was selected. The coefficient of the determination (R^2) of the fitted regression between the actual and predicted D_b values was calculated. Following the methodology of De Vos

et al. (2005) a validation of the predicted D_b was carried out for the 39 horizon samples extracted for validation.

Results and Discussion

The selection of the best PTF for each horizon was applied calculating the best fitted regression model (R^2). Green colours show the PTF selected in each case.

Table 1. Available information for each horizon is listed about the number of sample (n) and the coefficient of determination (R^2) of the fitted regression (when available).

		Bernoux (1998)	Kaur (2002)	Kaur (2002) intrinsic	Leonavičiūtė (2000) (A)	Leonavičiūtė (2000) (B)	Leonavičiūtė (2000) (BC-C)	Leonavičiūtė (2000) (E)	Manrique & Jones (1991)	Jeffrey (1970)	Tamminen & Starr (1994)
HORIZON	n										
Ap	114	0.46	0.57	0.57	0.56	0.42	0.42	0.40	0.57		
Ap1	30	0.57	0.75	0.60	0.74	0.54	0.52	0.52	0.70		
Ap2	16	0.40	0.36	0.25	0.36	0.30	0.35	0.26	0.36		
Apg	22	0.59	0.69	0.50	0.69	0.59	0.55	0.55	0.69		
Ah	16	0.34	0.34	0.42	0.36	0.13	0.17	0.43	0.31		
Ag	13	0.34	0.59	0.38	0.58	0.60	0.59	0.55	0.63		
Bw	54	0.09	0.32	0.21	0.35	0.33	0.10	0.36	0.28		
Bg	59	0.21	0.22	0.04	0.19	0.25	0.19	0.25	0.92		
Bs	7	0.35	0.64	0.43	0.79	0.50	0.65	0.57	0.31		
Bt	9	0.59	0.59	0.96	0.59	0.82	0.84	0.78	0.96		
Btg	15	0.57	0.59	0.21	0.40	0.65	0.18	0.63	0.69		
BC	15	0.09	0.55	0.26	0.41	0.58	0.28	0.55	0.59		
C/Cl/Cr	21	0.06	0.22	0.12	0.09	0.33	0.03	0.27	0.34		
Cg	12	0.02	0.71	0.52	0.63	0.39	0.33	0.41	0.64		
Btg	15	0.41	0.07	0.24	0.09	0.26	0.33	0.26	0.19		
E	10	0.40	0.61	0.78	0.62	0.52	0.44	0.57	0.49		
O	24								0.45	0.22	0.49

Conclusions

For almost half of the horizons, the Manrique & Jones PTF showed to be the best-fit. Thereafter, the Bernoux PTF was best-fit for four horizons. The Kaur, Leonavičiūtė (B), Leonavičiūtė (BC-C) and the Jeffrey PTFs did not present a best-fit for any horizon. In some cases, the results for the best-fit PTF did not yield a very strong correlation (e.g.<0.4 Manrique and Jones, Bg horizon).

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Integrating soil characteristics, land management and soil microbial communities

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Introduction

Microorganisms are the drivers of nutrient cycling, in particular improving the ability of plants to absorb nutrients, but also protecting from environmental stress and disease. Despite the vital role that soil microbes play, we understand only a fraction of their ecosystem function in relation to improving plant growth and soil health. A better knowledge of the impact of environmental factors on microbial community structure and potential function will lead us to closer understanding of the differences in soil productivity. An extensive dataset of microbial, physicochemical, soil type and land use parameters were collected in this project in conjunction with the Irish Soil Information System project with the aim of identifying the main environmental drivers of soil microbial biomass and functionality in Ireland.

Materials and Methods

Soil samples were collected from surface horizons of 156 soil pits, exposed around Ireland during a national soil survey (2012-2013). Standard soil chemical and physical parameters described by Doran and Parkin (1996) were analysed in the lab after soils were dried and sieved to 2 mm. Soils for microbial analysis were stored at 4°C until arrival in the laboratory. Following sieving to 2 mm, soils were incubated at 20°C for one week prior to analysis. The fumigation extraction method was applied using a Shimadzu TOC-TN analyser for measuring microbial biomass ($\mu\text{g C g}^{-1}$ dry soil) nitrogen (N_{mic}), carbon (C_{mic}) and extractable extracellular carbon (C_{ext}). For the calculations, a conversion factor of 0.45 was used (Solaiman, 2007). The MicroRespTM (Creamer *et al.*, 2009) method was used to analyse carbon respiration from 7 carbon substrates and water (Fig. 1). Respiration rates were calculated ($\mu\text{g CO}_2\text{-C g}^{-1} \text{ h}^{-1}$) from an independent calibration curve after 6 hour incubation at 25°C. For statistical analysis all non-normal variables were log transformed and soils were grouped into 11 soil types (Irish Soil Classification System), 2 land-use types (improved and unimproved grassland) and 3 drainage categories (poor, moderate, well). The Pearson correlation and regression modelling using Statistica 12 (StatSoft Inc., 2010) as well as Canoco 4.5 were applied to identify significant correlations and environmental predictors for microbial biomass and function. Anova (with post hoc Tukey HSD for unequal n) was used to identify differences between land-use, soil type and drainage categories. The level of significance accepted for all analysis was $p < 0.05$.

Results and Discussion

Abiotic properties such as MC (%), OM (%), N (%) and pH significantly enhanced the response of the microbial community to a range of soil carbon sources

(Fig. 1). These properties (except pH) were also strong predictors of C_{mic} , N_{mic} and $C_{\text{mic}}/N_{\text{mic}}$ ratio, with pH for the latter showing a negative effect.

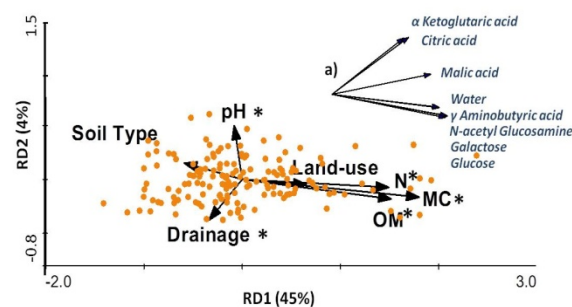


Fig. 1 Redundancy analysis of all respiration data using environmental soil properties to explain the variance between samples. RD percentage variation is displayed in parenthesis, * indicates significance of $p < 0.05$. a) Loading plot of carbon substrates used in MicroResp assay.

Interestingly soil types which are associated with poor drainage capacity (Alluvial, Groundwater- and Surface-water gleys) had a higher significant mean C_{mic} but lower respiration rates per mg biomass for all substrates compared to moderate and well drained soils. Poor drainage was also positively correlated to clay (%) and OM content but significantly negatively correlated to the $C_{\text{mic}}/\text{organic carbon}$ and $C_{\text{ext}}/C_{\text{mic}}$ ratio. These findings suggest that the microbial community in poorly drained soils may have adapted to prolonged periods of anaerobic conditions and therefore do not metabolize added substrates as efficiently. Average microbial biomass and respiration were higher for grassland unimproved compared to grassland improved soils. The ratio of basal to substrate induced respiration can be used as a measure of soil intrinsic substrate availability. This measure was significantly lower for grassland unimproved soils indicating a greater nutrient balance within these soils.

Conclusion

This study identified significant trends in microbial biomass and activity related to OM, N, MC, land use types and soil drainage categories. It also highlights that microbial parameters are sensitive to multiple environmental variables, and to understand and improve soil productivity these factors need to be considered.

Acknowledgement

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Phosphorus sorption and supply potential in grassland soils with contrasting chemical properties

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Introduction

An adequate supply of phosphorus (P) in agricultural soils is essential to meet the demands for crop growth and grazing animal health. However, the finite nature of this resource and Europe's dependence on fertiliser P imports is putting its supply under pressure as reserves are diminishing, (Cordell *et al.*, 2009). Whilst it has been accepted that no soil test for P availability is universal, recent research has indicated that increases in P use efficiency can be achieved with improvements in soil testing methods that incorporate soil properties into agronomic advice. Phosphorus sorption and buffering controls the supply of P in available form and the objectives of this present study were to examine the variation in these attributes across contrasting soils and discuss their significance in controlling soil P supply to plants in Irish soils.

Materials and Methods

One hundred and twenty soil samples (100 mm depth) were collected from a range of Irish soil associations, and across a range of soil test P levels (Morgan's P). Phosphorus buffering capacities were derived from sorption isotherm studies in which six solutions of P concentration were added to 2 g soil and the P sorbed calculated as the difference between initial and final P concentration. These data were fitted to the Langmuir isotherm equation: $C/X = 1/X_m \cdot b + C/X_m$, where X is P sorbed (mg P kg^{-1}) and C is the equilibrium P concentration (mg P l^{-1}). The linear Langmuir equation was then used to derive X_m , the sorption maximum (mg P kg^{-1}) and b, a constant related to the binding energy (l mg^{-1}). Maximum buffer capacity (MBC, kg^{-1}) was calculated as the product of X_m and b and represents uptake and supply functions in soil. Available P was measured using a P sink method (iron-oxide paper strip test), using one FeO-impregnated paper strip (100 x 20 mm) added to each soil sample of soil (1g) in 40 ml of 0.01M CaCl_2 solution and shaken for 16 h. Mehlich3 reagent was also used to extract P, Al, Fe, Ca. Soil pH was measured on all samples. Soil data were analysed using SAS Enterprise Guide V5 to construct correlation and regression. The NLMIXED procedure in SAS was used for change-point analysis and broken-line regression.

Results and Discussion

Langmuir sorption buffer capacities (MBC) and binding energies (b) were strongly correlated with soil pH and extractable aluminium (Al). A broken-line regression fitted to the relationship between MBC and Al and derived a change-point value for Al above which MBC increased linearly (Fig. 1). Soils above the change point were predominantly acidic to neutral with non-calcareous parent material and exhibited higher

buffering capacities compared to calcareous soils. These soils were examined further by calculating ratios of Mehlich3-Al and P (Al/P) to represent ability to supply P, and the relationship with available P is presented in Fig. 2. High ratios of Al/P were associated with low P availability, characteristic of high P fixing soils. A threshold value of Morgan's P ($\sim 7.3 \text{ mg l}^{-1}$) revealed Al/P ratios below which soils began to supply P more freely. The change-point for Morgan's P fell within the current target index for P availability (Fig. 2) however, the confidence interval was more compatible with the previous agronomic P indices used for grassland.

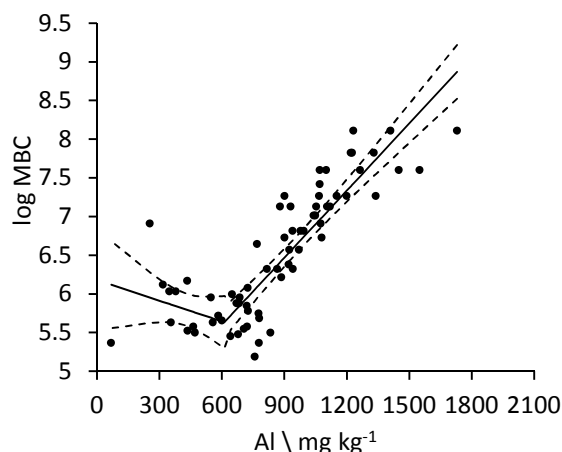


Fig. 1. Relationship between MBC and Al in soils.

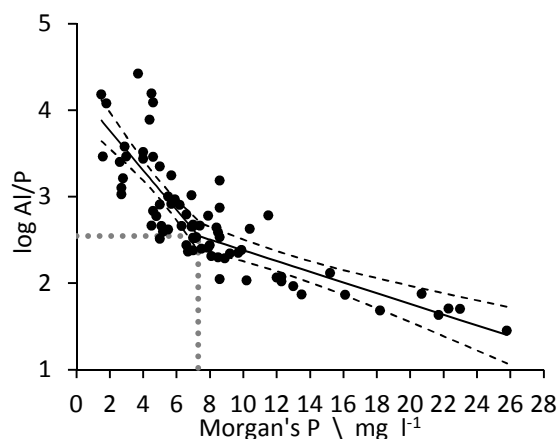


Fig. 2. Variation in Al/P with available P in acidic to neutral soils.

Conclusions

This work highlighted the important influence of soil properties, such as extractable Al, on the P supply potential in soils. It showed differences in P dynamics between acidic and calcareous soils and indicated that soil properties should be considered in conjunction with traditional soil tests in future P management strategies.

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Effects of meteorological and soil data on unsaturated time lag estimates

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Introduction

The European Union Water Framework Directive (WFD) requires member states to attain good water status within designated reporting periods, the first of which is 2015. However, the efficacy of mitigation measures (e.g. the Nitrates Directive) can only be assessed after elucidation of total time lag (t_T) (unsaturated (t_u) and saturated (t_s)) (Fenton *et al.*, 2011). This study focuses on t_u . The objective of this study was to determine the effects of 1) hourly versus daily meteorological data resolution, and 2) simple to complex soil hydraulic parameter analyses on estimated t_u using the Hydrus 1D numerical model.

Methods

For objective 1, transport of a conservative tracer through a soil profile was simulated in Hydrus 1D for 12 soil textural classes, using either daily or hourly meteorological data. A soil profile with depth of 50 cm was modelled with atmospheric and free-drainage boundary conditions imposed at the top and bottom of the profiles, respectively. For objective 2, the same methodology was applied (using the meteorological data time step identified in objective 1) to nine real soil profiles from Co. Waterford. For this objective, simulations were repeated for each soil profile using hydraulic parameters derived from: A) textural class, B) particle size distribution, C) a partial soil water characteristic curve (SWCC) excluding the arduous -15 bar pressure step, or D) a full SWCC. The resulting solute breakthrough curves were divided to indicate initial breakthrough (IBT, yr) which informs monitoring campaigns, centre of mass (COM, yr) which identifies the predominant effect of mitigation measures on water quality and full exit (Exit, yr) used in estimation of long term t_T .

Results and Discussion

For objective 1, differences between hourly and daily meteorological data in IBT at 0.5 m never exceeded 0.01 yr. For COM, differences ranged between 0.02 and 0.28 yr, as clay content increased. For Exit, differences of 0.10 to 0.42 yr were observed. For these two latter markers, daily data overestimates t_u , relative to hourly data. These results suggest that where the latter components of solute transport are of primary concern, hourly data should be preferred, which in practice are readily available from synoptic recording stations.

For objective 2, IBT estimates, according to the four complexity levels, showed minor differences (av. 0.08 yr) (Fig. 1). However, generic soil data (Options A and B) underestimated t_u by 0.28 to 0.97 yr, compared to when the full soil dataset (Option C) was employed (Fig. 2). Underestimation of t_u by using such data could result in unrealistic expectations regarding the attainment of WFD goals. Excluding the -15 bar pressure step from the SWCC, Option C typically had a minor effect on t_u (av. 0.08 yr) compared to Option D, suggesting that its omission may be justified.

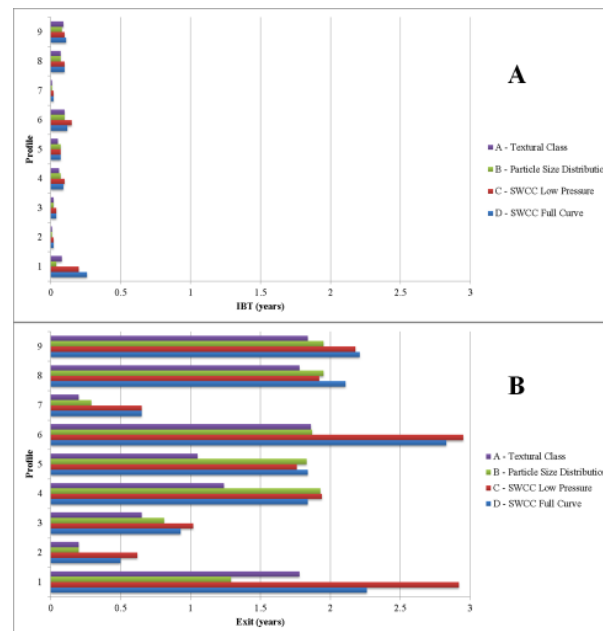


Fig. 1: A) Initial breakthrough (IBT) and B) full tracer exit at base of soil profile for nine Waterford soils using various soils data inputs (A-D).

Conclusions

For a holistic assessment of t_u , hourly rather than daily meteorological data are recommended. However, for assessing IBT alone, daily data are sufficient. With respect to soil data complexity, where IBT is of primary interest, generic soil data are sufficient. However, within the context of the WFD where the period between implementation of mitigation measures and subsequent reporting periods are short, COM and total solute exit are of interest to policymakers. Measurement of the SWCC is required to accurately predict these components of t_u . Underestimation of solute exit poorly reflects the prolonged leaching of contaminants at low concentrations. Furthermore, these results do not preclude greater t_u in particularly deep or slow draining soil profiles. Full details of this study are available in Vero *et al.* 2014.

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Using sediment fingerprinting to target soil erosion management strategies

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Introduction

Cost-effective management of soil erosion and in-stream sediment is important to prevent the deterioration of soil and freshwater resources. Knowledge of the relative contribution of sediment from different erosional sources is an important element in better management, but quantification of these is traditionally resource intensive. Novel techniques such as sediment fingerprinting offer an alternative approach to identify sources and estimate specific contributions. Distinctive physico-chemical properties, or 'tracers', are used to define signatures for each potential source. Sediments transported to a river sampling point therefore comprise a mixture of upstream sources, which can be variously characterised as either surface soils versus channel banks (or spatially differentiated on the basis of geology and/or land use). Sediment fingerprinting mathematically 'un-mixes' delivered sediment to its upstream sources, providing quantitative estimates of relative contributions. This study aims to identify sediment sources to inform soil management strategies in a 10 km² poorly-drained grassland agricultural catchment in Ireland

Materials and Methods

Source sampling targeted seven potential field and non-field sources; eroding channel banks (n=55), road verges (n=44), topsoils (n=35), subsoils (n=32), tracks (n=6), in-field drains (n=2) and eroding ditches (n=5). Non-field sources were surveyed across the catchment and active erosion areas sampled. Field samples were considered sufficiently representative of catchment soil types and land uses. For one year, commencing in March 2012, eroded sediments were captured using time-integrated suspended sediment samplers, with composite samples typically spanning 6-12 weeks. Soil and sediment samples were dried at 40°C, manually ground and sieved to 125 µm, representing the most biogeochemically active 'fine fraction', and to minimise effects of particle size enrichment. Mineral magnetic measurements were used to characterise each sample. Magnetic susceptibility (high and low frequency), anhystereic and isothermal remanence (40 mT, 100 mT, 300 mT and 1 T) were conducted and six ratios describing magnetic grain size and character were established. These data were statistically un-mixed using the FR2000 algorithm. Estimated source contributions were applied to the measured sediment load (using high-resolution turbidity and discharge data) relating to each sampler installation period.

Results and Discussion

Using the magnetic tracers, multiple discriminant analysis (Fig. 1) identified three 'parent' source groups: channel banks (channel banks and ditches), roads (road verges and tracks) and fields (topsoils, subsoils and in-

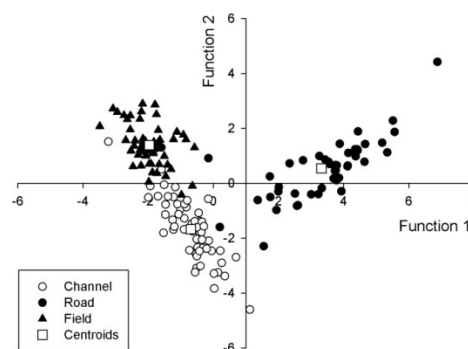


Fig 1. Multivariate discriminant diagram – illustrating the statistical 'separation' of source groups

field drains). Sediment loads were seasonally dependent through the monitoring period (Fig. 2). Winter sediment loads (October to February) were greater than summer sediment loads except for the May to July 2012 period. This is attributed to greater rainfall over the winter months. Over the whole monitoring period, 57% of sediment was attributed to channel sediments, 25% to fields and 18% to roads. During winter months, channel sources were dominant; because of greater stream power combined with seasonal weathering of bank forming materials. Greater contributions of field sediment during summer months suggest a combined effect of intensive stock grazing reducing protective vegetation cover, greater soil compaction and source area expansion due to excessive rainfall amounts. Marginal areas of arable land use could also be important contributors. Channel bank contributions during summer months may be reduced by increased riparian and in-stream vegetation.

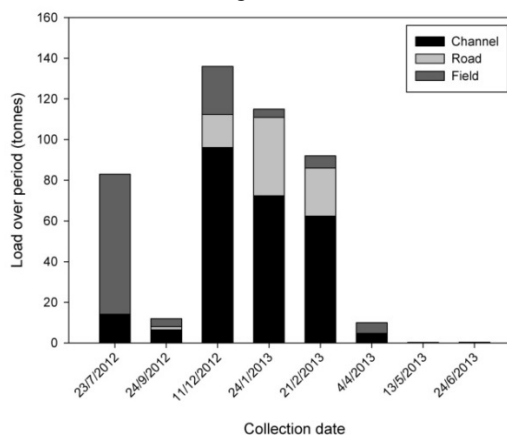


Fig 2. Load specific un-mixing of suspended sediment sources

Conclusions

Sediment fingerprinting is a valuable tool. In this poorly drained grassland catchment, channel banks contributed the largest proportion of sediment to the river channel and are, therefore, a management priority. Soil erosion and export from fields was seasonally important, and should not be neglected.

Acknowledgements

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Visual drainage assessment: A standardised approach to land drainage design in the field

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Introduction

Ideally, land drainage design should be based on a full characterisation of soil physical and hydraulic properties and the input of such data to standard steady-state drainage design equations to elucidate appropriate drain spacing and depth (Skaggs *et al.*, 2012). In spite of the availability of in-situ and lab based methods for quantifying soil drainage properties (Bouwer and Rice 1983; Van Beers, 1983), such methods are usually disregarded by practitioners in the field due to inexperience and time and monetary constraints. As such most drainage scheme designs have no scientific basis and are formulated in accordance with local common practice and the experience of the contractor(s) employed to install the drainage system. This approach may or may not be effective dependent on site specifics. Some expert practitioners have developed methods of deciphering pertinent soil characteristics and designing drainage systems in the field. However such methods are subjective and as a result non-transferable. The design method established herein is called visual drainage assessment (VDA) and provides a standardised mechanistic method of effective land drainage design in the field that is accessible to all stakeholders involved in land drainage. The objectives of the study were to compare designs developed using a) the VDA method b) an optimal method and c) a fixed generic design for sites on six poorly drained farms in south-west Ireland.

Material and Methods

The spacing and depth prescribed by the three design methods for each site were compared by model estimate of discharge (mm/day) and watertable (WT) control (minimum WT depth, m) capacity. Discharge and WT depth data were analysed using ANOVA with design method as a fixed effect. The VDA method is based on nine visual indicators (water seepage, texture (sand/silt/clay %), absence or presence of pan layers, structure, porosity, plasticity, stone content, colour/mottling and root development) chosen to permit inference of soil permeability or to identify characteristics that inhibit or promote particular drainage techniques. Multiple (typically 2-3 per site) soil test pits (2.5-3.0 m deep) were excavated at representative locations on each site and examined with respect to each of the indicators. Discrete soil horizons were classified as highly, moderately or poorly permeable based on indicator characteristics and appropriate drain depth and spacing were then prescribed. For the optimal method, saturated hydraulic conductivity (k_s) (measure of permeability) data obtained from soil samples collected from a range of depths in soil test pits were used as inputs to standard drainage design equations to establish optimum depth

and spacing, assuming a design drainage discharge value of 12 mm/day and a minimum WT depth of 0.45 m. A fixed generic drainage design (0.8 m deep drains at 15 m) was also prescribed for each site.

Results and Discussion

The VDA methodology delivered a reasonable estimation of the permeability of various soil horizons. All VDA designs were similar to the optimal design at each site in terms of prescribed drain depth and spacing (Table 1). Mean estimated drainage discharge capacity from the VDA (13.3 mm/day) and optimal (12.0 mm/day) designs were significantly higher ($P < 0.001$, s.e. 1.42 mm/day) than from the generic designs (0.5 mm/day). Mean estimated minimum WT depth from the VDA (0.49 m) and optimal (0.45 m) designs were significantly higher ($P < 0.001$, s.e. 0.057 mm/day) than from the generic designs (0.0 m).

Table 1. Estimated drainage system performance and comparison of drainage design methods at each site

Site	Design method	Spacing (m)	Depth (m)	Drainage discharge ¹ (mm/day)	Minimum WT depth ² (m)
1	VDA	15.0	1.60	15.6	0.73
	Optimal	17.2	1.50	12.0	0.45
	Generic	15.0	0.80	1.0	0.00
2	VDA	15.0	1.70	10.7	0.29
	Optimal	14.1	1.50	12.0	0.45
	Generic	15.0	0.80	0.6	0.00
3	VDA	20.0	1.70	11.7	0.42
	Optimal	19.8	1.60	12.0	0.45
	Generic	15.0	0.80	0.9	0.00
4	VDA	1.4	0.60	14.3	0.60
	Optimal	1.6	0.50	12.0	0.45
	Generic	15.0	0.80	0.1	0.00
5	VDA	1.5	0.45	13.9	0.45
	Optimal	1.7	0.50	12.0	0.45
	Generic	15.0	0.80	0.1	0.00
6	VDA	1.5	0.45	13.7	0.44
	Optimal	1.6	0.50	12.0	0.45
	Generic	15.0	0.80	0.0	0.00

Note: VDA = Visual drainage assessment, WT = watertable, ¹assuming a minimum WT depth of 0.45 m, ²assuming a rainfall recharge of 12 mm/day

Conclusions

The VDA methodology described provides the industry with a standardised method of approaching land drainage design in the field where the permeability of the soil is not measured but interpreted by visually and manually examining the soil profile. The estimated performance of drainage systems designed by VDA was much better than that attainable by generic design and was similar to that achievable by the optimal design. The method needs to be developed further and validated over a wider range of site and soil conditions.

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An Investigation into the Impact of an Aggregate Isolation Procedure on Microbial Community Composition

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Introduction

Soil aggregates, or more particularly, the intra-aggregate space, provide a habitat for soil micro-biota. Determining soil microbial community composition and functionality at the aggregate scale may be a critical factor in understanding the C and N biogeochemical cycling potential of soils (Bach and Hofmockel, 2014). The 'wet-sieving' approach is the most common method of aggregate isolation. This method involves submerging air-dried soils in distilled water (slaking), causing air trapped in the soil matrix to form a pressure gradient resulting in a breakdown of all but the most stable aggregates (Elliott, 1986). This method is commonly used for studies on microbial community composition (e.g. Mummey and Stahl, 2004; Kong *et al.*, 2011; Davinic *et al.*, 2012). Despite this, few studies have addressed how the various steps in this process (drying, sieving, re-wetting and slaking) will, in combination, affect the microbial community of the soil in question. In this study, we investigated the effect of the wet-sieving process on microbial community composition and related these findings back to the microbial community composition of the bulk soil.

Materials and Methods

Soil horizon samples (300g) were taken from three grassland sites in the Mid-Western region of Ireland in August 2014 and stored at 4°C during transportation. The samples were subsequently homogenised and sieved (8 mm) and a subsample stored at -80°C. This was the bulk soil sample (BSS). The remainder was dried at 40°C for 1 week. Approximately 80 g of dried soil was fractionated through a series of >2 mm, >250 µm and > 53 µm sieves to obtain large macroaggregate, macroaggregate and microaggregate fractions respectively. Material < 53 µm was deemed the silt and clay fraction. Each of the obtained soil fractions were dried at 50°C for 1 week, weighed, and a subsample stored at -80°C. DNA was extracted from soil samples using the Powerlyzer® Powersoil® DNA isolation kit (MO BIO Laboratories Inc. USA). The diversity of the bacterial community was analyzed via 16S rRNA gene based PCR and subsequent Denaturing Gradient Gel Electrophoresis (DGGE). Bulk soil samples were compared against its corresponding 'combined fractions' sample (CFS) (where the 16S rRNA gene of each individual fractions was amplified separately and combined post-PCR). Resultant DGGE profiles were analysed using phoretix advanced 1D software (Nonlinear Dynamics) and an UPGMA (unweighted pair group with arithmetic mean) dendrogram was constructed.

Results

The DGGE community profile from the CFS did show changes when compared against its corresponding BSS, with each forming distinct clusters on an UPGMA dendrogram (Fig. 1).

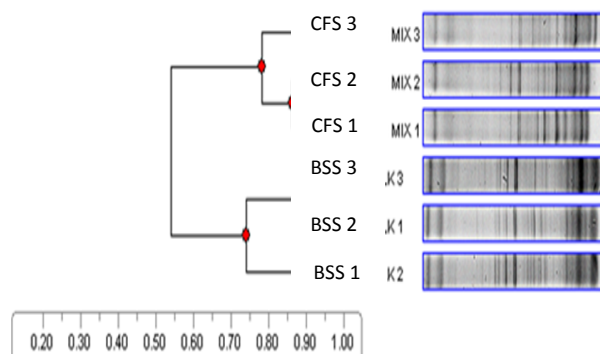


Fig. 1. UPGMA dendrogram of the DGGE fingerprints of 16S rRNA gene fragments of BSS (BULK) and corresponding CFS (PCR MIX).

Conclusions

Changes in bacterial community composition were reported after soil fractionation. The variation reported here, however, more likely resulted from separate PCR reactions for each fraction (i.e 'rare' species being PCR amplified in the fraction sample which would not have been in the BSS) than any inherent changes incurred during the fractionation procedure. This experiment will be repeated with a greater number of replicates using terminal restriction fragment length polymorphism (T-RFLP). Characterizing changes to the aggregate microbial community incurred from this method is critical for further studies examining the role of this community in soil biogeochemical cycles.

Acknowledgements

We would like to acknowledge the Teagasc Walsh Fellowship scheme for financial support

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The production potential of multispecies swards at varying annual nitrogen inputs in the post establishment year

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Introduction

In order to achieve an increase in food output from grassland-based ruminant production systems in the future it will be necessary to increase grassland productivity without increasing inputs such as chemical fertilisers (Foley *et al.*, 2011). Multispecies swards (by increasing species richness) can increase biomass production from lower inputs of nitrogen (N) compared to conventional monospecies perennial ryegrass (PRG) swards (Nyfeler *et al.*, 2009). However, the suitability and longevity of multispecies swards in a frequently defoliated system are largely unknown. The aim of this study was to quantify the annual growth performance of multispecies mixes in the post establishment year at varying levels of N input and identify if functional group inclusion caused transgressive over-yielding.

Materials and Methods

Eight pasture mixes were selected using a constrained simplex-centroid design with different proportions of nine species from three functional groups; three grasses, three legumes and three herbs. The constraint imposed on the design was that there must be at least 40% grass in each mixture (no more than 60% legume or herb). The three grasses were PRG (*Lolium perenne*), timothy (*Phleum pratense*) and cocksfoot (*Dactylis glomerata*), the three legumes were white clover (*Trifolium repens*), red clover (*Trifolium pratense*) and birdsfoot trefoil (*Lotus corniculatus*), and the three herbs were plantain (*Plantago lanceolata*), chicory (*Cichorium intybus*) and yarrow (*Achillea millefolium*). The 8 pasture mixes were repeated at three levels of species richness, with one, two or three species per functional group. For example, level 1 had one species from each functional group and level 2 had two species from each functional group (8 mixes x 3 levels of richness = 24 mixes in total). The design was replicated at four different nitrogen (N) fertiliser application rates (0, 45, 90 and 135 kg N/ha/y), resulting in a total of 96 plots (24 mixes x 4 N rates). The plots were sown at UCD Lyons Estate Research Farm in August 2013. In the post establishment year the plots were harvested to a known height (4 cm) every 28 days from the 9 April to the 23 October 2014 in a simulated grazing routine. Total plot fresh yield was weighed by the Haldrup forage harvester (Logster, Denmark) and a sample of herbage was taken and dried at 45°C for 72 hours for dry matter (DM) determination. The design of the experiment facilitated the analysis of interactions between the three functional groups. The null hypothesis stated that there would be no diversity effect while the alternative hypothesis stated that there would be a positive diversity effect. The analysis is based on multiple linear regressions and was conducted using Minitab 16.

Results and Discussion

There were positive interactions between species from the functional groups i.e. there was a diversity effect (Fig 1). Legume containing mixes contributed to an increase in annual production compared to when grasses or herbs were included in the mix for the post establishment year ($P < 0.0001$) across the four N treatments (Fig 1). Fig 2 shows the contour response plane for the autumn DM production from harvest 6 (21 August) to harvest 8 (23 October) across the four N levels. Autumn DM production was > 3000 kg DM/ha when legumes were dominant in the mix and 500 kg DM/ha when grasses and herbs were dominant in the mix. There was also an increased yield in response to N especially in the grass dominant mixes ($P < 0.001$).

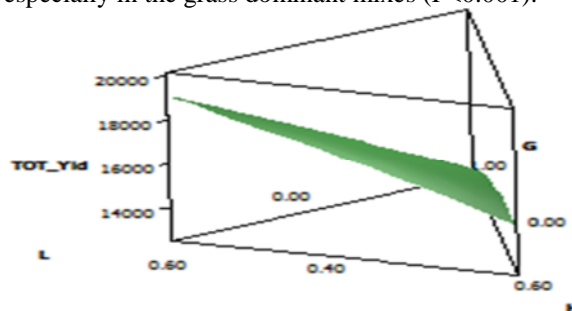


Fig. 1. Surface response plane for total annual production (TOT_Yld kg DM/ha) across the four N treatments, where G=grass; L=legume; H=herb

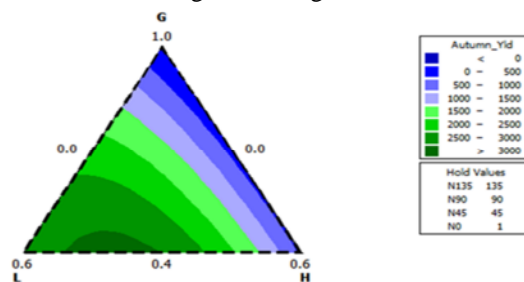


Fig. 2. Contour response plane for autumn yield (Autumn_Yld kg DM/ha) across the 4 N treatments, where G=grass; L=legume; H=herb

Conclusion

In the post establishment year, legumes contributed to an increase in DM production compared to when grasses or herbs were dominant in the mixture. Transgressive over-yielding resulted in higher biomass yield at low inputs of fertiliser N in legume containing swards. Further quantification of yield over subsequent years is required to elucidate persistency of this effect.

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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 m² 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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Milk production responses of lactating dairy cows to sward structure differences between perennial ryegrass varieties

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Introduction

Improved efficiency of animal production from grass is the ultimate goal of forage grass breeding for most temperate regions (Wilkins and Humphreys, 2003). Perennial ryegrass varieties form the basis of pasture production in many temperate regions. Sward structure can vary between varieties and has been shown to affect milk production of grazing dairy cows (Wims *et al.*, 2013), though a significant effect on milk production does not always occur (Cashman *et al.*, 2014; Tas *et al.*, 2006). Quantification of animal responses to sward structural differences is a critical step in comparing perennial ryegrass varieties for on-farm value. The objective of this study was to compare the milk production performance of dairy cows when grazing four perennial ryegrass varieties varying in sward structure at two herbage allowances.

Materials and Methods

Four perennial ryegrass varieties comprising two diploids (D) and two tetraploids (T) were sown as monocultures. Varieties included AstonEnergy (T), Delphin (T), Glenroyal (D) and Tyrella (D). Seven cows (two primiparous and five multiparous) were assigned to each variety from 1 July to 28 July at two herbage allowance: 15 and 20 kg DM/cow/day. This resulted in 8 treatments (4 varieties × 2 allowances). Cows were blocked based on lactation number (3.0), milk yield (18.5 kg/d), milk solids (1.4 kg/d), protein (33.7 g/kg), fat (40.5 g/kg) and lactose (47.6 g/kg), and body weight (549 kg) and body condition score (3.0; based on a scale of 1 to 5, 1=emaciated, 5=extremely fat). Fresh grass was allocated to cows daily. Pre- and post-grazing sward heights were measured daily (50 heights per treatment) directly before and after grazing using a rising plate meter with a steel plate (diameter 355mm, 3.5 kg/m²; Jenquip, Fielding, New Zealand). Pre-grazing free-leaf-lamina (FLL) was measured from the highest ligula (longest leaf sheath) to the top of the leaf using a hand-ruler on 100 random tillers across each

offered treatment twice weekly. Approx. 40 g of representative herbage was sampled from each treatment twice weekly to ground level; samples were then cut to the weekly post-grazing height per respective treatment and separated manually into leaf and stem fractions. Fractions were then dried for 16 h at 90°C for DM determination. Individual milk yields were recorded at individual AM and PM milking. Milk solids (protein, fat and lactose) were measured twice weekly. Animal variables were analysed using PROC MIXED in SAS 9.3, with grass allowance, variety, their interactions and pre-experiment covariate included in the model as fixed effects and animal included as a random effect.

Results and Discussion

Although the four varieties had a similar herbage mass (kg DM above 4cm from 12m², not shown), significant variety differences were recorded in all parameters (Table1). AstonEnergy and Delphin were grazed to a lower residual height (4.1, 4.2 cm) compared to the highest, Glenroyal (+0.6 cm; P<0.001). AstonEnergy also had higher FLL (P<0.001), higher leaf (P<0.001) and lower stem (P<0.05) contents than Glenroyal. Importantly, AstonEnergy supported a higher milk yield (+1 kg/cow/d; P<0.05) and milk solids (+0.1 kg/cow/d; P<0.05) than Glenroyal. Delphin was most similar to AstonEnergy in sward structure and gave the same milk production, whereas Tyrella was broadly equivalent to an average of the examined varieties and also supported an intermediate milk output. Increasing herbage allowance from 15 to 20 kg DM/cow/day gave the expected increase milk yield and solids, but also increased the post-grazing sward height (Table1).

Conclusion

Varieties differing in leaf:stem ratio and free-leaf-lamina length by the magnitudes observed in this study were sufficiently different to induce milk production and grass utilisation differences in grazing cows. This could be used to supplement assessments of their on-farm value.

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Table1. The effect of perennial ryegrass varieties and herbage allowance on milk production, pre- and post-grazing sward height, pre-grazing free-leaf-lamina, leaf and stem proportion (1 July – 28 July)

Herbage DM allowance:	15 kg	20 kg	Aston-Energy	Delphin	Glenroyal	Tyrella	SED	Allowance	Variety
Milk yield (kg/cow/d)	15.1 ^a	16.7 ^b	16.3 ^a	16.3 ^a	15.3 ^b	15.7 ^{ab}	0.26	***	*
Milk solids (kg/cow/d)	1.24 ^a	1.35 ^b	1.31 ^a	1.35 ^a	1.23 ^b	1.28 ^{ab}	0.03	***	*
Post-grazing SH (cm)	3.8 ^a	4.9 ^b	4.1 ^a	4.2 ^a	4.7 ^c	4.4 ^b	0.19	***	***
Pre-grazing FLL (cm)	17.5	17.5	18.7 ^{ab}	19.9 ^a	14.1 ^c	17.4 ^b	0.37	NS	***
Leaf (%)	74.0	77.0	82.0 ^a	78.5 ^{ab}	68.0 ^c	74.0 ^b	0.01	NS	***
Stem (%)	17.0	15.0	12.0 ^a	15.5 ^{ab}	19.5 ^b	16.0 ^b	0.01	NS	*

SH = Sward height; FLL = free-leaf-lamina; ^{a-c} Means within a row with different superscripts differ (* = P<0.05; ** = P<0.01; *** = P<0.001)

Finishing autumn-born bulls from pasture in the first half of the grazing season using concentrates

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Introduction

Incorporating a grazing period into suckler bull beef systems comprising spring-born, late-maturing breed types, can reduce production costs but these animals generally require an intensive finishing period indoors pre-slaughter in order to achieve adequate carcass fat cover at a young age (O’Riordan *et al.*, 2011). There may be greater scope for finishing autumn-born bulls at the same age, but off high nutritive value ‘spring grass’, as they are more mature and thus, should have a greater propensity for fat deposition in comparison with more immature spring-born bulls (Owens *et al.*, 1993). The objective of this study was to determine the effects of concentrate supplementation level in the first half of the grazing season on growth and carcass characteristics of autumn-born suckler bulls in contrast with a high concentrate indoor finishing system.

Materials and Methods

Eighty weaned, Charolais and Limousin sired suckler bred bulls (512 days old, s.d. 34.5; 554 kg, s.d. 45.1) previously offered grass silage and one of three concentrate supplements over 90 days, were blocked according to breed type, previous supplement type and weight and, from within block, randomly assigned to one of four finishing treatments: 1) Grass Only (G0); 2) G0 plus 0.25 of predicted dry matter intake (DMI) offered as concentrates (G25) (3 kg fresh weight), 3) G0 plus 0.5 of predicted DMI offered as concentrates (6 kg) (G50) or 4) Barley-based concentrates indoors *ad libitum* with grass silage to appetite (ALC). Bulls were turned out to pasture on 7 April. To ensure that the response to concentrates at pasture was not confounded with differences in herbage allowance or quality, the three grazing groups were allocated herbage of similar pre-grazing height (11.8cm) and mass (2300 kg DM/ha) in adjacent sub-paddocks which differed in area, such that, post-grazing herbage height and herbage mass per hectare was similar for each treatment. Pasture organic matter digestibility (OMD) was 791 g/kg DM. Average residency period per sub-paddock was 5.4 days. Pre- and post-grazing sward heights (rising plate meter), herbage mass (lawnmower cuts) and estimated herbage disappearance per group were measured. Concentrates

were offered once daily in the morning in troughs. Animals were weighed on consecutive days pre-turnout, every three weeks throughout and pre-slaughter. Rumen fluid samples (stomach tube) were obtained on one occasion from each animal two hours after concentrate feeding. For logistical reasons bulls were slaughtered on two days, a week apart. Post-slaughter, carcass weight, conformation and fat score were recorded and the 6-10 ribs joint was dissected 48 hours later. Data were statistically analysed using the GLM procedure of SAS. The model contained fixed effects of diet, slaughter day, their interactions and block.

Results and Discussion

The ALC group had greater ADG, estimated carcass weight gain, slaughter and carcass weight, carcass fat score, rib joint weight and fat proportion, and ultrasonic fat depth at the rib, lumbar and rump than the grazing treatments (Table 1). Bulls offered G50 had a greater ADG ($P<0.05$) and slaughter weight ($P<0.01$) than G0, with G25 being intermediate ($P>0.05$). Carcass weight and carcass gain per day was higher for G50 ($P<0.05$) than G25 and G0, which did not differ ($P>0.05$). Rib joints were lighter ($P<0.05$) for G0 than G25 and G50, which did not differ ($P>0.05$). Rumen pH was greater for the three grazing treatments versus indoors ($P<0.05$). Mean post-grazing sward heights were 4.70, 4.94 and 4.89 cm for G0, G25 and G50 respectively. Corresponding estimates for daily herbage disappearance per animal were 8.67, 7.06 and 4.15 kg DM, and for daily total DMI were 8.67, 9.46 and 8.95 kg. Supplementation for G25 and G50 reduced grass intake by 0.67 and 0.94 kg DM per kg DM concentrate offered. The substitution effect from G25 to G50 was 1.21 kg herbage DM per kg DM concentrate offered.

Conclusion

Proportionately, daily live weight and estimated carcass weight gain for G0 was only 0.52 and 0.56 that of ALC. Supplementation at G50, but not G25, increased these proportions to 0.64 and 0.73, respectively. Concentrate supplementation at pasture did not enhance carcass fat score and all pasture treatments were inadequately finished; mean carcass fat score of <6 (2+).

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Table 1. Effect of concentrate supplementation level on the growth and carcass traits of grazing, autumn-born suckler bulls

	G0	G25	G50	ALC	SEM	<i>p</i> -value
Average daily gain (kg)	0.90 ^a	1.02 ^{ab}	1.10 ^b	1.73 ^c	0.065	*
Slaughter weight (kg)	635 ^a	648 ^{ab}	664 ^b	706 ^c	6.3	**
Kill out proportion (g/kg)	578 ^{ab}	566 ^a	583 ^b	575 ^{ab}	5.3	*
Carcass gain per day (kg)	0.59 ^a	0.56 ^a	0.77 ^b	1.05 ^c	0.055	*
Carcass weight (kg)	367 ^a	367 ^a	387 ^b	406 ^c	5.4	**
Carcass conformation (1-15)	9.5 ^{ab}	8.9 ^a	9.9 ^b	9.9 ^b	0.33	*
Carcass fat (1-15)	5.0 ^a	5.6 ^a	5.4 ^a	8.2 ^b	0.25	***
Ribs joint weight (kg)	8.74 ^a	9.46 ^b	9.49 ^b	10.77 ^c	0.221	*
Bone proportion (g/kg)	223 ^a	230 ^a	217 ^a	205 ^b	5.5	*
Fat proportion (g/kg)	41 ^a	53 ^a	47 ^a	134 ^b	6.2	***
Lean proportion (g/kg)	740 ^a	716 ^b	738 ^{ab}	659 ^c	8.5	*

Concentrate supplementation of suckler bulls at pasture: Effects on growth, carcass and meat quality characteristics

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Introduction

Traditionally suckler bull production systems were based on high concentrate diets. O’Riordan *et al.* (2012) showed that production costs could be reduced by incorporating a grazing period during the growing-finishing period followed by an indoor *ad libitum* concentrate finishing period. As grazed grass is considerably cheaper than grass silage or concentrates (Finneran *et al.*, 2010), finishing bulls directly off pasture may be economically attractive. A primary challenge for forage-based bull systems is to achieve adequate carcass fat cover at a young slaughter age (O’Riordan *et al.*, 2012). The objective of this study was to determine growth, carcass and selected meat quality characteristics of bulls either at pasture with or without supplementation or indoors on *ad libitum* concentrate.

Materials and Methods

Forty spring-born (7 March, s.d 39.1 days), suckler bulls with a mean live-weight of 477 kg (s.d 37.2), circa 15.5 months of age, were blocked for sire breed, date of birth and initial weight and assigned at random to one of 4 treatments for a 130 d finishing period from 28 June to 5 November; (1) Grazed grass only (GO), (2) GO plus 1.6 kg dry matter (DM) barley-based concentrate (C) daily (GCL), (3) GO plus 3.2 kg C DM C daily (GCH) and, (4) Indoors *ad libitum* C and grass silage (AL). At pasture animals were rotationally grazed on 9 paddocks per treatment group (2.92 bulls/ha). Bulls were 20 months old at slaughter. Post-slaughter, carcass weight (CW), conformation and fat score were recorded. The left side of each carcass was cut at the 5/6 rib 48 hours (h) post-slaughter and allowed to bloom for 1 h. *M. longissimus dorsi* (LD) pH and temperature and colour

(Lightness, redness (a) and yellowness (b)) of LD and carcass fat were recorded. A sample of LD was taken for chemical analysis. Data were analysed using the Mixed Model procedure of SAS. The model contained the fixed effect of treatment with block as a random effect. Linear and quadratic relationships in response to C feeding at pasture were determined. An a priori contrast between GCH and AL was examined.

Results and Discussion

Increasing C inclusion in the diet at pasture linearly increased average daily gain (ADG), slaughter and CW, carcass conformation and fat score. Slaughter weight ($P<0.05$), CW and ADG ($P<0.001$) were higher for AL than GCH. Conformation ($P=0.073$) and fat ($P>0.05$) scores were not different between AL and GCH. Kill-out proportion was greater ($P<0.05$) for AL than GCH. Increasing C inclusion in the diet at pasture linearly ($P<0.001$) increased ultimate temperature and linearly ($P<0.01$) decreased moisture proportion of the LD. Ultimate temperature was greater ($P<0.001$) for AL than GCH. Muscle colour of the LD was lighter ($P<0.01$), and fat content was higher ($P<0.001$) for AL compared to GCH. Carcass fat colour was less yellow ($P<0.01$) for AL than GCH.

Conclusion

While finishing bulls directly off pasture may be attractive to reduce production costs, both GO and GCL failed to meet the minimum market specification for carcass fat score of 6 (scale 1-15). However with increased supplementation (GCH) slaughtering off pasture is possible.

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Acknowledgements

Financial Support from the Kepak Group is gratefully acknowledged.

Table 1. Effect of concentrate level of finishing diet on growth, carcass and meat quality traits of suckler bulls

	GO	GCL	GCH	AL	SEM	Significance	
						GCH vs AL	¹ C Level
ADG (kg)	0.82	0.92	1.32	1.89	0.077	***	² L
Slaughter weight. (kg)	589	584	643	709	17.9	*	L
Carcass weight (kg)	306	317	340	395	11.3	***	L
Kill-out proportion (g/kg)	519	541	529	557	7.2	*	NS
Conformation score (1-15)	5.7	6.7	7.8	9.3	0.48	0.073	L
Fat score (1-15)	4.8	5.2	6.8	7.8	0.39	NS	L
<i>M. longissimus dorsi</i> : Ultimate pH (1-14)	5.72	5.70	5.79	5.68	0.045	NS	NS
Ultimate temperature (°C)	1.32	1.72	1.87	3.03	0.197	***	L
³ Lightness	25.8	24.5	25.0	28.2	0.77	**	NS
Saturation	24.8	25.1	25.1	25.9	0.38	NS	NS
Moisture (g/kg)	760	757	750	741	3.6	**	L
Fat (g/kg)	12.5	9.9	15.4	25.0	2.2	***	NS
Protein (g/kg)	210	214	214	222	3.9	NS	NS
Fat yellowness	16.6	15.7	16.2	14.1	0.53	**	NS

¹Linear or quadratic response to C at pasture ²Linear ³Lightness, scale 0 (black) to 100 (white); Yellowness, scale + ‘b’ (yellow) to – ‘b’ (blue)

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 temperate 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°C 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.

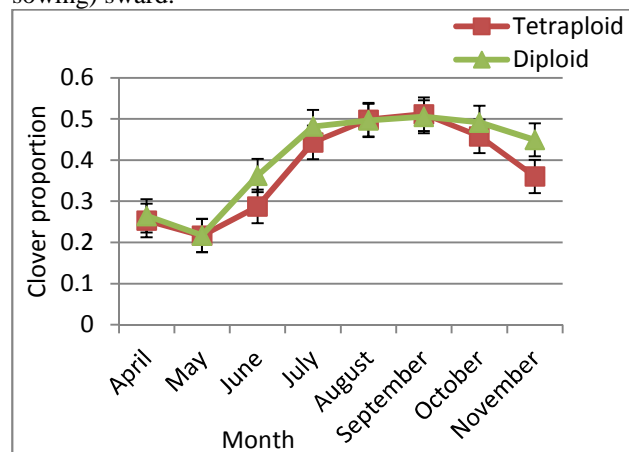


Fig. 1. Clover proportion (expressed by mean values; standard error represented by error bars) of diploid and tetraploid swards

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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The effects of supplementation with Co, alone or in combination with vitamin B12 and Se, on blood metabolites and on trace elements in blood and other tissues of lambs grazing autumn pasture

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Introduction

A high level of lamb performance is achievable from grazed grass offered as the sole diet (Keady and Hanrahan 2009a, 2009b, 2010). However, many producers are unable to finish lambs from grazed grass alone. Whilst the reasons for this inability probably include poor grassland management and parasite control, mineral deficiency is an issue in some sheep producing areas in Ireland. In a connected study Keady *et al.* (2015) concluded that supplementing lambs with Co alone or in combination with vitamin B12 and Se increased lamb performance and that the response to supplementation increased as the grazing season progressed. The aim of this study was to determine the effects of supplementation with Co alone or in combination with vitamin B12 and Se on blood composition and tissue reserves. The effect of period of time since administration of supplement commenced was also examined.

Materials and Methods

Recently weaned lambs (n=67) were randomly allocated to one of 3 supplementation treatments on 12 July: no supplement (control), Co (Cobalt) or Co plus vitamin B12 and Se (VitMin). The Co treatment contained cobalt sulphate (2.1 mg/ml) only. The VitMin treatment contained B12 (200 µg/ml), cobalt acetate (10 mg/ml) and selenium selenite (0.25 mg/ml). Lambs on the Co and VitMin treatments received 10 ml and 2.1 ml of drench, respectively, fortnightly until 18 November. Lambs were managed in a rotational grazing system on predominantly perennial ryegrass swards without concentrate supplementation. Lambs were slaughtered on either 6 November or 18 December. The day prior to slaughter a blood sample was removed from the jugular vein for determination of protein, urea, beta-hydroxybutyrate (BHB), Se, Cu and glutathione peroxidase (GSHPX) concentrations. Following

slaughter tissue was removed from the liver and the kidney cortex for determination of Co and Se concentrations, respectively. The data were analysed as a randomised study using Proc MIXED of SAS to accommodate heterogeneous residuals for some traits, with fixed effects for treatment, slaughter date, sex and birth type.

Results and Discussion

The effects of supplementation and kill date on blood composition and tissue reserves are presented in Table 1. Supplementation with either Co alone or with VitMin increased blood protein and liver Co concentrations. Relative to lambs supplemented with Co, those supplemented with VitMin had higher blood concentrations of Se and GSHPX and higher liver Co concentration. The lambs slaughtered on the 6 Nov and 18 Dec received their last treatment drench 14 and 30 days prior to slaughter, respectively. Delaying slaughter date, and thus increasing the time interval from the last treatment drench, increased protein concentration and reduced BHB and urea concentrations in the blood, and reduced Co in the liver. Blood protein and the concentrations of Cu in blood and liver increased with delayed kill date. There was a significant treatment x kill date interaction for Co concentration in liver. For the control, Co and VitMin treatments liver Co concentrations were 0.11, 1.02 and 1.36 µmol/l, and 0.23, 0.44 and 0.62 µmol/l for kill date 5 Nov and 18 Dec, respectively.

Conclusions

Supplementation with Co, alone or in combination with vitamin B12 and Se, increased liver Co concentration. The concentration of Co in liver declined by 55% following a 30-day period without supplementation.

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Table 1. The effects of treatment on blood and tissue composition

Tissue	Component	Treatment (T)			s.e.	Kill date (D)		s.e.	Significance		
		Control	Cobalt	VitMin		6 Nov	18 Dec		T	D	TxD
Blood	Total protein (g/l)	78.3 ^a	83.3 ^b	81.7 ^b	0.40	77.9	84.3	2.36	*	***	NS
	Urea (mmol/l)	9.8	10.1	10.0	0.55	10.5 ^b	9.4 ^a	0.56	NS	**	NS
	BHB (mmol/l)	0.41	0.37	0.33	0.047	0.40 ^b	0.34 ^a	0.045	NS	*	NS
	Se (µmol/l)	1.0 ^a	1.1 ^a	1.7 ^b	0.14	1.3	1.2	0.13	***	NS	NS
	Cu (mmol/l)	16.7	15.5	16.0	0.39	14.7 ^a	17.5 ^b	1.20	NS	**	NS
	GSHPX (units/ml)	154 ^a	162 ^a	292 ^b	27.5	200	205	0.9	**	NS	NS
Liver	Co (µmol/l)	0.17 ^a	0.73 ^b	0.99 ^b	0.081	0.83 ^b	0.43 ^a	0.067	***	***	***
	Cu (mmol/l)	1.45	1.81	1.66	0.190	1.43 ^a	1.85 ^b	0.180	NS	**	NS
Kidney	Se (µmol/l)	17.8	17.5	16.8	1.35	17.8	16.9	1.26	NS	NS	NS

Effect of perennial ryegrass ploidy and nitrogen input on white clover content and stolon mass under intensive grazing

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Introduction

Perennial ryegrass (PRG) is the most widely used compatible grass with white clover (WC) in temperate pastures. Contribution to dry matter (DM) yield by WC is consistent with its content in grass-clover mixtures (Camlin, 1981). Competition between PRG and WC can result in an interaction in clover content. Tetraploids have a more open growth habit resulting in a higher compatibility with WC compared to diploids (Frame and Boyd, 1986). In addition, nitrogen (N) fertiliser can also affect competition and productivity in grass-clover mixtures (Elgerasma *et al.*, 2000). Identifying suitable grass-clover mixtures for grazing swards is essential in order to maximise potential of WC. The objective of this experiment was to evaluate the effect of PRG ploidy and nitrogen application rate on WC content and stolon mass under an intensive grazing regime.

Materials and Methods

In June 2012, a randomised complete block design with 5 replicates was sown in 18 m × 3 m plots. Eight PRG varieties (4 diploids and 4 tetraploids) were each sown with WC at 37 kg/ha for tetraploids and 34 kg/ha for diploids, with the inclusion of Crusader WC (medium leaf) at 5 kg/ha. Two rates of N were applied: 250 (HN) and 100 (LN) kg N/ha. Rotation length was adjusted for N application rate (HN - 21 days; LN - 30 days), giving nine grazing rotations at HN and eight at LN from 18 Mar. to 14 Nov. 2014. Seasonal clover measurements were in spring (Feb-Apr), mid-season (May-July) and autumn (Aug-Nov). Each plot was sampled above 4 cm for clover content, at four points across a diagonal at each grazing. Samples were mixed and a 70 g subsample separated into grass and clover fractions and dried at 90°C for 16 hours. Tiller density of PRG varieties and WC stolon mass were measured in January, May and October 2014. Three sods (10 cm x 10 cm) were sampled per plot, tillers were counted, and stolons were removed, washed and dried at 40°C for 48 hours. Data were analysed using PROC MIXED in SAS (2011) with block, nitrogen, ploidy and their interactions tested for in the model.

Results and Discussion

Nitrogen affected clover content ($P < 0.001$) by reducing it to 22% at HN, compared to 43% at LN (Table1). This nitrogen response also caused an interaction with ploidy whereby tetraploid varieties had a higher clover content (+6%; $P < 0.01$) than diploids (19%) under HN over the full grazing season, but this was not repeated at LN. These responses were present at each grazing as indicated by the significant differences in each growth period with the exception of spring. Perennial ryegrass tiller density was decreased ($-1614/m^2$; $P < 0.001$) but WC stolon mass was increased ($+42 g/m^2$; $P < 0.001$) as nitrogen decreased across the year (Fig.1). There was no significant effect of grass ploidy on WC stolon mass.

Conclusion

Under dairy cow rotational grazing white clover content was heavily reduced by a higher nitrogen application. Differences in clover compatibility were evident between diploids and tetraploids but this was only at higher nitrogen levels when grass growth competition was accentuated and tetraploid tolerance became an advantage. Competition from perennial ryegrass tillers within the sward was reduced under a low nitrogen scenario, thus resulting in higher clover content across all swards.

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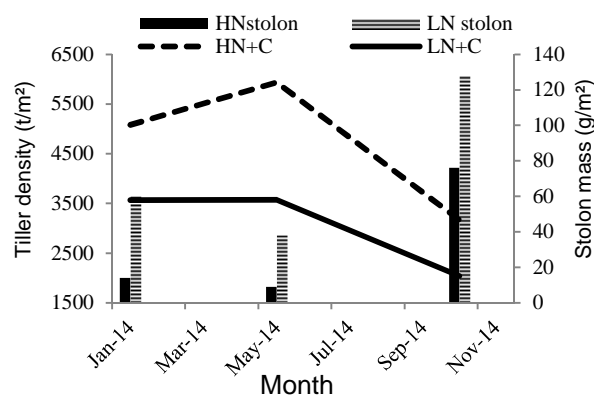


Fig. 1. Tiller density (t) and stolon mass (stolon) of perennial ryegrass and white clover swards under high and low nitrogen regimes (HN, LN)

Table1. The effect of ploidy and nitrogen on annual and seasonal clover content (%) in grass-clover swards

	250 kg N/ha			100 kg N/ha			SE	Ploidy	Nitrogen (N)	N × Ploidy
	Dip	Tet	Mean	Dip	Tet	Mean				
Annual	19 ^a	25 ^b	22 ^a	44	41	43 ^b	0.90	NS	***	**
Spring	7	7	7 ^a	22	20	21 ^b	0.87	NS	***	NS
Summer	18 ^a	23 ^b	20 ^a	45	42	44 ^b	1.06	NS	***	**
Autumn	29 ^a	38 ^b	33 ^a	54	51	52 ^b	1.50	NS	***	**

Dip = diploid; Tet = tetraploid; ^{a-b} Means within a row with different superscripts differ (** = $P < 0.01$; *** = $P < 0.001$)

Effect of seeding ratio of mixed red clover and perennial ryegrass on sward DM yield

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Introduction

Red clover (*Trifolium pratense* L.) is a short-lived (2-3 years) perennial that has recently come under renewed interest for its low input, high yield potential for conservation in Irish grassland enterprises (Weldon and O'Kiely, 2011). This is partly due to its ability to fix atmospheric N and high nutritive value that results in increased animal intakes compared to grass silage (Bertilsson and Murphy, 2003). Red clover has a lower water soluble carbohydrate concentration and buffering capacity than grasses which poses a challenge for adequate preservation as silage. Red clover is predominantly sown with a companion grass species which offers the potential to combine complementary yield, nutritive quality and ensilability characteristics of each species to match farming enterprise requirements. Altering the seeding ratio of red clover to grass provides a mechanism of controlling the relative contribution of each species in the sward and its associated level on yield, nutritive quality and ensilability characteristics. The current study examined the yield responses of three red clover/perennial ryegrass seeding ratios across three harvest years.

Materials and Methods

Red clover (RC; cv. Merviot) plots (7.0 m²) were sown at Crossnacreevy in 2009 with one of two companion perennial ryegrasses (PRG; cv. Millennium/AberGlyn) in three seeding ratios by weight (3:30; 6:27; 9:24; RC:PRG) at a constant rate of 47 kg/ha in a randomised complete block design (n = 3). Plots were harvested to 5cm height in a four-cut system (cut 1 – early June; cut 2 – late July; cut 3 – early September; cut 4 – mid October) in each of the three years following sowing. For each harvested plot the DM yield was measured and a sub-sample (c. 500g) was taken to determine the contribution of each species by botanical separation. Statistical analyses were carried out using GENSTAT (v 16.0). The effect of companion species was not significant at every harvest and was subsequently pooled. Within each harvest year and replicate the DM yield was calculated as a total of four silage cuts. An ANOVA with single factor for seeding ratio was carried out for total annual yield in each harvest year.

Results and Discussion

Red clover was the dominant species in the sward in 'Year 1' despite its low contribution in the sowing rate. The reported low persistency of red clover (Weldon and O'Kiely 2011) was evident in the study whereby clover content fell each year, yet it still comprised over 60% of the harvested herbage in the third harvest year (Table 1). The resultant yields fell by more than half, from an average of 17.0 to 7.2 t/ha DM, between years 1 to 3. An expected decline due to the presence of red clover did not appear to be compensated for by the companion grass. This could in part be due to the low nitrogen application rate of the current study or the competitive nature of the red clover prevented the adequate establishment of perennial ryegrass. Seeding ratio had a negligible effect on the clover content, however there was a significant yield response, in which the lowest clover sowing ratio was lowest yielding and the two higher ratios did not differ except in the third year. Increasing the red clover seeding ratio from 3:30 to 6:27 or 9:24 increased annual yields by 3.3, 2.0 and 0.8 t/ha DM respectively over the course of the three years. The current study highlights the complex relationship between red clover and ryegrass in mixed swards whereby it is not simply the sum of the sown components as in ryegrasses (Gilliland *et al.*, 2011). Management variables such as differing companion grass varieties/species, varying cut timing or strategic use of applied nitrogen, may provide better mechanisms for controlling sward composition and performance.

Conclusions

Under the applied cutting and nitrogen regime altering the seeding ratio did not appear to influence the proportion of clover in the sward but did not adequately explain the large yield differences between the seeding treatments. Increasing the proportion of clover in the seed mixture tended to increase the yield, however given the long known benefits of red clover silage for milk production (Castle and Watson, 1974) further study of these topics is a priority.

Acknowledgements

PTS staff for maintenance and harvesting of field trials.

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Table 1. Total DM yield (t/ha) of mixed red clover and perennial ryegrass swards over three harvest years

Sowing Ratio (RC:PRG)	Year 1		Year 2		Year 3	
	Total yield	RC ¹ (%)	Total yield	RC ² (%)	Total yield	RC (%)
3:30	14.75 ^a	97.3	14.48 ^a	86.2	6.61 ^a	65.6
6:27	17.57 ^b	97.8	15.85 ^b	82.5	7.86 ^b	67.2
9:24	18.55 ^b	98.2	16.13 ^b	85.1	7.03 ^a	66.2
Significance	P<0.001		P<0.05		P<0.05	
S.E.D	0.567		0.574		0.414	

PRG – perennial ryegrass; RC – red clover. Different superscript letters indicate significant difference at P<0.05. Different superscript letters indicate significant difference at P<0.05. Data available ¹ at one cut; ² at three cuts.

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 separately and where necessary combined to generate total DM yield. Least squares means for the different varieties 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 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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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 m² 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.

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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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

Treatment	Period 1 (Early; 25Feb-9Mar)			Period 2 (Late; 19Mar-30Mar)			SEM	CD	Per	CD× Per
	Early	Mid	Late	Early	Mid	Late				
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

The effect of lime on soil phosphorus availability and grass production at two contrasting field sites

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Introduction

Lime and Phosphorus (P) are essential soil inputs for efficient high yielding grassland production systems. Historically, constrained use of P inputs on farms, coupled with increased fertiliser P prices has resulted in low fertiliser P use (and lime use) and a decline in soil P fertility nationally (Lalor and Wall, 2013). As beef and dairy production systems intensify, farmers will rely more on soil P reserves to produce sufficient grass of adequate P content to meet animal dietary requirements. Therefore strategies to improve soil P fertility under constrained P use are needed. The aim of this study was to investigate the temporal effects of P and lime on soil test P (STP), soil pH, grass production and herbage P concentration at two grassland sites in Ireland.

Materials and Methods

This experiment commenced in spring 2014 on two pre-existing grassland experiments at Johnstown Castle (JC), Co. Wexford and Moorpark (MP), Co. Cork with contrasting soil types (moderately drained loam & well drained sandy loam respectively). Previous P and lime treatments on these experimental sites resulted in gradients in soil pH and STP levels within each site (Sheil et al., 2014). The present study investigates the effects of applying different rates of P and lime across the initial soil pH (Fig. 1) and STP gradients. Experimental treatments began in late April 2014. The new superimposed treatments were applied in a factorial design with 4 rates of P x 2 rates of lime in completely randomised blocks with four replicates per treatment. Fertilizer P (0, 20, 40, 60 kg ha⁻¹ yr⁻¹ as 16% P) was applied at the start of the year. Lime (0 [NL] and 5t ha⁻¹ [L]) as ground limestone, was applied to plots within each soil pH gradient (4 pH gradients) at the start of the year on each site. Nitrogen (300 kg ha⁻¹ yr⁻¹) and S were applied to all plots as Sulpha CAN (26.6%N, 5%S). The plots were harvested 8 times in 2014 to simulate grazing management and grass DM yields and herbage P concentrations determined. A generalised linear mixed modelling approach was used to analyse the data using the PROC GLIMMIX procedure of SAS 9.3. The sources of variation in the model were lime, fertiliser P, initial soil pH, STP and site, and block was treated as a random effect.

Results and Discussion

Pre-existing experimental treatments on both sites resulted in unique gradients in soil pH and soil P indices at each site. Initial soil pH and STP were consistently lower across all lime treatment combinations at JC compared to MP (Fig. 1). The interactions of site x P rate x lime were significant ($P < 0.05$) and site x initial soil P and site x initial soil pH were significant

($p < 0.001$). There were no interactive effects between P, lime, initial pH or STP on grass DM yield.

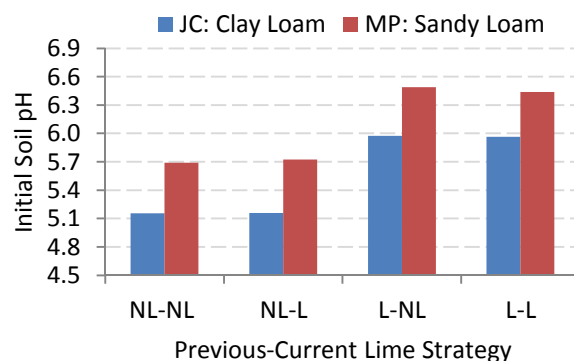


Fig. 1. Mean initial soil pH and the Previous-Current lime treatment regimes at each site (JC and MP).

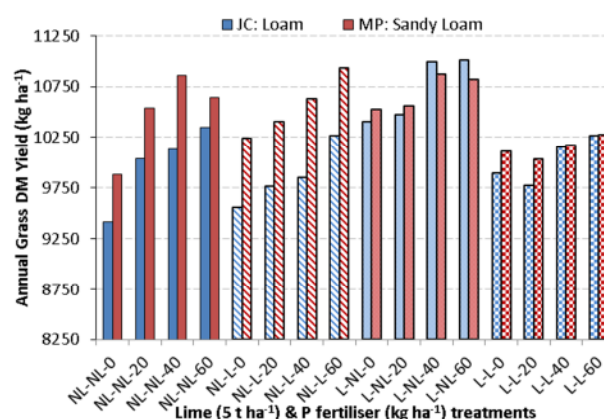


Fig. 2. Annual grass DM yield for the different lime and P fertiliser treatment combinations at each site.

At the start of this experiment only the L-NL and L-L were at (MP) or near (JC) the optimum soil pH (6.3) for grassland. The L-NL treatments produced the highest grass yields when the respective P treatments were compared by lime strategy. Suboptimal soil pH on treatments NL-NL and NL-L, as a result of under-liming, appears to have hampered grass production, possibly by restricting P availability at lower P application rates. Over-liming (L-L) also limited grass production as P may have been precipitated as Ca-P.

Conclusions

Liming for pH correction plays a pivotal role in regulating soil P availability and fertiliser P use efficiency in grassland systems. Optimising soil pH in combination with STP is necessary to optimise grass yield potential from soil P resources.

Acknowledgements

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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).

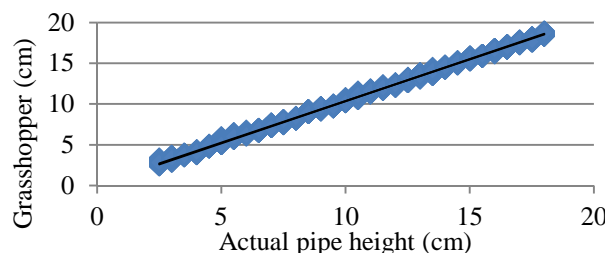


Fig. 1. Relationship between actual pipe heights and pipe heights measured by the Grasshopper (150 measures taken at each of 32 pipe heights)

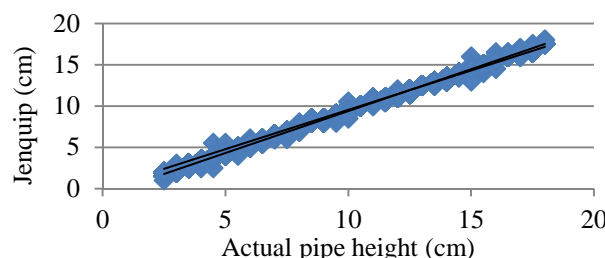


Fig. 2. Relationship between actual pipe heights and pipe heights measured by the Jenquip (150 measures taken at each of 32 pipe heights)

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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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.

Acknowledgements

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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 (CI250) or 150 kg N/ha/yr (CI150) 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 CI150 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 \times 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 CI150 than CI250. This increase in CI150 WC content coincided with the reduction in N fertiliser application to CI150, 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 CI150 and CI250 treatments (Table 1). From mid-June to the end of the lactation, milk production was greater on CI250 and CI150 compared to Gr250; similar to Riberio Filho *et al.* (2003) and Egan *et al.* (2013).

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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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 (CI150 and CI250, respectively) and average sward clover content on CI150 and CI250.

	CI150	CI250	Gr250	S.E. ¹	TRT	Year	Wk.	TRT ² \times Wk.	TRT \times 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

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

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 1. 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 CO₂-equivalent (CO₂-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 CO₂-eq/kg of FPCM (range 0.60-2.18 kg of CO₂-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.

Table 2. Correlations¹ 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

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.

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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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, emery content, mass of liveweight (LW), and mass of carcass weight (CW). System expansion was also used.

Results and Discussion

Table 1 illustrates the effect of different allocation methods on the CF in CO₂ 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 CO₂-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 CO₂-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 CO₂-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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Table 1. The effect of method of allocating GHG emissions in CO₂-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
Emery	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

A comparison of late-maturing suckler-bred bulls and steers in two contrasting production systems

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Introduction

There is a lack of published data on direct comparisons of late-maturing suckled bulls and steers. While production of steers predominates, there has been an increase in male cattle slaughtered as young bulls from ca. 0.05 to ca. 0.20 of the national male kill (O'Riordan *et al.*, 2011). Traditionally, bulls were produced indoors at relatively young ages (14 months +) on high concentrate diets, whereas steers are commonly produced in a more extensive system at pasture after two to three grazing seasons and are slaughtered at relatively older ages (24-30 months) (O'Riordan *et al.* 2011). O'Riordan *et al.* (2012) demonstrated the feasibility of incorporating a grazing period into a suckler bull production system prior to finishing indoors. The production of steers at a younger age may lead to the avoidance of carrying extra animals for a second winter period. The objective of this experiment was to compare the performance of bulls and steers in two finishing systems which focused on avoiding a second winter finishing period.

Materials and Methods

Sixty weaned, spring born (4 March s.d. 27.8 days) Charolais and Limousin sired suckler bulls ca. 8 months old (363 kg s.d. 23.0 kg) were blocked on sire breed, birth date and initial weight and from within block assigned to a 2 (Gender (bull or steer) – GEN) × 2 (System (pasture or *ad libitum* concentrate diets) – SYS) factorial arrangement of treatments (n=15 animals/treatment). Half of the males were castrated 14 days before the start of the study. Animals were offered grass silage (dry matter digestibility (DMD 688 g/kg)) *ad libitum* (GS) plus 3 kg concentrate (862 g/kg rolled barley, 60 g/kg soya bean meal, 50 g/kg molasses and 28 g/kg minerals / vitamins) daily for the first winter, targeting an animal growth rate of ~0.6-0.7 kg/day (Marren *et al.*, 2013). Animals were housed on slatted floor pens, in groups of 5 (3 pens per treatment) according to treatment and treatment pens were randomly assigned within the shed. First winter duration was 127 days, at the end of which two

treatments (1 Bull and 1 Steer) remained indoors on *ad libitum* concentrates while two other treatments (1 Bull and 1 Steer) were turned out to pasture (April 24th) where they rotationally grazed a *Lolium perenne* dominant sward (2.28ha per treatment (6 paddocks)) for 98 days. Following re-housing animals were gradually adapted (during a 3-week period) to an *ad libitum* barley-based concentrates (formulated as above) plus GS to appetite (DMD 677g/kg) diet. Animals were slaughtered at ~19 months of age. Indoor feed intake was recorded on a pen basis and animals were weighed at 3-week intervals. Post-slaughter, carcass weight, carcass conformation and fat score were recorded. Data were analysed using the mixed models procedure of SAS. The model contained fixed effects of GEN and SYS and their interaction with block as a random effect.

Results and Discussion

There were no GEN × SYS interactions recorded (P>0.05) for the traits presented. Pre-grazing herbage mass and post grazing sward heights were 1720 kg DM/ha and 4.65 cm, respectively. Bulls had significantly greater performance than steers for all variables measured (Table 1). Compared with pasture, live-weight gain (LWG) was higher (P<0.01) on *ad libitum* concentrates. When subsequently housed, pasture fed animals had higher (P<0.001) LWG than animals housed fulltime. *Ad libitum* concentrate groups had significantly higher LWG during the growing period and significantly lower gains during the finishing period. Carcass weight was not affected (P>0.05) by SYS, whereas carcass fat scores were higher (P<0.01) on *ad libitum* concentrates.

Conclusion

Under the conditions of this study, bulls significantly out-performed steers on all variables measured with the exception of fat score. Market specifications for carcass fat score were met by all finishing strategies.

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Table 1. Effect of gender and diet on the performance of suckler bulls and steers

Gender (GEN)	Bull		Steer		s.e.m	Significance	
	Grazed	Indoors	Grazed	Indoors		GEN	SYS
System (SYS)							
Post-turnout weight (kg)	438 ^a	464 ^b	433 ^a	468 ^b	12.3	NS	***
LWG Growing (kg/day)	1.49 ^a	1.82 ^b	1.28 ^c	1.64 ^a	0.074	**	***
LWG Finishing (kg/day)	1.79 ^a	1.33 ^b	1.51 ^b	0.87 ^c	0.105	***	***
Slaughter weight (kg)	711 ^{ac}	728 ^a	651 ^{bc}	683 ^c	17.5	***	0.125
Kill-out proportion (g/kg)	571 ^a	575 ^a	559 ^b	560 ^b	4.7	**	NS
Carcass weight (kg)	406 ^a	419 ^a	364 ^b	382 ^b	9.9	***	0.088
Fat score (1-15)	6.7 ^a	7.9 ^b	7.6 ^a	8.6 ^b	0.37	*	**
Conformation score (1-15)	9.9 ^{ac}	10.2 ^a	8.9 ^b	9.1 ^{bc}	0.33	**	NS

Effect of production system on compositional and sensory qualities of bull beef

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Introduction

Grazed grass is cheaper than grass silage which in turn is cheaper than concentrates (Finneran *et al.*, 2011). Including a period of silage feeding together with grazing prior to concentrate finishing of suckler bulls could improve economic profitability compared to concentrate feeding alone. Little information is available on the effects of these alterations of the production system on the eating quality of the beef. The objective of the study was to examine the influence of different production systems, involving grass silage alone or followed by grazed grass prior to a finishing period on concentrates, on the compositional and sensory characteristics of bull beef.

Materials and Methods

Charolais and Limousin sired suckler bulls (n=180) were assigned to three production systems (PS). The PS were: *ad libitum* concentrates to slaughter (C), grass silage *ad libitum* for 120 days followed by C (GSC), or grass silage *ad libitum* for 120 days, followed by 100 days grass at pasture and finally to C (GSPC). For each PS there were three target CW viz. 360, 410 and 460 kg. *Longissimus thoracis* (LT) muscle was excised (from the 10th rib area), and aged for 15 days at 2°C, before storage at -18°C prior to analysis. For resource reasons only 14 animals per treatment were used in the study. Compositional analysis and sensory analysis using a trained panel were undertaken. Data were analysed

using the mixed models procedure of SAS whereby PS, CW and their interactions were treated as fixed effects and animal was included as a random effect.

Results and Discussion

Moisture content was lower (P<0.001) for C and GSC (which did not differ) than GSPC (Table 1). There was an interaction (P<0.01) between PS and CW with respect to intramuscular fat whereby for 360 kg CW, C and GSC (which did not differ; P>0.05) were higher than GSPC; for 410 kg CW, C was higher than GSC and GSPC which did not differ, while for 460 kg CW, C was similar to GSC but higher than GSPC whereas GSC and GSPC did not differ. Texture/tenderness values were higher (P<0.001) for C and GSC (which did not differ) than GSPC. ‘Beefy flavour’ was higher (P<0.05) for C than GSPC. There was an interaction (P<0.01) between PS and CW with respect to ‘flavour liking’ whereby for 360 kg CW, C and GSC (which did not differ) were higher than GSPC, for 410 kg CW, C was similar to GSC but higher than GSPC where GSC and GSPC did not differ whereas for 460 kg CW, all PS were similar. ‘Overall liking’ was higher (P<0.001) for C and GSC (which did not differ) than GSPC.

Conclusion

A period at pasture prior to finishing on concentrates decreased the quality of the beef as assessed by a trained sensory panel which may be related to differences in marbling fat. We suggest that the absolute difference (0.5 units) would not be detected by untrained consumers.

Acknowledgement

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Table 1. Effect of production system and carcass weight on bull beef compositional and sensory qualities (n=14)

PS	C			GSC			GSPC			SE	Significance ¹		
	CW	360	410	460	360	410	460	360	410	460	PS	CW	I ²
Moisture ³		73.4 ^a	72.8 ^a	73.3 ^a	73.4 ^a	73.8 ^{ab}	73.0 ^a	74.7 ^b	74.6 ^b	73.8 ^{ab}	0.4	***	
Protein ³		23.3	23.2	23.4	23.5	24.0	23.7	22.9	23.5	23.5	0.3		
Fat ³		2.6 ^d	3.2 ^d	2.5 ^{cd}	2.6 ^d	1.3 ^{ab}	1.6 ^{bc}	0.6 ^a	0.8 ^{ab}	1.5 ^b	0.3	***	**
Ash ³		1.1	1.1	1.0	1.1	1.11	1.1	1.1	1.1	1.1	0.0		
Texture/tenderness ⁴		4.8 ^{cd}	4.3 ^{bcd}	4.4 ^{cd}	4.4 ^{bcd}	3.8 ^{ab}	4.6 ^d	3.9 ^{abc}	3.7 ^a	3.9 ^{abc}	0.2	***	*
Juiciness ⁴		5.1	4.9	4.8	5.0	5.1	5.1	5.0	4.8	4.9	0.1		
Beefy flavour ⁴		4.5 ^b	4.5 ^b	4.5 ^b	4.6 ^b	4.2 ^a	4.4 ^{ab}	4.3 ^a	4.2 ^a	4.4 ^{ab}	0.1	*	*
Abnormal flavour ⁴		2.7 ^{bcd}	2.5 ^{abc}	2.4 ^{ab}	2.4 ^a	2.8 ^d	2.7 ^{bcd}	2.7 ^d	2.7 ^{cd}	2.6 ^{abcd}	0.1		*
Flavour liking ⁴		5.0 ^{bc}	5.2 ^{bc}	5.2 ^{bc}	5.5 ^c	5.0 ^{ab}	5.3 ^{abc}	4.8 ^a	4.8 ^a	5.0 ^{abc}	0.1	***	**
Overall liking ⁴		4.7 ^c	4.6 ^{bc}	4.6 ^{bc}	5.0 ^c	4.4 ^{ab}	4.9 ^c	4.0 ^a	4.0 ^a	4.3 ^{ab}	0.1	***	*

¹: * p<0.05, ** p<0.01, *** p<0.001; ²: interaction effect; ³: chemical composition (g/100 g); ⁴: sensory characteristics, scale 1-8 (8 extremely tender/juicy/intense flavour/liked)

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.

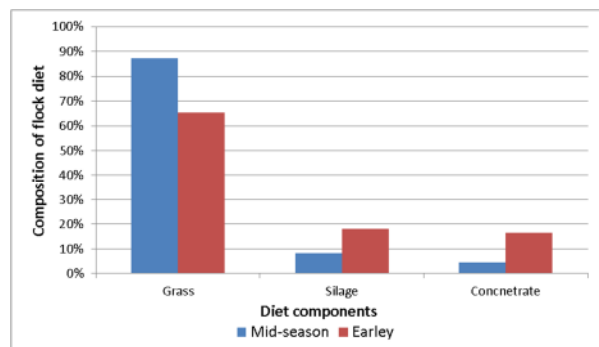


Fig. 1. Proportion of grass, silage and concentrate in the diet of early and mid-season lambing flocks

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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A neural network model of Irish farmers' perceptions of land mobility

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Introduction

Land has always been one of the most important and controversial assets in Ireland and land mobility continue to be a critical issue to the future success of the Irish agricultural sector (FH2020). The Irish agricultural sector is still portrayed by a low level of land mobility and late transfer pattern with small farms and an older farming population. Policies and schemes applied to the agricultural sector to improve the land mobility situation appear to be failing to have the desired effect. The overall objective of this study is to assess the Irish farmers' perceptions of land mobility measures and identify potential solutions that could improve land mobility and smooth land transfer in the Irish agricultural sector.

Materials, Methods & Model

The data used in this study comes from a Macra na Feirme survey conducted in 2012 on a random sample of 421 Irish farmers aged over 50 years to determine the future plans related to land transfer, farming and land ownership (Bogue, 2012). Of these farmers, those that had no identified successor (N=201) answered more detailed questions on land transfer and mobility and these formed the basis for the analysis. Collected data was analysed by using the Interactive Activation and Competition (IAC) neural network analysis (McClelland, 2014; McClelland and Rumelhart, 1988). IAC models are useful for showing the supporting and competing constraints between different factors in a problem domain and can reveal generalisations over data sets describing individuals. Here the model was applied to farmers' perceptions, their properties (e.g., location, age, sex), and land transfer/mobility measures. An IAC network consists of a collection of nodes representing features of interest (e.g., farmer age, sex, location, farmer perception that mobility will not reduce tax) and excitatory links between these nodes indicating that these features are related in a particular case (i.e., the properties/responses of a particular farmer in the survey). Nodes are also organized into pools, indicating that these feature-nodes are mutually exclusive with inhibitory links between them (e.g., the sex pool has two mutually exclusive nodes, male vs female). As such, the network as a whole represents the properties and response choices of the farmers in the study and the inhibitory or excitatory relationships between these factors. For example, when one feature-node (e.g., a land transfer option) is activated (i.e., clamped) it propagates activation through the network, and the relationship between this node and other nodes in the network can be assessed.

Results

The results show that land transfer is mainly related to the farmer's personal and family characteristics with a complex interaction of factors affecting the land transfer decision. The traditional and intense relationship with the male heir stands out as a key factor. The results also highlight that, on average, land mobility and transfer measures are connected to the farmer's internal processes; his perceptions of different land mobility solutions, as well as personal characteristics (age group) and economic resources (size of the farm, enterprise type). However, the models depict high discrepancy between the farmers' beliefs and their final decision on land transfer. The key finding is that even though farmers believe that land mobility measures, such as incentives for young farmers and early retirement schemes, could help to improve land mobility in Ireland, they are not sure these measures would actually 'work' in the long run in terms of influencing the final decision as to whether or not to transfer the land. This finding exposes the fact that whilst farmers suggest a range of possible measures they do not necessarily trust these measures themselves and fears about placing their land in others hands' predominates.

Conclusion

In this study we have addressed land mobility issues as perceived by Irish farmers that could help nurture change in land transfer patterns. The benefits of applying some of these measures could result in better social and economic conditions for encouragement of young farmers and security for elderly farmers who wish to retire. However, our findings show that implementation of the measures, such as early retirement and incentive schemes for young farmers, should be a part of a larger network and policy change. More specifically, a more dynamic, coherent and creative approach that involves farmers and incorporates their views on land transfer is needed to be able to encourage land mobility and early land transfer. One new creative initiative that could help rectify this situation is Macra na Feirme's "matchmaking" site that assists farmers interested in leasing land to find land-owners by matching their needs and helping them in drawing up a lease agreement tailored to the desires of both parties.

Acknowledgments

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The production of suckler bulls at 16 months of age: a comparison of pasture and indoor finishing

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Introduction

Recent changes to market specifications have encouraged the production of bull beef at under 16-months of age. These young bull beef systems are generally based on a high concentrate diet offered indoors. Late-maturing, spring-born suckler-bred bulls may be finished at less than 16 months of age on a diet consisting of 50:50 high nutritive value grass silage: concentrate (Drennan and McGee (2009). However, grazed pasture is considerably cheaper than grass silage or concentrates (Finneran *et al.*, 2012); it is, thus, desirable to investigate the role of grazing in the production of these young bulls. The objective of this study was to determine the performance and fat scores of young suckler-bred bulls finished (at under 16 months of age) either indoors on a high concentrate diet or on a 50:50 ratio of grass silage and concentrate; or at pasture with or without concentrate supplementation.

Materials and Methods

Sixty weaned, spring-born (25 March, s.d. 28.4 days) Charolais and Limousin sired suckler bred bulls ca. 8 months old (357 kg live weight, s.d. 25.3 kg) were blocked on sire breed, weight, and birth date and from within block assigned to one of four treatments. The treatments at pasture were: 1) Grass only (G0), or 2) Grass plus 0.5 of predicted dry matter intake (based on 1.9 % of body weight) offered as concentrates (~5kg fresh weight) (G50) with indoor treatments, 3) offered Grass silage (DMD 677 g/kg) plus 5kg concentrates or 4) *ad-libitum* concentrates. All concentrates were of the same formulation (below). Animals on each treatment (n=15) were assigned to three pens (five animals/pen) in a slatted floor shed. The first winter diet consisted of *ad libitum* grass silage (GS) (Dry Matter Digestibility (DMD) 695 g/kg) plus 2 kg concentrate (862 g/kg rolled barley, 60 g/kg soya bean meal, 50 g/kg molasses and 28 g/kg minerals & vitamins) daily for 128 days. On day 86 of the winter, two treatment

groups that were assigned to remain indoors, began their 121 day finishing treatments. At the end of the winter (128 days), the remaining animals (n=15/treatment) were turned out to pasture (April 8th) where they rotationally grazed a *Lolium perenne* dominant sward for 79 days. Grazing treatments were stocked at approximately 5.85 animals/ha (~2500 kg LW/ha at turn-out) with area allowance reducing for the supplemented group so as to achieve the same (~5cm) target post-grazing sward height. These animals remained at pasture until slaughter. All animals were slaughtered on the same date where 88.3% of the animals were under the age of 16 months. Animal liveweight was recorded at approximately 3-week intervals. Post-slaughter, carcass weight, conformation and fat score were recorded. Data were analysed using the mixed models procedure of SAS with a model including terms for finishing strategy and block.

Results and Discussion

The *ad-libitum* concentrate group had a significantly greater performance across all production and carcass traits measured (Table 1). There was a tendency for (p=0.08) for concentrate supplementation to increase live-weight gain (LWG) at pasture. Compared with unsupplemented pasture, indoor finishing on a 50:50 grass silage/concentrate diet significantly improved slaughter and carcass weight, fatness and conformation. Carcass weight, conformation and fat score increased significantly with increasing concentrate input.

Conclusion

Under the conditions of this study, it was not possible to produce suitably finished (fat score 2+ (6 on 1-15 scale)) animals at 16 months of age from pasture either with or without supplementation.

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Acknowledgements

DAFM Research Stimulus Fund (11/SF/322)

Table 1. Effect of finishing strategy on the production of bulls at approximately 16-months of age

	Finishing strategy				SEM	Sig.
	GO	G50	Silage + 5kg	<i>Ad-libitum</i> concentrates		
LWG Winter (kg/day)	0.74	0.75	-	-	0.041	-
Live weight – End winter (kg)	421 ^a	423 ^a	447 ^b	463 ^b	6.9	**
LWG Finishing (kg/day)	1.31 ^a	1.47 ^a	1.38 ^a	1.85 ^b	0.065	***
Slaughter weight (kg)	496 ^a	513 ^a	556 ^b	601 ^c	9.3	***
Kill-out proportion (g/kg)	559 ^a	562 ^a	568 ^a	594 ^b	4.7	***
Carcass weight (kg)	277 ^a	289 ^a	315 ^b	357 ^c	6.1	***
Fat Score (1-15)	3.6 ^a	4.2 ^a	6.0 ^b	7.3 ^c	0.29	***
Conformation (1-15)	7.7 ^a	8.5 ^b	8.6 ^b	10.0 ^c	0.25	***

Effects of castration on lamb quality 1: carcass proportions and meat quality characteristics

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Introduction

Traditionally, castration of male lambs has been a common practice in Ireland. However, Hanrahan (1999) and Keady *et al.* (2015) have reported that intact lambs had better growth rate and produced less fat than castrated lambs. It is important to know whether these production benefits of non-castration have any negative effects on carcass quality, which would affect the returns to processors, or on meat quality characteristics, which would affect customer acceptance. Hence, the aim of this study was to evaluate the carcass proportions and meat quality characteristics of intact and castrated males reared in grass-based systems.

Materials and Methods

Ten twin pairs of male lambs (sired by Suffolk rams), born in March, were allocated to this study. Within 24 h of birth, 1 lamb per set of twins, chosen at random, was castrated, using a rubber ring, while the other lamb was left intact. The ewes and their lambs were put to pasture and received no concentrate supplementation. The flock was managed in a rotational grazing system. Lambs were weaned at 14 weeks of age and slaughtered on 26 September at a mean age of 189 days (s.d. 7.5). Two hours prior to slaughter, fat and muscle depth were measured over the eye muscle at the 11th rib using an ultrasonic scanner (Concept MLV, with 3.5 MHz transducer, Dynamic Imaging Co., UK). Carcass weight was recorded immediately after slaughter. The pH and temperature of the *Longissimus thoracis et lumborum* (LTL) were monitored once per hour for 5 h. After 24 h in the chill at 2°C, the carcasses were again weighted and split into foresaddle, middle and hindsaddle. Fat and muscle depth were recorded over the eye muscle at the 11th rib using a caliper. The LTL muscles from both sides were excised, cut into 2.5 cm steaks and stored in vacuum package bags. Samples used for LTL composition were then frozen at -20°C. Samples used for Warner-Bratzler shear force (WBSF) were aged for 10 days at 2°C and frozen at -20°C until further analysis. The methods for meat quality measurements were described by Hamill *et al.* (2012) with some modifications for lamb. Traits measured on the LTL included drip loss, lean colour (L*, a* and b*), intramuscular fat (IMFat), moisture and protein N concentration, analysed using a Leco N analyser, WBSF and cook loss. Data on carcass proportions and LTL composition were analysed using Proc GLM (SAS), including the MANOVA option, to fit a model with effects for sex category.

Results and Discussion

Multivariate analysis for carcass proportions yielded a significant treatment difference ($P < 0.001$). This reflected the fact that for entire males a higher

proportion of the carcass was in the foresaddle with lower proportions in middle and hindsaddle when compared with castrates. The treatment means for carcass proportions are in Table 1. The results for the MANOVA analysis of ultrasonic fat (UFat), ultrasonic muscle depth (UMD), fat depth, muscle depth, intramuscular fat, moisture and protein concentrations, and cook loss are presented in Fig. 1. The evidence for a treatment difference approached significance ($P = 0.09$) and the means indicate that entire males were less fat than castrates.

Table 1. Effects of castration on carcass proportions and meat quality characteristics.

	Treatment		SE	Sig
	Castrate	Entire		
Carcass wt.(kg)	19.7	19.3	0.56	NS
Chill loss (g/kg)	12.1	22.0	2.18	NS
Hindsaddle (kg)	6.8	6.5	0.17	**
Middle (kg)	5.6	5.2	0.21	**
Foresaddle (kg)	7.2	7.4	0.21	**
Drip loss (g/kg)	15.9	16.8	1.68	NS
L*	35.2	35.6	0.75	NS
a*	13.9	13.0	0.37	NS
b*	11.9	12.0	0.28	NS
WBSF (N)	24.1	22.1	1.69	NS

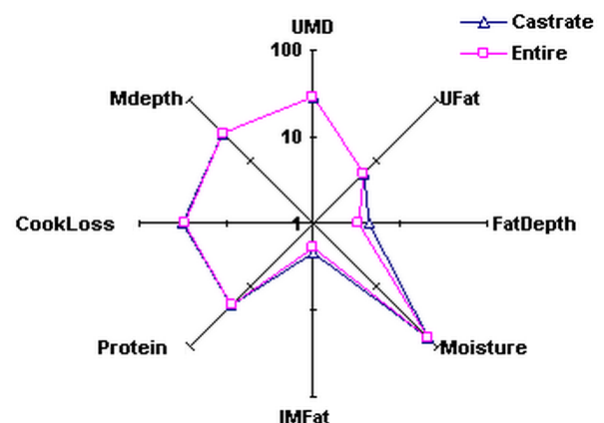


Fig. 1. Summary plot of effects of castration on LTL composition (axes are log₁₀ scale).

Conclusion

The only effect of castration on carcass or meat quality characteristics was a significant increase in the relative proportion of the middle and hindsaddle, with a concomitant reduction of the foresaddle.

Acknowledgements

The authors gratefully acknowledge funding from DAFM under the Research Stimulus Fund (Project 11/SF/311).

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Effects of castration on lamb quality 2: sensory attributes

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Introduction

Traditionally, male lambs born in mid-season, grass-based production systems are castrated. However, Hanrahan (1999) and Keady *et al.* (2015) reported that leaving male lambs entire increases growth rate so they reach slaughter weight at a younger age and yield leaner carcasses. There are no data available on the effects of castration on the eating quality of meat from lambs reared on pasture as the sole diet under Irish conditions. Therefore, the objective was to evaluate the effects of castration on sensory attributes of cooked meat from lambs reared in grass-based systems.

Materials and Methods

Ten twin pairs of male lambs (sired by Suffolk rams), born in March, were allocated to this study. Within 24 h of birth, one lamb per twin set, chosen at random, was castrated using a rubber ring while the remaining lamb was left intact. The ewes and their lambs were turned onto pasture and received no concentrate supplementation. The flock was managed in a rotational grazing system. Lambs were weaned at 14 weeks of age and slaughtered on 26 September at a mean age of 189 days (s.d. 7.5). After 24 h in the chill at 2°C the *longissimus thoracis et lumborum* (LTL) muscles from both sides were excised, cut into 2.5 cm steaks, stored in vacuum package bags and aged for 10 days at 2°C. Samples were then frozen until sensory assessment. Samples were thawed at 4°C overnight, cut into steaks (20 mm thick) and grilled until an internal temperature of 74°C was reached. The cooked steaks were cut into blocks (2 cm³) for the evaluation. Trained assessors (n=10) rated each sample for abnormal flavour intensity and lamb flavour intensity (1 = extremely weak to 8 = extremely strong), juiciness (1 = extremely dry to 8 = extremely juicy), texture (1 = extremely tough to 8 = extremely tender); flavour liking and overall liking were evaluated on an 8-point hedonic scale. The flavour profile of the samples was assessed on a 100 mm unstructured intensity line scale (0 = nil to 100 = extreme) for the following attributes: fatty, sweet, dairy, livery, acidic, metallic, grassy, bitter, kidney, ammonia, fishy, soapy and rancid. Sensory data involved 19 variables and these were analysed using multivariate procedures (Proc GLM; SAS) so that Type I error rate was controlled; the variables were divided into 4 subgroups for these analyses: variables assessed on an 8-point scale formed a group while the variables evaluated on the continuous line scale were divided into 3 groups (5 variables with the highest maximum, 5 variables with the lowest maximum and the remaining 3 variables). The initial model included effects for both sex category and dam.

Results

Multivariate analysis yielded no evidence for a treatment difference for attributes evaluated on the hedonic scale ($p = 0.4$) or for the groups consisting of the flavours 'Fatty, Livery, Sweet, Dairy, Acidic' ($p = 0.3$) and 'Metallic, Grassy, Bitter' ($p = 0.6$). The treatment difference for the final group, 'Soapy, Fishy, Rancid, Kidney, Ammonia', approached statistical significance ($p = 0.06$) reflecting higher scores for 'Fishy' and 'Rancid' and lower scores for 'Soapy' and 'Kidney' for castrates relative to entire males. The treatment means for the sensory attributes measured on a 1 to 8 scale are displayed in Fig. 1 while the means for the flavour profile variables (0 to 100 line scale) are in Fig. 2. It should be noted that the intensity of the flavour profile components were all less than 10 except for 'Fatty' 'Sweet' and 'Dairy'. The absence of any overall difference between the groups is evident.

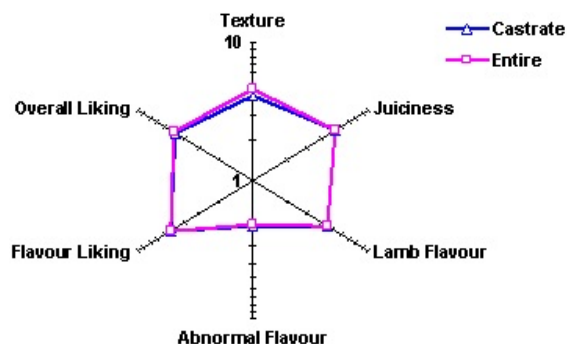


Fig. 1. Summary plot of sensory attributes measured on a 1 to 8 scale (axes are log₁₀ scale).

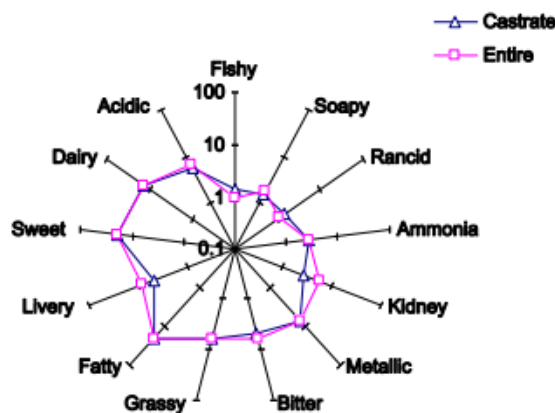


Fig. 2. Summary plot of flavour profile measured on 0 to 100 line scale (axes are log₁₀ scale).

Conclusion

There was no evidence from this study that would require rejection of the null hypothesis that there is no difference in sensory perception between LTL muscle from entire and castrate lambs. Thus the results do not support the view that there are consumer acceptance issues from leaving male lambs entire so as to exploit their higher growth performance in this grass-based production system.

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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 (120m² 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.

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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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

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.

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

Stocking rate (SR)	Low		Medium		High		SEM ¹	P-Value	
Animal genotype (B)	HF	JX	HF	JX	HF	JX		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

SEM¹ = Standard error mean

MS² = Milk solids (fat plus protein)

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.

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
<i>Somatic cell count</i>	7	6 to 7	7	6.75 - 7
<i>Milk composition</i>	7	6 to 7	7	6 to 7
<i>Protein composition</i>	6	6 to 7	6	6 to 7
<i>Protein functionality</i>	6	5 to 7	6	6 to 7
<i>Consistency in milk composition across lactation</i>	6	5 to 7	6	5 to 7
<i>Fat composition</i>	6	6 to 7	6	5 to 6
<i>Sensory attributes</i>	6	4 to 6	5	4.25 - 6
<i>Environmental traits</i>	5	5 to 6	5	4 to 6
<i>Animal welfare</i>	6	5 to 7	5	2 to 6

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

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.

Acknowledgements

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

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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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 (6.17)	6674 (6.32)	4.07 (0.003)	4.11 (0.003)	3.57 (0.001)	3.57 (0.003)
2	6695 (6.45)	6580 (6.38)	4.03 (0.003)	4.04 (0.003)	3.52 (0.001)	3.52 (0.003)
3	6512 (6.18)	6530 (6.27)	4.01 (0.003)	4.00 (0.003)	3.49 (0.001)	3.49 (0.003)
4	6164 (6.08)	6467 (6.24)	3.97 (0.003)	3.93 (0.003)	3.44 (0.001)	3.44 (0.003)

Maternal performance of high and low replacement index cows during their first lactation

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Introduction

Successful suckler systems are dependent on cows maintaining a 365 day calving interval, producing a live calf each year and efficiently converting grazed pasture to milk production. Following this, weaning output is the best indicator of a cow's maternal performance. Milking capability of the beef cow is the driving force of calf weaning weight (Boggs *et al.*, 1980). Animals identified as high genetic merit for maternal traits through the Replacement Index should be superior for milk production and fertility traits, therefore driving the overall system performance and ultimately profitability. Consequently, the objective of this study, carried out at Teagasc Grange, was to compare the performance of high and low replacement index cows during their first lactation.

Materials and Methods

Data were available from 82 cows and their progeny; 50 and 32 cows of high and low index, respectively. Animals were selected from high reliability (>70%) Angus and Limousin sires on the basis of their Replacement index; €148 and €46 for high and low index sires, respectively. Sires selected for the study were commonly used across the dairy and suckler herd (42 and 40 dairy beef crossbred and suckler cows, respectively). Cows calved for the first time at 24 months of age in spring 2014 with a mean calving date of 21 March. Animals were managed under a rotational grazing system with an average pre- and post- grazing height of 11.6 (s.d. 1.9) cm and 4.1 (s.d. 0.8) cm respectively. Cow and calf live weight and cow body condition score (BCS; 0 to 5) were recorded every three weeks. The weigh-suckle-weigh technique was used at 120 and 156 days in milk to establish cow milk yield during the grazing season (McGee *et al.*, 2005). Gradual weaning commenced on 20 October and was completed over a five day period. At weaning calf weight and quality were recorded. Calf quality was

determined on a 1 to 5 scale as outlined in the DAFM Suckler Cow Welfare Scheme (ICBF, 2008). The effect of cow genetic merit (high or low) and cow origin (dairy or beef) on cow and calf performance was analysed using a mixed model in PROC HP MIXED (SAS Inst. Inc., Cary, NC). Fixed effects included for all traits were genetic merit of the cow, cow type and the replacement index of the cow's sire nested within genetic merit. Depending on the trait under investigation (i.e. cow or calf trait) the heterosis coefficient and recombination loss coefficient of the cow or calf were included as fixed effects. For all calf traits, sex and sire were included as fixed effects. For calf live weight, age and the interaction between age and sex were included as fixed effects. Within all cow and calf traits the sire of the cow was included as a random effect.

Results and Discussion

Live weight and BCS were similar across genotypes (Table 1). Cows originating from the beef herd were 46 kg heavier ($P<0.001$) at weaning and had a greater BCS ($P<0.001$) throughout lactation. Genetic merit had no effect on milk yield whereas a significant difference ($P<0.001$) was found within cow origin. Dairy cross cows had a 2.1 kg/d increase in milk yield over the beef cows. Calf birth weight and quality showed no difference within genetic merit or origin. Weaning weight ($P<0.01$) and average daily gain ($P<0.05$) were greater for dairy bred cows than beef sourced cows, but no genetic merit influence was observed. No difference in the proportion of calf weight to cow weight was observed between cow genetic merit but a cow origin effect was detected with calves from dairy bred cows achieving 50% of cow weight at weaning compared to 40% for the calves from beef cows ($P<0.001$).

Conclusion

Results from the current study suggest that genotype had no effect on cow's maternal performance during her first lactation. It does however show that origin of the cow has an influencing effect on certain traits.

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Table 1: Effect of genetic merit and cow origin on cow live weight, body condition score and progeny performance.

	Genetic Merit		s.e. ¹	P-value	Cow Origin		s.e.	P-value
	High	Low			Dairy	Beef		
Cow live weight (kg)	554	560	8.9	0.6108	514	560	9.2	<0.001
Body condition score (BCS) ²	2.70	2.73	0.033	0.6570	2.58	2.85	0.043	<0.001
Milk yield (kg/d)	6.7	6.4	0.29	0.4410	7.6	5.5	0.29	<0.001
Calf birth weight (kg)	39	41.4	1.41	0.2390	40.8	39.6	1.19	0.3660
Weaning weight (kg)	248	242	6.4	0.5465	257	234	5.9	<0.01
Calf ADG ³ (kg)	0.96	0.97	0.021	0.8679	1.00	0.94	0.020	<0.05
Calf quality (1 to 5)	3.16	3.04	0.069	0.2459	3.06	3.14	0.065	0.4389
Prop. calf to cow (%)	46	44	1.4	0.2239	50	40	1.3	<0.001

¹Weighted standard error of the mean, ²BCS= 0 emaciated to 5 extremely fat, ³ADG = average daily gain

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 at 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.

Table 1. Least squares phenotypic mean¹ (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	750 ^c	1222 ^d
se	0.33	0.02	0.33	0.83	3.2

¹Reference 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

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.

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The effect of stocking rate and prolificacy potential on carcass output and lamb performance from pasture based production systems.

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Introduction

Lamb production in Ireland is largely driven by the seasonal pattern of grass production. Currently the national average carcass output is 189 kg/ha on Irish sheep farms and is limited by low stocking rate and prolificacy levels (NFS, 2013). A target of 468 kg carcass/ha at a stocking rate of 13 ewes/ha (1.8 lambs weaned per ewe joined) is considered achievable from pasture-based systems of lamb production (Teagasc Roadmap, 2013). The aim of the current study was to investigate the effect of stocking rate and prolificacy potential (based on breed type) on lamb average daily live weight gain, days to slaughter (DTS), carcass weight and carcass output (kg/ha).

Materials and Methods

The two-year study commenced in October 2011 and finished in October 2013. A total of 360 primiparous hogget ewes comprising of two breed types, differing in prolificacy potential (PP) (Hanrahan, 1994), were assembled: medium prolificacy (MP) - Suffolk X ewes (target weaning rate of 1.5 lambs/ewe, n=180), and high prolificacy (HP) - Belclare X ewes (with a target weaning rate of 1.8 lambs/ewe, n=180). Within breed type, ewes were blocked by live weight (kg) and body condition score (BCS - scale 1-5), and randomly assigned in year one, to one of three stocking rate (SR) pasture systems: a low SR (LSR; 10 ewes/ha), a medium SR (MSR; 12 ewes/ha), and a high SR (HSR; 14 ewes/ha). Ewes were mated to Charollais rams over a 6 week period. Following lambing, ewes and their progeny were rotationally grazed without concentrate supplementation. Lamb growth rates were recorded from birth to weaning and from weaning to finishing. Lambs were weighed at two week intervals from six

weeks of age. Lambs were weaned at 14 weeks and drafted for slaughter once pre-defined live weight targets of 42, 43, 44, 45 and 46 kg were reached in the months June, July, August, September and October, with the aim to produce a carcass of 19-20 kg. Post weaning a leader-follower grazing system was operated with lambs gaining access to fresh grass ahead of the ewes. The effects of SR and PP on pre-weaning average daily gain (ADG) from 0 to 14 weeks, carcass output, carcass weight, kill-out percentage, post weaning and total lifetime ADG were analysed using linear mixed models (PROC HP MIXED, SAS Institute 2012) with ewe included as a random effect.

Results and Discussion

Data presented represent the mean of two production years (2011/12 to 2012/13). Interactions were observed for 0 to 14 week ADG, with the HSR-HP lambs having a lower ADG (232 g/day) compared to the mean ADG of 257 g/day achieved by the other treatments (P<0.05). HSR MP lambs had a lower carcass weight of 19.2 kg (-0.4 kg) relative to the other treatments (P<0.05). There was significant differences in carcass output between SR and PP treatments (P<0.001), with the exception of the HSR MP and MSR MP treatments which produced equal amounts of carcass (mean 419.6 kg). High SR lambs were slower (P<0.001) to reach slaughter (+23 days) compared to low SR lambs (209 days). Stocking rate had no significant effect on kill-out percentage.

Conclusions

Increased carcass output (kg/ha) from pasture-based production systems is achievable through increased stocking rate and prolificacy levels despite lower individual lamb growth. Further investigation is required into the longer term effects of such systems on carcass output and lamb performance.

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Table 1. The effect of stocking rate and prolificacy level on carcass output and lamb performance,

Parameter	Stocking Rate (SR)				Prolificacy (PP)			P-value		
	LSR	MSR	HSR	SEM	MP	HP	SEM	SR	PP	PP × SR
0-14 week ADG	269 ^a	256 ^b	247 ^c	2.8	261	253	2.3	***	**	*
Post weaning ADG	199 ^a	177 ^b	175 ^b	11.2	180	187	3.0	***	NS	NS
Total lifetime ADG	242 ^a	221 ^b	215 ^b	9.7	230	225	3.0	***	*	NS
Days to slaughter	209 ^a	224 ^b	232 ^c	11.2	220	224	3.5	***	NS	NS
Carcass weight (kg)	19.7	19.6	19.6	0.25	19.5	19.8	0.07	NS	***	*
Kill-out percentage	44	44	44	0.005	43	44	0.002	NS	***	NS
Carcass output (kg/ha)	332 ^a	393 ^b	453 ^c	0.2	366	418	0.2	***	***	***

ADG: Average daily gain (grams)

* P<0.05; ** P<0.01; *** P<0.001; NS = P>0.05

^{a,b,c} Within rows, superscripts indicates significant differences (P<0.05)

An investigation into the effect of breed and gender on production traits of male lambs during indoor finishing

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Introduction

The Scottish Blackface (SB) breed accounts for approximately 22% of the national ewe flock, producing mainly store lambs. The collapse of Mediterranean markets has resulted reduced market options for these light hill lambs. In hill areas there is little scope to finish these lambs off pasture. Little work has been carried out on examining production traits of hill lambs when intensively finished on high concentrate diets. The objective of this study was to compare the performance of castrated and ram lambs of the SB breed with Texel (TX) lambs when fed a high concentrate diet for a 36 day period prior to slaughter.

Materials and Methods

A total of 80 spring-born male lambs were used in a 2 × 2 factorial design with two breeds (SB (n=40) and TX cross (n=40)) and gender (castrate (n=40) and ram (n=40)) study carried out in two replicates. Lambs were castrated using a scrotal ring within 48 hr of birth. Lambs were individually penned (182cm × 122cm) for the duration of the 36 day indoor finishing period. Following a 10 day introduction period to full concentrate feeding, lambs were offered 100 g DM of grass silage and free access to concentrate feed at all times. The concentrate used was a 75% cereal-based lamb ration with 15% crude protein and an energy value of 1.0 UFL (feed unit)/kg fresh weight. Individual lamb feed intakes were recorded daily. Lambs were ultrasonically scanned for muscle depth and fat thickness on day 0 (start of finishing period) and day 35 and were slaughtered on day 36.

Post slaughter carcass weight, carcass conformation and fat grade were recorded. Carcass conformation and fat scores were recorded using the EUROP system by experienced personnel. Data were analysed using PROC GLM of SAS with terms for breed, gender and their interactions included in the model.

Results and Discussion

Results are presented in Table 1. Data from two lambs (one SB and one TX) were removed from the study due to poor daily feed intakes (>3 standard deviations from the mean). For all variables measured, with the exception of weight at the start of the feeding period (P<0.001), feed conversion efficiency (FCE) (P<0.05), average daily gain (ADG) (P=0.10) and ultrasonic fat (P=0.06), there were no breed × gender interactions. Feed conversion efficiency was lower for TX rams compared to TX castrates, whereas for SB, FCE was similar in castrates and rams. There was a tendency for higher ADG in TX rams compared TX castrates (P<0.10), whereas ADG was similar in SB castrate and SB ram lambs. Kill-out proportion and carcass fat score was lower (P<0.01) in ram lambs compared to castrates. TX lambs had higher feed intakes, higher kill-out proportion and produced heavier, leaner, superior conformed carcasses than SB lambs (P<0.001). TX lambs had superior muscle gain compared SB (P<0.001), whereas there was no significant difference in fat gain between the breeds. A total of 35/39 (90%) and 39/39 (100%) of the SB and TX lambs, respectively, produced carcasses >18 kg. Across both breeds ADG was highly correlated to average daily feed intake during the 36 day feeding period (R²=0.44).

Conclusions

Texel cross lambs had superior growth rates and feed conversion efficiency and carcass attributes compared to SB lambs. Notwithstanding this, SB lambs meet the specification of the French market (18kg+ carcass) though castrated lambs may become over-fat if not selected for slaughter on time.

Acknowledgement

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Table 1. Effect of lamb breed (B) and gender (G) on production and carcass traits.

Variable	Scottish Blackface		Texel Cross		SEM	Significance		
	Castrate	Ram	Castrate	Ram		B	G	B x G
Starting liveweight (kg)	35.2	38.1	39.6	39.1	0.45	***	*	***
Final liveweight (kg)	43.6	46.5	50.5	52.1	0.82	***	**	NS
Cold carcass weight (kg)	19.8	20.7	24.4	24.2	0.38	***	NS	NS
Kill-out proportion (g/kg)	454	445	482	465	0.01	***	**	NS
Carcass fat score (1-5)	4.3	3.7	3.8	3.1	0.12	***	***	NS
Carcass conformation score (1-5)	2.8	2.8	3.7	3.7	0.13	***	NS	NS
Daily feed intake (fresh weight-kg)	1.37	1.36	1.62	1.62	0.044	***	NS	NS
Average daily live weight gain (g)	230	230	299	356	18.8	***	NS	P=0.10
FCE (kg feed/kg liveweight gain)	6.24	6.80	5.86	4.80	0.385	**	NS	*
Ultrasonic fat (mm) at day 35	0.73	0.73	0.80	0.64	0.048	NS	P=0.06	P=0.06
Ultrasonic muscle (mm) at day 35	29.3	28.6	32.3	32.8	0.44	***	NS	NS
Ultrasonic fat gain (mm)	0.17	0.20	0.27	0.20	0.049	NS	NS	NS
Ultrasonic muscle gain (mm)	4.53	4.13	6.90	7.10	0.394	***	NS	NS

N.S= P>0.05, * =P<0.05, ** = P<0.01, *** = P<0.001, F at score (1-5), where 1 is lean and 5 is fat. Carcass conformation (E=5, U=4, R=3, O=2, P=1).

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: $Y = \mu + \text{genetic group} + \text{cow}(\text{genetic group}) + \text{feeding treatment} + \text{parity} +$

calving day + genetic group \times 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 \times 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. 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.

References

Ramsbottom, G., Cromie, A.R., Horan, B., & Berry, D.P. (2012) *Animal* 7: 1031-1039

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)

* = $P<0.05$, ** = $P<0.01$, *** = $P<0.001$

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 banded 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:

$$r_{X,Y} = \frac{\mathbf{a}'_X \mathbf{G}_{XY} \mathbf{a}_Y}{\sqrt{\mathbf{a}'_X \mathbf{G}_{XX} \mathbf{a}_X \mathbf{a}'_Y \mathbf{G}_{YY} \mathbf{a}_Y}}$$

where \mathbf{a} is the vector of economic weight, and \mathbf{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.

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

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.

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Comparative live weight, body condition score at breeding and reproductive performance of heifers of high and low replacement index

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Introduction

Profitable suckler systems in Ireland are dependent on cows calving in spring (Crosson *et al.*, 2009), maintaining a 365 day calving interval with compact calving, and producing a live calf each year. However, current industry figures show that suckler cows are producing 0.83 calves per cow per year with a calving interval of 395 days (ICBF, 2014). Genetic evaluations provide information to aid in breeding decisions that increase the performance of progeny. With the inception of a new Replacement Index by ICBF in 2012, availability of maternal genetic evaluations should enable breeders to improve current industry performance and ultimately improve maternal efficiency of the beef sector. Therefore, the objective of this study was to compare the live weight, body condition score at breeding and reproductive performance of high and low replacement index heifers sourced from both the dairy and beef herd.

Materials and Methods

Data were available from 107 first parity cows; 67 and 40 heifers of high and low index, respectively. Heifers were selected from high reliability (>70%) Aberdeen Angus and Limousin sires commonly used across the dairy and suckler herd (53 and 54 dairy beef crossbred and suckler heifers, respectively). The Replacement index was €148 and €46 for high and low index sires, respectively. Heifers calved for the first time in spring 2014 at 24 months of age. Live weight and body condition score (BCS; 0 to 5) were recorded every three weeks. Breeding commenced on 29 April and lasted 13 weeks. Tail paint and vasectomised bulls were used as aids for heat detection. Heifers were

artificially inseminated for six weeks and stock bulls thereafter. Reproductive variables included: calving to service interval, 24 day submission rate, pregnancy rate to first service, six week in-calf rate, final in-calf rate, calving to conception interval and the number of services per cow. All pregnancy traits were defined based on trans-rectal ultrasound imaging (Aloka 210D * II, 7.5 MHz) 70 days after the end of the breeding season. The effect of cow genotype and cow origin on cow live-weight, BCS and reproductive performance was analysed using mixed models in PROC HP MIXED (SAS Inst. Inc., Cary, NC). Sire of the cow was included as the random effect. Analysis of binary fertility data was undertaken using PROC GENMOD assuming a logit link function. Fixed effects included in all models were genotype of cow (high or low), cow origin (dairy or beef), heterosis and recombination loss of the cow and the replacement index of the cow's sire nested within genetic merit group.

Results and Discussion

Live weight and BCS at breeding were similar across genotypes (Table 1). Heifers from the beef herd were 66 kg heavier ($P<0.001$) and had 0.21 of a greater BCS at breeding ($P<0.001$). Age at first calving had no genotypic or dam origin effect. Pregnancy rate, calving to conception interval, pregnancy to first service, number of services per cow, calving to service interval and estimated calving interval were similar for cow genotype and origin of dam. High merit replacement heifers had a greater submission rate ($P<0.001$) and tended to have a greater six week in calf rate ($P=0.072$). Heifers originating from the dairy herd had a greater submission rate ($P<0.001$) than beef heifers.

Conclusion

Results from the current study suggest that genotype had no effect on live weight, BCS at breeding or most reproductive traits investigated. Heifers sourced from the dairy herd had lower live weights and BCS at breeding but had a greater submission rate in the first 24 days of the breeding season.

References

Crosson, P., McGee, M. & Drennan, M.J. (2009) *Proc. Agric. Res. Forum* p68.
ICBF (2014) Irish Cattle Breeding Federation Ltd.

Table 1. Effect of genetic merit and cow origin on live weight, body condition score and reproductive performance.

	Genetic Merit		s.e. ¹	P-value	Cow origin		s.e. ¹	P-value
	High	Low			Dairy	Beef		
Live weight (kg)	519	530	0.7	0.4818	491	557	9.6	<0.001
Age at first calving (d)	757	767	4.9	0.1672	756	768	5.2	0.1244
BCS at breeding ²	2.72	2.68	0.029	0.3210	2.60	2.81	0.032	<0.001
Calving to service interval (d)	61	65	3.4	0.4988	63	63	3.3	0.9965
Submission rate in first 24 days (%)	72	38		<0.001	70	39		<0.01
Pregnancy to first service (%)	44	48		NS	53	39		NS
6 week in-calf rate (%)	57	39		0.072	54	41		NS
Pregnancy rate (%)	89	84		NS	91	81		NS
Calving to conception interval (d)	82	82	4.6	0.9840	80	84	4.7	0.5432
No. of services per cow	1.82	1.67	0.131	0.4322	1.66	1.83	0.142	0.4504
Expected calving interval (d)	368	365	4.3	0.5850	365	368	4.5	0.6753

¹Weighted standard error of the mean, ²BCS = body condition score range: 0 = emaciated, 5 = extremely fat

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. Contemporary group was defined as herd-gender-season of slaughter; gender in the present study refers to bull, steer, or heifer. Only contemporary 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 at 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 mean¹ 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

¹Reference 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

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The effect of replacement rearing regime on body measurements of ewes differing in prolificacy

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Introduction

Plane of nutrition offered to flock replacements during different phases of the rearing regime may impact on body development and consequently compromise ewe size and development at maturity. Furthermore ewe mature body size differs within and between genotypes. Ewe mature body size impacts on maintenance requirements and, consequently, costs of production. There is paucity of information on the relationship between ewe weight and frame size at different stages during the rearing phase. The aim of the current study was to evaluate the effects of plane of nutrition offered during different stages of the rearing phase on body size of ewes, differing in prolificacy, until first joining at 18 months. The prediction of ewe live weight from body measurements was also examined.

Materials and Methods

A total of 292 ewe lambs, consisting of 4 genotypes [Chamoise × Scottish Blackface (CSBF), Belclare × SBF (BelSBF), Belclare (carrying either the GDF or BMP genes for increased ovulation) × SBF (BelMGSBF) and Belclare (Bel)] were randomly allocated, within genotype, over 3 years to 4 treatments in a 2 × 2 design as follows: 2 daily allowances of extended grazed herbage (deferred grazing) dry matter [0.75 (L) or 1.75 (H) kg/head] during winter 1 (23 Nov. to 1 Apr.); 2 summer planes of nutrition achieved by set stocking at sward heights of 4 cm (L) or 6 cm (H) from 2 Apr. to 1 Sept. Withers height, body length, heart girth and cannon bone circumference were recorded at the start of the extended grazing (6 months), end of extended grazing (12 months) and the end of summer

grazing (18 months). Ewes were weighed at joining in Oct. at ~19 months of age. The data were analysed with treatments and genotype as fixed effects using Proc GLM of SAS.

Results and Discussion

Mean withers height, body length, body girth and cannon bone circumference at 6 months were 59.4 cm, 48.9 cm, 76.3 cm and 7.44 cm, respectively. Increasing the plane of nutrition offered during the first winter increased all body measurements at 12 months and body girth and length at 18 months (Table 1). Increasing plane of nutrition offered during the second summer increased all body measurements except withers height at 18 months. There were no interactions between winter and summer nutrition levels. The effects of ewe genotype on body measurements are presented in Table 2. Relative to the BelSBF, the CSBF had smaller body frame at each time point whilst Bel was larger. The BelMGSBF ewes had generally larger frames at 18 months than BelSBF; differences were significant for withers height, body girth and cannon circumference.

An analysis of the relationship between body measurements at 6, 12 and 18 months and weight at joining yielded significant ($P<0.001$) linear relationships for each age. The prediction equations for weight at joining were as follows:

$-46.6 + 0.496H + 0.246L + 0.508G + 2.44C$ ($R^2=0.43$)
using body measurements at 6 months;

$-64.9 + 0.338H + 0.407L + 0.585G + 4.24C$ ($R^2=0.52$)
using body measurements at 12 months;

$-84.3 - 0.057H + 0.529L + 1.030G + 3.58C$ ($R^2=0.73$)
using body measurements at 18 months;

where H = height (cm), L = length (L), G = girth (cm) and C = cannon bone circumference (cm).

Table 1. Effects of plane of nutrition on body measurements to first joining

		Winter 1 (W1) nutrition				s.e.	Significance		
		High		Low			W1	S	W1xS
		High	Low	High	Low				
Summer (S) nutrition									
Weight at joining (kg)		58.4	52.2	53.6	48.0	0.53	***	***	NS
Withers height	12 months		61.3		60.2	0.18	***	-	-
	18 months	64.0	63.5	63.4	63.2	0.26	0.06	NS	NS
Body girth	12 months		80.4		74.9	0.21	***	-	-
	18 months	87.7	83.3	84.2	80.5	0.45	***	***	NS
Body length	12 months		50.5		47.8	0.21	***	-	-
	18 months	53.5	51.5	51.8	50.3	0.24	***	***	NS
Cannon bone circum. (cm)	12 months		7.62		7.46	0.023	***	-	-
	18 months	8.25	7.94	8.23	7.86	0.034	NS	***	NS

Table 2. Effects of ewe genotype on body measurements to first joining (Relative to BelSBF)

		Ewe genotype			
		BelSBF	CSBF	Bel	BelMGSBF
Weight at joining (kg)		56.5	-7.7***	+8.4***	+0.5
Withers height (cm)	12 months	62.1	-4.7***	+4.1***	+0.3
	18 months	64.7	-4.3***	+3.7***	+1.3***
Body girth (cm)	12 months	79.1	-4.5***	+5.3***	+0.4
	18 months	85.7	-5.7***	+3.2***	+1.4**
Body length (cm)	12 months	50.3	-3.2***	+2.2***	-0.1
	18 months	53.2	-3.6***	+3.4***	+0.6
Cannon bone circum. (cm)	12 months	7.65	-0.38***	+0.58***	+0.15**
	18 months	8.23	-0.44***	+0.46***	+0.22***

Conclusions

Ewe genotype had a greater impact on body size than plane of nutrition offered during the rearing phase. Significant relationships between body measures and weight at joining were identified.

The effect of replacement rearing regime on the performance of 2-tooth ewes differing in prolificacy

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Introduction

The plane of nutrition during different phases of the rearing regime may impact on ewe body development and performance. The aim of this study was to evaluate the effects of plane of nutrition during the first winter, the second grazing season and subsequent first pregnancy on ewe performance and that of their progeny, using breeds differing widely in prolificacy.

Materials and Methods

A total of 292 ewe lambs, over 3 years, representing 4 genotypes [Chamoise \times Scottish Blackface (C \times SBF), Belclare \times SBF (Bel \times SBF), Belclare (carrying either the GDF or BMP genes for increased ovulation \times SBF (BelMG \times SBF) and Belclare (Bel)] were randomly allocated, within genotype, to a 2 \times 2 \times 2 factorial design as follows: 2 daily allowances of herbage (deferred grazed) dry matter (DM) [0.75 (L) or 1.75 (H) kg] during winter 1 (23 Nov. to 1 Apr.), 2 summer planes of nutrition achieved by set stocking at sward heights of 4 (L) or 6 (H) cm from 2 Apr. until 1 Sept. and 2 planes of nutrition [medium or high feed-value grass silage] while housed during pregnancy (1 Dec. to lambing in mid Mar.). From 1 Sept. until housing ewes were managed at pasture as one flock and joined (17 Oct.) with a panel of Suffolk rams. Total concentrate (conc) allowances of 13, 20, 28 and 31 kg were offered to ewes carrying singles, twins, triplets and quadruplets, respectively, over final 6 weeks of pregnancy. Ewes were put to pasture post lambing and managed in a rotational-grazing system; those rearing 1 or 2 lambs received no conc. Ewes rearing 3 lambs were offered conc (0.5 kg/day) for 5 weeks post lambing and their lambs had access to conc (300 g/

lamb/day) until weaning. All lambs were grazed as one flock post weaning, without conc. The data were analysed as a factorial design with treatment and genotype as fixed effects using the GLM and MIXED procedures of SAS for ewe and lamb traits (dam random), respectively.

Results and Discussion

The DM, DM digestibility and ME concentrations of the deferred-grazed herbage and the medium and high feed-value grass silages were 145, 208 and 267 g/kg; -, 693 and 752 g/kg; and 10.0, 10.8 and 11.6 MJ/kg DM respectively. During winter 1 intake and utilisation rate for herbage organic matter were 0.31 and 0.61 kg/day and 48.6 and 39.2 % for the L and H treatments, respectively. Whilst altering plane of nutrition during winter 1 and summer 2 significantly altered live weight at joining by up to 7.7 kg there was no effect on litter size or number of lambs weaned per ewe joined (Table 1). Increasing plane of nutrition in winter 1 increased lamb birth weight, tended to increase weaning weight, and reduced age at slaughter. Altering summer 2 nutrition level had no effect on ewe prolificacy or on lamb performance. Increasing plane of nutrition during winter 2 increased ewe weight at lambing, and lamb weight at birth and weaning. For the L and H winter 2 nutrition levels ewe mortality and barrenness were 5 and 1%, and 3 and 0%, respectively. Relative to the Bel \times SBF ewes: C \times SBF were lighter at joining and lambing, and produced fewer lambs, which were lighter at birth and weaning; progeny from Belclare ewes were heavier at weaning; BelMG \times SBF ewes produced more lambs, which were lighter at birth but a similar weight at weaning (Table 2). There was no evidence for treatment by ewe genotype interactions.

Conclusions

Increasing the plane of nutrition offered during pregnancy had the greatest impact on progeny performance, followed by the plane of nutrition offered during the first winter.

Table 1. The effects of treatment on ewe and lamb performance

	Winter 1 (W1) nutrition				s.e.	Winter 2 (W2)			s.e.	Significance			
	High		Low			High	Low	W1		S	W1xS	W2	
	High	Low	High	Low									
Summer (S) nutrition	High	Low	High	Low									
Weight (kg) - joining	61.1	57.0	57.1	53.4	0.55				***	***	NS		
- lambing	54.6	51.2	50.5	49.7	0.71	54.8	48.0	0.57	***	***	NS	***	
Body condition - joining	3.74	3.56	3.53	3.30	0.041				***	***	NS	NS	
Litter size	2.01	2.12	2.08	2.10	0.088	2.09	2.06	0.059	NS	NS	NS	NS	
Number reared/ewe joined	1.68	1.74	1.58	1.72	0.090	1.71	1.65	0.066	NS	NS	NS	NS	
Lamb weight (kg) - birth	4.36	4.27	4.14	4.10	0.090	4.40	4.04	0.065	*	NS	NS	***	
- weaning	28.3	29.5	29.0	28.0	0.49	29.3	28.1	0.37	NS	NS	*	**	
Age at slaughter (days)	196	196	202	205	4.2	198	201	3.4	*	NS	NS	NS	

Table 2. The effects of ewe genotype on ewe and lamb performance (Relative to Bel \times SBF)

	Mean for		Deviation from Bel \times SBF	
	Bel \times SBF	C \times SBF	Belclare	BelMG \times SBF
Weight (kg) - joining	56.5	-8.1***	+8.9***	+1.0
- lambing	49.6	-5.6***	+11.5***	+2.9*
Body condition score - joining	3.65	-0.14*	-0.42***	-0.04
Litter size	1.97	-0.49***	+0.13	+0.49***
Number reared per ewe joined	1.68	-0.60***	-0.03	+0.39*
Lamb weight (kg) - birth	4.42	-0.48**	+0.00	-0.45***
- weaning	29.1	-3.8***	+1.3*	+0.08

Effects of supplementary concentrate type and protein level on growth of suckler-bred weanling bulls offered grass silage

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Introduction

Providing feed for livestock is the single greatest cost in Irish beef farming; this cost is highest during the indoor winter period as grass silage and/or concentrates, the predominant feedstuffs offered, are more expensive than grazed grass (Finneran *et al.*, 2010). Winter feed costs could be reduced by utilising alternative more cost-effective concentrate feed ingredients, such as soya hulls. High protein ingredients are increasingly expensive and the growth response of cattle to (crude) protein supplementation on grass silage-based diets can be marginal (Huuskonen *et al.*, 2014). The objective of this study was to examine the effects of: (i) replacing barley with soya hulls; and, (ii) protein level of a barley-based concentrate on intake and performance of weanling bulls offered grass silage.

Materials and Methods

Two hundred and fifty five weaned, Charolais and Limousin sired suckler-bred bulls (411 kg, s.d. 63.3) born in either autumn 2012 (n=120) or spring 2013 (n=135) were blocked by sire breed and weight and, from within block, randomly assigned to one of three concentrate supplement types: 1. Barley/soya-based control (BS) (86.2% rolled barley, 6% soyabean meal) 2. Soya hulls-based (SH) (93.3% SH) or 3. Barley-based (B) (92.2% B). All concentrates contained 5% molasses and were balanced for minerals and vitamins. The BS and SH concentrates were formulated, based on published feed tables, to have similar protein - PDIE (true protein digestible in the small intestine when energy limits microbial protein synthesis) levels on a dry matter (DM) basis. Bulls were penned in groups of five (n=17 for intake-related measurements) in slatted floor sheds and offered grass silage (700 g/kg DMD; 130 g/kg DM CP) to appetite and 1.7 kg concentrate DM daily for 90 days. They were weighed on consecutive days at the beginning and end of the

trial and every three weeks throughout. Ultrasonic fat and muscle depths were also measured at the beginning and end. On one occasion, blood samples were obtained pre- and 2 hours post-, and rumen fluid (stomach tube) samples 2 hours post-, concentrate feeding. Intake was measured on a pen-basis. Data were statistically analysed using the mixed models procedure of SAS. The model contained fixed effects of diet and animal type (spring-born or autumn-born), and the random effect of block. For end of trial ultrasonic measures of body composition, initial values were included as covariates.

Results and Discussion

Average daily live weight gain (LWG) of bulls offered B was 74 g lower (P<0.05) than SH and tended to be 61 g lower (P=0.09) than BS; LWG did not differ (P=0.69) between BS and SH (Table 1). The increase of 1.5g LW per 1g/kg DM increase in dietary CP concentration is consistent with the value (1.4) found by Huuskonen *et al.* (2014) in their meta-analysis. Concentrate type had no effect (P>0.05) on final weight, DM intake or feed efficiency. Bulls offered SH had lower ultrasonic fat depths at the lumbar and had greater ultrasonic muscle depth (P<0.05) than BS and B, which did not differ (P>0.05). Rump fat depth was lower (P<0.05) for SH than B, with BS being intermediate (P>0.05). Post-feeding rumen pH and concentrations of plasma non-esterified fatty acids (P<0.05) and urea were higher, and plasma β -hydroxybutyrate were lower (P<0.01), for SH compared to BS and B, which did not differ (P>0.05).

Conclusion

Although feed nutrition databases indicate that the energy value of soya hulls is lower than barley (and soybean meal), under the conditions of this study this was not the case. The growth response in barley-fed animals to additional protein was small.

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Table 1. Effect of supplementary concentrate type on intake, performance and blood variables in weaned suckler bulls

	Barley/Soya (BS)	Barley (B)	Soya Hulls (SH)	SEM	p-value
Final weight (kg)	488	483	489	6.0	ns
Average daily gain (kg)	0.862 ^{ab}	0.801 ^a	0.875 ^b	0.0240	*
Rib fat depth (mm)	2.16	2.19	2.15	0.025	ns
Lumbar fat depth (mm)	2.12 ^a	2.07 ^a	1.99 ^b	0.032	*
Rump fat depth (mm)	2.36 ^{ab}	2.41 ^a	2.27 ^b	0.050	*
<i>Longissimus dorsi</i> depth (mm)	65.3 ^a	64.1 ^a	67.1 ^b	0.576	*
β -hydroxybutyrate (mmol/litre)	0.21 ^a	0.20 ^a	0.18 ^b	0.008	**
Glucose (mmol/litre)	4.16	4.19	4.23	0.043	ns
Urea (mmol/litre)	3.63 ^a	3.61 ^a	3.85 ^b	0.086	**
Non-esterified fatty acids (mmol/litre)	0.20 ^a	0.22 ^a	0.27 ^b	0.016	*
Rumen pH	6.96 ^a	6.88 ^a	7.09 ^b	0.035	*
Silage DM intake (kg/head/day)	5.28	5.21	5.30	0.250	ns
Feed conversion ratio (kg DM/kg ADG)	6.17	6.48	6.17	0.161	ns

Effect of replacing barley with increasing levels of wheat dried distillers grains on intake, growth and carcass traits of beef cattle

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Introduction

Feed provision accounts for over 75% of direct costs in beef production; concentrates are generally the most expensive feedstuff (Finneran *et al.*, 2010). In addition to cereals, a wide variety of feed ingredients are used in beef rations in Ireland. Due to global demand for renewable energy, by-products such as distillers dried grains (DDG) are becoming more available on the feed market (Leupp *et al.*, 2009). The two most common sources of DDG imported into Ireland at present are maize distillers and to a lesser extent wheat distillers (WD). Very little research has been carried out evaluating WD as a feed ingredient for beef cattle. The objective of this experiment was to evaluate the partial replacement of barley and complete replacement of soyabean meal in a barley-soya ration with increasing levels of WD on intake and performance of beef cattle.

Materials and Methods

Fifty nine weaned, spring-born (12 March) Charolais sired steers ca. 12 months old with a mean (SD) bodyweight of 361 (24.9) kg were blocked on live weight and, from within block, randomly allocated to one of five concentrate treatments. The concentrates were barley-soya-based control (862 g/kg rolled barley, 60 g/kg soyabean meal, 50g/kg molasses and 28 g/kg minerals/vitamins), and replacement of barley (+ all soya bean meal) with 200, 400, 600 and 800 g/kg fresh weight WD (crude protein 319g/kg DM; oil B 55g/kg DM). Steers were individually offered (Calan gate system) 3.0 kg dry matter (DM) of the respective concentrates as a supplement to moderate digestibility grass silage (DM digestibility, 642 g/kg; CP 135 g/kg DM) offered to appetite during a 70-day

'growing' phase (GP) and, following a 26 day dietary adaptation period, were offered the same concentrates *ad libitum* plus 3 kg grass silage (fresh weight basis) daily during a 86-day 'finishing' phase (FP). Animals were weighed at the beginning and end of the GP and FP, and every 14 days throughout. Post-slaughter, carcass weight and, carcass conformation and fat score were determined. Data were analysed using the mixed models procedure of SAS. The model contained the fixed effect of treatment and block was included as a random effect. Linear and quadratic response terms to WD inclusion level were included in the model.

Results and Discussion

During the GP, increasing inclusion level of WD resulted in a linear increase in average daily gain (ADG) ($P < 0.001$) and a linear decrease in feed conversion ratio (FCR – kg DM/kg ADG) ($P < 0.001$). In contrast, during the FP, ADG decreased linearly ($P < 0.01$) and FCR increased linearly ($P < 0.05$) with increasing WD inclusion. Carcass fat score decreased linearly ($P < 0.05$) as WD inclusion increased. Inclusion of WD had no effect ($P > 0.05$) on slaughter weight, carcass weight and kill-out proportion.

Conclusion

Results indicate that the nutritive value of WD is superior to a barley-soya ration at inclusion rates up to 800g/kg when offered as a supplement to grass silage of moderate nutritive value, but not when offered in a high concentrate diet.

Acknowledgements

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Table 1. Effect of inclusion level of wheat distillers in a barley-soya based ration on intake and performance of steers

	Wheat distillers inclusion level g/kg					SEM	Significance ¹
	0	200	400	600	800		
<i>Growing Phase</i>							
ADG (g/kg)	0.87	1.00	1.08	1.11	1.13	0.054	L
DM intake (kg)	6.91 ^a	6.90 ^a	6.76 ^{ab}	6.77 ^{ab}	6.50 ^b	0.167	*
FCR (kg DM/ kg ADG)	8.43	7.21	6.34	6.13	5.98	0.468	L
<i>Finishing Phase</i>							
ADG (g/kg)	1.31	1.37	1.07	1.04	1.09	0.071	L
DM intake (kg)	10.00	10.21	10.16	9.98	9.96	0.285	NS
FCR (kg DM/ kg ADG)	8.15	7.64	9.81	10.22	9.60	0.571	L
Slaughter weight (kg)	559	560	559	543	546	10.9	NS
Carcass weight (kg)	304	313	310	301	302	6.4	NS
Kill-out proportion (g/kg)	545	559	554	553	554	0.5	NS
Fat score (1-15)	7.5	7.4	7.0	6.5	6.5	0.34	L
Conformation score (1-15)	8.0 ^a	9.0 ^b	8.2 ^{ab}	7.8 ^a	8.4 ^{ab}	0.37	*

¹ L=linear response & Q=quadratic response ($P < 0.05$)

Sensory characteristics of muscle from heifers fed a lipid supplement in a grass or concentrate-based ration

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Introduction

Consumer interest in the relationship between diet and health has focussed attention on increasing the concentration of conjugated linoleic acid in beef. Supplementation with a combination of plant and marine oil is effective in this regard (Moloney *et al.*, 2007). A potential adverse effect of this strategy is an alteration in the sensory characteristics of beef due to excessive lipid oxidation which may be ameliorated by dietary anti-oxidants (Richardson *et al.*, 2005). The objective of this study was to determine the sensory quality of muscle from heifers either at pasture or fed a concentrate ration when offered a lipid supplement with or without vitamin E.

Materials and Methods

Sixty Charolais-sired suckler heifers were used. The animals were blocked on body weight (BW) and assigned at random within block to either unlimited grazed grass (G), a restricted amount of G and 2.5 kg /425 kg BW of a lipid supplement that contained 293 g sunflower seeds and 67 g fishoil/kg (GSF), a restricted amount of G and this supplement but with 400 IU vitamin E added (GSFV), 6 kg/425 kg BW of a concentrate ration that contained (g/kg) rolled barley 412, soyabean 168, citrus pulp 338, linseed oil, 37, molasses 20 and a mineral/vitamin mix 25 (C), restricted C with 2.5 kg /425 kg BW of the above supplement with (CSF), or without vitamin E (CSFV). The strategy was to achieve a similar carcass weight for all treatments. Cattle were slaughtered after 160 days. *M. longissimus dorsi* muscle from the 10th rib area was aged for 14 days post slaughter and stored frozen pending analysis by a 10 member trained sensory panel. Panellists rated steak, cooked to an internal temperature of 74°C, using a 0-100mm line scale where low values are low ratings and high values are higher ratings for a particular trait.

Data were analysed as a randomised block with a factorial arrangement of treatments. Effects of ration type, supplement type and their interaction were included in the model.

Results

Data are summarised in Table 1. Carcasses from G heifers tended (P < 0.1) to be lighter than carcasses from GSF heifers, while carcasses from CSFV heifers tended (P < 0.1) to be lighter than carcasses from C and CSF heifers. Inclusion of a lipid supplement *per se* increased (P < 0.05) the intramuscular fat concentration. The score for “greasy” was higher (P < 0.05) for muscle from heifers offered grass-based rations compared to muscle from heifers offered concentrate-based rations. Inclusion of a lipid supplement increased (P < 0.05) the score for “acidic” flavour of muscle but not when it contained vitamin E. There was no difference (P > 0.05) between treatments for scores for “tenderness” or “juiciness”, or for “overall beef” or “abnormal flavour” of muscle. There was no difference (P > 0.05) between treatments for scores for the specific flavour descriptors of “bloody”, “livery”, “metallic”, “bitter”, “sweet”, “rancid”, “fishy”, “dairy” and “cardboard” of muscle or on overall muscle liking/acceptability.

Conclusion

There was little difference in beef sensory characteristics whether cattle were finished on grass or a concentrate-based ration and had a similar pre-slaughter growth rate. While a lipid supplement increased intramuscular fat concentration it did not influence overall acceptability of beef.

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Table 1. Carcass weight and muscle characteristics

Base ration (R)	Grass			Concentrate			SED	Significance ²		
Supplement (S) ¹	None	SF	SFV	None	SF	SFV		R	S	R × S
Carcass (kg)	252	264	261	270	271	256	6.4	NS	NS	†
IMF (g/kg) ³	1.33	2.18	2.63	2.19	2.62	2.68	0.447	NS	*	NS
Tenderness ⁴	57.8	59.5	61.5	59.7	57.2	60.6	5.66	NS	NS	NS
Juiciness ⁴	45.8	46.6	44.8	45.2	46.3	49.3	3.28	NS	NS	NS
Beef ⁴	42.3	41.9	43.9	42.6	43.2	37.4	2.68	NS	NS	†
Abnormal ⁴	20.4	20.6	17.9	18.5	20.3	24.0	2.70	NS	NS	†
Greasy ⁴	16.4	15.1	17.5	12.8	14.1	13.9	1.66	*	NS	NS
Acidic ⁴	12.3	16.1	13.7	12.4	15.9	13.7	2.08	NS	*	NS
Vegetable ⁴	15.3	16.2	15.6	13.4	18.3	17.3	1.81	NS	†	NS
Overall acceptability ⁴	32.6	35.0	33.4	32.5	34.6	31.7	3.14	NS	NS	NS

¹ SF=supplement of sunflower and fishoil; SFV=SF + vitamin E. ² * = p < 0.05, † = P < 0.1; ³ IMF=Intramuscular fat, ⁴ 100 mm line scale: 0 (least) – 100 (most).

Effect of removal of in-feed antibiotics on performance and health indicators of pigs during the first weaning stage

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Introduction

High usage of antibiotics (AB) in both human and animals is associated with an increase in levels of AB resistance worldwide (Burow *et al.*, 2014). Antibiotic use in feed is typically high in weaned pigs to control pathologies (Cromwell, 2002; De Bryne *et al.*, 2014). Strategies that help reduce the use of AB need to be further studied. The aim of this study was to quantify the consequences for the health and performance of pigs for the first 5wk post-weaning of removing AB from their feed and relying instead on targeted parenteral administration of AB to tackle disease.

Materials and Methods

This study was carried out on a commercial farrow-to-finish farm (300 sows) (Sept. – Nov. 2014). The farm tested positive for Porcine Reproductive and Respiratory Syndrome and influenza. Six weekly batches of 140 pigs weaned at 28 ± 2 d of age were individually weighed, tagged and sorted into 2 groups of approximately 70 pigs with similar body weight (BW: 9.2 ± 0.56 kg). Each group was randomly allocated to one of the following treatments each week: in-feed medication (ANTI, n=6) whereby sulfadiazine-trimethoprim (Pfizer Ltd., Sandwich, UK) was included in the diet following manufacturer instructions (14.4mg/kg BW/d; for 5 d/wk) and no in-feed medication (NONE, n=6) whereby no AB were included in the pigs diet. At the end of the first weaner stage (i.e. after a period of 4 wk and 4 d) the pigs were weighed and moved to the second weaner stage accommodation. Feed intake of the groups was recorded daily during the 1st weaner stage as well as all mortalities and all parenteral administration of AB following the recommendations of the private veterinary practitioner. Average total gain (ATG), average total feed intake (ATFI) and feed conversion ratio (FCR) were calculated. The total number of parenteral AB treatments (i.e. AB injections) was calculated as a percentage of the number of animals in the group. Data were analysed by general linear models using the GLM procedure SAS 9.3 (Cary, NC, USA). In all models, treatment was used as a fixed classification factor and initial mean BW was used as a covariate. Each group of 70 animals was considered the experimental unit. Alpha level for determination of significance was 0.05.

Results and Discussion

Pigs in the ANTI group showed higher ATFI ($P = 0.051$) and ATG ($P = 0.033$) than pigs in the NONE group (Fig. 1) indicating that even when used at therapeutic doses AB have growth promotion effects. However, the FCR did not differ between the two treatments (1.50 ± 0.077 ; $P = 0.484$) which shows that the NONE pigs were as efficient as the ANTI pigs. As expected removal of in-feed AB increased the percentage of parenteral AB treatments of NONE pigs ($P = 0.040$; Fig. 1). However, the mortality rate was not different between the two treatments ($2.0 \pm 1.79\%$; $P = 0.854$).

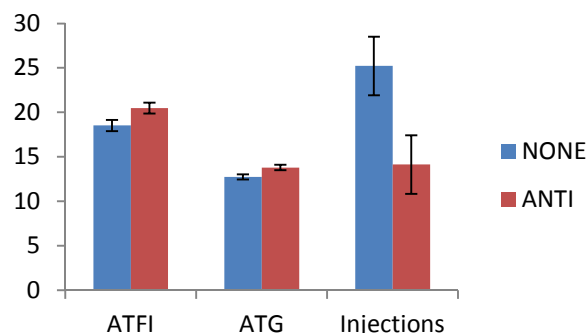


Fig. 1 Effect of removal of in-feed antibiotics on feed intake (ATFI; g/animal), body weight gain (ATG; g/animal) and percentage of animals receiving parenteral treatments (Injections) between antibiotic group (ANTI) and non-antibiotic group (NONE) during first weaner stage (32d). $P < 0.05$ in all cases.

Mean initial BW was correlated to the percentage of parenteral AB treatments ($r = 60.7$; $P = 0.016$) and tended to be correlated to the mortality rate ($r = 56.3$; $P = 0.070$). This result reflects the strong relationship between BW and disease.

Conclusion

Pigs that received no in-feed antibiotics during the 1st weaner stage had reduced feed intake and weight gain, and received more parenteral AB treatments than pigs which received antibiotics in their feed. However, the mortality rate and FCR were unaffected. A change from in-feed to parenteral use of AB could reduce the total amount of AB doses used in weaned pigs.

Acknowledgments

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High-throughput sequencing of the faecal microbiome in pigs divergent for residual feed intake

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Introduction

Changes in the profile of the intestinal microbiome are known to affect body mass and adiposity (Sekirov *et al.*, 2010). As the digestive tract is sterile at birth, the sow's faecal microbiota provides the inoculum that determines the microbial profile of the offspring later in life (Kelly *et al.*, 2007). The hypothesis of this study was that pigs divergent for residual feed intake (RFI) have different faecal microbial profiles from weaning to slaughter at ~145 kg. We also investigated the influence of the sow on the development of faecal microbiota of the offspring.

Material and methods

Entire litters from seven sows were individually housed with feed intake and weight recorded every 2 weeks between weaning and slaughter. At day 139 post-weaning (pw) 32 pigs were selected within litter and gender as having the best (n=12), poorest (n=10) and average (n=10) RFI. RFI was calculated as the residual from a regression of average daily feed intake (ADFI) on gender, average daily gain (ADG), mid-test metabolic weight and their interactions with gender and back fat ($R^2=0.87$). Faeces were collected from pigs at weaning, day 42 pw and day 139 pw for microbiota profiling using high-throughput 16S rRNA gene sequencing, on the Illumina MiSeq platform. Data were analysed using a mixed model, with RFI category, day pw, gender and sow as main effects, and day as a repeated variable. Statistical significance was reported at $P \leq 0.05$. Least squares means are presented as relative abundance (% of the total number of sequence reads). Means separation was performed using the Tukey-Kramer adjustment for multiple comparisons.

Results and discussion

RFI category or gender did not affect the relative abundance of the faecal bacterial phyla in pigs ($P > 0.05$; major phyla are shown in Table 1). However, the relative abundance of the main bacterial phyla changed as pigs aged ($P < 0.05$; Table 2).

Firmicutes decreased numerically from weaning to day 42 pw and then increased to day 139 pw (an overall time effect was observed). *Bacteroidetes* and *Spirochaetes* increased from weaning to day 42 pw and *Proteobacteria* decreased from weaning to day 42 pw. *Synergistetes* decreased from weaning to day 42 pw and increased thereafter ($P < 0.05$). Dam affected the relative abundance of the major phyla ($P < 0.05$), except *Firmicutes* and *Synergistetes* ($P > 0.05$). Most of the minor phyla (abundance $< 1.5\%$) either increased or did not change with age (data not shown).

Table 2. The effect of time post-weaning on the relative abundance of the main faecal bacterial phyla in pigs

	Weaning	Day 42	Day 139	SEM	P
<i>Bacteroidetes</i>	30.8 ^b	43.1 ^a	39.7 ^a	2.82	<0.01
<i>Firmicutes</i>	51.8	46.9	50.2	3.40	0.04
<i>Proteobacteria</i>	5.56 ^a	2.48 ^b	1.96 ^b	0.598	<0.01
<i>Spirochaetes</i>	0.85 ^b	4.13 ^a	4.16 ^a	0.542	<0.01
<i>Synergistetes</i>	2.92 ^a	0.08 ^c	0.17 ^b	1.325	<0.01

^{a,b,c}Values within a row with a different superscript are different ($P < 0.05$). Values are presented as least squares means of the bacterial relative abundance (% of the total number of sequence reads).

Conclusions

The relative abundance of the faecal bacterial phyla in pigs was not different between RFI categories. However, the microbiota profile changed with age, likely as a result of the adaptation of microbiota to the nutrient profile of the diets and maturation of the intestinal microbiota to a stable, adult-type community. The sow had a major influence on the intestinal microbiota profile of offspring, confirming the importance of microbial colonisation at birth and early in life on the pig's microbiota profile later in life. No gender difference was observed for the faecal microbiota at the phylum level.

Acknowledgements

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Table 1. Major faecal bacterial phyla in pigs divergent for RFI

	Weaning			Day 42 post-weaning			Day 139 post-weaning				P		
RFI category	Good	Medium	Poor	Good	Medium	Poor	Good	Medium	Poor	SEM	RFI	Sow	Gender
<i>Bacteroidetes</i>	28.4	30.0	34.1	44.2	41.3	43.8	39.4	39.5	40.3	5.00	0.59	0.01	0.39
<i>Firmicutes</i>	50.5	51.0	54.0	47.2	45.8	47.9	49.9	50.4	50.3	6.02	0.86	0.23	0.68
<i>Proteobacteria</i>	4.83	7.20	4.93	2.50	2.62	2.32	1.81	2.21	1.88	1.214	0.15	0.02	0.17
<i>Spirochaetes</i>	0.67	1.21	0.75	3.65	6.64	2.89	4.91	3.68	3.98	1.144	0.09	0.03	0.33
<i>Synergistetes</i>	5.33	4.16	1.10	0.09	0.08	0.08	0.15	0.30	0.10	2.632	0.23	0.28	0.90

Values are presented as least squares means of the bacterial relative abundance (% of the total number of sequence reads)

Can the digestible undegradable protein supply offered to ewes during late pregnancy affect lamb performance?

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Introduction

The plane of nutrition offered to ewes in late pregnancy influences lamb birth weight and subsequent performance (Keady and Hanrahan, 2009a, b). Nutrient requirements of ewes increase as pregnancy advances, particularly during the final 6 weeks, due to foetal growth and mammary development (Thomson and Thomson, 1940). We hypothesized that digestible undegradable protein (DUP) supplementation in late pregnancy might reduce the extent of periparturient relaxation of immunity (PPRI) and affect foetal organogenesis with a subsequent effect on dam performance and lamb growth. Hence, our aim study was to evaluate the effects of concentrate DUP concentration and concentrate level offered to ewes in late pregnancy on the performance of their progeny.

Materials and Methods

Eighty eight pregnant ewes (Belclare and Belclare x Scottish Blackface) that were carrying twins or triplets were allocated to 4 dietary treatments for the final 6 weeks of pregnancy. The dietary treatments were 2 concentrates differing in (DUP) concentration and offered at 2 levels; grass silage was offered *ad libitum*. The concentrate was formulated using either protected soyabean meal (Sopralin; Trouw Nutrition, Belfast), or other by-products as the protein source. Concentrates were formulated to contain similar crude protein (206 g/kg of dry matter (DM)) and ME (12.5 MJ/kg DM) concentrations. The estimated DUP concentrations were 94 and 29 g/kg DM, for high and low DUP concentrates, respectively. The high DUP concentrate contained 365, 170, 170, 150, 70, 50 and 25 kg/t of barley, soya hulls, sugar-beet pulp, sopralin, soyabean meal, molasses, and minerals and vitamins, respectively. The low concentrate contained 335, 240, 175, 80, 80, 50, 25 and 5 kg/t of barley, rapeseed meal, maize gluten, soya hulls, sugar-beet pulp, molasses, minerals and vitamins, and urea, respectively. Twin

and triplet bearing ewes offered the low and high concentrate feed levels received 18 and 25 kg, and 30 and 35 kg, respectively, over the last 6 weeks of pregnancy. Ewes with triplets had one lamb removed at lambing so that all ewes were put to pasture with 2 lambs. Ewes plus lambs were managed as one flock at pasture and received no concentrate supplement. Anthelmintic treatment (Ivermectin; Oramec, Merial Animal Health Ltd) was administered at 5, 14, and 21 weeks of age as per manufacturer's instructions. All lambs were slaughtered on 7th Oct (mean age 205 days). Data were analysed using Proc GLM for ewe traits, and Proc MIXED for lamb traits with fixed effects for treatment, litter size and sex, and ewe as a random term for lamb traits.

Results and Discussion

The pH and concentrations of DM, ammonia nitrogen, crude protein and DM digestibility of the grass silage were 4.1, 212 g/kg, 78 g/kg N, 114 g/kg DM and 659 g/kg DM, respectively. The effects of concentrate DUP concentration and concentrate feed level on lamb performance are presented in Table 1. Neither the concentration of DUP in the concentrate nor concentrate feed level offered in late pregnancy altered lamb weight at birth, weaning or slaughter. Carcass weight and carcass fat score were also unaffected.

Conclusions

The lack of effect on lamb performance may be because DUP supplementation late in pregnancy does not affect the foetal organogenesis essential for the development of an efficient immune response to parasites. While DUP supplementation earlier in pregnancy may influence development of the immune system this is not relevant under Irish husbandry conditions.

Acknowledgements

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Table 1. Effect of concentrate DUP concentration and feed level offered to ewes in late pregnancy on performance of their progeny.

(DUP) Concentrate level (CL)	Low		High		s.e.	Significance		
	Low	High	Low	High		DUP	CL	CL × DUP
Lamb weight (kg)								
– birth	4.71	4.65	4.65	4.52	0.156	NS	NS	NS
– weaning	29.5	30.3	29.3	28.8	0.744	NS	NS	NS
– slaughter	43.8	44.8	43.7	43.0	0.95	NS	NS	NS
Lamb gain (g/day)								
– birth to weaning	255	270	258	250	7.18	NS	NS	NS
– birth to slaughter	193	202	195	191	4.00	NS	NS	NS
– weaning to slaughter	132	134	135	131	5.01	NS	NS	NS
Carcass weight (kg)	17.2	17.7	17.3	17.1	0.52	NS	NS	NS
Carcass fat classification	2.33	2.34	2.26	2.48	0.10	NS	NS	NS

Replacement of barley with increasing levels of maize dried distillers grains: intake, growth and carcass characteristics of beef cattle

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Introduction

Feed represents the largest variable cost on Irish beef farms and of the main feedstuffs used, concentrates are generally the most expensive (Finneran *et al.*, 2012). Concentrates are usually offered to beef cattle either as a supplement to forage or to appetite. Due to increased production of biofuels globally (Klopfenstein *et al.*, 2007) there is a greater supply of associated protein rich by-products such as distillers dried grains (DDG), available for animal feed. The main form of DDG imported into Ireland is 'corn' or maize dried distillers (MD) and it is one of the primary feed ingredients used in cattle rations (ca. >250,000 tonnes annually). The objective of this experiment was to evaluate the partial replacement of barley and complete replacement of soyabean meal in a barley-soya ration with increasing levels of MD on intake, growth and carcass traits of beef cattle.

Materials and Methods

Fifty seven weaned, spring-born (12 March) Charolais sired steers (360, s.d. 25.0 kg) ca. 12 months old were blocked on live weight and, from within block, randomly allocated to one of five concentrate treatments. The concentrates were barley-soya-based control (862 g/kg rolled barley, 60 g/kg soyabean meal, 50g/kg molasses and 28 g/kg minerals/vitamins) and replacement of barley (+ all soya bean meal) with 200, 400, 600 and 800 g/kg fresh weight MD (crude protein 289 g/kg DM; oil B 94 g/kg DM). Steers were individually offered (Calan gate system) 3.0 kg dry matter (DM) of the respective concentrates as a supplement to grass silage (DM digestibility, 642 g/kg;

CP 135 g/kg DM) offered to appetite during a 70-day 'growing' phase (GP) and, following a 26 day dietary adaptation period, were offered the same concentrates *ad libitum* plus 3 kg grass silage (fresh weight basis) daily during a 86-day 'finishing' phase (FP). Animals were weighed at the beginning and end of the GP and FP, and every 14 days throughout. Post-slaughter, carcass weight, conformation and fat score were determined. Data were analysed using the Mixed models procedure of SAS. The model contained fixed effect of treatment and block was included as a random effect. Linear and quadratic response terms response terms to MD inclusion level were included in the model.

Results and Discussion

During the GP, increasing the inclusion level of MD resulted in a linear increase in average daily gain (ADG) ($P<0.001$) and a quadratic ($P<0.05$) decrease in feed conversion ratio (FCR – kg DM/kg ADG). In contrast, during the FP, ADG decreased linearly ($P<0.05$) but there was no effect ($P>0.05$) on FCR. Inclusion of MD had no effect ($P>0.05$) on slaughter weight. With increasing MD inclusion level, kill-out proportion increased linearly ($P<0.05$), whereas carcass fat score decreased linearly ($P<0.01$).

Conclusion

Results indicate that the nutritive value of MD is superior to a barley-based ration at inclusion rates up to 800g/kg when offered as a supplement to grass silage of moderate nutritive value, but not when offered in a high concentrate diet.

Acknowledgements

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Table 1. Effects of maize distillers inclusion level in a barley-based concentrate on intake and performance of steers

	Maize distillers inclusion level g/kg					SEM	Significance ¹
	0	200	400	600	800		
<i>Growing Phase</i>							
ADG (g/kg)	0.87	1.11	1.19	1.17	1.33	0.056	L
DM intake (kg)	6.91	6.90	6.93	6.74	6.68	0.167	NS
FCR (kg DM/ kg ADG)	8.4	6.3	5.8	5.7	4.9	0.47	Q
<i>Finishing Phase</i>							
ADG (g/kg)	1.31	1.25	1.26	1.17	1.13	0.071	L
DM intake (kg)	10.00 ^{ab}	9.92 ^{ab}	10.25 ^a	9.67 ^{ab}	9.29 ^b	0.285	*
FCR (kg DM/ kg ADG)	8.1	8.2	8.4	8.4	8.5	0.57	NS
Slaughter weight (kg)	559	564	571	563	552	10.9	NS
Carcass weight (kg)	304 ^a	308 ^a	319 ^b	317 ^a	312 ^a	6.4	*
Kill-out proportion (g/kg)	545	547	559	562	563	0.5	L
Fat score (1-15)	7.5	8.2	7.4	7.1	6.4	0.34	L
Conformation score (1-15)	8.0 ^a	8.1 ^a	8.5 ^{ab}	9.1 ^b	8.4 ^{ab}	0.37	*

¹ L=linear response & Q=quadratic response ($P<0.05$)

Intake and performance of beef cattle offered barley-based concentrates with increasing inclusion levels of soya hulls

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Introduction

Feed accounts for over 75% of direct costs on Irish beef farms with concentrates the most expensive feedstuff (Finneran *et al.*, 2010). In addition to cereals a wide range of feed ingredients are incorporated into beef rations in Ireland. This includes by-products from further processing of oilseeds, such as soya hulls (SH). Soya hulls are an imported feed by-product used in Ireland (ca. >300,000 tonnes annually). There is relatively little research published evaluating the inclusion of SH in beef cattle diets. The objective of this study was to evaluate intake and performance of beef cattle when barley was replaced in the diet with increasing levels of soya hulls.

Materials and Methods

Fifty seven weaned, spring-born, Charolais and Limousin sired steers ca. 13 months (458, s.d. 30.9 kg) were blocked on breed and live weight and, from within block, randomly allocated to one of five concentrate treatments. The control concentrate was barley-soya based (862g/kg rolled barley, 60g/kg soya bean meal (SBM), 50g/kg molasses and 28g/kg minerals/vitamins). For the other concentrates 200, 400, 600, and 800 g/kg of barley were replaced with SH (crude protein 105 g/kg DM), on a fresh weight basis. Concentrates had a similar protein concentration (PDI - true protein digestible in the small intestine) on a dry matter (DM) basis. Steers were individually offered (Calan gate system) 3.0 kg DM of the respective concentrates as a supplement to moderate nutritive value grass silage (DM digestibility, 640 g/kg; crude protein 126 g/kg

DM) offered *ad libitum* during a 71 day growing study (GS). At the end of this phase steers were offered grass silage only to appetite for 21 days to ensure that gut-fill variances did not impact on live weight. They were then blocked on weight and GS treatment and randomly re-assigned to the one of the five concentrates as outlined earlier. Following a dietary adaption period, the concentrates were offered *ad libitum* plus 3kg fresh weight grass silage daily during a 70-day finishing study (FS). Animals were weighed at the beginning and end of the GS and FS, and every 14 days throughout. Post-slaughter, carcass weight and conformation and fat score were determined. Data were analysed using the MIXED procedure of SAS. The model contained the fixed effect of treatment and block was included as a random effect. Linear and quadratic response terms were included in the model.

Results

During the GS there was a linear decrease ($P<0.001$) in average daily gain (ADG) and linear increase ($P<0.001$) in feed conversion ratio (FCR – kg DM/kg ADG) as inclusion levels of SH increased (Table 1). During the FS there was a linear decrease in ADG and slaughter weight ($P<0.01$) and, an increase in DM intake (DMI) ($P<0.01$) and FCR ($P<0.001$) with increasing SH inclusion. There was a quadratic (curvilinear) response in carcass weight ($P<0.05$).

Conclusion

Results suggest that based on growth rate and carcass weight the maximum inclusion level of SH in a barley-based beef ration is ca. 200g/kg.

Acknowledgements

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Table 1. Effect of soya hulls inclusion level in a barley-based concentrate on intake and performance of steers

	Soya hull inclusion level (g/kg)					Significance ¹	
	0	200	400	600	800	SEM	
<i>Growing study</i>							
ADG (g/kg)	0.78	0.78	0.67	0.60	0.70	0.046	L
DMI (kg)	7.26	7.46	7.35	7.37	7.32	0.155	NS
FCR (kg DM/ kg ADG)	9.72	10.03	11.09	13.25	10.86	0.764	L
<i>Finishing study</i>							
ADG (g/kg)	1.44	1.45	1.17	1.19	1.04	0.089	L
DMI (kg)	11.12	11.7	11.71	12.81	11.9	0.399	L
FCR (kg DM/ kg ADG)	7.89	8.58	10.47	11.34	11.85	0.729	L
Slaughter weight (kg)	676	675	662	650	644	14.7	L
Carcass weight (kg)	382	393	374	366	367	7.7	Q
Kill-out proportion (g/kg)	562 ^{ab}	572 ^a	562 ^{ab}	550 ^b	564 ^{ab}	6.8	**
Conformation score (1-15)	9.0	9.3	8.7	8.6	8.9	0.45	NS
Fat score (1-15)	8.6 ^a	8.4 ^a	7.8 ^a	8.8 ^a	6.7 ^b	0.56	***

¹ L=linear response & Q=quadratic response ($P<0.05$)

Effect of substituting barley with maize on the performance of suckler-bred bulls offered a high concentrate diet

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Introduction

In feed nutrition databases maize is often assigned a higher nutritive value than barley (INRA, 2004). Processed maize grain is usually included in cattle rations to increase performance and, mainly due to anecdotal evidence, to increase the rate of fat deposition, and thus achieve earlier ‘finish’. There are inconsistent effects of replacing processed barley with processed maize on cattle growth (Koenig and Beauchemin, 2005; Keane, 2008) and carcass fatness (Tiffany and Spears, 2005; Koenig and Beauchemin, 2005; Keane, 2008). Processed maize grain is generally available in two main forms; ground (meal) and flaked-toasted. The objective of this study was to examine the effects of partially replacing barley with maize meal or flaked maize on intake, growth and carcass characteristics of suckler-bred bulls offered a high concentrate diet.

Materials and Methods

Sixty weaned, Charolais and Limousin sired suckler bred bulls (554 kg, s.d. 43.6; 515 days old, s.d. 35.8), previously offered grass silage and one of three concentrate supplements over 90 days, were blocked according to breed type, previous supplement type and weight and, from within block, randomly assigned to one of three concentrates: 1. Barley-based control (BC) (86.2% rolled barley (B), 6% soyabean meal,); 2. Maize meal (MM50) (42.6% B, 42.6% MM, 7% soyabean meal) or 3. Flaked maize (FM50) (42.6% B, 42.6% FM, 7% soyabean meal). All concentrates contained 5% molasses and 2.8% minerals & vitamins, and were formulated to have similar levels of protein (PDI – true protein digestible in the small intestine). Following gradual adaptation, concentrates were offered to appetite with grass silage *ad libitum* over an 86

day mean finishing period. Animals were housed in groups of four in slatted pens (n=5 for intake-related measurements). They were weighed on consecutive days at the beginning of trial, every three weeks throughout and pre-slaughter. Rumen fluid samples (stomach tube) were obtained on one occasion from each animal 2 hours post-feeding. For logistical reasons bulls were slaughtered on two days, a week apart. Post-slaughter, carcass weight, conformation and fat score were recorded. The 6-10 ribs joint was dissected 48 hours post-slaughter. Data were statistically analysed using the GLM procedure of SAS. The model contained fixed effects of diet, slaughter date, their interactions, and block.

Results and Discussion

Carcass (P<0.05) and ribs joint (P<0.01) weights were greater for bulls offered MM50 compared to BC, with FM50 being intermediate (P>0.05) (Table 1). Carcass fat score tended to differ (P=0.06) between concentrates with BC fattest and FM50 thinnest. Concentrate dry matter intake (DMI) was higher (P<0.05) for FM50 than MM50, with BC being intermediate (P>0.05). Silage DMI was lower (P<0.05) for FM50 compared to BC and MM50, which did not differ (P>0.05). Feed conversion ratio was poorer (P<0.05) for BC than MM50, with FM50 being intermediate (P>0.05).

Conclusion

Bulls offered maize meal (but not flaked maize) had superior carcass weight and feed efficiency compared to those offered rolled barley. Maize inclusion in the diet did not enhance carcass fat deposition.

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Table 1. Effect of concentrate type on the performance and carcass traits of finishing suckler bulls

	BC	MM50	FM50	SEM	p-value
Daily live weight gain (kg)	1.81	2.04	1.87	0.094	0.08
Slaughter weight (kg)	708	732	713	8.9	0.06
Carcass weight (kg)	406 ^a	420 ^b	409 ^{ab}	4.6	*
Kill-out proportion (g/kg)	574	574	574	4.6	ns
Carcass conformation (1-15)	9.9	10.4	9.8	0.27	ns
Carcass fat (1-15)	8.3	7.7	7.4	0.32	0.06
Ribs joint weight (kg)	10.75 ^a	11.46 ^b	11.21 ^{ab}	0.181	**
Lean proportion (g/kg)	658	669	664	8.1	ns
Fat proportion (g/kg)	136	124	130	7.7	ns
Bone proportion (g/kg)	205	205	205	3.4	ns
Rumen pH	6.07	6.04	6.02	0.091	ns
Dry matter intake: Concentrate (kg/day)	10.3 ^{ab}	9.4 ^a	10.4 ^b	0.32	*
Silage (kg/day)	1.45 ^a	1.45 ^a	1.30 ^b	0.039	*
Total (kg/day)	11.76	10.85	11.71	0.333	0.09
Feed conversion ratio (kg DMI/kg ADG)	6.39 ^a	5.33 ^b	6.08 ^{ab}	0.267	*

Effect of dietary restriction and compensatory growth on growth hormone and systemic insulin-like growth factor-1 synthesis in Holstein-Friesian bulls

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Introduction

The somatotrophic axis is of critical importance in the control of nutrient utilisation and partitioning for growth and development in cattle (Bauman, 1992). Systemic insulin-like growth factor-1 (IGF-1) concentrations are reduced during dietary restriction and increase upon re-alimentation and subsequent compensatory growth (Hornick *et al.*, 2000). However it is not known if the documented variation in IGF-1 concentration is due to altered sensitivity of the pituitary gland to synthesise growth hormone. The objective of this study was to establish pituitary sensitivity to synthesise growth hormone through administration of its precursor, growth hormone releasing hormone (GHRH) during dietary restriction and subsequent re-alimentation in Holstein-Friesian bulls.

Materials and Methods

This study utilised animals as part of a previous study by Keogh *et al.* (2012). Briefly, 30 Holstein-Friesian bulls were assigned to one of two groups: (i) restricted feed allowance for 125 days (RES; n=15) followed by *ad libitum* access to feed for 55 days or (ii) *ad libitum* access to feed throughout (ADLIB; n=15). The first 125 days was denoted as Period 1 and the subsequent 55 days, Period 2. During Period 1 RES were managed to achieve a target mean daily growth rate of 0.6 kg/day. On days 89 and 35 of periods 1 and 2 respectively, a GHRH challenge was performed on all bulls. Indwelling catheters were fitted and all animals were infused with GHRH (20 µg/ 100 kg body weight) in sterile 0.9% (9 g/L) saline at a rate of 10 µg of GHRH per mL of saline. Blood samples were collected at -15, -5, 0, 5, 10, 15, 20, 30, 45, 60, 75, 90, 105 and 120 minutes relative to GHRH infusion. Blood samples were subsequently centrifuged and the resulting plasma assayed for both growth hormone and IGF-1 concentrations, using an enzyme-linked immunosorbent assay and radioimmunoassay, respectively (Taylor *et al.*, 2006). Area under the curve (AUC) analysis was carried out on each animal's growth hormone and IGF-1 plasma

concentration data to quantify the hormonal response to GHRH infusion. Area under the curve data were transformed if necessary and statistically analysed using the MIXED procedure of SAS with terms for treatment and period, as well as their interaction included in the model, as appropriate.

Results and Discussion

Average daily gain (ADG) for Period 1 was 0.6 kg/day for RES and 1.9 kg/day for ADLIB treatment. During re-alimentation an ADG of 2.5 and 1.4 kg/day was observed for the RES and the ADLIB groups, respectively. Least square means of AUC data are presented in Table 1. There was no effect of either treatment or period on the growth hormone response to GHRH administration ($P > 0.05$). However, a treatment x period interaction ($P < 0.05$) was evident for IGF-1 response, which was lower in RES animals in Period 1, and subsequently greater in these animals in Period 2. The lack of difference in growth hormone response to GHRH administration indicates that there are no alterations in pituitary sensitivity to GHRH in the production of growth hormone during dietary restriction. The resultant lowered concentration of IGF-1 is in agreement with previous reports (Hornick *et al.*, 2000) and indicates an uncoupling of the somatotrophic axis in response to dietary restriction, which was subsequently not evident by day 35 of re-alimentation.

Conclusion

The lack of difference in growth hormone response to GHRH administration indicates that the sensitivity and capacity of the pituitary gland to synthesise growth hormone is not affected by dietary restriction or compensatory growth. However, the lower IGF-1 response in RES animals suggests an uncoupling of the axis during dietary restriction which had apparently recovered early into re-alimentation.

Acknowledgements

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Table 1. Effect of treatment (T) and period (P) on growth hormone (GH) and IGF-1 AUC following GHRH administration.

Hormone	RES		ADLIB		SEM	Significance		
						T	P	T×P
GH (mmol.min.L ⁻¹)	9024.65	8195.66	8368.13	8414.38	407.828	NS	NS	NS
IGF-1 (mmol.min.L ⁻¹)	49017	60973	64486	57898	3944.365	NS	NS	*

* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; NS = $P > 0.05$.

Effect of feed restriction and compensatory growth on insulin signalling in bovine skeletal muscle

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Introduction

Compensatory growth (CG) is an accelerated growth phenomenon observed in cattle upon re-alimentation following a prior dietary restriction (Hornick *et al.*, 2000). Compensatory growth is commonly exploited by cattle producers to reduce overwintering costs of beef cattle (Keane and Drennan, 1994). Although it is well established that dietary restriction incurs a reduction and CG an increase in systemic insulin concentrations (Hornick *et al.*, 2000), it is not known whether dietary restriction and CG affect glucose uptake and insulin signalling (IS) in insulin responsive tissues. The objective of this study was to examine transcriptional differences of genes of the IS pathway within *M. longissimus dorsi* (LD) tissue in Holstein Friesian bulls, following (i) a period of restricted feed intake and (ii) during re-alimentation induced CG.

Materials and Methods

This study utilised tissue collected as part of the study of Keogh *et al.* (2012). Briefly, 30 Holstein-Friesian bulls were assigned to one of two groups: (i) restricted feed allowance for 125 days (RES; n=15) followed by *ad libitum* access to feed for 55 days or (ii) *ad libitum* access to feed throughout (ADLIB; n=15). The first 125 days was denoted as Period 1 and the subsequent 55 days, Period 2. During Period 1 RES animals were managed to achieve a target mean daily growth rate of 0.6 kg/day. *M. longissimus dorsi* biopsies were harvested from all bulls on days 120 and 15 of periods 1 and 2 respectively. Total RNA was isolated using the TRIzol procedure and subsequently purified using the Qiagen RNeasy clean up kit. RNAseq libraries were prepared from the isolated total RNA and RNA sequencing and bioinformatic analysis performed on resultant reads as outlined by Keogh *et al.* (2014).

Results and Discussion

Average daily gain (ADG) for Period 1 was 0.6 kg/d for RES and 1.9 kg/d for ADLIB. During the first 15 days of re-alimentation an ADG of 4.1 and 1.2 kg/d was observed for the RES and ADLIB, respectively (ADG for entire Period 2 was 2.5 and 1.4 kg/d for RES and ADLIB respectively). At the end of Period 1, 9 genes of the IS pathway were differentially expressed. Following a period of re-alimentation and CG, 6 IS genes were differentially expressed. Genes differentially expressed at each time point are presented in Table 1. Following a period of dietary restriction, greater expression of *GLUT4* and *PRKCZ* suggested greater insulin sensitivity for intracellular glucose uptake. Insulin sensitivity in LD was further established through down regulation of the phosphoinositide phosphatases: *PTEN* and *SHIP*. Although an indication towards insulin sensitivity was recorded in LD tissue following dietary restriction, the

downstream anabolic effects of IS were interrupted, with a potential for the inhibition of protein (*4E-BP1*), glycogen (*PPP1R3A*) and fatty acid (*ACLY*) synthesis observed. This may have reflected an adaptive response to reroute energy towards tissue maintenance and away from anabolic tissue deposition. During re-alimentation, the observed sensitivity during feed restriction had subsided. Greater expression of the FoxO genes: *FOXO1*, *FOXO3* and *FOXO4* during re-alimentation may have reflected the greater feed intake during Period 2. Up-regulation of the FoxO genes may have potentially been necessary during CG in order for cells to cope with the greater concentrations of IS by controlling reactive oxygen species and potential damage from sudden extra processing of a greater abundance of nutrients (Nemoto *et al.*, 2004).

Table 1. Differentially expressed genes of the IS pathway in skeletal muscle during dietary restriction (Period 1) and CG (Period 2).

Gene	Fold change ¹	P value
Period 1:		
<i>ACLY</i>	-3.676	1.95E-06
<i>4E-BP1</i>	2.175	5.87E-10
<i>GRB10</i>	1.322	0.000187
<i>SHIP</i>	-1.293	0.000231
<i>PPP1R3A</i>	-1.466	0.005161
<i>PRKCZ</i>	1.33	0.002892
<i>PTEN</i>	-1.469	0.001709
<i>c-RAF</i>	1.258	0.00052
<i>GLUT4</i>	1.611	9.89E-08
Period 2:		
<i>ACLY</i>	1.846	0.007759
<i>FOXO1</i>	2.008	0.000358
<i>FOXO3</i>	1.385	0.008536
<i>FOXO4</i>	1.391	0.000227
<i>SHIP</i>	1.306	0.001877
<i>GRB10</i>	1.456	9.04E-05

¹Fold changes are in RES compared to ADLIB animals

Conclusion

The pattern of differentially expressed genes following a period of dietary restriction indicates a greater sensitivity in skeletal muscle to IS as well as an inhibition towards the anabolic effects of IS. However, evidence of continued muscle sensitivity to insulin was not apparent early into re-alimentation and CG.

Acknowledgements

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Effects of finishing strategy, genotype and level of concentrate supplementation on the performance of dairy bulls slaughtered at 15 months of age

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Introduction

Current UK market specifications dictate that dairy bulls be slaughtered at less than 16 months of age (Matthews, 2011). Previously, Ashfield *et al.* (2014) reported that the 15 month bull production system was the least profitable dairy calf to beef system, largely due to the high input costs. Since concentrates constitute 0.75 of total variable costs for bulls in this system (Prendiville *et al.*, 2012) the objective of this study was to investigate alternative finishing strategies for dairy bulls slaughtered at 15 months of age.

Materials and Methods

Data were available for 51 spring born Holstein-Friesian (HF) and 34 Jersey × Holstein-Friesian (JEX) bulls. Calves were assigned to a 2 level of concentrate supplementation (1 kg and 2 kg per head daily (LA and HA, respectively) during the 1st season at pasture) × 2 finishing strategy (concentrates *ad libitum* (AL) and grass silage *ad libitum* supplemented with 5 kg of concentrate (SC) dry matter (DM) per head daily) × 2 genotype (HF and JEX) factorial arrangement of treatments. Bulls were housed on November 3rd. The AL treatment group was adapted to concentrates *ad libitum* over a 3 week period. Straw was offered *ad libitum*. The SC treatment group was adapted to grass silage *ad libitum* (72 dry matter digestibility) and 5 kg DM of concentrate per head daily over a 7 day period. Bulls were penned on a slatted floor shed, group fed for 205 days (s.d. 15.1) and slaughtered in May/June. Concentrates offered consisted of 580 g/kg barley, 260 g/kg beet pulp, 100 g/kg soya bean meal, 40 g/kg molasses and 20 g/kg minerals. Bulls were weighed fortnightly throughout the study. Post-slaughter carcass weight, conformation score and fat score were recorded. Data were analysed using the Mixed model procedure of SAS. Fixed effects were finishing strategy, genotype and level of concentrate

supplementation and their interactions. Initial live-weight was included as a covariate.

Results and Discussion

No interactions were observed for the traits presented. Estimated finishing concentrate dry matter intakes (DMI) were 1.5 and 1.0 tonne for AL and SC, respectively and 1.2 and 1.3 tonne for LA and HA, respectively. The estimates of DMI were similar for both genotypes. Average daily gain (ADG) during the 1st season at pasture was greater ($P<0.01$) for HA than LA (Table 1). At housing, HA were 17 kg heavier than LA ($P<0.05$). Live weight at slaughter and carcass weight, conformation score and kill-out proportion did not differ between HA and LA. Fat score was greater for HA compared to LA ($P<0.05$). Average daily gain during the finishing period was greater for LA than HA ($P<0.05$). The AL treatment group had a greater live weight at slaughter ($P<0.001$), carcass weight ($P<0.001$) and ADG during finishing ($P<0.001$) than SC. Conformation score ($P=0.054$) tended to be greater for AL compared to SC. Kill-out proportion and fat score did not differ between AL and SC. Live weight at slaughter, carcass weight and ADG during finishing were greater for HF compared to JEX. Conformation score was greater for HF compared to JEX ($P<0.05$). Kill-out proportion and fat score did not differ between genotypes.

Conclusions

While both treatments groups failed to meet the required market specifications from a carcass weight perspective, results from the current study suggests that supplementing dairy bulls with concentrates on a grass silage *ad libitum* diet resulted in lower carcass weights, conformation score and fat score than bulls finished on a concentrate *ad libitum* diet.

Acknowledgements

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Table 1: Effects of finishing strategy, genotype and concentrate supplementation level on the performance of dairy bulls

	Supplementation level (S)		Finishing strategy (F)		Genotype (G)		SEM ⁷	P-value		
	LA ¹	HA ²	AL ³	SC ⁴	HF ⁵	JEX ⁶		S	F	G
Initial live-weight (kg)	85	83	86	83	90	79	2.8	0.364	0.303	<0.001
Housing weight (kg)	212	229	222	218	226	215	6.7	<0.05	0.537	0.093
Slaughter weight (kg)	452	467	479	440	475	444	9.4	0.117	<0.001	<0.01
Carcass weight (kg)	229	239	245	223	243	225	5.3	0.063	<0.001	<0.01
Kill-out proportion (g/kg)	516	521	521	516	520	517	3.3	0.095	0.155	0.255
Conformation score (1-15)	4.68	4.74	4.93	4.50	4.91	4.52	0.221	0.872	0.054	<0.05
Fat score (1-15)	4.86	5.45	5.39	4.92	5.14	5.18	0.250	<0.05	0.062	0.925
ADG ⁸ 1 st season (kg/day)	0.78	0.89	0.84	0.82	0.83	0.83	0.036	<0.01	0.644	0.871
Finishing ADG (kg/day)	1.28	1.21	1.34	1.14	1.29	1.20	0.038	<0.05	<0.001	<0.05

¹1 kg/head/day; ²2 kg/head/day; ³concentrates *ad libitum*; ⁴grass silage *ad libitum* and 5 kg DM of concentrate per head daily; ⁵Holstein-Friesian; ⁶Jersey × Holstein-Friesian; ⁷standard error of the mean; ⁸average daily gain

Fatty acid composition and consumer assessment of burgers made from tissue from cattle fed a plant or marine oil supplement

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Introduction

Consumer interest in the relationship between diet and health has focussed attention on increasing, in beef, the concentration of omega (n)-3 polyunsaturated fatty acids (PUFA) (particularly eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA)) and conjugated linoleic acid (CLA). Since omega-3 fatty acids associate preferentially with muscle membranes (Noci *et al.*, 2005), addition of fat in the manufacture of processed beef products dilutes the nutritional value of omega-3 enriched beef. However, CLA associates preferentially with fat tissue (Noci *et al.*, 2005) and therefore CLA-enriched fat could be used as an ingredient in the manufacture of healthy beef products. The objective was to manufacture a beef burger enriched in both CLA and omega-3 and to test the retention of these fatty acids during cooking and the consumer reaction to the cooked product.

Materials and Methods

Spring-born beef (Holstein-Friesian heifers (n=48)) were assigned, at four months old, to either a standard grass-based production system, or within that system to continued supplementation with a safflower oil (to promote CLA deposition) or ruminally protected fish oil (to promote EPA and DHA deposition)-containing concentrate. Following slaughter at 25 months of age, *longissimus dorsi* (LD) muscle and subcutaneous adipose tissue (AT) was collected and fatty acid composition determined as described by Noci *et al.* (2005). For control (CON) burgers, samples of AT and LD that clustered around the mean value for CLA and EPA+DHA, respectively, were pooled. For enriched burgers (ER), pools of AT were based on samples with the highest CLA concentration and pools of LD were based on samples with the highest EPA+DHA concentrations. Each pool of tissue was separately minced, total lipid concentration (TL) was measured and burgers (4 batches/treatment) were formulated to a

200g lipid/kg industry standard and rapidly frozen at -30°C. Subsequently, fatty acid analysis was performed on uncooked burgers and burgers cooked on a George Foreman Grill (5 min, each side). Cooked burgers were offered to 15 consumers in triangle tests for difference detection and in pair tests for preference. Fatty acid data were analysed according to a split plot design with batch and type in the main plot and cooking in the sub-plot. Consumer data were analysed as described by Roessler *et al.* (1978).

Results

The fatty acid composition of burgers is presented in Table 1. The TL concentration of the burgers was close to the target. Enriched burgers were higher (P<0.05) in PUFA, CLA and EPA + DHA concentrations compared to CON. With respect to EPA + DHA, the ER burgers could be labelled a “source of” omega-3 PUFA (EU, 2010). Cooking decreased (P< 0.05) TL concentration but increased (P<0.05) EPA + DHA concentrations. Cooking decreased (P<0.05) the concentrations of monounsaturated and saturated fatty acids in CON but not in ER. More consumers correctly detected a difference between burgers (9 v 6, P=0.05) and while the preference did not differ at the 95% confidence level, there was a difference in preference (11 preferred CON) at the 90% confidence level.

Conclusions

In this pilot study, a beef burger with a higher concentration of “healthy” fatty acids after cooking, than a conventional product, was considered different and tended to be less preferred by consumers.

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Table 1. Concentration (mg/100g) of total lipid (TL) and fatty acids¹ in control and nutritionally enhanced beef burgers

	CLA	EPA	DHA	EPA+DHA	PUFA	MUFA	SFA	TL
Control								
Raw	99.3	7.2	3.8	11.0	567	7866 ^a	6309 ^a	22064
Cooked	70.7	14.9	4.7	19.6	496	5780 ^b	4534 ^b	17348
Enriched								
Raw	495.1	36.0	20.5	56.5	1231	6047 ^b	4147 ^b	20126
Cooked	460.4	49.6	27.2	76.8	1265	5905 ^b	4116 ^b	19035
Significance								
Burger (B)	*	*	**	**	*	NS	*	NS
Cooking (C)	NS	*	*	**	NS	**	**	*
B & C	NS	NS	*	NS	NS	*	**	NS
sed	52.70	3.70	3.00	6.50	130.5	821.4	568.0	2586.9

¹CLA=conjugated linoleic acid, EPA=eicosapentaenoic acid, DHA=docosahexaenoic acid, PUFA=total polyunsaturated fatty acids, MUFA=total monounsaturated fatty acids, SFA=total saturated fatty acids

Effect of ranking pigs on residual feed intake (RFI) on growth and other measurements for feed efficiency.

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Introduction

FCR is traditionally used to measure feed efficiency (FE) in pigs. However, other measurements of feed efficiency may be more suitable (Moore *et al.*, 2009). The aim of this study was to determine if RFI (the difference between the observed feed intake and the intake predicted on observed growth), residual gain (RG; the difference between the observed growth rate and growth predicted on observed feed intake) and residual intake and gain (RIG; the difference between RG and RFI) are viable alternatives, as they consider individual requirements for maintenance and growth and are not as dependent on production parameters as FCR.

Material and methods

Individual performance [average daily feed intake (ADFI), average daily gain (ADG) and back fat thickness] was measured weekly from day 42 post-weaning to slaughter for 4 batches of pigs (32 litters; N=322 pigs); 2 batches at Teagasc, Moorepark, Ireland and one batch each at AFBI, Hillsborough, Northern Ireland and Vetmeduni, Vienna, Austria. Two common boars were used across sites to investigate the effect of paternal ancestry on growth performance. All animals were offered feed manufactured to a common formulation and nutrient specification, with individual ADFI being recorded using electronic feeding stations. RFI and RG were calculated by location on a contemporary group basis using PROC GLM in SAS (SAS, Cary, NC, USA), as a regression of ADFI on ADG for RFI, ADG on ADFI for RG, mid-test

metabolic weight and their interactions with gender, gender alone and back fat. RIG was calculated as the difference between RG and RFI (standardised by dividing by their standard deviation within batch). One hundred and thirty two pigs were ranked as high, low and average RFI within litter and gender and data (ADG, ADFI, FCR, RFI, RIG, body weight), were analysed using PROC MIXED in SAS, with main effects as RFI rank, gender, RFI rank \times gender, location, and boar. The number of days on trial was included as a covariate, as slaughter age differed by site. Data are presented as LS means \pm pooled SEM. Significance was at $P \leq 0.05$.

Results and discussion

Site and boar significantly affected ADG, ADFI, FCR and BW at birth, day 42 post-weaning and at slaughter ($P < 0.05$, data not shown). While the boar also affected RFI and RIG, location did not ($P > 0.05$; data not shown), indicating that selection of animals was similar across sites. Low RFI pigs had lower ADFI ($P < 0.05$), similar ADG and improved FCR ($P < 0.05$) than high RFI pigs. Males had higher ADG, better FCR and higher slaughter BW than females ($P < 0.05$).

Conclusions

RFI was useful in ranking FE in pigs, but FCR followed a similar trend for identifying extremes. RFI may be a useful tool for genetic selection and selection on FE across production sites, however, FCR is a more easily obtained measure and may be more practical in most other circumstances. Although diets were formulated to a common specification and fed to a common regime across sites, location had a major influence on pig growth performance and FE.

Acknowledgements

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Table 1. Effect of gender and RFI ranking on pig growth and feed efficiency between day 42 post-weaning and slaughter at ~ 100kg

Parameter	Gender		SEM	P value	RFI rank			SEM	P value
	Male	Female			Low	Average	High		
ADG (g)	1129	1089	19.6	0.03	1104	1121	1102	24.5	0.69
ADFI (g)	2394	2418	45.0	0.57	2268 ^c	2408 ^b	2542 ^a	56.2	<0.01
FCR (feed:gain)	2.11	2.22	0.024	<0.01	2.04 ^c	2.14 ^b	2.31 ^a	0.030	<0.01
RFI (g)	-8.8	-18.8	16.53	0.51	-132.1 ^c	-21.0 ^b	111.5 ^a	20.63	<0.01
RIG (g)	63	356	314.5	0.32	2032 ^a	320 ^b	-1724 ^c	394.9	<0.01
Birth BW (kg)	1.70	1.61	0.056	0.09	1.66	1.71	1.61	0.070	0.27
D42 BW (kg)	33.7	32.8	0.76	0.18	33.3	33.2	33.3	0.95	0.98
Final BW (kg)	101.0	97.8	1.52	0.02	99.1	99.9	99.2	1.89	0.88

*No gender \times RFI interactions were observed

Establishment of critical timing of progesterone supplementation on corpus luteum and embryo development in beef heifers

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Introduction

Concentrations of progesterone (P4) in the first week post insemination are associated with embryo survival in beef (Diskin and Sreenan 2005) and dairy heifers (Parr *et al.*, 2012). An experimental model to induce low endogenous P4 on days 3 and 4 in heifers has been previously validated (Beltman *et al.*, 2009). The effects of administration of exogenous P4 to animals with a compromised CL on subsequent CL function and embryo development are unknown. The objective of the experiment was to elucidate if the negative effects of induced low P4 on CL and embryo development could be reversed by supplementing P4 for different time periods during the early luteal phase.

Materials and Methods

A total of 81 reproductively normal, two year old beef heifers with an initial (mean \pm SEM) live weight and body condition score of 511 ± 5.13 kg, and 3.52 ± 0.04 , respectively, were used across three replicates. All heifers had ad libitum access to grass silage and each heifer was offered 2 kg concentrates per day. Oestrous cycles were synchronized by using 2 injections (2mls) of a synthetic prostaglandin F_{2α} analogue (PGF, Estrumate; Intervet/Schering-Plough Animal Health) administered 11 days apart. Heifers displaying standing oestrus were artificially inseminated (AI) using frozen-thawed semen from 1 high fertility bull. All inseminations took place within 12 hours of standing oestrus. (Day of oestrus = day 0) Following AI, heifers were randomly assigned to 1 of 4 treatments:

Control: received no hormonal treatment following AI.

LP: Administration of PGF (Estrumate, 2ml) on days 3, 3.5 and 4 and no further treatment

PGP4-7: Administration of PGF on days 3, 3.5 and 4 and a CIDR (1.38g P4; Pfizer Animal Health UK) inserted on day 4 and removed on day 7.

PGP4-10: Administration of PGF on days 3, 3.5 and 4 and a CIDR inserted on day 4 and removed on day 10.

Following slaughter (Day 16), the reproductive tracts of all heifers were collected. The uterine horn ipsilateral to the CL was dissected and flushed with phosphate buffered saline to determine the presence of an embryo. Embryo length was measured using an optical callipers. For each heifer, the entire CL was dissected from the ovary, and weighed. Concentrations of P4 were measured twice daily on days 0, 3, 4, 7 and 10. The effects of treatment on CL weight and embryo length (following log transformation) were determined by ANOVA. Progesterone data was analysed using repeated-measures ANOVA (PROC MIXED) with terms for treatment, day and interaction included.

Results and Discussion

There was no difference in concentrations of P4 (Fig. 1) on day 3, 3.5 and 4 between the four treatments ($P > 0.10$). Concentrations of P4 were lower in LP heifers on day 7 ($P < 0.03$) and 10 ($P < 0.05$) compared to control heifers. Concentrations of P4 in heifers administered PGP4-7 were similar to LP heifers on day 7.5. However, concentrations of P4 were lower in heifers administered PGP4-7 ($P < 0.03$) and PGP4-10 ($P < 0.0001$) in comparison to LP heifers on day 10.5. Embryos (log transformed, Table 1) in LP heifers were significantly smaller than PGP4-7 and PGP4-10 heifers ($P < 0.005$). There was no difference in CL weight between LP heifers and heifers administered PGP4-7 and PGP4-10 ($P > 0.10$).

Table 1. Embryo and corpus luteum characteristics following recovery on day 16.

Treatment (No. animals)	Back-transformed embryo length (mm)	Log embryo length (mm)	CL weight \pm s.e.m (g)
Control (15)	73.42 ± 17.07	4.21 ± 0.19	5.01 ± 0.42
LP (21)	53.87 ± 15.04	3.58 ± 0.17^a	3.87 ± 0.33^x
PGP4-7 (22)	80.57 ± 15.95	4.29 ± 0.18^{ab}	3.80 ± 0.37^x
PGP4-10 (23)	115.78 ± 17.64	4.45 ± 0.19^{ab}	2.93 ± 0.45^x

^{ab} $P < 0.005$; ^x $P > 0.10$

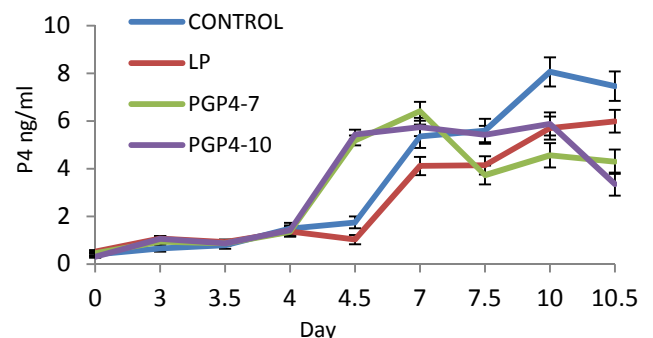


Fig. 1. Circulating concentrations of P4 on days 0 to 10.5 in control, LP, PGP4-7 and heifers administered PGP4-10 (Day 0 = Day of oestrus)

Conclusions

Concentrations of P4 on day 10.5 were lower in both groups supplemented with P4 compared to LP heifers. Evidence is also provided that supplemental P4 did not reverse the negative effects of induced low P4 on CL development. However, embryo length on day 16 was enhanced by exogenous P4 supplementation.

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The relationship between tympanic temperature and onset of oestrus and ovulation in beef heifers

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Introduction

In seasonal pasture-based systems of production, such as those operated in Ireland, use of AI requires accurate oestrus detection in order to achieve a 365-day calving interval. The two main factors affecting this interval are submission rate (the proportion of eligible cows put forward for insemination) and conception rate (proportion of inseminated cows which become pregnant). The main driver of submission rate, currently around 60% nationally, is accurate oestrus detection. Furthermore, in the beef suckler herd, in part due to the labour involved in oestrus detection, less than 17% of calves are born from AI, potentially hampering genetic progress. The aim of this study was to investigate the feasibility of using fluctuations in body temperature, as measured by the tympanic temperature in the ear using the Boviminder® ear tag, to predict the onset of oestrus and ovulation. In order to maximise oestrous activity, beef heifers which had their oestrous cycles synchronized were used. This strategy maximizes the number of animals in oestrus at the same time which is known to increase the activity (i.e., number of mounts) per animal.

Materials and Methods

Crossbred beef heifers ($n=44$, mean age 23.5 ± 0.39 months, mean weight 603.30 ± 5.68 kg) were housed indoors on straw for the duration of the experiment and were fed a diet consisting of grass and maize silage supplemented with a standard beef ration. All heifers were fitted with a Boviminder® ear tag approximately two weeks before the start of the oestrous synchronization protocol to allow acclimatization and to establish a baseline activity threshold. The device recorded the temperature of each heifer, accurate to one-tenth of a degree Fahrenheit, every 10 min and transmitted the data via a base station located in the shed over the internet where it could be accessed remotely on a PC. The oestrous cycles of all heifers were synchronised using an 8-day progesterone-releasing intravaginal device (PRID, 1.55 g P4, Ceva Sante Animal, Libourne, France) with intra-muscular administration of a prostaglandin F2 α (PGF2 α) analogue (5 ml Enzaprost; Ceva) given on the day before P4 device removal. Heifers were checked for signs of oestrus at 4-hour (h) intervals (i.e., 6 times per day) commencing 30 h after device withdrawal. Oestrus onset was defined as the time when the heifer first stood to be mounted by a herd mate. Duration of oestrus was defined as the time between the first and last standing events. Beginning 12 h after the onset of oestrus, the ovaries were scanned by ultrasound at 4-h intervals to determine the time of ovulation, defined as the time when the preovulatory follicle was no longer visible minus two hours. Temperature was recorded every 10 min and averaged to hourly means for the following 4 periods relative to oestrus (time 0): Period I: -48 h to -7

h, Period II: -6 h to +6 h, Period III +7 h to ovulation, and Period IV: ovulation to 48 h post ovulation. Data were analyzed using a Mixed Model ANOVA in a completely randomized design to observe effects of induced oestrus on tympanic temperature. Correlation methodologies were also used as appropriate.

Results

The mean (\pm standard deviation) interval from removal of the PRID insert to onset of oestrus activity was 46.6 ± 14.7 h. The mean duration of oestrus was 16.0 ± 5.67 h and the mean interval from oestrus onset to ovulation was 27.9 ± 7.68 h which is in agreement with the published literature (Walker et al., 1996).

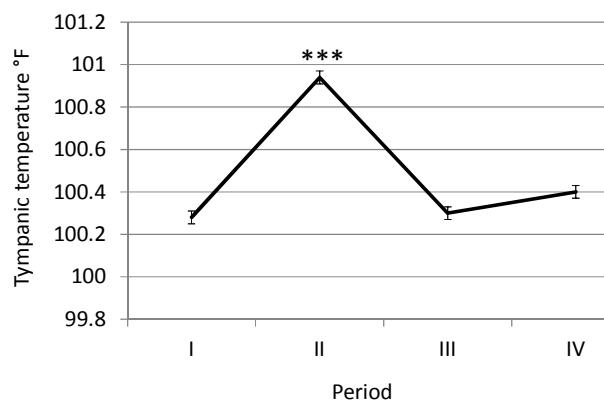


Fig. 1. Change in tympanic temperature relative to onset of oestrus in beef heifers. See text for description of periods. Values represent mean \pm S.E.

Daily ambient temperature averaged $66.2 \pm 1.2^{\circ}\text{F}$ (mean \pm SD) during the study. Highest tympanic temperatures ($100.95 \pm 0.03^{\circ}\text{F}$) were observed in Period II around oestrus onset, whereas lowest temperatures were observed in the 48 h preceding oestrus onset ($100.28 \pm 0.03^{\circ}\text{F}$; Period I) and around ovulation ($100.30 \pm 0.2^{\circ}\text{F}$; Period III), respectively ($P<0.001$). Indeed, around the time of oestrus onset (Period II) mean temperature was 0.66°F ($P<0.001$) higher compared with Period I (animal baseline temperature). Diurnal temperature rhythms were similar ($P > 0.10$) before (Period I) and after oestrus (Period III). Coefficient of correlation between body temperatures and rectal temperatures was $r = 0.48$ ($P<0.05$).

Conclusions

A significant elevation in tympanic temperature was associated with the oestrus in beef heifers and was followed by a decline in temperature leading up to ovulation approximately 28 h later.

Acknowledgements

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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.

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.

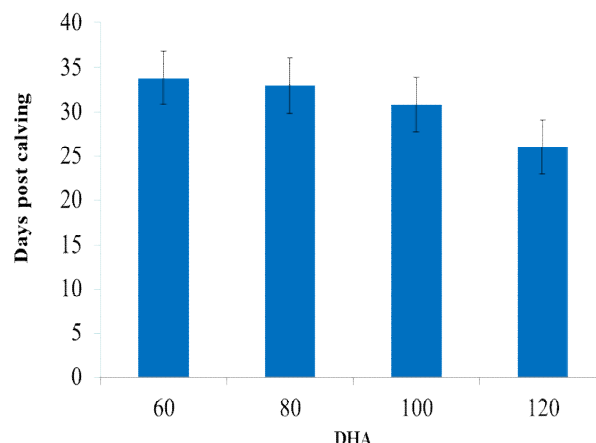


Figure 1 Main effect of daily herbage allowance on the commencement of luteal activity.

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

Metabolite	DHA_Duration								S.E.M	DHA*dur
	60_2	60_6	80_2	80_6	100_2	100_6	120_2	120_6		
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 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 β -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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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). 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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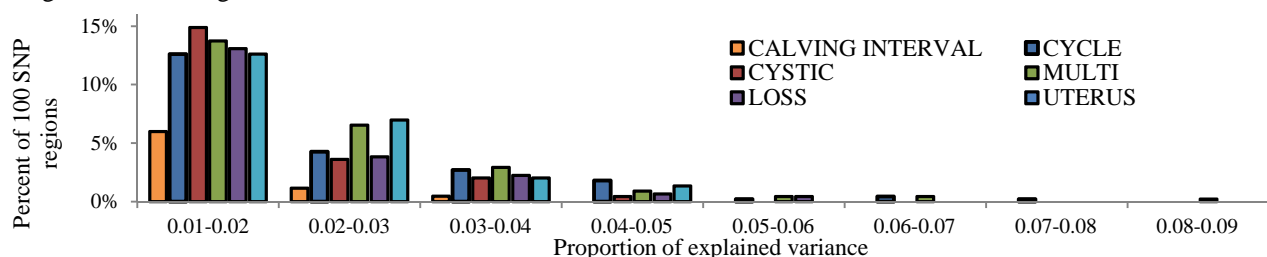


Fig. 1. The percentage of 100 SNP regions that explain greater than 1% of the variation in calving interval, CYCLE, CYST, MULTI, UTERUS, and LOSS traits.

Effect of breed, plane of nutrition and age on systemic gonadotrophin and testosterone concentrations, following a GnRH challenge in young dairy bulls

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Introduction

The advent of genomic selection has led to additional pressure to obtain adequate quantities of semen from young dairy bulls. The onset of puberty in the bull is thought to be regulated by the intensity of early gonadotrophin-releasing hormone (GnRH) pulsatility in the hypothalamus, which in turn is affected by plane of nutrition during calf-hood (Brito *et al.*, 2007). Our aim was to determine the effect of plane of nutrition and age on GnRH-induced release of luteinising hormone (LH), follicle stimulating hormone (FSH) and testosterone (TT) in pre-pubertal bulls of two contrasting dairy breeds, offered two diverse planes of nutrition.

Material and Methods

Holstein-Friesian (F) and Jersey (J) bull calves with a mean (\pm SD) age and bodyweight of 19 (\pm 8.2) days and 46 (\pm 9) kg, respectively were sourced from commercial dairy farms and subsequently assigned to either a high (H) or low (L) plane of nutrition based on breed, age, sire and weight. Calves were individually fed milk replacer and concentrate using an electronic feeding system (Förster-Technik SA 2000, Engen, Germany). After five days acclimatisation F-H (n=9) and J-H (n=8) received 1200 g and 800 g of milk replacer, respectively, together with concentrate *ad libitum*. F-L (n=11) were allocated 500 g of milk replacer plus a maximum of 1 kg of concentrates while J-L (n=6) were allocated 350 g of milk replacer plus a maximum of 1 kg of concentrates. Treatment diets were designed using National Research Council (2001) guidelines; targeting growth rates of 1.2kg/day and 0.5kg/day, for high and low treatments respectively. Animals were weaned at a mean age (S.D.) of 83 (10.5) days. Following weaning F-H and J-H were offered *ad libitum* concentrates, while F-L received 1.7 kg and J-L 1.4 kg concentrate daily. All animals had daily access, on average, to 0.5 kg of straw. Animals were turned out at 16 weeks of age where F-H and J-H received grass and concentrates *ad libitum* while F-L and J-L both received grass *ad libitum* plus 0.5 kg concentrate. Intensive blood sampling (every 15 min for 3 h) was conducted using indwelling, intravenous catheters; at 4, 6 and 8 months of age.

GnRH (Buserelin Receptal®; Intervet Ireland) was administered (0.05 mg/kg liveweight, i.v.) after the third blood sample was taken. Blood samples were collected at 15 min intervals (n=9) for gonadotrophins (LH, FSH) and at 30 min intervals (n=4) for TT. Serum was collected and stored at -20°C before analysis. All three hormones were analysed using RIA. Scrotal circumference (SC) measurements were taken fortnightly beginning at turnout. Area under curve (AUC) was calculated and data were subjected to a repeated measures ANOVA (PROC MIXED, SAS v9.3). Terms for breed, plane of nutrition and age together with their interactions, as appropriate, were included in the statistical model.

Results and Discussion

There were no interactions detected amongst the main factors for systemic concentrations of either LH or FSH ($P>0.05$). LH was higher for animals on the high plane of nutrition ($P<0.05$) while there was a tendency for this hormone to decrease with age ($P=0.06$, Table 1). There was no effect of either breed or treatment on FSH. FSH concentrations also declined with age ($P<0.05$). A three-way interaction of treatment x breed x age ($P<0.001$, Table 1) was detected for TT. All animals had low concentrations of TT at 16 weeks, this increased dramatically at weeks 24 and 32, with J having consistently higher concentrations of TT than FR. A treatment x age interaction was detected for SC ($P<0.001$). SC increased as animals got older, across both treatments, however it was consistently larger for H animals ($P<0.001$). No effect of breed was detected for SC ($P>0.05$).

Conclusions

This study demonstrates that young bulls on a high plane of nutrition have a larger store of LH, particularly in the first 16 weeks of life. This was consistent with higher TT production in the pre-pubertal period and coincided with increased testicular development. FSH appears to be unaffected by breed or level of nutrition. The data suggest earlier sexual maturation in animals maintained on a high plane of nutrition throughout calf-hood.

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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Table 1. Effect of breed (B), treatment (T) and age (A) on gonadotrophin and testosterone response (AUC) to three GnRH challenges.

Hormone (ng/ml)	B			T			A (weeks)				Significance ¹			
	H-F	J	SED	H	L	SED	16	24	32	SEM	B	T	A	B*T*A
FSH	5.17	5.5	0.52	5.0	5.6	0.52	6.3 ^a	5.0 ^b	4.7 ^b	0.25	NS	NS	*	NS
LH	44.3	47.3	4.36	50.6	42.0	4.4	51.2	46.3	39.7	2.14	NS	*	0.06	NS
TT	18.14	28.6	4.18	33.2	13.7	4.18	5.6	32.7	31.9	2.44	*	***	***	***

¹*= $P<0.05$, **= $P<0.01$, ***= $P<0.001$. ^{a, b} = superscripts with same letter are not significantly different ($P>0.05$)

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 10⁶ sperm per dose (n=6 bulls), and X-SS frozen semen, at 2.1 x 10⁶ 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 °C, snap frozen in liquid nitrogen and stored at -80 °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).

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 *in 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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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

Effect of the sperm surface protein β -defensin 126 on the ability of bull sperm to penetrate cervical mucus *in vitro*

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Introduction

β -defensins are antimicrobial peptides which have been reported to play a role in sperm function in primates and rodents. In the bull, β -defensin 126 (BD126) mRNA and protein have been exclusively detected in the cauda epididymis where it is incorporated onto the sperm surface. A mutation of the BD126 gene has been linked to subfertility in men, where sperm having normal motility and morphology exhibited a reduced ability to penetrate through mucus *in vitro* (Tollner *et al.*, 2011). Since the role of this protein has not been investigated in cattle, the aim of this study was to determine the effect of BD126 on the ability of bull sperm to penetrate through cervical mucus *in vitro*.

Material and Methods

Testes were collected from bulls at a local abattoir and transported to the laboratory at ambient temperature. Sperm from the cauda epididymis were recovered by retrograde flushing of the vas deferens with phosphate buffered saline. To obtain sperm from the corpus, the epididymis was dissected from the testis and minced. Cauda and corpus sperm from three bulls were each pooled and washed in Hepes-buffered Tyrode's medium, concentration assessed using a haemocytometer and diluted to 4×10^6 sperm per mL. Epididymal fluid (EF) from the cauda was obtained by centrifugation of freshly extracted sperm at $14,000 \times g$ for 10 min. Bovine EF has been previously shown to contain BD126, as do cauda sperm; however, corpus sperm lack this protein. Addition of BD126 antibody (Atb) blocks the binding of this protein to the sperm surface. The aim of Experiment 1 was to assess the effect of BD126 on the ability of sperm to penetrate mucus *in vitro*. Corpus sperm were incubated for 1 h with EF, with (Treatment 1; Corpus+EF+Atb) or without (Treatment 2; Corpus+EF) BD126 Atb; untreated corpus (Treatment 3; Corpus) and cauda sperm (Treatment 4; Cauda) were used as controls. Following incubation, the fluorescent stain Hoechst 33342 was added to each sample to aid in visualising sperm. Flattened capillary tubes (Composite Metal Services Ltd., Ilkley, UK) were marked at 10 mm intervals between 10 and 90 mm and filled with frozen-thawed cervical mucus collected from cows in oestrus. Two capillary tubes were placed vertically in an Eppendorf containing 250 μ L of each sample and were incubated for 30 min at 37°C before placing them on a hot plate to immobilise and kill the sperm. Sperm were counted across the width of the tube, one field of view wide, at each 10 mm interval using a fluorescent

microscope. The total number of sperm in each tube was used for statistical analysis. Four replicates were completed with two capillary tubes representing each treatment in each replicate. The aim of Experiment 2 was to assess if the differences in mucus penetration observed in Experiment 1 were due to sperm motility parameters. The same treatments used in Experiment 1 were assessed for total motility and progressive linear motility using a computer assisted sperm analysis system (Sperm Class Analyser; MicroOptic, Barcelona, Spain). Data were assessed for normality of distribution and analysed using a one-way Analysis of Variance in the STATGRAPHICS Centurion package (version XVI). The model included the main effects of treatment, replicate and their interactions.

Results and Discussion

A higher number of cauda than corpus sperm penetrated cervical mucus ($P < 0.001$; Fig 1). Addition of EF increased the ability of corpus sperm to migrate through mucus ($P < 0.05$; Fig 1), as evidenced by an increased number of total sperm in the capillary tube. When the BD126 Atb was added to corpus sperm in combination with EF it did not alter the number of sperm migrating through the mucus compared to the corpus with EF alone, suggesting that other factors within EF affect the ability of sperm to penetrate mucus. In Experiment 2, as expected, cauda sperm had higher motility than corpus sperm ($P < 0.001$). Addition of EF (with or without the BD126 Atb) to corpus sperm did not affect any of the motility parameters.

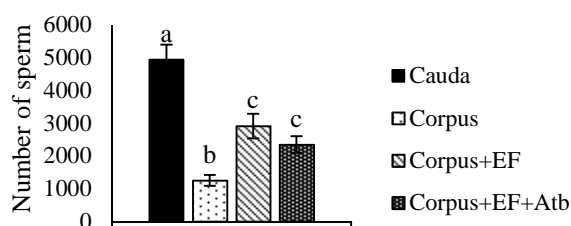


Fig. 1: Total number of sperm penetrating cervical mucus (from 20 mm to 90 mm) after treatment of corpus sperm with epididymal fluid (EF) with or without BD126 antibody (Atb). Values with different superscripts differ ($P < 0.05$).

Conclusions

Incubation of bull sperm from the corpus epididymis, known to lack BD126, with EF which contains BD126, resulted in enhanced sperm migration through cervical mucus, which was not due to an increase in motility. The lack of an effect of incubation with the BD126 Atb on sperm motility under the conditions of this study may reflect the concentration used and/or the efficacy of the Atb to inhibit the actions of BD126.

Acknowledgements

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The effect of dietary polyunsaturated fatty acid supplementation on semen volume and quality in young post-pubertal dairy bulls

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Introduction

Sperm utilise polyunsaturated fatty acids (PUFA), in particular n-3 and n-6 PUFA to maintain the membrane fluidity required for normal sperm cell function (Wathes *et al.*, 2007). As ruminants cannot synthesize these fatty acids *de novo*, they require dietary supplementation (Mattos *et al.*, 2000). Recent work by our group has shown some positive effects of dietary supplementation of n-3 PUFA on semen quality in rams (Fair *et al.*, 2014); however, limited data exist for bulls. The aim of this study was to examine the effects of dietary supplementation with both n-3 and n-6 PUFA on semen volume and aspects of semen quality in young post-pubertal dairy bulls.

Material and Methods

Holstein-Friesian (n=43) and Jersey (n=7) bulls with a mean \pm s.e.m. age and bodyweight of 420.1 ± 5.86 days and 382 ± 8.94 kg, respectively, were blocked on breed, weight, age and semen quality (based on the outcomes of two pre-trial ejaculates) and randomly assigned to one of three treatments, namely (i) a non-supplemented control (CTL, n=15), (ii) rumen protected safflower (n-6 PUFA, n=15), (iii) rumen protected n-3 PUFA enriched fish oil (n-3 PUFA, n=20). Both fats were added at 2% of dietary dry matter and all three diets were isonitrogenous (160g/kg crude protein). Diets included: 25% rolled barley, 20% maize, 15% soyabean, 17% beet pulp, 12% soyhulls, 4% oil, 2% minerals, 5% molasses. Animals were housed in a slatted floored shed and fed individually using an electronic feeding system (Calan Inc., Northwood, New Hampshire). Animals were allowed two weeks acclimatisation to the facility followed by ten days acclimatisation to these diets, and were then offered diets *ad libitum* for 12 weeks. All animals received 5 kg (fresh weight) of grass silage daily. Semen was collected using an electro-ejaculator (Pulsator, Lanes, CO, USA) at weeks -2, -1, 0, 10, 11 and 12 relative to the beginning of the trial period (week 0). On collection, semen volume and progressive linear motility (PLM), using a phase contrast microscope incorporating a heated stage (100 sperm per assessment), were recorded. Sperm concentration was measured using a photometer (Minitub, Germany)

calibrated for bovine semen. Semen was then diluted to 80×10^6 sperm per ml in Bioxcell (IMV, L'Aigle, France) and loaded into 0.25 ml straws (IMV, L'Aigle, France). Straws were cooled gradually from room temperature to 4°C over a period of 90 min and allowed to equilibrate at 4°C for 3 h. They were then frozen to -140°C over 9 min (-15.5°C/min) in a programmable freezer (Planar, Birmingham, UK) followed by immersion and storage in liquid nitrogen until use. Post-thaw PLM (n=1 straw per collection for each bull) was assessed as described earlier, after thawing by immersion into a beaker of water at 37°C. Data were analysed by means of repeated measures ANOVA using the mixed procedure of statistical analysis software (SAS, version 9.3). Fixed terms for treatment and week along with their interactions, where appropriate, were included in the model. Week was included in the analysis as a repeated term.

Results and Discussion

All values represent mean \pm s.e.m. Concentrate intake across the three treatments did not differ with bulls on the CTL, n-6 PUFA and n-3 PUFA treatments consuming; 10.9 ± 0.37 kg, 11.1 ± 0.31 kg, 11.0 ± 0.35 kg respectively, on a fresh weight basis. The average daily gain between treatments was also similar, with CTL, n-6 PUFA, n-3 PUFA gaining 1.4 ± 0.19 , 1.4 ± 0.17 and 1.6 ± 0.29 kg per day, respectively. No effect of week was detected after 70 days feeding therefore these data (three successive collections beginning on week 10), were pooled. There was no effect of treatment ($P>0.05$) on semen concentration, PLM or drop in post-thaw PLM (Table 1). Throughout the trial period, the average volume of semen collected at each ejaculation did not differ between treatments ($P>0.05$).

Conclusions

Dietary supplementation with either n-3 or n-6 PUFA to young post-pubertal bulls had no effect on gross measurements of semen quality. Further investigation into post-thaw *in-vitro* quality parameters of sperm from these treatment groups is on-going.

Acknowledgements

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Table 1. Effect of dietary treatment on semen volume and quality after 70 days feeding (average of three collections)

	Treatment						P-value
	CTL	SEM	n-6 PUFA	SEM	n-3 PUFA	SEM	
Volume (ml)	3.9	0.30	3.5	0.29	3.6	0.26	0.64
Concentration ($\times 10^6$)	1069.3	94.04	1139.3	91.42	1132.72	79.24	0.83
Progressive linear motility (%)	78.8	2.31	82.2	2.27	78.3	1.93	0.39
Drop in PLM post- thawing (%)	20.0	4.02	23.5	4.05	17.2	3.54	0.50

Role of sperm sialic acid in sperm-oocyte interaction

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Introduction

The importance of sialic acid in sperm-oocyte interaction has recently been highlighted as zona-pellucida (ZP) glycoproteins containing sialic acid have been reported to be essential for the sperm-ZP binding (Pang *et al.*, 2011). It has also been demonstrated that although sperm capacitation leads to a partial loss of these monosaccharides, around 80% of the sperm sialome remains intact after this process (Ma *et al.*, 2012). This study tested the hypothesis that sialic acid present on the sperm surface has a role in sperm-oocyte interaction and that successful fertilisation requires recognition of sialic acids from both the sperm and oocyte to occur.

Material and Methods

Ovaries from cows and heifers were collected at a commercial abattoir and surface visible follicles (>2 mm) were aspirated to recover cumulus-oocyte complexes (COCs). Good quality COCs were matured in groups of 50 for 24 h at 39 °C under an atmosphere of 5% CO₂ in air with maximum humidity, following which they were fertilised with 1 x 10⁶ Percoll-selected motile sperm. The aim of Experiment 1 was to determine if removal of sialic acid (using 5 mg/mL *Clostridium perfringens* type V Neuraminidase; NMase, an enzyme that cleaves off terminally positioned sialic acid) from sperm or COCs would affect fertilisation success. Groups of 50 matured COCs were randomly allocated to the following experimental treatments: (i) NMase COCs (COCs incubated for 1 h with NMase and fertilised with untreated sperm; n=127 COCs) (ii) NMase sperm (COCs fertilised with sperm incubated for 1 h with NMase; n=124 COCs), or (iii) control (untreated COCs, fertilised with untreated sperm; n=144 COCs). Approximately 20 h post fertilisation, cumulus cells were removed from presumptive zygotes and washed in phosphate buffered saline before being transferred to groups of 25 in culture drops. Culture dishes were kept at 39 °C under an atmosphere of 5% CO₂ and 5% O₂ in air with maximum humidity. Cleavage was assessed 48 h post fertilisation and blastocyst development was recorded on Days 6, 7 and 8 (Day 0 = day of fertilisation) and expressed over the total number of oocytes fertilised. The aim of Experiment 2 was to determine the effect of increasing the duration of incubation with NMase on sperm only. COCs were fertilised with sperm incubated with or without (control) NMase for 1 h (Sperm NMase 1 h, n=172 COCs; Control 1hr, n=193 COCs), or 5 h (Sperm NMase 5 h, n=192 COCs; Control 5 h, n=181 COCs). Following incubation, sperm were washed before fertilisation. Presumptive zygotes were cultured and cleavage and blastocyst development were assessed as described earlier. A third experiment (Experiment 3) was conducted to determine the effect of increasing the duration of incubation with NMase on COCs only. COCs were with or without (control) NMase for 1 h

(COCs NMase 1 h, n=118 COCs; Control 1 h, n=129 COCs), or 5 h (COCs NMase 5 h, n=133 COCs; Control 5 h, n=121 COCs). Following incubation, COCs were washed before fertilisation with untreated sperm. Presumptive zygotes were cultured and cleavage and blastocyst development were assessed as described earlier. Data were assessed for normality of distribution and analysed using a one-way Analysis of Variance in the STATGRAPHICS Centurion package (version XVI). The model included the main effects of treatment, replicate and their interactions.

Results and Discussion

In Experiment 1 treatment of COCs with NMase decreased the percentage of cleaved oocytes ($P<0.001$) and the percentage total blastocysts ($P<0.001$; Fig 1). This trend was also evident when sperm were treated with NMase, ($P<0.001$). As expected increasing the duration of incubation of COCs with NMase decreased fertilisation rate ($P<0.001$; data not shown). However, Experiment 2 demonstrated that increasing the duration of incubation of sperm with NMase also decreased fertilisation rate ($P<0.05$; Fig. 2).

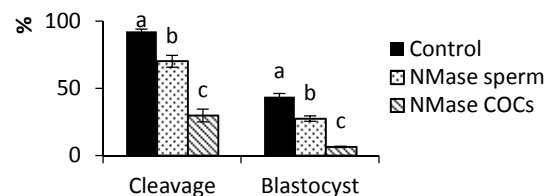


Fig. 1. Effect of NMase treatment on cleavage and blastocyst rates at Day 8. Values with different superscripts differ significantly within each category

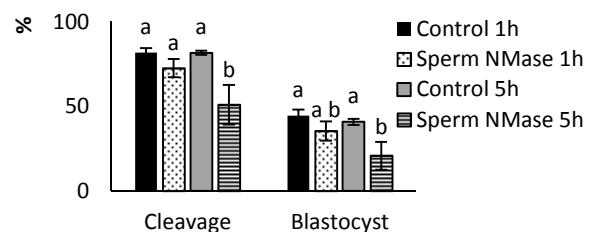


Fig. 2. Effect of increased time of incubation of sperm with NMase on cleavage and blastocyst rate at Day 8. Values with different superscripts differ ($P<0.05$) within each category

Conclusions

Removal of sialic acids from the oocyte and sperm using NMase had a negative effect on fertilisation rate. Increasing duration of incubation of sperm with NMase decreased its ability to fertilise untreated oocytes, indicating a possible role of sperm sialic acids in the sperm-oocyte interaction.

Acknowledgements

We gratefully acknowledge support from the Department of Agriculture, Food and the Marine under the Research Stimulus Fund (Project 11/S/104).

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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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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.1000bulls.genomes.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

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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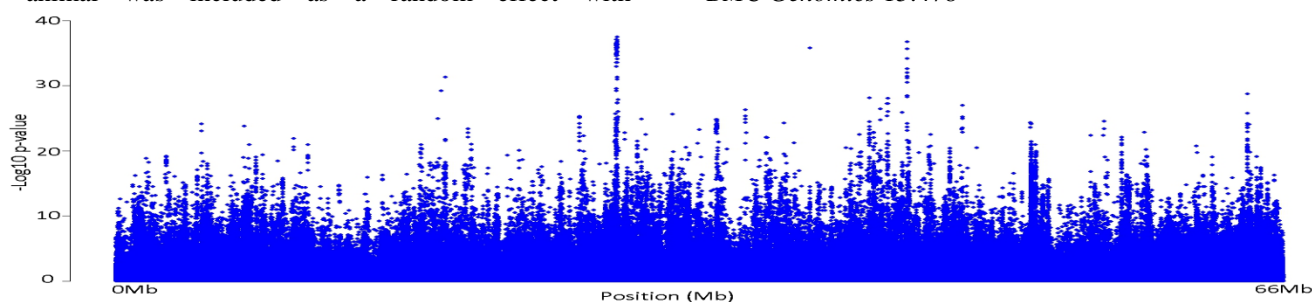


Fig. 1. Single SNP regression results on BTA 18 using imputed sequence data for calving interval in a Holstein-Friesian breed.

Interleukin-8 SNP associated with both somatic cell score and calving interval in Holstein-Friesian cattle

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Introduction

Interleukin 8 (IL8) is a pro-inflammatory chemokine, which regulates neutrophil migration and activation. As neutrophils are the major cell type present in blood, and represent the first line of defence against pathogens, IL8 has a critical role in animal health. Increased somatic cells in milk are predominantly composed of neutrophils and for this reason, we hypothesized that genetic variation in the bovine IL8 gene could represent a genetic marker for improving animal health. IL8 is likely to have a critical role in determining the response to most, if not all, infectious diseases in cattle. Understanding the evolutionary selection pressures acting upon this gene may also shed light on any potential antagonistic relationships that may exist between selection for reduced SCC (as a marker of mastitis) and other health or production traits of agricultural interest. The aim of this study was to investigate the association of the IL8 SNP with fertility and udder health in Holstein-Friesian cattle.

Materials and Methods

IL8 promoter SNP rs110291328 (A/G) was selected for genotyping as this mutation is a potential causative variant with multiple regulatory elements located in close proximity. This SNP was added to the research component of the custom International Dairy and Beef SNP chip for cattle breeding (IDB; Mullen *et al.* 2013). Genotypes and phenotypes were obtained from the Irish Cattle and Breeding Federation (ICBF). A total of 3310 Holstein-Friesian cows with IDB call rates $\geq 90\%$ were available for analysis. Phenotypes (expressed as PTAs) were deregressed and parental contributions removed following the protocol described in Garrick *et al.* 2009. The association between the SNP and calving interval and somatic cell score were individually quantified using mixed models (EMMAX, Kang *et al.* 2010) accounting for relationships between animals using a genomic relationship matrix (GRM). The GRM was constructed using 16,488 SNP on the IDB. P values were adjusted using a Bonferroni correction.

Results and Discussion

Significant associations between the IL8 SNP were detected with both somatic cell score and calving interval (CIV) [adj $P < 0.01$]. The G allele substitution was associated with increased somatic cell score (0.05; SE: 0.02) and reduced calving interval (-4.96 days; SE: 1.65). This is the first report of a significant association between this critical gene and important production related traits in Irish cattle. Moreover, the divergent relationship identified between this SNP and two important traits - SCS and CIV suggests a genetic component that may contribute to the antagonistic relationship between immune and fertility traits.

Like most immune genes, IL8 has been shaped by strong evolutionary pressure due to exposure to bacterial and viral pathogens. Genetic variation in this gene has previously been associated with susceptibility to Tuberculosis and *E. coli* infection in humans (Jiang *et al.*, 2003; Ma *et al.*, 2003). Previously, our work uncovered 29 novel polymorphisms (SNPs) in the promoter region of the bovine IL8 spanning 2.1 kb upstream of the transcription start site (Meade *et al.*, 2012). This region controls IL8 expression levels and therefore the activation of the innate immune response to infection. We also showed that the genetic variation segregates into only two distinct versions (haplotypes), which varied across different breeds and displayed significantly different capacity to drive IL8 expression in bovine mammary epithelial cells *in vitro* (Meade *et al.*, 2012). This significant association reported here supports the functional experiments that we have performed showing that the haplotype encompassing this SNP confers higher IL8 gene and protein expression in both mammary and uterine epithelium cells *in vitro*. Furthermore, the same haplotype confers significantly higher IL8 gene and protein expression in calves stimulated with the bacterial endotoxin, LPS. It is likely therefore that reduced IL8 expression contributes to the increased CIV detected with the association study, perhaps via increased susceptibility to uterine infection.

Conclusions

Significant associations of this bovine IL8 promoter SNP with both somatic cell score and calving interval were identified. On-going functional characterization of both IL8 haplotypes is being performed to assess the role these variants play in neutrophil recruitment profiles and susceptibility to uterine and mammary infection in cattle.

Acknowledgements

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Bioeconomic modelling of alternative calving dates, production systems and grazing season lengths for Irish suckler farms

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Introduction

Of the predominant feedstuffs readily available for Irish suckler systems, efficiently managed grazed grass is the cheapest, followed by grass silage which, in turn, is cheaper than concentrates (Finneran *et al.*, 2011). Consequently, in order to maximise profitability of suckler systems, a long grazing season with a corresponding short indoor winter feeding period is desirable. Previous research indicated that, earlier calving and turn-out to pasture in spring generally improves farm net margins (Crosson *et al.*, 2009). The objective of this study was to evaluate the profitability of alternative calving dates, grazing season lengths and production systems for suckler farms.

Materials and methods

To evaluate technical and financial performance, the Grange Beef Systems Model (Crosson *et al.*, 2009) was used. This is a whole-farm budgetary simulation model which simulates the primary farm activities that occur on suckler beef farms. Three systems of production using late-maturing cow breed types were modelled; suckler calf-to-weanling, suckler calf-to-steer/heifer beef and suckler calf-to-bull/heifer beef. Grass based herbage availability was set at 9 t dry matter (DM) per hectare (ha) with a total land area of 40 ha. Five alternative calving dates were analysed representing cows calving from January to May in spring-calving systems and one calving date (September) representing autumn-calving systems. Three alternative grazing season lengths were modelled representing sites with short grazing season lengths (15 April to 15 October), medium length grazing seasons (15 March to the 31 October) and long grazing seasons (15 February to 15 November). In spring-calving systems cows were turned out at calving or when the grazing season commenced, whichever occurred later. In the spring and autumn calving calf-to-weanling systems, calves were sold on 31 October and 30 June, respectively. In the calf-to-beef scenarios steers (bulls) and heifers were finished at 24 (16) and 20 months of age, respectively.

Results and discussion

February and March-calving systems had the highest margins with calving and turnout dates closely aligned so that a high proportion of the total diet of the cow is grazed grass. In contrast, May-calving was least profitable since output was low (particularly for weanling systems) and costs are greater (calving after the start of the grazing season so that a higher proportion of the total diet of the cow is grass silage). January calving was less profitable than February or March calving since calved cows are indoors for longer and require higher levels of relatively expensive concentrate supplementation. September-calving was only comparable in profitability with spring-calving systems in the calf-to-weanling scenario. A key factor in this regard was the higher price received for older autumn-born weanlings. For calf-to-beef systems, autumn-calving was much less profitable owing to a lack of the same price premium. Grazing season length was a key determinant of profitability with long grazing seasons returning 2.3 times higher net margin than short grazing seasons. On average, calf-to-steer beef systems had higher gross margins and similar net margins when compared to calf-to-weanling systems; calf-to-bull beef systems had higher gross and net margins than either alternative production system.

Conclusions

Profitability of suckler beef production systems is heavily influenced by length of grazing season and calving date. Longer grazing seasons increase profitability by replacing more expensive grass silage and concentrates with grazed grass. Calving too early (e.g. January) is less profitable as calved cows require higher quality (more expensive) grass silage and/or concentrate supplementation. September calving was found to be less profitable than early spring-calving systems.

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Table 1. Effect of month of calving, grazing season length and production system on technical and financial performance of suckler farms

Scenario	Month of calving ¹						Grazing season length ²			Production system ³		
	Jan	Feb	Mar	Apr	May	Sep	Short	Med	Long	Wean	Steer	Bull
Cows calving (number)	66.6	66.5	69.1	70.3	73.3	63.0	69.9	68.5	69.0	77.3	57.2	69.9
Cattle sold (number)	50.8	51.6	53.7	54.6	57.0	48.9	54.2	53.1	53.5	60.3	44.0	54.1
Liveweight output (kg/ha)	190	190	183	172	166	197	177	179	185	549	0	0
Carcass output (kg/ha)	359	358	359	355	367	330	355	357	367	77	456	530
Grass grazed (t DM/ha)	5.9	6.0	6.0	5.8	5.6	5.1	5.0	5.9	6.7	5.8	5.8	5.6
Profitability (€/ha)												
Gross output	1,754	1,766	1,755	1,701	1,744	1,776	1,718	1,732	1,782	1,564	1,711	1,973
Gross margin	951	973	968	874	814	695	791	919	1,038	827	864	947
Net margin ⁴	311	399	388	293	217	84	195	326	443	251	268	327
Net margin (+/- €/ha)												
Purchase price (+/- 10%)	12.7	11.5	10.4	10.2	13.7	14.9	12.7	11.4	11.0	7.2	11.7	17.9
Beef price (+/- 10%)	54.9	54.8	54.2	52.7	53.4	52.7	53.2	53.6	55.1	62.7	45.6	53.0

¹Month of calving represents cows calving on the 15th day of the respective months. ²Grazing season length of finishing animals are dictated by the requirement for indoor finishing. ³Production system: Wean = all progeny surplus to heifer replacement requirements are sold post-weaning on 31 October. Steer: male progeny are finished as steers at 24 months of age and heifer progeny are finished at 20 months of age. Bull: male progeny are finished as bulls at 16 months of age and heifer progeny are finished at 20 months of age. ⁴Excluding owned land and labour.

The relationship between Thoroughbred (TB) racehorse ownership and Irish racecourses

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Introduction

Dukes (2013) reported that improving the value proposition that racehorse owners are offered is paramount to the Thoroughbred (TB) industry's long-term vitality. The current study forms part of a larger project designed to determine the investment opportunities, overall attractiveness and other potential merits of racehorse ownership using Porter's (1980) Five Forces Model. The model asserts that industry structure, represented through five competitive forces, ultimately shapes profit potential. To our knowledge, this is the first time that the application of the Porter model has been used in connection with racehorse ownership analysis. This paper focuses the bargaining power of buyers (racecourses). Irish racecourses typically buy the performance of racehorses from owners in exchange for the opportunity to achieve prize money or 'black type' honorifics. The bargaining power of buyers increases where (1) buyers are more concentrated than suppliers; (2) fees constitute a sizeable part of buyers' costs; (3) buyers' profits are low; (4) sellers are fungible and; (5) market information is freely available (Porter, 1980). Secondary data (Figure 1) demonstrates the power of Irish racecourses as buyers relative to their main suppliers (racehorse owners). It highlights how racecourses' prize money has been reduced by a disproportionately large amount relative to the largest reductions experienced by racecourses, namely government contributions and attendances.

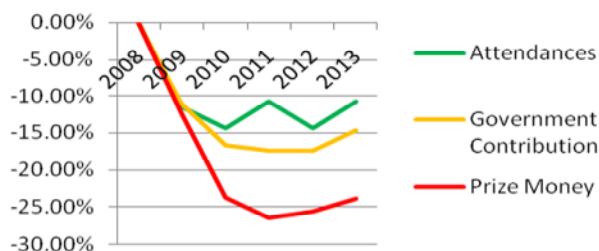


Fig. 1. Attendances, Government Contributions and Prize Money on Irish Racecourses (HRI, 2014)

The literature also evidenced the relative lack of power of overseas racecourses. Net prize money per horse in training is superior in Britain (Indecon, 2012) and total prize money in France is four times greater than Ireland (HRI, 2014; IFHA, 2014). The objective of the current study was to examine the buyer-supplier relationship that exists between TB owners and Irish racecourses.

Materials and Methods

In-depth interviews were undertaken with racehorse owners (n=3) from each of three subpopulations, stratified by experience (≤ 1 , 5-10, and ≥ 20 years). These were conducted using a validated questionnaire, designed to facilitate both quantitative and qualitative analysis of participants' relationships with all five forces. Interviews were recorded and transcribed.

Results and Discussion

Table 1. Key Issues Identified by Research Participants

	Owner \leq 1 yr exp.	Owner 5- 10 yrs exp.	Owner \geq 20 yrs exp.
Prize money [IRE vs abroad]	X	X	X
Benefits-in-kind [IRE vs abroad]	X	X	X
Entry Fees		X	X
Tax-free status	X	X	

Pertinent results are summarised in Table 1. Benefits-in-kind (for example, hospitality) are uncommon in buyer-supplier interactions and were typically absent from the literature. Yet their presence influences the power dynamics within the dyad and a successful attempt to quantify them would advance knowledge in the area. When pressed, all participants specified that prize money was the single biggest concern dictating future investment decisions. Furthermore, all acknowledged the potential to improve their competitive position (prize money) and shift bargaining power away from the Irish racecourses (buyers) by racing abroad. The results were applied to Porter's (1980) model where manipulation of supply was identified as a potential strategy for improving owners' (suppliers) bargaining power. Also, drawing from co-opetition theory (Brandenburger and Nalebuff, 1996), forward integration was isolated as a potential aid to owners seeking influence over the price achieved for their product. This may require capital outlay, but not such to put it beyond large owners or groups of smaller owners. In practice, incremental improvements of competitive positioning will probably begin with an effective lobbying strategy. However, such a strategy may be more effective if aligned with credible alternative competitive opportunities such as above.

Conclusions

This paper demonstrates how the Irish TB industry can continue to thrive in a different economic environment by applying suitable economic models to reinvent traditional practices. This can stimulate the requisite investment to fortify and grow a valuable indigenous industry.

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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 (3,526 CFU/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.

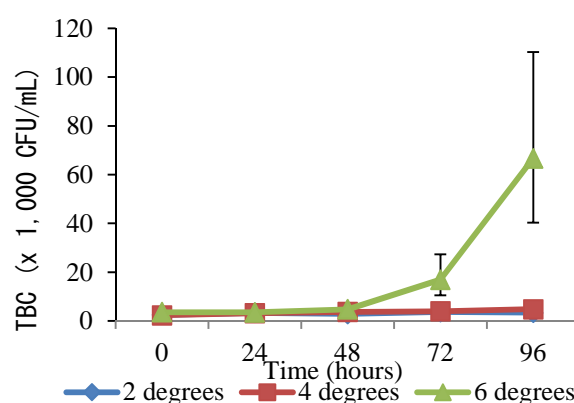


Fig. 1. Effect of storage time and temperature on the total bacterial count of bulk tank milk.

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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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 Netherlands) hot oil bath on a 3.4 g milk aliquot; milk pH was assessed with a SevenCompactTM 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. 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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Table 1: Number of records (n) and fit statistics for the technological milk traits in cross and external validation.

Trait	Cross Validation					External Validation						
	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

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 than 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 (RMSE_c) and external validation (RMSE_v), 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).

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

Trait (µg/ml)	Cross Validation			External Validation				
	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 ¹Traits were log transformed prior to analysis.

Attitudes of Northern Irish Producers and Advisors toward knowledge exchange and innovation transfer

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Introduction

Knowledge exchange, technology transfer and information sharing are fundamental to the sustainable development of the agri-food industry in Northern Ireland (NI). Published studies from outside of NI recognise that many factors contribute to the adoption of new policies / codes of practice / technologies (e.g. Roux *et al.*, 2006; Vanclay, 2004). Understanding the main factors influencing adoption is fundamental to improving technology uptake. Rates of adoption of new knowledge are affected by 1) the attitudes of both the knowledge provider and the receiver, as well as 2) the effectiveness of transfer arrangements. The aim of this study was therefore to investigate Northern Irish producers' and advisors' specific attitudes toward knowledge exchange and innovation transfer arrangements in order to improve these services.

Materials and Methods

Two comprehensive questionnaires were generated in consultation with researchers across all sectors of the NI agriculture industry with the aim of evaluating the main factors influencing producers' & advisors' attitudes toward knowledge exchange techniques. During 2011/12 producers were surveyed, this survey was conducted face-to-face with a stratified random sample of 553 NI producers across all sectors; this sample was representative of the structure of the NI agri-food industry equating to 2.3% of the NI farm population based on census data. During 2013/14 the second survey was conducted online based on a list of over 600 industry representatives, a link to the survey was also placed on the Knowledge Transfer Partnership website. A total of 153 responses were received from agri-food industry researchers, agri-sales representatives and advisors. The majority of these respondents were local to NI/UK but 13 respondents worked internationally to at least some degree. For ease of analysis all primary producer responses were categorised as 'Producers' and all respondents who were employed in a research/advisory etc. role were categorised as 'Providers'.

Results and Discussion

The diversity in farming enterprises among the sample was echoed in the diverse and wide range of useful events/techniques made use of by producers and providers e.g. evening meetings, agricultural shows, farm walks, open days, seminars/conferences, press articles, discussion groups, leaflets/booklets in post, focus farms and the internet. Both producers and providers showed a distinct difference in the 'usefulness' ratings of these potential events/techniques (Table 1). 'Usefulness' is defined as: "the potential ability to improve the farm business/ ability for the event / technique to actively transfer knowledge / innovation". In all cases; those who actually used the source within the past 3 years rated such information sources significantly more 'useful' compared with those who had not recently used them ($P \leq 0.05$ Pearson Chi

Sq). It is however not possible to distinguish whether this lack of 'usefulness' is preconceived with respondents consequently not making use of such sources of information, or whether 'usefulness' ratings are based on recent experience.

Table 1. Proportion using five selected comparable events/techniques and associated 'usefulness' ratings

Event / Technique	Providers			Producers		
	% Using event / technique	Average usefulness rating ¹		% Using event / technique	Average usefulness rating ²	
		Users	Non-users		Users	Non-users
Discussion between producers/providers	94.8	2.7	1.2	52.7	3.9	2.8
Farming Press	96.9	2.2	0.3	93.2	3.9	2.7
Farm events	93.8	2.3	0.7	42.6	4.0	2.8
Leaflets/booklets/handouts	93.8	2.1	0.7	78.0	3.4	2.7
Television/Radio	49.5	1.5	0.4	83.6	3.2	2.5

¹ Scale: 0 'not useful' to 3 'very useful'; Median = 1.5

² Scale: 1 'very poor' to 5 'excellent'; Median = 3

Table 1 also reveals two additional notable points; 1) there appears to be some disparity in the usage level of certain events/techniques between producers and providers and 2) in relation to producers; some of the most usefully rated events/techniques emerge as some of the least often used. This highlights a degree of divergence between the techniques promoted by providers and the ability/willingness of producers to attend/make use of the information; producers appear to make greater use of less time-intensive information sources such as the farming press, TV/radio and guidance leaflets/booklets thus suggesting that time constraints prevent farmers from taking advantage of the events/techniques which they find most useful.

Conclusions

There is clear disparity in the usage rates of valuable information sharing techniques between key stakeholders within the agri-food industry. Producers are aware of which sources could be most valuable to their business, but they appear less able to make use of them due to time and/or financial pressures. Addressing producers' ability to adopt new knowledge and innovation will enable more effective and wide-reaching technology transfer in the future.

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New entrants into Irish racehorse ownership

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Introduction

Racehorse owners drive economic activity in the Irish Thoroughbred (TB) industry (Dukes, 2013). The objective of the current study was to examine the behaviour of new entrants to racehorse ownership. This is one element of a larger academic project seeking ways to improve investment attractiveness of racehorse ownership. The research examines the industry through Porter's (1980) Five Forces Model, which asserts that industry structure, represented through five competitive forces will determine profit potential. This paper focuses on the threat of new entrants and how it affects the returns available to TB owners. Porter (1980) posits that the threat of new entry (rather than its occurrence) constrains profitability because prices (prize money) must remain low to deter entry and incumbents are often forced to make additional investments to secure their industry position. The literature identified capital investment and registration fees with Horse Racing Ireland as the only barriers to entry into TB ownership. According to Porter (1980), the threat of entry is directly related to industry growth. The effect of the TB industry's slow growth is graphically depicted from 2008 to 2012 in Figure 2. Industry growth is operationalised through prize money levels, while the threat of new entry is operationalised as a reflection of actual entry, one year in advance of its occurrence. All figures are expressed as a fraction of 2007 levels.

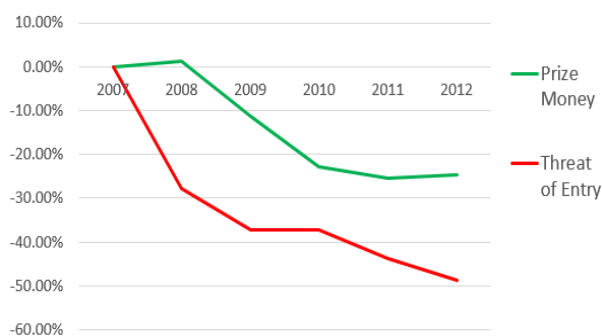


Fig. 1. Irish TB Industry Decline and the Threat of New Entry (HRI, 2014)

Materials and Methods

In-depth interviews were undertaken with one racehorse owner from each of three subpopulations, stratified based on experience levels (≤ 1 , 5-10 and ≥ 20 years). This meant that each participant's original investment in TB racing had occurred during a different decade. Therefore, the sample generates a more holistic picture of the process through which new entrants become involved in the industry than would otherwise have been possible. Interviews were recorded and transcribed. Both quantitative and qualitative questioning explored participants' relationships with each of the five competitive forces. Interviews meant that the research could also explore non-rational motivators (Creswell, 2009) for ownership investments, for example, 'thrilling possibilities' (HRI, 2015). Furthermore, the research

instrument allowed for the thematic analysis of participants' calculated thoughts. Their ownership experience meant that their knowledge and insights had potential to contribute to the research outcomes.

Results and Discussion

The results indicated a consensus among participants that the prize money available was the most important factor driving their investment decisions. It is likely that new owners are motivated in the same way. Therefore, the threat of new entry can be expected to escalate in line with prize money. Furthermore, all participants stated that they required assistance from an existing stakeholder when entering racehorse ownership. This suggests that insider knowledge may be a barrier to entry for new owners. This insight is not currently available in the literature. Identifying where the concept is relevant and variables through which it can be operationalised is a logical next step. Two participants highlighted their discontent with Horse Racing Ireland and the Association of Irish Racehorse Owners' active attempts to recruit new owners to the sport. Typically, state intervention seeks to protect indigenous incumbents, although it is quite uncommon for a representative organisation to deprioritise the incomes of those that it represents. It may be an attempt to vitalise a stagnant industry, but this will require further research. Indeed, all of the issues raised warrant further research as their identification and pursuit has potential to advance knowledge and fortify the economic positions of existing owners. For example, this paper offers evidence in support of shifts in prize money as a valid operationalisation of industry expansion and contraction. This means that owners can now anticipate a greater competitive threat from new entrants as prize money rises and strategise accordingly. Finally, using actual entry as a proxy for the pre-occurring threat of entry was very much a first step in the concept's operationalisation. Future research may be able to boost the construct validity, perhaps by plotting a more accurate estimation of the time lapse or considering the influence of environmental factors (e.g. the reintroduction of stallion taxes).

Conclusions

Should the TB industry follow national and international trends and return to economic growth, existing owners must protect their own investments during the process. By applying suitable economic models to anticipate and react to competitive threats, owners can fortify their own positions and fuel the recovery of the wider TB horse industry.

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Contribution of the horse industry to the economy of a rural community in Ireland

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Introduction

The horse industry is a major contributor to the economy, rural diversity and culture of Ireland. It is important to rural Ireland as it provides jobs and economic activity where other opportunities are limited. It can be divided into three broad sectors the Thoroughbred industry (TB), the Sport Horse industry (SH) and the subsidiary services that support both of industries. In 2012 the direct economic contribution from the TB industry in Ireland was approximately €1.1 billion (Hartnell *et al.*, 2013). The direct economic contribution from the SH industry was in excess of €708 million per annum (Fahy *et al.*, 2013). The objective of this study was to quantify the contribution of the horse industry to rural communities with a particular focus on expenditure, land usage, employment and business activities.

Materials and methods

The study was conducted using a personally administered questionnaire. All equine enterprises with contact details in Co Limerick were targeted (n=321). These enterprises contributed to the local economy through direct business activities and/or their use of subsidiary goods and services. The final population represented 63% of all TB studs, 62% SH studs, 48% race horse trainers, 20% individual SH owners and 67% equestrian centres documented in Co Limerick. The questionnaire examined: number and type of horse, enterprise type and services offered, employment, land use/management and overall expenditure. Data was analysed using non-parametric tests in SPSS. An expenditure model was used to evaluate the overall economic contribution. This model calculates the multiplier effect of expenditures; this is then added to total expenditure to determine the economic impact to the rural community.

Results and Discussion

The total annual expenditure for enterprises in this study was approximately €8.3 million with €7.2 million classified as on-farm and €1.1 million classified as off-farm expenditure (Table 1).

Table 1. Annual on-farm and off-farm expenditure

On-farm	Expenditure (€)	%Total
Service/employment	3,844,091	49
Horse upkeep	2,591,761	40
Land/buildings	800,980	11
Total on-farm	7,236,832	100
Off-farm		
Transport	189,414	16
Racing	796,875	71
Competition	95,845	9
Hunting	35,580	3
Pony club	5,380	0.7
Riding club	3,630	0.3
Total off-farm	1,126,724	100

Total economic impact from all enterprises calculated using the expenditure model was €21 million/annum. TB enterprises incurred significantly higher expenditure/annum (€9,528,627vs€2,960,522; $P<0.001$) and significantly higher expenditure/horse/annum (€6,500vs€2,140; $P<0.001$) (Table 2).

Table 2. Annual economic contribution (€) of TB and SH enterprises

	TB	SH
On-farm expenditure	5,645,089	1,593,759
Off-farm expenditure	956,934	169,969
Induced expenditure	2,926,538	1,196,794
Total expenditure	9,528,627	2,960,522
Expenditure per horse	6,500	2,140
Economic Contribution	16,007,982	5,004,370

The study participants utilised 5,033 ha of grassland, 82% was in the ownership of the participants, 18% was leased from other landowners. A total of 70% of participants were registered farmers and kept other livestock. Horses represented 36% of all LUs. The majority of land (69%) was owned by those that grazed horses in combination with cattle and/or horses in combination with both cattle and sheep. These mixed enterprises also leased the majority of land (72% of land leased). Only small proportions of land (16% of owned land and 15% of leased land) were exclusively grazed by horses. A total of 44% of enterprises employed staff. The TB sector employed significantly more staff compared to the SH sector ($P<0.001$). A total of 33% of enterprises were family run, 64% of these enterprises relied solely on labour from family members. The TB and SH industries represented 60% and 40% of family run enterprises, respectively. There were 154 FTEs in paid employment, 70% and 30% of these were employed in the TB and SH industries, respectively. A total of 149 FTEs were in unpaid employment, 38% and 62% represented the TB and SH industries, respectively. A total of 81 % of enterprises engaged in some form of business activity, 72% were involved in the sale and purchase of horses and 48% offered a range of services. The most frequently offered included: breaking (18%), livery (14%), racehorse training (12%), boarding mares (12%), sales preparation (11%) and tuition (10%).

Conclusions

The results of this study provide some preliminary data on the economic contribution of the TB and SH industries to a typical rural community in Ireland. A significant proportion of land in the rural area was grazed by horses only and horses in combination with both cattle and sheep. The reliance on labour input from family members was prevalent in the region particularly those enterprises involved in the SH industry.

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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 voluntarily 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.

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

	Group 1	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

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.

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

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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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

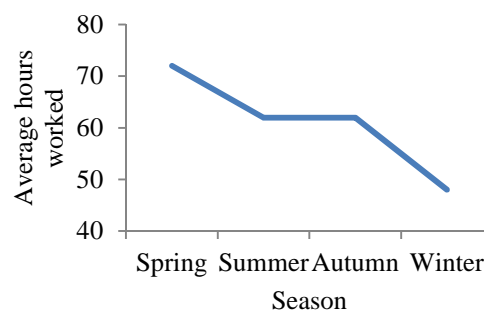


Fig. 1. Seasonal variation in weekly labour input of main operator on Irish dairy farms

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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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 thermophilic 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 thermophilic bacteria. However, some milk processors in Ireland have implemented more stringent TBC (<30,000 cfu/ml) and thermophilic (<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, thermophilic 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 thermophilic 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 thermophilic counts in bulk milk (Magnusson

et al., 2006). The thermophilic 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 unprepared 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	date
^a TBC (cfu/ml)	3,152	1,678	0.10	**
^a Thermophilic (cfu/ml)	11	5	**	*
^a SCC (cells/ml)	156,000	102,000	0.09	NS
^a SRC (cfu/ml)	NS	NS	NS	NS
^b <i>B. cereus</i> (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 thermophilic 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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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 (RMSE_c) and external validation (RMSE_v), 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 2: Pearson correlations¹ 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

¹Correlations 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

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

Trait ¹	n	Cross validation		External validation				
		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

Bovine genetic disease and major gene frequencies: A national perspective on crossbred and purebred cattle

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Introduction

To aid cattle genomics in Ireland a low cost, custom bovine Illumina single nucleotide polymorphism (SNP) genotype panel (International Dairy & Beef panel; IDBv1 panel) was developed for Ireland in 2012 (Berry *et al.*, 2013). The IDB was updated in 2014 (IDBv2) to contain probes for 7 disease haplotypes, 96 Mendelian diseases and traits, and 34 gene alleles of major phenotype effect). Here we report the initial allele frequencies of the 65 validated probes across an initial 90,606 genotyped animals from the Irish crossbred and purebred beef and dairy populations. Knowing an animal's genetic disease and major gene status will allow for more informed breeding decisions. By genotyping breeding stock with the IDBv2, lethal disease carrier x carrier matings can be avoided thus removing the financial cost from having an affected calf born. Knowledge of the MG status provides the opportunity to increase the frequency of desired traits, for instance polled vs horned cattle. As more disease and MG probes on the IDBv2 become validated the genetic information will become available for farmers to use.

Material and Methods

Causative mutations for multiple Mendelian traits, disorders, and alleles of large phenotype effect were included on the IDBv2 (Mullen *et al.*, 2013). DNA from confirmed carriers was obtained from multiple international collaborations or via purchased semen straws; these were used to validate the diagnostic probes. Genotyped animals were from the Beef Genomics Scheme, parentage validation for Herdbook registration, and multiple Irish Cattle Breeding Federation and Teagasc research programs. Genotyping was performed at Weatherbys Ireland using standard Illumina procedures. An animal's purebred (N=26,994) or crossbred (N=63,612) status was determined via its pedigree information on the ICBF database.

Results and Discussion

Of the 47 validated Mendelian disease and trait probes, carrier animals were identified in Ireland for all but 6 of them (Table 1). No animals were identified that were homozygous for a lethal disease (e.g. Paunch Calf Syndrome), while carrier and affected animals were identified for non-lethal Mendelian traits such as coat colour (Table 1).

Conclusion

Genetic disease and major gene alleles are present in the Irish cattle population. They are not confined to just purebreds and many are at a higher frequency in the

crossbred population (Table 1). The use of genotyping assays like the IDBv2 would all cattle farmers to determine the carrier status of their animals. Once the carrier status is known mating strategies can be developed to increase genetic gain while avoiding carrier by carrier mating for genetic diseases.

Table 1. Percent carriers in purebred and crossbred cattle in Ireland

Mendelian Trait Name	Pure	Cross
Beta Mannosidosis	-	0.02%
Black Colour E	1.76%	36.44%
BLAD	0.07%	0.29%
Brachyspina	0.17%	0.50%
Citrullinaemia	-	0.09%
Complex Vertebral Malformation	0.21%	0.97%
Congenital Muscular Dystonia 1	0.10%	0.29%
Congenital Muscular Dystonia 2	0.02%	0.12%
Crooked Tail Syndrome	0.14%	0.71%
Dilutor 3	2.95%	8.98%
Dun	0.00%	0.02%
HH1	0.19%	0.54%
HH3	0.36%	0.97%
HH4	0.10%	0.05%
Hypotrichosis KRT71	0.30%	0.37%
JH1	0.01%	0.04%
Kappa Casein	44.45%	47.70%
MH2	0.01%	0.06%
Mulefoot	0.00%	0.05%
Osteopetrosis	0.02%	0.00%
Paunch Calf Syndrome	0.01%	0.00%
Polled Celtic	1.07%	13.33%
Polled Holstein	0.09%	0.06%
Protoporphyria	1.69%	0.45%
Pseudomyotonia 632	0.00%	0.01%
Pseudomyotonia 857	0.00%	0.01%
Red Factor e	5.40%	35.03%
RNF11	0.33%	0.27%
Silver Char Dilutor 1	0.32%	19.30%
Spinal Muscular Atrophy	-	0.01%
STAT1	24.48%	28.22%
STAT3 19069	34.33%	44.58%
STAT3 25402	38.72%	47.63%
STAT5 13244	43.58%	47.48%
STAT5 13319	13.74%	12.25%
STAT5 13516	43.63%	47.52%
Tibial Hemimelia Improver	0.07%	0.25%

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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 ≥ 10 g/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 $>4^{\circ}\text{C}$ 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 \times 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).

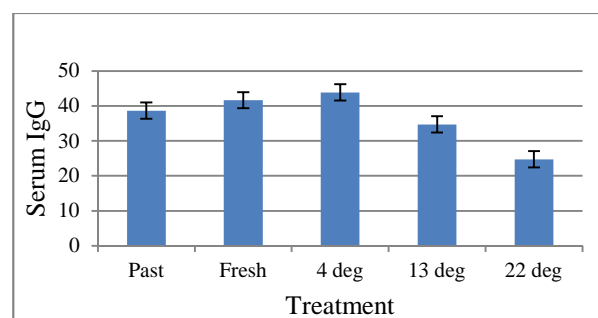


Fig. 1. Comparison of calf serum IgG concentrations at 24 hours when calves were offered colostrum with varying bacteria levels

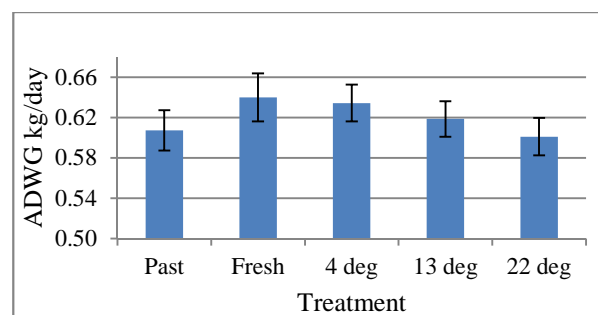


Fig. 2. Comparison of pre-weaned calf ADWG between colostrum with varying bacteria levels

Conclusions

Colostrum with high levels of bacteria had a negative effect on IgG absorption in the pre-weaned dairy calf. Colostrum should be stored $\leq 4^{\circ}\text{C}$ to minimise bacterial growth and improve subsequent passive transfer of immunoglobulins.

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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: $SCS = \log_{10}(SCC \times 1000)$. 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. 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 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

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

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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 \times Friesian, $n=38$; Norwegian Red, $n=6$), parity (2.40 ± 1.61), calving date (17 Feb 14, ± 16 d) 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: $2 \times$ treatment durations (2wk or 6wk), and $4 \times$ 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 7×24 h 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.

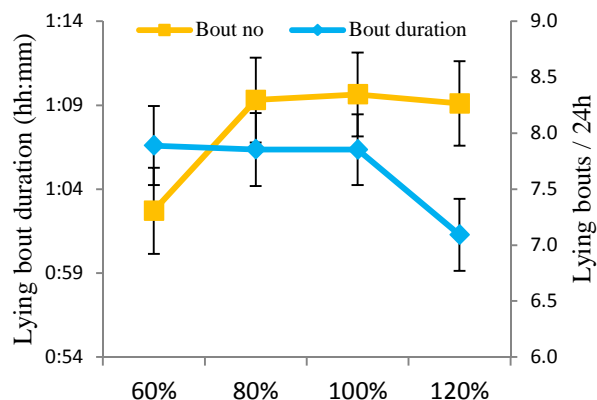


Fig. 1. Lying bout duration and no. lying bouts across DHA allowances

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.

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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Effect of floor type on welfare variables and performance of beef bulls

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Introduction

Consumer concerns have sometimes been expressed about the welfare, in particular cleanliness and lameness, of beef cattle housed on concrete slatted floors. An alternative to bare concrete slatted floors is covering them with rubber mats (RM) (Gygax *et al.*, 2007). There is limited published research comparing the welfare and performance of beef cattle on concrete slats and RM. Graunke *et al.* (2011) carried out a study comparing the welfare and performance of growing and finishing bulls on concrete slats and RM and found that bulls on concrete slats had a greater number of hoof lesions. In the same study, Graunke *et al.* (2011) reported a greater daily live weight gain for growing bulls up to 400kg on RM than concrete slats, however, during the finishing phase, there was no difference in performance between the two floor types. The objective of the present study was to evaluate the effect of concrete slats with and without RM on the performance and welfare of finishing bulls.

Materials and Methods

Seventy-two Charolais and Limousin crossbred beef bulls, (441 (s.d. 45.1) kg) were blocked by breed and live weight and assigned to one of four treatments: 1) Old concrete slats, 2) New concrete slats, 3) Old concrete slats with RM attached and 4) New concrete slats with RM attached. The old concrete slats were *in situ* for 30 years and were in good condition with no obvious defects. The new concrete slats were installed one month before the study began. Rubber mats (Durapak Agri. Ltd., Cork) were fitted to the respective pens by a commercial technician. Each treatment had 3 pens of 6 bulls. Bulls were fed a grass silage and rolled barley based total mixed ration on a 54:46 dry matter (DM) basis. Feed was weighed into each pen daily and refusals were weighed twice weekly (n=3 for intake measurements). At the beginning of the study, bull’s hooves were inspected for the presence of lesions. Bulls were weighed and assessed for cleanliness every three weeks and slaughtered after 148 days. Bulls were blood sampled on d 0 and d 148. Whole blood (K₃EDTA)

samples were analysed using an ADVIA haematology analyser (Bayer Healthcare, Siemens, UK). Total leukocyte, neutrophil, lymphocyte, eosinophil and monocyte percentage, red blood cell number and haemoglobin concentrations were measured. Post-slaughter, carcass weight, carcass gain, conformation and fat score, kidney and channel fat and hide weight were recorded and hooves were inspected for lesions. Statistical analyses were performed using the mixed model procedure of SAS 9.3. The model included the fixed effect of slat, mat, their interactions and block. Cleanliness scores had multiple observations and were analysed using repeated measures ANOVA. If the interaction term was not significant ($P>0.05$), it was subsequently excluded from the final model.

Results and Discussion

There was no slat × mat interaction for any of the performance or slaughter characteristics measured ($P>0.05$) (Table 1). Average daily live weight gain ($P<0.01$), estimated carcass gain ($P<0.05$), kidney and channel fat weight ($P<0.05$) and hide weight ($P<0.01$) were greater in bulls housed on RM than on concrete slats. Carcass weight, kill out %, conformation score and fat score were not affected by treatment ($P>0.05$). Bulls on RM had more hoof lesions than those on concrete slats ($P<0.01$). There was no difference ($P>0.05$) in performance, carcass traits or hoof lesions between old and new concrete slats. There were mat × time and slat × time interactions for cleanliness scores. Bulls on both floor types got dirtier from d 0 to 42. After that, bulls on concrete slats got dirtier until d 63 but by slaughter there was no difference between treatments. Floor type had no effect on any of the haematological variables measured ($P>0.05$).

Conclusions

The results indicate that housing bulls on RM improved daily live weight and carcass gain. In terms of animal welfare, the haematology results indicate that floor type had no effect on the immunological status of the bulls. While there was no evidence of lameness in bulls on RM, the increased number of hoof lesions suggests that animal welfare may be compromised.

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Table 1. Performance characteristics, carcass traits and hoof lesion scores of bulls on different floor types

	Mat		Slat		SEM	Sig.		
	Yes	No	Old	New		Mat	Slat	Mat×Slat
DM intake (kg/day)	9.4	9.4	9.5	9.3	0.15	NS	NS	NS
Slaughter weight (kg)	649	623	640	632	10.6	0.08	NS	NS
Live weight gain (kg/day)	1.41	1.24	1.35	1.31	0.04	<0.01	NS	NS
Carcass weight (kg)	364	352	359	358	6.83	NS	NS	NS
Est. carcass gain (kg/day)	0.79	0.71	0.75	0.75	0.03	<0.05	NS	NS
Kidney and channel fat (kg)	8.17	7.31	8.06	7.41	0.30	<0.05	NS	NS
Hide weight (kg)	51.4	47.4	50.0	48.8	0.99	<0.01	NS	NS
Lesion score	16.3	11.3	14.8	12.8	0.99	<0.01	NS	NS

Can the supply of digestible undegradable protein offered to ewes during late pregnancy affect lamb parasitism?

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Introduction

Evidence on the prevalence of anthelmintic resistance has led to greater interest in alternative parasite control strategies such as protein supplementation (Houdijk *et al.*, 2005). While it has been reported that an increase in dietary supply of metabolisable protein (MP) can reduce faecal egg count (FEC) in artificially infected periparturient ewes (Houdijk *et al.*, 2000, Sakkas *et al.*, 2012), little is known about the effect of intrauterine protein availability on “fetal programming” and on development of the immune response later in life. The aim of the present study was to determine whether quality of protein, using supplements differing in digestible undegradable protein (DUP), offered to ewes in late pregnancy affects the development of resistance to gastrointestinal nematodes (GIN) in the progeny when exposed to natural GIN challenge.

Materials and Methods

Four treatments were offered as follows: 2 concentrates differing in DUP concentration (94 and 29 g/kg dry matter (DM)) each offered at 2 feed levels as described by Sebastiano *et al.* (2015). Individual faecal samples for FEC measurement were collected, per rectum, from all lambs at 10, 12, 14, 16, 20, 21 and 29 weeks of age. Blood samples were collected by jugular venepuncture at 10, 12, 14, 16, 20, 24 and 26 weeks of age for the determination of serum IgA and IgE antibodies specific for *Teladorsagia circumcincta*. Anthelmintic treatment (Ivermectin; Oramec, Merial Animal Health Ltd) was administered at 5, 14, and 21 weeks of age as per manufacturer’s recommendations. At slaughter the abomasum was recovered from 12 animals (6 males and 6 females) per treatment and the worm burden was determined. All data were analysed using Proc MIXED (SAS[®]) to fit a model that had fixed effects for sire breed, sex, treatment, age at sampling and their interactions, with individual as random. Prior to analysis, worm burden, antibody and FEC data were transformed to square root (SQRT(x+1), logarithms (ln(x +1) and ln (x +25)), respectively, to stabilise the variance.

Results and Discussion

The effects of DUP concentration in the concentrate

Table 1. Total abomasal worm burden and total *Teladorsagia circumcincta* and *Trichostrongylus axei* burden by diet (Least squares means on square root scale)

diet (Least squares means on square root scale)								
Concentrate level (CL)	Digestible undegradable protein (DUP)					Significance		
	Low		High		s.e.			
	Low	High	Low	High		DUP	CL	CLxDUP
Total worm burden	85	94	88	91	8.17	NS	NS	NS
<i>T.circumcincta</i>	68	74	70	68	7.59	NS	NS	NS
<i>T.axei</i>	49	57	51	58	4.28	NS	NS	NS

supplement and concentrate feed level offered during late pregnancy on worm burden, FEC and serum IgE and IgA concentrations are presented in Table 1 and Figures 1 and 2, respectively. Neither DUP concentration nor feed level offered in late pregnancy altered progeny worm burden, FEC or serum *T. circumcincta* specific IgE and IgA concentrations.

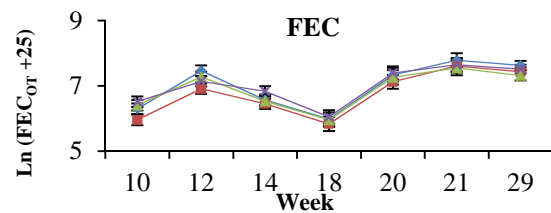


Fig 1. FEC of “other trichostrongyles” (least squares mean \pm s.e.) ♦ (High DUP 30 kg), ■ (High DUP 18 kg), ▲ (Low DUP 30kg), x (Low DUP 18kg)

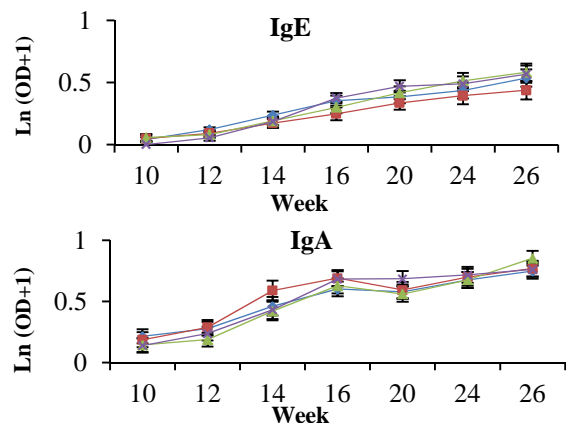


Fig 2. Least squares mean OD values (\pm s.e.) for serum IgE and IgA ♦ (High DUP 30 kg), ■ (High DUP 18 kg), ▲ (Low DUP 30kg), x (Low DUP 18kg)

Conclusions

The development of the immune response in lambs to GIN is not affected by the level of DUP in the maternal diet in late pregnancy.

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Weight as a basis for targeted selective anthelmintic treatment of lambs

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Introduction

The existence of gastrointestinal nematodes (GIN) resistant to anthelmintics (AR) threatens the anthelmintic-dominant approach to the control of GIN. In Ireland there is evidence for AR to benzimidazole and levamisole on approximately 80 and 40 % of farms, respectively (Good *et al.*, 2012). In light of this and the recent introduction of two novel anthelmintic drugs, namely, monepantel and derquantel to the market, the challenge to the industry is clear: safeguard anthelmintic efficacy. The adoption of practices that can slow the development of resistance is required (Abbot *et al.*, 2012; Good, 2008). The maintenance of refugia, the proportion of the parasite population that escapes exposure to anthelmintic, is important in delaying the build-up of AR in worm populations (van Wyk, 2001). Conventionally, anthelmintics are delivered on a whole group basis. One proposal for maintaining refugia is part-flock treatment (Abbot *et al.*, 2012). There is a need for information on which individuals in the flock should be left untreated and an assessment of any negative effects of this strategy on animal performance. Results from a previous study on the effects of selective treatment of lambs post weaning revealed a potential negative effect on lamb growth rate in the absence of treatment. As the parasite challenge in that study was low, it was considered necessary to repeat the study under conditions of greater parasite challenge (Good *et al.*, 2008). Therefore, the aim of the present study was to evaluate the effect of anthelmintic treatment at weaning on lamb performance under a range of conditions (i.e., different flocks and years)

Materials and Methods

The study was undertaken over 2 years and involved 3 farms with multiple breeds. The breeds involved were Belclare (n=243), Texel (n=106), Suffolk (n=56) and Ile de France (n=41) and the farms were located in Galway (Teagasc, Athenry research farm (2013 & 2014), Wicklow[†] (2013) and Kilkenny[†] (2014). Weaned lambs were weighed and assigned to one of 3 weight class: light, medium or heavy. The light and heavy lambs were used in the study and were randomly assigned to one of 2 anthelmintic regimes (\pm anthelmintic; STARTECT, Zoetis, administered in accordance with manufacturer's instructions) and co-grazed on 'contaminated' pastures. Lambs were

weighed, faecal and blood (haematology and pepsinogen) sampled and assessed for dags and body condition at day 0 and again after 4 weeks. Animals treated with anthelmintic were faecal sampled 14 days post treatment to check drug efficacy. Strongyle eggs in faeces were counted (FEC) using the modified McMaster (ANON 1986) (on day 0 and 28) and FECPAK methodologies (day 14). FEC were distinguished as *Nematodirus* (FEC_{NEM}), and 'other trichostrongyles' (FEC_{OT}), excluding *Strongyloides papillosus*. Data at week 4 were analysed using the Proc MIXED of SAS[®] and a model that included breed, sex, treatment (dosed or undosed), weight class and treatment by weight class interaction as fixed effects, initial weight, within weight group, as a covariate and farm-by-year as a random term. The FEC data were log transformed prior to analysis to normalise residuals.

Results and Discussion

Results are presented in Table 1. The results for FEC clearly show that lambs were exposed to GIN infection. Mean FEC_{NEM} and FEC_{OT} were 33 and 464 at Day 0. FEC measurements at 14 days post treatment indicated 100% efficacy of the anthelmintic used. Treatment was significant for FEC_{OT}, FEC_{NEM} (P<0.001) and dag score (P < 0.05) at Day 28; dosed lambs had lower values than undosed lambs. Treatment also had a significant effect on final live weight (P<0.001); undosed lambs were 1.2 (s.e. 0.20) kg lighter than lambs that had been dosed. There was no evidence for an interaction between treatment and weight class (P > 0.6). Breed effects on dag score (P<0.001) largely reflected a higher score for Suffolk lambs (2.9). Mean dag score at Day 28 was 1.9, 2.4, 2.0 for Belclare, Ile de France and Texel, respectively.

Conclusions

As weight class did not affect FEC and since heavy lambs are likely to be sold earlier and taking account of withdrawal period, it would be appropriate to selectively choose lighter lambs for treatment.

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Table 1. Least squares means for final live weight, dag and body condition scores. Geometric means for FEC_{OT}

Group	Weight (s.e)	Dag	BCS	FEC _{NEM} (CI)	FEC _{OT} (CI)
Heavy-Dosed	43.1 (0.58)	2.2	3.2	12 (2, 24)	116 (38, 269)
Heavy-Undosed	41.9 (0.58)	2.5	3.0	29 (15, 47)	1213 (549, 2648)
Light-Dosed	35.4 (0.56)	2.1	2.9	16 (7, 30)	133 (50, 312)
Light-Undosed	34.3 (0.56)	2.6	2.9	35 (21, 54)	1336 (617, 2863)

Comparison of two methods to determine bovine colostrum quality on farm

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Introduction

The immunoglobulin (Ig) concentration of bovine colostrum can vary significantly (Morrill *et al.*, 2008). This variation can contribute to an inadequate intake of colostrum Ig, leaving calves at greater risk of ill health. Laboratory testing is considered to be the most accurate method for determining colostrum Ig concentration. This can be expensive, and results are not immediately available to inform decision making within the first hours of the calf's life. Therefore, the objective of this study was to compare a digital Brix refractometer (DBR) and colostrometer (CM) to a laboratory test for determining the immunoglobulin G (IgG) content of colostrum.

Materials and methods

Colostrum samples were collected from 20 dairy farms throughout Northern Ireland from February 2013 to February 2014. Colostrum samples were taken by the farmer at the first milking postpartum and stored in a fridge (~4°C). Subsequent colostrum samples were collected every 3 days and brought to AFBI Hillsborough. Samples were analysed using a DBR (Bellingham and Stanley Optiduo, Basingstoke, UK, range 0-54%) and CM (KRUUSE Colostrum Densimeter, Langeskov, Denmark). Samples analysed using the CM were warmed in a water bath to 20°C before testing. The samples were frozen at -20°C after analysis using the DBR and CM. The colostrum samples were removed from the freezer and thawed in a fridge (4°C) overnight, centrifuged, fat removed and then refrozen (-20°C) until analysis. Colostrum samples were thawed at 4°C overnight, after which the IgG concentration was determined using an ELISA kit for bovine IgG from Bio-X Diagnostics (Jemelle, Belgium). A spearman rank correlation between Elisa IgG and DBR and CM results was performed using Genstat version 16.0. Epidemiological diagnostic test characteristics, sensitivity, specificity, positive prediction value (PPV), negative prediction value (NPV) and accuracy were calculated for different DBR and CM results for an ELISA IgG concentration of 50 mg/ml.

Results and discussion

Table 1. Comparison of digital Brix refractometer (DBR) and colostrometer (CM) cut-off values to represent good quality (50 mg IgG/ml) colostrum

DBR cut-off value (%)	Sensitivity	Specificity	PPV ¹	NPV ²	Accuracy
23	0.70	0.76	0.76	0.70	0.73
24	0.64	0.86	0.84	0.69	0.75
25	0.52	0.92	0.87	0.64	0.71
CM cut-off value					
1050	0.75	0.59	0.67	0.69	0.67
1055	0.64	0.80	0.77	0.67	0.72
1060	0.34	0.86	0.73	0.55	0.59

¹PPV = Positive predictive value, ²NPV = Negative predictive value.

A total of 123 colostrum samples were tested by the three methods. The mean Elisa IgG value was 50.79 mg/ml. The DBR mean value was a Brix score of 23%. The CM had a mean specific gravity value of 1052. The correlation between the Elisa IgG and DBR was 0.72 ($p < 0.001$), which is similar to that found by Biemann *et al.* (2010). The correlation between the Elisa IgG and CM was 0.51 ($p < 0.001$), which is lower than that found by Chigerwe *et al.* (2008). The sensitivity, specificity, PPV, NPV and accuracy for a range of cut-off values for the DBR and CM are presented in Table 1. For the DBR, the highest sensitivity and NPV was found for a Brix score of 23% whereas the highest specificity and PPV was found for a Brix score of 25%, leading to the highest accuracy for a Brix score of 24%. Biemann *et al.* (2010) stated a Brix score of 22% was the most accurate cut-off for quality colostrum. The highest sensitivity and NPV for the CM was found at 1050, the highest specificity at 1060 and the highest PPV and accuracy at 1055. Godden (2008) stated a value of 1050 represented the cut-off value for quality colostrum when using a CM. The difference between the cut-off values found between this study and other studies could be explained by the use of an ELISA kit which requires fat removal, whereas, the other studies used radial immunodiffusion assays and fat was not removed. Further analysis is needed to determine the effect this might have on the results.

Conclusion

The DBR had a higher correlation with Elisa IgG than the CM. However, both methods provide a quick and easy way to determine colostrum IgG concentration on farm. Using an ELISA kit and removing fat for the laboratory analysis the cut-off value for good quality colostrum (50 mg IgG/ml) was 24% and 1055 for the DBR and CM, respectively.

Acknowledgements

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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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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 annual 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%

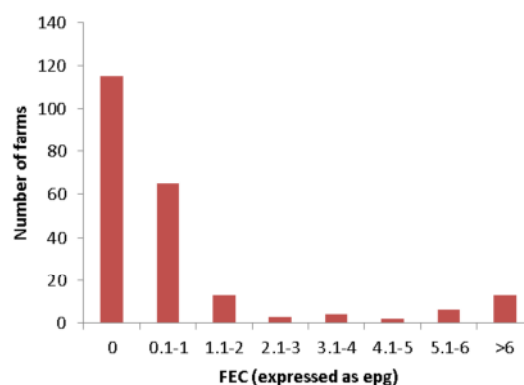


Fig. 1: Number of farms with differing FEC status.

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

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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.

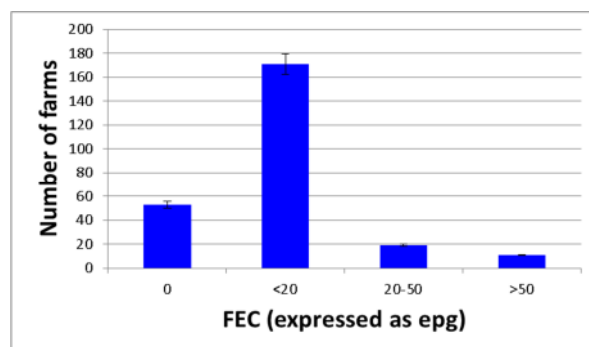


Fig 1. Number of farms with differing FEC status.

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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Widespread failure of anthelmintic drench tests on Irish farms in the sheep technology adoption program

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Introduction

In 2013, as part of a nationwide sheep technology adoption program (STAP), over 1,800 sheep producers carried out drench tests. 19.5% percent met the criteria for a drench test with a high level of anthelmintic treatment failure on Irish sheep farms observed (Keane *et al.*, 2014). In 2014, sheep producers were again given the opportunity to test the efficacy of their anthelmintic treatment by means of a drench test.

Materials and Methods

The drench tests were carried out as reported in 2014 (Keane *et al.*, 2014), between 1st of June and the 19th of September on spring born lambs. In brief, to carry out the drench test: the same group of lambs was faecal sampled before and after anthelmintic treatment. The interval between samples was 7 days for Levamisole (LEV) and 14 days post treatment for Benzimidazole (BZ) and Macrocytic Lactones (ML). The faecal samples and treatment information was then sent to DAFM approved laboratories to determine the Faecal Egg Counts (FECs) using the modified McMaster method. FEC were categorized as *Nematodirus* spp. (FEC_{NEM}) and other trichostrongyles excluding *Strongyloides papillosus* (FEC_{OT}). Data were collated and analysed with SPSS 16. To calculate a reduction, a pre-treatment FEC of ≥ 200 eggs per gram (epg) is required in addition to the post-treatment faecal sample taken between 10-14, 4-7 or 14-18 days for BZ, LEV and ML, respectively, with an effective anthelmintic treatment deemed as resulting in a reduction in FEC $>95\%$ (Coles *et al.*, 1992).

Results and Discussion

The response to both years of this task is summarised in Table 1. While there were fewer participants in 2014 when compared to the previous year, it is noteworthy that a higher level of compliance with was observed. In 2014, 50% of participants carried out the task as required as opposed to only 30% in 2013. Sheep producers chose BZ, LEV and ML in 41.3%, 23.3% and 34% of cases, respectively. The remaining 1.4% of producers used an unsuitable product. Results of the drench tests carried out in 2014 are summarised in Table 2. Only 51% of 524 compliant drench tests were effective against Trichostrongyles. There was a significant difference in the efficacy of the three drugs (χ^2 test; $P < 0.001$) against these species. BZ products are the most popular with producers despite being the least effective, resulting in a reduction of $>95\%$ in only 29% of cases. The LEV products were the least popular drug and were effective in 56% of cases. The ML products were the most efficacious providing a $>95\%$

reduction in 71% of cases. In contrast, all drug groups were highly effective against *Nematodirus* spp., with only two BZ tests considered ineffective. 109 drench tests were completely effective against *Nematodirus* spp. Of these, 95 met the criteria to also calculate a Trichostrongyle egg reduction. While being completely effective against *Nematodirus*, evidence for inefficacy against Trichostrongyles following BZ, LEV and ML was observed in 75%, 32% and 17% of tests, respectively. This evidence suggests that the treatment failure is as a result of anthelmintic resistance as opposed to an inappropriate dosing technique. These results agree with those of last year and previous work carried out on the topic in Ireland (Good *et al.*, 2012).

Table 1. Response to STAP drench task 2013, 2014

Information	2013	2014
Total participants	1893	1274
Fully compliant drench tests	527	640
FEC _{OT} pre sampling ≥ 200 epg	369	524
NFEC _{NEM} pre sampling ≥ 200 epg	115	111

Table 2. Summary results of drench test 2014

Drench	%	FEC _{OT}		FEC _{NEM}	
		%	n	%	n
BZ	95 - 100	29	59	96	45
	81 - 94	15	32	2	1
	51 - 80	26	54	0	0
	0 - 50	30	62	2	1
	Total	100	207	100	47
LEV	95 - 100	56	59	100	22
	81 - 94	16	17	0	0
	51 - 80	14	15	0	0
	0 - 50	13	14	0	0
	Total	100	105	100	22
ML	95 - 100	71	151	100	42
	81 - 94	9	18	0	0
	51 - 80	10	21	0	0
	0 - 50	10	22	0	0
	Total	100	212	100	42

Conclusions

In 2014, there was an improvement in the level of compliance with the test instructions. As in the previous year approximately half of all treatments administered were inefficacious and BZ remains the most popular drug despite its consistently poor performance against Trichostrongyles. While it is not possible to definitively conclude that treatment failure in the majority of cases is due to anthelmintic resistance, data from a cohort of flocks suggest that it is responsible.

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Can digestible undegradable protein supply offered to ewes in late pregnancy affect the periparturient parasite egg count of mature ewes?

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Introduction

Gastrointestinal nematode parasites are currently controlled by a combination of pasture management and anthelmintics. In Ireland as elsewhere, there is clear evidence for anthelmintic resistance in nematode populations to all 3 non-prescription anthelmintic groups on the market (Good *et al.*, 2012). This has been a key driver of research on the development of sustainable solutions for parasite control. The temporary loss of acquired immunity to gastrointestinal nematodes that is indicated by an increase in faecal egg output in late pregnancy is a well-established phenomenon and is important in the epidemiology of nematode parasites in sheep (Barger, 1993). There is some evidence to suggest that faecal egg output by parasitised ewes is reduced in response to increased dietary metabolisable protein supply (Donaldson *et al.*, 1998; Houdijk *et al.*, 2005). The aim of the present study was to evaluate the effects of the quantity of digestible undegradable protein (DUP) offered to ewes in late pregnancy on the parasite egg count during the periparturient period for ewes with a natural parasite challenge.

Materials and Methods

Four treatments were offered in the current study, to 88 twin-bearing ewes, during the last 6 weeks of pregnancy; viz., 2 concentrates with different DUP concentrations (94 and 29 g/kg dry matter) and offered at 2 levels (18 or 30 kg) as described by Sebastiano *et al.* (2015). Ewes were penned in groups of 4/5 and offered silage *ad libitum* with free access to water. Ewes did not receive anthelmintic treatment. Strongyle faecal egg counts (FEC) were determined from faecal samples, using modified McMaster methodology (ANON, 1986), collected (per rectum) from each ewe at 6 and 3 weeks pre-lambing, at lambing and at 1, 3, 4, 5, 6, 7, 8, 9 and 10 weeks post lambing. Faecal egg counts were distinguished as *Nematodirus* (FEC_{NEM}), *Strongyloides papillosus* (FEC_{SPAP}) and 'other trichostrongyles' (FEC_{OT}). Ewes and their lambs were managed as one flock at pasture and received no concentrate supplementation. Data were analysed using Proc MIXED of SAS®. The model had fixed effects for treatment, sample week, litter size and treatmentxweek interaction and animal within treatment as a random term. Prior to the analysis the FEC data were transformed to logarithms (ln (X+25)) to normalize the residuals.

Results and Discussion

As FEC_{NEM} and FEC_{SPAP} were negligible only the results of FEC_{OT} are reported. The effect of week on FEC_{OT} was highly significant (P<0.001). The dietary treatment (i.e., concentration of DUP in the concentrate and level of concentrate offered to ewes during late pregnancy) did not affect the FEC_{OT} (Figure 1) observed in ewes with a natural parasite challenge. There was no evidence for any effect of litter size or any treatment by week interaction (P>0.05).

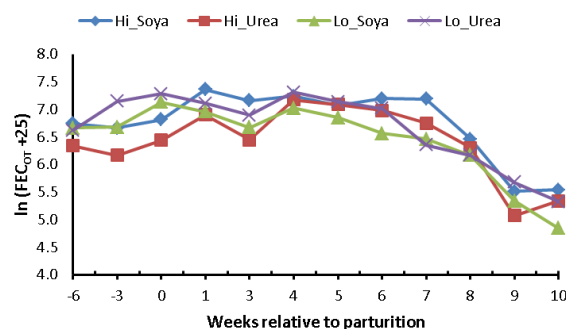


Fig. 1. Faecal egg count for 'other trichostrongyles' (least squares means, log scale) ♦ (High DUP 30 kg), ■ (High DUP 18 kg), ▲ (Low DUP 30kg), × (Low DUP 18kg)

Conclusions

The faecal egg count of ewes, with a natural parasite challenge, during the periparturient period cannot be modulated by DUP supply during late pregnancy within the wide range examined in this study and thus will not confer any benefit through a reduction in the parasite challenge on pasture

Acknowledgements

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The relationship between tail lesion scores and viscera condemnations in slaughter pigs

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Introduction

Tail biting is a behavioural vice performed by pigs which causes poor welfare, poor performance and carcass condemnation (Taylor *et al.*, 2010). Tail biting and the resulting damage provides routes for the spread of infection which explains why tail damage is associated with other disease lesions (Schröder-Petersen & Simonsen, 2001). The relationship between carcass abscission, and tail biting is well-documented (Huey, 1996). However, the relationship between tail lesion severity and disease lesions responsible for viscera condemnation is less well investigated. The aim of this study was to investigate this relationship in Irish slaughter pigs.

Materials and Methods

The study was conducted during April 2012 in an Irish abattoir. The following data were collected at the evisceration point from every 3rd pig slaughtered over 7 days: farm identification, sex, tail lesion score and viscera inspection outcome. Tail lesions were scored according to a 0 to 4 point scale (Fig. 1). Disease lesions responsible for lung (pleurisy, pneumonia and abscess), heart (pericarditis) and liver (ascariasis) condemnation were recorded based on the decision of the veterinary inspector (VI). The cold carcass weight (CCW) was also collected. Data on 3,143 pigs from 61 different batches were available. Batch was the experimental unit and data from each batch were averaged before analysis. Batches with less than 20 pigs were excluded from the dataset. An overall tail lesion (TL) score was given to each batch, with each score weighted according to severity. The effect of VI, sex, TL score and CCW and the lesions responsible for viscera condemnation were assessed using PROC GLM. The reasons for viscera condemnation were included as fixed effects. Statistical differences were reported when $P \leq 0.05$.



Fig 1. Tail lesion scoring: no lesion (score 0), mild (score 1), moderate (score 2) and severe (score ≥ 3).

Results and Discussion

Tail lesions (score ≥ 1) were found in 72% of the study population, with 2.3% affected by severe tail lesions. A total of 1,114 cases of diseases associated with viscera condemnation were recorded, with approximately 71% being related to lung diseases, 8% to heart disease and 16% related to liver disease. Descriptive data are shown in Table 1. Batch size ranged from 20 to 108 pigs, with an average of 51.5 ± 20.9 pigs per batch. At least one batch presented 0% for each of the diseases associated

with viscera condemnation. Pleurisy (13.7%) followed by pneumonia (10.4%) showed the highest prevalence but the prevalence of ascariasis showed the greatest variation between batches (0 to 75%).

Table 1. Mean \pm S.D., min and max values for batch size, TL score, CCW and diseases associated with viscera condemnation within batches.

	Mean	Min	Max
TL score	0.98 \pm 0.41	0.22	2.13
CCW (kg)	79.6 \pm 4.68	63.00	89.85
Pleurisy (%)	13.7 \pm 13.42	0.00	61.11
Pneumonia (%)	10.4 \pm 12.17	0.00	55.81
Pleuropneumonia (%)	1.7 \pm 3.65	0.00	20.59
Abscess (%)	0.3 \pm 0.97	0.00	7.14
Pericarditis (%)	2.8 \pm 3.94	0.00	22.22
Ascariasis (%)	7.3 \pm 15.59	0.00	75.00

There were inconsistencies between the VIs in the detection and identification of several disease lesions as VI was associated with condemnations for pneumonia, pleuropneumonia, pericarditis and ascariasis (Table 2). Sex was not associated with any of the reasons for condemnation in spite of the sex effect on tail lesion severity (Harley *et al.*, 2014). The lack of an association between TL and abscess may have been due to the low numbers of lungs condemned for this reason in comparison to the work by Huey (1996). CCW were associated with pleurisy, pneumonia, pleuropneumonia and ascariasis.

Table 2. *P*-values for associations between variables.

	VI	Sex	TL	CCW
Pleurisy	0.2094	0.3658	0.0551	0.0015
Pneumonia	0.0461	0.8177	0.0019	0.022
Pleuropneumonia	0.0055	0.1441	0.0008	<.0001
Abscess	0.475	0.9663	0.9835	0.2543
Pericarditis	0.0102	0.286	0.509	0.2127
Ascariasis	0.0293	0.4682	0.1014	0.0062

Conclusions

There is a high prevalence of tail and disease lesions leading to viscera condemnations in Irish slaughter pigs. There is a need for standardisation of criteria for identifying the latter to reduce variation between VI. Several disease lesions were associated with reduced pig performance as reflected in carcass weights. The relationship between tail lesion scores and the lung diseases supports the association between poor health and poor welfare on pig farms.

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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 ($P<0.0001$) 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 ($P=0.052$).

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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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

The effects of soil loosening on herbage dry matter yield from grassland sites in Northern Ireland

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Introduction

Due to increased tractor size and higher stocking rates in beef and dairy systems, the risk of soil compaction on grassland is perceived to be a problem on many intensive farms. A relatively small number of studies have been carried out on the benefits of mechanical soil loosening on grasslands in the UK and Ireland, with benefits usually being evaluated in terms of grass yield. Results from previous studies have shown both yield increases and decreases (Bhogal *et al.*, 2011; Frost, 1988). In response to concerns over soil compaction raised by farmers in Northern Ireland (NI), the extent of soil compaction on grassland soils across NI was assessed. As part of this assessment a three-year study on grass yield response to soil loosening at five intensively managed sites was commenced. Results from the first year of this work are presented here.

Materials and Methods

Five grassland sites were selected across NI to take into account regional variations in soil and climatic conditions. The soil types of the five sites ranged from clay loam to heavy clay and were described by the farmers as being moderately compacted. In autumn 2013, an area of approximately 45 m × 5 m was marked out and divided into 6 equal blocks on each site. Within each block, the three treatments Not Loosened control (NL), Autumn Loosened (AL) and Summer Loosened (SL) were randomly allocated (each plot was 2.5 × 5 m). Soil loosening was carried out with a tractor mounted McConnel Grassland Shakaerator with a working width of 2.5 m, three lifting tines (at 0.6 m centres) and a working depth of approximately 0.3 m. The AL treatment was carried out in autumn 2013. Due to wet weather in spring it was not possible to carry out the SL treatment until after the first harvest in 2014. There were three main harvests in 2014 with a fourth autumn “clean off” cut included on 3/5 sites due to strong grass growth on those sites in early autumn (measured by rising plate meter). Plot harvesting coincided with grass harvesting times on each farm in order to reflex grass management at each site. The first harvests took place from 21/05 – 05/06, the second harvests took place 09/07 – 30/07 and the third harvests 26/08 – 04/09. The fourth “clean off” cut was taken in early October on the sites identified with strong grass growth. Grass yields were measured by cutting a 5 m × 1 m strip of grass from each plot using a pedestrian-controlled reciprocating-blade grass mower (Agria). The cut grass was raked, gathered, bagged and weighed on-site. Grass dry matter (DM) content was determined by drying the herbage at 100°C for 24 hours. Grass DM yield data were statistically analysed using a general analysis of variance (ANOVA) using Genstat for Windows version 12. The model accounted for treatment as a single factor with site location providing replication for each harvest

Results and Discussion

Table 1 shows the effects of soil loosening on grass DM yield (kg DM/ha) averaged across the five sites. At the first harvest (May 2014) the DM yield for AL was lower (~8%) than the NL control (P=0.005). However, at the second harvest the DM yield for AL was higher (~10%) than the NL control (P<0.001). At Harvest 2 (July 2014), which was the first harvest after treatment SL had been applied, SL had a significantly lower (~12%) DM yield *c.f.* the NL control. At the third harvest (Aug./Sept 2014), the yields for both AL and SL were not different (P>0.05). The fourth harvest (Oct. 2014) on these sites showed no effects (P>0.05) from soil loosening on grass DM yield.

Table 1. Effects of soil loosening on grass dry matter yield (kg DM/ha) in harvests following loosening

Harvest	1	2	3	4 ^b
Control	8787	5793	3205	1992
Autumn (AL)	8058	6353	3224	1969
Summer (SL)	^a	5119	3299	2044
S.E.M.	246.6	230.2	76.5	55.7
P value	0.005	<0.001	0.43	0.39

^a Treatment SL was applied after the first harvest so was not statistically compared with the autumn treatment

^b Harvest 4 was done on 3/5 sites (site specific)

Grass DM yields at the harvest that immediately followed soil loosening were lower (P<0.01) than those from the NL control. Sward surface damage was observed on all the loosened plots post soil loosening. The SL treatment, which was carried out during a dry period, resulted in the worst visual damage as a result of soil cracking and surface damage on all sites (very pronounced on one site in particular) and this was reflected in greatly reduced DM yields at the next harvest. The DM yields at the third harvest following AL treatment (second harvest following SL treatment) were not significantly (P>0.05) different. In this work the positive and negative effects of soil loosening on DM yield were relatively small and short term and were in agreement with previous work in NI (Frost, 1988).

Conclusions

The first year's results indicate that soil loosening in autumn and after the first harvest reduced grass yields in the following harvest, increased them in the next harvest, and appeared to have no further effect in any later harvest. Thus, the benefits of the soil loosening treatments as applied seemed relatively short term.

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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 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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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	

Is it economically beneficial to sow forage maize under plastic mulch in Northern Ireland?

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Introduction

In Ireland, maize (*Zea mays*) has been identified as a high-risk fodder crop having potential to be both the cheapest and the most expensive conserved feed, with variability in yield being the largest risk factor. The use of plastic mulch can reduce this variability and increase nutritive quality (Finneran *et al.*, 2012), but Northern Ireland is a peripheral maize growing region with soil and air temperatures often limiting factors. Plastic mulch generates increased soil temperature in May and June (Farrell and Gilliland, 2011), which is a critical growth and developmental period that strongly influences overall DM yield and nutritive quality (Meehan and Gilliland, 2012). The cost of sowing with plastic mulch incurs an additional cost of approximately €300/ha (Finneran *et al.*, 2012), compared to approximately €600/t (Personal Communication) of purchasing maize starch as animal feed. Therefore, the increase in value of the harvested crop must be greater than the initial investment to justify the use of plastic mulch. Finneran *et al.* (2012) reported that the economic viability of plastic mulch use was dependent on the seasonal growing conditions and justifies further assessment under the marginal growing conditions in Northern Ireland. The aim of this research was to assess whether plastic mulch is an economically beneficial strategy for maize production in Northern Ireland.

Materials and Methods

Maize recommended list maize variety trials were established and managed in accordance with UK national list testing procedures (www.defra.gov.uk). Replicated (n = 3) plots of four rows, spaced 75 cm apart, were sown at a sowing rate of 100k seeds/ha to a depth of 3 cm and spaced 13cm apart in both open and plastic mulch systems. In 2010, three cultivars were sown and five cultivars in both 2011 and 2013. Plastic mulch used in the plastic mulch treatment, where two coverings of 6µm photodegradable covered rows 1 & 2 and rows 3 & 4, respectively. Fresh yields were based on samples of 100 plants from each of three replicates and oven dried at 60°C for 36 hours to obtain dry matter content. A two-way ANOVA was carried out for

each year with plastic mulch (with/without) and variety as factors. The costs of utilizable dry matter (€/ t UDM) were estimated based on the assumptions of Finneran *et al.* (2012).

Results and Discussion

Although there was a wide range in DM yield over the three years, ranging from 7.7 t ha⁻¹ to 18.8 t ha⁻¹, the starch content was always significantly higher with plastic mulch (Table 1). In 2011 mulch increased the DM yield by 1.9 t ha⁻¹ (P<0.001), had a negative effect in 2010 (-1.8 t ha⁻¹; P<0.05) and had no significant effect in 2013. These different DM yield responses were determined by the overall growth potential of each harvest year, whereby in the highest yielding year (2010; warmest June) the plastic mulch suppressed DM yield, possibly due to the earlier maturation and cob development. In the year with intermediate DM yields (2013; intermediate June temperature) there was no significant effect and the lowest yielding year (2011; coolest June) plastic mulch had a positive effect. This influenced the production cost per utilizable dry matter, whereby using plastic mulch was only cheaper in the year with the lowest maize yields which concurs with the findings of Finneran *et al.* (2012). However as the primary reason for growing maize is to produce a high energy, starch rich feed the use of plastic mulch always provided a greater yield of starch and at a lower production cost per tonne of starch.

Conclusions

The three growing seasons examined are representative of the varied range of weather conditions in Northern Ireland. Dependent on the seasonal growing conditions, DM yield was not always higher under the plastic mulch treatment. As maize nutritive value has a significant influence on animal productivity and thus profitability of the farm enterprise. Therefore due significantly increased starch yield and reduced starch production costs per unit product sowing maize under plastic mulch was always economically beneficial.

Acknowledgements

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Table 1. Mean annual yields and costs for forage maize grown in Northern Ireland in three growing seasons

Year (<i>June Temp. °C</i>)	2010 (<i>14.3</i>)			2011 (<i>11.8</i>)			2013 (<i>13.1</i>)		
	Open	Plastic	Sig.	Open	Plastic	Sig.	Open	Plastic	Sig.
DM yield (t ha ⁻¹)	18.8	17.0	P<0.05	7.7	9.6	P<0.001	12.1	12.0	N.S.
Production cost (€/ t UDM)	123	158	-	300	285	-	187	225	-
Starch yield (t ha ⁻¹)	5.2	6.3	P<0.01	1.8	3.7	P<0.001	2.8	5.0	P<0.01
Production cost (€/ t starch)	336	319	-	1016	500	-	626	348	-

Sig – Significant difference between sown without plastic mulch (Open) and with plastic mulch (Plastic)

The effect of stocking rate and ewe prolificacy potential on grass utilisation per hectare, per ewe and per kilogram of lamb carcass produced

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Introduction

Within grass-based systems of lamb production higher stocking rates and ewe prolificacy levels have the potential to greatly increase lamb output/ha. Maximising the quantity of grazed grass utilised has the potential to greatly increase profitability at farm level (Davies and Penning, 1996). The aim of this study was to investigate the effect of increasing ewe stocking rate and prolificacy level on grass utilisation on a per hectare, per ewe and per kilogram of lamb carcass produced basis.

Materials and Methods

Data from a two-year sheep farm systems experiment, established in October 2011, was used. A total of 360 ewes comprising of two breed types, differing in prolificacy potential (PP) (Hanrahan, 1994), were assembled: medium prolificacy - Suffolk crossbred ewes (n=180) with a target weaning rate of 1.5 lambs/ewe, and high prolificacy - Belclare crossbred ewes (n=180) with a target weaning rate of 1.8 lambs/ewe. Within breed type, ewes were blocked by live weight (kg) and body condition score (BCS, 1-5), and randomly assigned to one of three pasture-based systems differing in overall stocking rate (SR): low SR (10 ewes/ha, SR1), medium SR (12 ewes/ha, SR2), and high SR (14 ewes/ha, SR3). Ewes were mated in October each year to lamb in early March. Following lambing, ewes and their progeny were rotationally grazed until weaning at 14 weeks of age. Post-weaning a leader-follower system was operated. Pre- and post-grazing herbage mass was recorded for each grazing. Nitrogen (N) fertiliser was applied at a rate of 13kg

N/ewe (130, 156 and 182 kg N/ha for each of the Low, Medium and High SR groups, respectively). Lamb carcass output/ha produced from grazed grass alone as well as total carcass output/ha were quantified for each system. The difference between total carcass output/ha and carcass output/ha from grazed grass was the quantity of carcass produced by supplementing lambs with silage and concentrates due to insufficient grass availability as dictated by weekly grass budgets. Data were analysed using the GLM procedure in SAS. Included in the model were effect of stocking rate and prolificacy potential and their interaction.

Results and Discussion

Increasing stocking rate significantly increased the quantity of grass utilised within the system (Table 1). There was an interaction between SR and PP for grass utilised/ewe whereby there was a significantly higher level of utilisation by high PP ewes compared to medium PP ewes (877 v. 833 kg DM) at low SR, but they did not differ at medium or high SR. An interaction also occurred between SR and PP level for carcass output/ha from grazed grass only; no significant difference was observed between medium SR HP and high SR HP groups (396 v. 406kg carcass), whereas there was a difference between SR in the MP groups. Interactions also occurred between medium SR HP and high SR MP groups whereby no significant differences were detected between these groups for total carcass output/ha, (419 v. 420 kg carcass) or for kg DM required/kg carcass produced (27.5 v. 28.0 kg DM).

Conclusions

Increasing lamb carcass output per hectare from grass-based systems may be achieved more efficiently by increasing the prolificacy potential of the flock first, and then, increasing the stocking rate.

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Table 1. Effect of stocking rate and ewe prolificacy on grass utilised per hectare, per ewe and per kg of carcass output

Parameter	Stocking Rate (SR)			Prolificacy (PP)		sed	P-value		
	Low	Medium	High	Medium	High		SR	PP	Inter.
Grass utilised/ha (kg DM)	8553 ^a	9618 ^b	11178 ^c	9789	9777	44.9	<0.001	NS	NS
Grass DM utilised / ewe (kg)	855 ^a	802 ^b	799 ^b	821	816	4.5	<0.001	NS	<0.001
Carcass output/ha from grazed grass only (kg)	322 ^a	373 ^b	381 ^c	337	380	7.6	<0.001	<0.001	<0.001
Total carcass output/ ha (incl. supp.) (kg)	332 ^a	393 ^b	453 ^c	366	418	9.3	<0.001	<0.001	<0.001
Grass DM utilised / kg carcass (kg)	25.9 ^a	24.6 ^b	24.8 ^b	26.8	23.4	7.67	<0.01	<0.001	NS
Total kg DM req'd / kg carcass	26.7 ^a	25.9 ^b	29.5 ^c	29.0	25.7	7.67	<0.001	<0.001	<0.001

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 \pm s.d.) calving date (February 17 \pm 15.5 d), breed, parity (2.4 \pm 1.61), pre-experimental milk yield (22.6 \pm 4.20 kg), body weight (BW) (469 \pm 68.2 kg) and body condition score (BCS) (3.09 \pm 0.193). From within block cows were randomly allocated to one of eight treatments in a randomised complete block design with a 4 \times 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 \times 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

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:

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

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

where NEI is daily net energy intake, NEL is daily net energy requirements for lactation, $\sum_{i=1}^2 DIM^i$ is days in milk included as a continuous variable with a linear and quadratic effect, $BW^{0.75}$ is metabolic live-weight, BCS is body condition score, ΔBW^+ describes animals gaining live-weight, ΔBW^- describes animals losing live-weight, while ΔBCS^+ describes animals gaining BCS, and ΔBCS^- 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 (ECE_{adj}), and 2) also consider the energy requirement for maintenance in the numerator (ECE_{adj2}):

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

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

where the b's represent the associated regression coefficients from the aforementioned REI model.

Partial efficiency of milk production (PEMP) and a similar trait $PEMP_{Nut}$ were defined as:

$$PEMP = \frac{NEL}{NEI - bBW^{0.75}} \quad PEMP_{Nut} = \frac{NEL}{NEI - NEM}$$

where NEM is daily net energy required for maintenance calculated as $(1.4 + 0.6 \times (\text{live-weight}/100)) \times 1.2$. 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 $PEMP_{Nut}$.

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

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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).

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

¹r < |0.03| were not different from zero

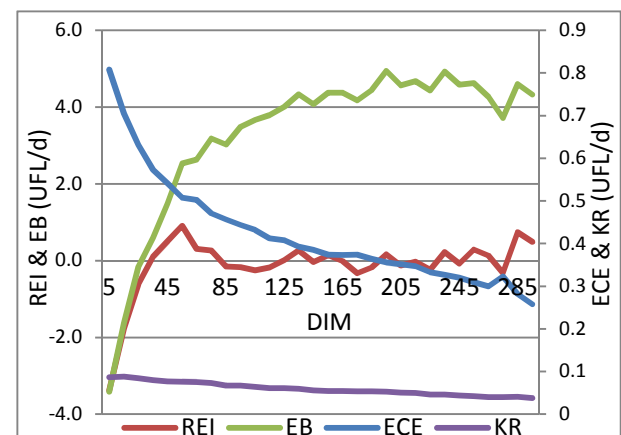


Fig. 1. Efficiency traits across lactation

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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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 286,082m³/farm/year (range 117,860 – 435,583m³). The average volume of water available

through rainfall occurring on the farms was 751,514m³/farm/year (348,106 – 1,177,567 m³).

Table 1. 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. Of 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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Effect of white clover seed inclusion rates with tetraploid, diploid and mixed perennial ryegrasses under simulated grazing and animal grazing

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Introduction

There is renewed interest in the inclusion of white clover (*Trifolium repens* L.; clover) into grazing systems in recent years. However, in Ireland there is no specific recommended clover seed inclusion rate for mixed perennial ryegrass (*Lolium perenne* L.; PRG) clover pastures. In temperate regions such as Ireland, PRG is the favoured companion grass for sowing with clover (Brock and Hay, 1996). A tetraploid PRG may be more compatible than a diploid PRG as a companion grass, as tetraploid PRG usually has a more open erect growth habit than diploid (Frame and Boyd, 1986), which may favour clover growth and persistence. The objective of this study was to examine the effect of white clover seed inclusion rate in a ryegrass-clover seed mixture on sward clover content for a tetraploid, diploid or mixed tetraploid-diploid PRG sward under contrasting managements.

Materials and Methods

In June 2013, 120 plots were sown in a 2 × 3 × 5 randomised complete block design with four replicates per treatment at Teagasc Moorepark. There were two managements (MAN) – simulated grazing (5 m × 1.5 m; SIM) and animal grazing (8 m × 3 m; ANI). Three PRG sward types – tetraploid (cv. Kintyre), diploid (cv. Aberchoise) and a 50:50 tetraploid:diploid mix (cv. Kintyre and Aberchoise); and five white clover (cv. Iona) seed rates (SR) – 0, 2.5, 5.0, 7.5 and 10 kg/ha. The PRG sowing rate was 27.5 kg/ha. All plots received 150 kg of inorganic nitrogen (N)/ha/y. The plots were defoliated seven times in 2014 (March to October). Pre-grazing herbage mass (> 4 cm; HM) was determined using an Etesia mower prior to each defoliation event (SIM MAN or ANI MAN). A subsection of the ANI plots were harvested for DM yield and the remainder was grazed. Sward clover content was measured in March, June, August and October. Herbage 4 cm above ground level was sampled at random locations in each plot. A 70 g sub-sample was removed and separated into grass and clover fractions and dried at 40°C for 48 h to determine DM proportions. Data were analysed using PROC MIXED in SAS with terms for SR, PRG sward type, management, rotation and associated interactions.

Results and Discussion

There was a significant (p<0.05) interaction between

SR×PRG sward type, PRG sward type×MAN and SR×MAN for HM (Table 1). Herbage mass was greatest on the tetraploid swards at SR 0 and 2.5, and it was greatest on the diploid swards at SR 5.0 and 7.5, with the mixed PRG sward having the greatest HM at SR 10. The HM on the diploid and mixed PRG swards was greater than the tetraploid sward under SIM MAN, and the tetraploid sward had the greatest HM under the ANI MAN. The SR×MAN interaction resulted in greater HM for the ANI MAN for 0 and 2.5 SR; while the SIM MAN had the greatest HM at 5.0 and 7.5 SR; there were no difference between MAN for the 10.0 SR. Wims et al. (2010) also found HM differences between simulated and animal grazing. Clover content was similar on SR's 2.5, 5.0, 7.5 and 10 (0.171 ± 0.013 g/kg DM) (Table 1). There was a SR×MAN interaction for clover content. When SR 0 was excluded, SR 5.0 with ANI MAN had lower clover content than all other SR and MAN. The ANI MAN had higher clover content on SR 2.5, 7.5 and 10.0 compared to the SIM MAN at the same SR. These results are in contrast to Evans and Williams (1987) who found higher clover content under simulated grazing compared to animal grazing. There was a three way interaction between SR×PRG×MAN for clover content. When SR 0 was excluded, SR 5.0 ANI MAN sown with the diploid PRG had lower clover content than all other SR, MAN and PRG. Frame and Boyd (1986) previously reported that clover content was greater when sown with tetraploid PRG; this effect was not observed in this experiment.

Conclusions

Tetraploid swards performed better under the ANI MAN and at the lower clover SR, while the diploid sward had greater HM on the SIM MAN and at the higher clover SR. Sward clover content in a one year old mixed sward seems to find an equilibrium balance regardless of PRG seed mixture or clover seed inclusion rate at sowing. Greater consideration must be taken when choosing PRG sward type and white clover seed inclusion rate.

Acknowledgements

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Table 1. Effect of white clover seed inclusion rate on dry matter yield and sward white clover content.

White clover seeding rate	0.0	2.5	5.0	7.5	10.0	SE ¹	Rot ²	SR ³	PRG ⁴	MAN ⁵	SR × PRG	PRG × MAN	SR × MAN
Herbage mass (kg DM/ha)	1488	1555	1569	1553	1583	26.2	***	NS	*	NS	***	**	**
White clover (g/g)	0	0.17	0.16	0.17	0.18	0.13	***	***	NS	NS	NS	NS	*

SE¹= standard error; Rot²= Rotation; SR³= seeding rate; PRG⁴= perennial ryegrass; MAN⁵= management;

Using principle component analysis to select representative calibration sample sets for near infrared spectroscopy prediction of crude protein

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Introduction

Near infrared reflectance spectroscopy (NIRS) is a secondary technique that utilises predictive calibration models to relate spectral data to laboratory reference values. These predictive models are developed from a calibration set, therefore the selection of the calibration set plays a major role in the accuracy and reliability of these models. As the calibration set is rarely representative of all possible samples, it should at least be representative of the future samples that will likely be analysed (Shenk and Westerhaus, 1991). A large calibration set can increase the accuracy and robustness of calibration models, however there is a significant time and cost associated with obtaining reference data. Shenk and Westerhaus (1991) proposed the use of principle component analysis (PCA) of spectral data to select a representative sub-set of samples. PCA describes the main principle components that explain the variation in the spectral data. From this, the neighbourhood H statistic (NH) is calculated as the mahalanobis distance between neighbouring spectra. An individual spectrum is selected to represent a local subset of samples within a defined mahalanobis distance. This process is repeated until there are no samples closer to each other than the defined distance. Shetty *et al.* (2012) reported that using procedures to select representative calibration sets could reduce the number of samples requiring reference analysis by up to 80% with a minimal loss in accuracy of calibration models. The aim of this research was to assess the accuracy of NIRS calibration models for crude protein using calibration sub-sets selected using PCA.

Materials and Methods

The full calibration set consisted of 2076 ryegrass samples that were collected from harvested plots at Backweston, Co. Kildare and selected to ensure that the calibration set encompassed the range in climatic conditions, ryegrass species, developmental stage, ploidy, genotype and age of sward that occur in the Recommended List trials. Obtaining reference laboratory data and related spectra were carried out as described by Burns *et al.* (2013). A 1,4,4,1 derivation and standard normal variate and detrend scatter correction treatment were applied to the spectra prior to analysis. A PCA analysis was applied to the spectra whereby 18 principle components were selected to describe 99.78 % of variation in the spectra. The 'select' algorithm of Shenk and Westerhaus (1991) was applied, whereby a NH of 0.2, 0.4, 0.6 and 0.8 was applied to select sub-sets from within the full calibration (Figure 1). Predictive regression models and cross-validations were carried out as per Burns *et al.* 2013.

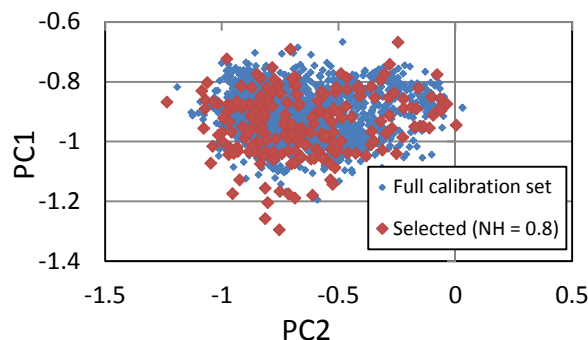


Fig. 1. Plot of principle component 1 (PC1) and principle component 2 (PC2) of the full calibration set and selecting samples using NH = 0.8.

Results and Discussion

Using the NH criteria of 0.2, 0.4, 0.6 and 0.8, subsets consisting of a 32 %, 73 %, 84 % and 90 % reduction in the full dataset were obtained, respectively (Table 1). The accuracy of the calibration models was broadly similar across all of the selected subsets, ranging from 0.979 - 0.983. The smallest calibration set (n = 210; NH = 0.8) provided the most accurate calibration model. However, there was a trend for decreased accuracy of the cross-validation as the calibration set size decreased, with the likelihood of an associated decrease in the robustness of these models as indicated by the increased SECV. Shetty *et al.* (2012) concluded that the methodology of sample selection is more important than the number of samples in the calibration set.

Table 1. NIRS calibration statistics for predicting crude protein (g/kg DM) based on calibration subsets selected using four neighbourhood H (NH) values.

NH	n	Mean	SEC	R ²	SECV
Full	2076	150.0	5.00	0.982	5.15
0.2	1414	147.2	5.34	0.980	5.53
0.4	556	145.9	5.53	0.979	6.03
0.6	323	147.0	5.64	0.980	6.68
0.8	210	147.0	5.36	0.983	6.37

SEC – Standard error of calibration; SECV – Standard error of cross validation

Conclusion

Using PCA to select representative calibration sub-sets is possible whilst also maintaining the accuracy of NIRS calibration models for predicting crude protein. There was a slight decrease in the robustness of the calibration models with a decrease in the size of the calibration set, however this must be considered in the context of associated cost and time savings.

Acknowledgements

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Evaluation of the effects of enzyme additives on fibre characteristics of grass silages

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Introduction

During conventional ensiling, under good management practices, a lactic acid bacterial fermentation will usually dominate, thus ensuring the maintenance of herbage nutritive value. Breakdown of plant fibre is one of the major limitations to biodegradability of ensiled herbage in both ruminant and biomethane production. Dehghani *et al.* (2012) found that silage additives such as fibrolytic enzymes reduce NDF contents of grass-clover silages. This reduction coupled with good preservation may improve the energy value of silages. The aim of this experiment was to evaluate four enzyme additives and quantify their effects on the fibre characteristics of ensiled grass silage.

Materials and Methods

Perennial ryegrass (*Lolium perenne* L.) and timothy (*Phleum pratense* L.) were each grown separately in four replicate blocks and precision-chop harvested at two dates in the primary growth, 29th May and 19th June 2013, for Harvest 1 and 2, respectively. Herbage were ensiled in laboratory silos for 119 days at 15 °C, with fibrolytic enzyme additives: (1) Control, (2) Phytase, (3) Cellulase-A, (4) Cellulase-B and (5) Xylanase. Enzymes were produced from solid state fermentation, dissolved in a 1% (v/v) detergent solution and on average applied at a rate of 1.5 ml kg⁻¹ of herbage DM, according to producer's specifications. After ensiling, silage sub-samples were dried at 40 °C for 48 h and milled through a sieve with 1 mm apertures. These were used for the determination of neutral detergent fiber (NDF), acid detergent fibre (ADF) and acid detergent lignin (ADL), and were expressed exclusive of residual ash. Data were analysed using a MIXED procedure (SAS 9.3) as a split-split-plot design with harvest as the main plot, species as the sub-plot, and enzyme treatment as the sub-sub-plot, with the effects of replicate block being accounted for within the main plot.

Results and Discussion

Perennial ryegrass mean (s.d.) pre-ensiling NDF was 482 (13.8) and 603 (33.9); and ADF was 267 (8.3) and 353 (21.9) for Harvest 1 and 2, respectively (in g kg⁻¹ DM). Timothy mean (s.d.) pre-ensiling NDF was 596 (18.1) and 673 (26.6), and ADF was 342 (13.5) and 389 (16.7) for Harvest 1 and 2, respectively (in g kg⁻¹ DM). Silage fibre results are presented in Table 1. Compared to the control (i.e. no enzyme additive) Cellulase-B and Xylanase decreased ($P<0.01$) both grass species NDF concentrations at Harvest 1. In Harvest 2, the NDF concentrations were decreased by the same enzyme additives ($P<0.01$) for perennial ryegrass but there were no effects of enzyme additives for timothy. The ADF concentrations were decreased by Xylanase ($P<0.01$) for both species at Harvest 1. In Harvest 2, the ADF concentrations were decreased by Xylanase ($P<0.01$) and tended towards being reduced by Cellulase-B

($P<0.0505$) for timothy. There were no effects of enzyme additive compared to the control for perennial ryegrass at Harvest 2. Silage ADL proportions were not affected ($P>0.05$) by any enzyme additive. Through the considerable reduction of NDF and moderate reduction of ADF compared to the control silage it appears that the more easily digestible parts of the fibre was degraded. This suggests that there was much greater cellulase than hemicellulase activity. Furthermore, the absence of an effect on silage ADL suggests that lignin also remained bound in the cell wall with the hemicellulose. Thus, the fibre fraction that is left behind may be more recalcitrant to subsequent digestion in the rumen or anaerobic digestion reactor (Dehghani *et al.*, 2012).

Table 1. Effect of harvest, species and enzyme on fiber characteristics (g kg⁻¹ DM) of ensiled herbage.

Harvest	Species	Enzyme	NDF	ADF	ADL
29 th May	PRG	Control	564	321	24
29 th May	PRG	Phytase	521	320	28
29 th May	PRG	Cellulase-A	539	318	23
29 th May	PRG	Cellulase-B	500	303	27
29 th May	PRG	Xylanase	473	268	27
29 th May	TIM	Control	661	408	31
29 th May	TIM	Phytase	626	399	29
29 th May	TIM	Cellulase-A	638	396	30
29 th May	TIM	Cellulase-B	599	388	34
29 th May	TIM	Xylanase	555	339	37
19 th June	PRG	Control	627	352	49
19 th June	PRG	Phytase	612	376	36
19 th June	PRG	Cellulase-A	603	367	35
19 th June	PRG	Cellulase-B	573	360	34
19 th June	PRG	Xylanase	555	334	37
19 th June	TIM	Control	654	402	45
19 th June	TIM	Phytase	630	397	45
19 th June	TIM	Cellulase-A	667	398	46
19 th June	TIM	Cellulase-B	621	373	44
19 th June	TIM	Xylanase	630	354	45
Standard error of the mean					
Harvest			2.4	5.6	2.0
Species			2.6	3.3	2.0
Enzyme			4.7	4.0	1.7
Harvest x Species			3.7	5.9	3.4
Harvest x Enzyme			7.0	6.9	3.3
Species x Enzyme			7.1	5.0	3.3
Harvest x Species x Enzyme			10.8	8.5	5.8
Levels of significance ^a					
Harvest			***	NS	NS
Species			***	***	NS
Enzyme			***	***	NS
Harvest x Species			***	***	NS
Harvest x Enzyme			*	*	NS
Species x Enzyme			NS	NS	NS
Harvest x Species x Enzyme			*	NS	NS

^a NS = not significant, * = $P<0.05$, *** = $P<0.001$.

Conclusions

Enzyme additives were effective at decreasing the NDF and ADF fractions of ensiled grasses. Compared to the control, Phytase and Cellulase-A seemed to have weak cellulase activity but Cellulase-B and especially Xylanase seemed to have a particularly strong cellulase activity. No enzyme exhibited marked ligninase activity relative to the control. Future research to assess the actual effects of this perceived fiber reduction in ruminants or anaerobic digestion reactors is required.

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An investigation to establish the effect of geographical location, film type and variety on the production of forage maize

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Introduction

There are numerous studies that show the beneficial effects of including maize silage in the diets of beef cattle (Keady *et al.*, 2008) and dairy cows (Burke *et al.*, 2007). Despite the advancements in suitable varieties of maize for growing in marginal conditions, low productivity and quality in poor growing seasons persists (Farrell and Gilliland, 2011) due to the variability in climatic conditions. The use of degradable mulch film technology has been shown to improve forage maize yields and composition (Keane *et al.*, 2003) and improve crop consistency. The objective of this study was to evaluate the effect of geographical location, film type and variety on the yield and quality of forage maize during a single growing season.

Materials and Methods

Plots were sown in the following four sites: Adare (South West), Cork (South), Dublin (North East), and Waterford (South East). Five varieties were chosen P7905, P7631, P7892, Benicia, PR39A98 and three film types: no film, film 1 (Samco Yellow) and film 2 (Samco Green). Therefore a 4 x 5 x 3 factorial arrangement. Both film types were 7 μ m, perforated (28 pinhole) photo-degradable mulch films, with film 1 being quicker to degrade post sowing compared to film 2. Plots were sown between 29th April and 2nd May 2013 using a two row Samco precision seeder at a seeding rate of 100,600 seeds ha⁻¹. Each plot measured 3.2m x 5m (16m²) with an average spacing of 80cm. Each plot was replicated three times. Each experimental block had an outside buffer of four rows of maize to prevent the effects of shading. Post emergence herbicide was applied eight weeks post sowing and best agricultural practice was followed throughout the growing season. Plots were harvested between 27th September and 9th October 2013, 5m of the two centre rows of each plot were harvested by hand in order to avoid edge effects and the fresh weight yield recorded. A sample of chopped whole plant was retained for dry matter determination and chemical composition. Chemical analysis was determined by Near Infrared Reflectance Spectrometry (NIRS) at AFBI, Hillsborough, Co. Down. In addition, a sub-sample of entire plants was retained for grain weight yield. Data was analysed using PROC MIX in SAS. The model accounted for site, film type, variety and replicate and all associated interactions.

Results and Discussion

There was a trend towards a site x variety interaction (P=0.1) (Fig. 1). The highest yielding variety in the South, PR39A98, was not the highest yielding variety at the other sites. There was a significant effect of site on the yield of whole crop forage maize (Fig. 1).

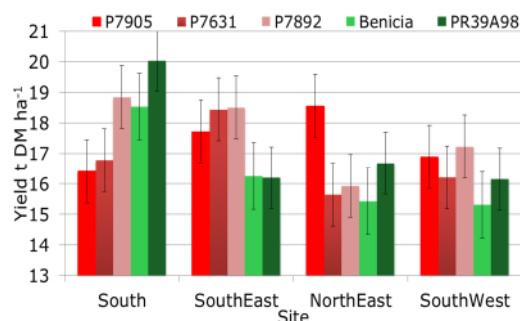


Fig. 1. The effect of site and variety on the yield (t DM ha⁻¹) of forage maize. Error bars =s.e.

Whole crop forage maize grown in the South and South East yielded significantly higher, (P<0.05) 18.13 and 17.42 t DM ha⁻¹, compared to whole crop forage maize grown in the North East and South West, 16.45 and 16.36 t DM ha⁻¹ respectively. Table 1 shows the effect of film treatment on whole crop yield and chemical composition of forage maize. Both film types significantly (P<0.001) increased whole crop yield, grain yield, DM %, ME content and starch % compared to forage maize grown in the open.

Table 1. The effect of film treatment on whole crop yield and chemical composition of forage maize

Film Treatment	Open	Film 1	Film2	SEM	Significance
Yield (t DM/ha ¹)	14.67	18.83	17.78	0.40	***
Grain yield (t DM/ha ²)	4.01	11.57	10.88	0.41	***
DM% ¹	23.71	32.73	31.6	0.57	***
Crude protein (%DM) ²	9.30	7.66	7.55	0.10	***
ME(MJ/kg DM) ²	11.64	12.22	12.51	0.14	***
Starch (%DM) ²	25.19	40.47	45.08	1.42	***
NDF(%DM) ²	44.96	40.94	30.47	0.76	***

***P<0.001. ¹LSM acrossall four sites, ²LSM for North East site only.

Conclusions

Geographical location, film and variety had a significant effect on the performance of forage maize grown in Ireland, a second year of this study has been completed which will allow final conclusions to be drawn.

Acknowledgements

We acknowledge Samco Agricultural Manufacturing and Enterprise Ireland for their financial support through the Innovation Partnership Programme 2013.

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A one year national survey of mycotoxins in Irish farm silages

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Introduction

Penicillium and *Fusarium* fungal species have been previously identified in 0.42 and 0.01 baled silage in Ireland, respectively. These moulds are toxigenic and can produce secondary fungal metabolites, namely mycotoxins. Mycotoxins can induce a range of detrimental ailments in livestock including abortions, vomiting, lameness, immuno-suppression, reduced feed intake and feed refusal (CAST, 2003). Monitoring feed for mycotoxins is requested by the European Food Safety Authority and this study includes all mycotoxins that are regulated in Commission Directive (EC) No. 32/2002 and recommendation (EC) No. 576/2006. The objective of this study was to identify the mycotoxin concentrations present in farm silages in Ireland during the winter of 2012-2013.

Materials and methods

Samples were collected from one silage feed face or round bale silage on each of 150 farms throughout Ireland. These silages consisted of baled grass silages (n=56) and pit silages (grass (n=88) and maize (n=6)). Samples were collected using a motorised corer system that was 60 cm in length and perpendicular to the surface of the bale or pit face. Core samples (n=2) were collected from the next bale or pit section ready for feeding. For mycotoxin and conventional chemical analysis, silage samples were dried at 40°C in a forced air circulation oven and milled (Retsch SM100) through a 1 mm pore sieve. A thorough cleaning protocol was used to avoid cross contamination. Mycotoxin analysis was by validated (Agilent 6460-1290) liquid chromatography tandem mass spectrometry (LCMS-MS) operating in both positive and negative electrospray ionisation modes. This 16 minute analytical run can detect 20 mycotoxins (andrastin A, aflatoxins B¹, B², G¹ and G², beauvericin, DON, HT-2, mycophenolic acid (MPA), roquefortines C and E, ochratoxin A, T-2, zearalanone, enniatins B, B¹, A and A¹, and fumonisins B¹ and B²) inclusive of all EU regulated mycotoxins concerned with feed. Chemical characteristic data were analysed using independent sample t-test and mycotoxin concentration data (non-normal distribution) were analysed using Mann Whitney test, with both tests accounting for baled vs pit silage.

Results and discussion

The herbage in baled silage appeared to be harvested at a more mature growth stage and underwent a more extensive wilting than pit silage, as evidenced by the numerically higher DM. This wilting restricted the lactic acid fermentation in baled silages compared to pit silages (Table 1). Both baled and pit silages contained mycotoxins from *Penicillium* and *Fusarium* moulds

(Fig. 1). Eight mycotoxins (roq. C, enniatin A, A1, B and B1, andrastin A, beauvericin and MPA) were present within the silages. Although baled and pit silages had similar mycotoxin profiles, pit silage had significantly higher concentrations of enniatin A1 (P< 0.01) and enniatin B1 (P< 0.01) than baled silage. MPA, which occurred in baled silage at a maximum concentration of 4.4 mg/kg DM, is well below other published values (Schneweis *et al.*, 2000). Singly, at the observed concentrations, the individual toxins do not pose acute toxicological risk to ruminants (EFSA 2014; Schneweis *et al.*, 2000). The possibility of additive or synergistic effects of co-occurring mycotoxins is unknown.

Table 1. Conventional chemical characteristics of farm silages collected in Ireland 2012 - 2013.

	Baled silage (n=56)		Pit silage (n=94)	
	Mean	SD	Mean	SD
DM ^a (g/kg)	291	85.3	239	49.2
pH	4.5	0.47	4.0	0.41
WSC ^b (g/kg DM)	48.5	49.55	9.2	7.96
DMD ^c (g/kg)	625	87.8	640	80.5
Lactic acid (g/kg DM)	82	139.0	101	38.6
Crude protein (g/kg DM)	118	18.7	126	21.8

^aDM= Dry matter; ^bWSC= Water soluble carbohydrates;

^cDMD= Dry matter digestibility

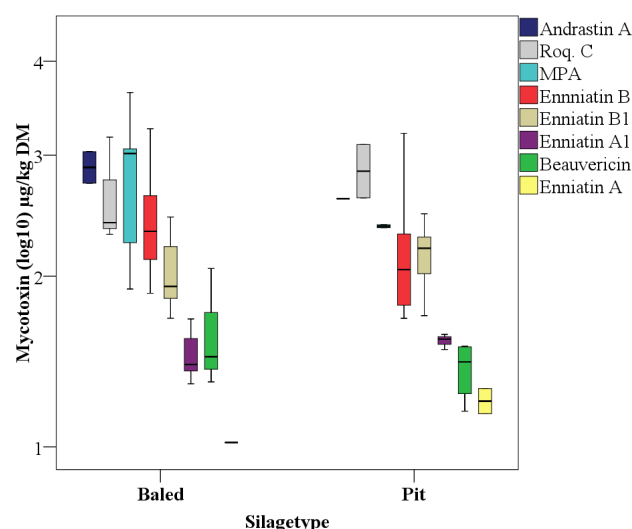


Fig 1. Box plots illustrating the mycotoxin profile found in silages sampled in Ireland 2012 - 2013.

Conclusions

Eight mycotoxins (roq. C, enniatins A, A1, B and B1, andrastin A, beauvericin and MPA) were detected within baled and pit silages collected during a 1 year national survey. None of the mycotoxins detected exceeded E.U. directive or recommendation limits.

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Mapping high nature value farmland distribution in Irish uplands

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Introduction

Uplands form large expanses of semi-natural landscape in Ireland, and topography (slope and aspect) helps to preserve such habitats. Upland habitats are unenclosed areas of land over 150 m altitude, and contiguous lowland areas of related habitats. A large part of such habitats are managed as commonage. High nature value (HNV) farmland is typically characterized by low intensity farming, which supports high biodiversity and a range of wildlife habitats (Baldock *et al.*, 1993). The resistance of semi-natural vegetation to change in such lands are mostly related to less intensive grazing practices on steeper slopes (Nadal-Romero *et al.*, 2014). This study is a part of an on-going research project to identify the distribution and extent of high nature value farmland in republic of Ireland (IDEAL-HNV). Current study aimed to investigate the HNV farmland distribution in upland areas for different topographical variations at different degrees of slope and aspects.

Materials and Methods

Initially, a coarse map for HNV suitability at townland scale was prepared using inputs like, percentage hedgerow cover, average livestock unit and Corine 2006 data (rescaled). A K-means clustering approach was applied to identify distinct groups based on these inputs. Data were standardised prior to clustering and the appropriate number of clusters determined by plotting the sum of square for a number of cluster solutions. The HNV map then intersected with upland coverage maps to calculate the total HNV distribution in upland areas (Fig. 1). HNV potential areas were classified into six grades (0-5) for quantitative representation of the distribution. Slope and aspect maps were prepared using 90m shuttle radar topographic mission elevation data. To understand the HNV distribution at different degrees of slope and aspects, the HNV map was plotted against seven divisions of slopes (at 10° difference) and for eight cardinal aspects (and flat, zero aspect).



Fig. 1. Green represents extent of uplands in Ireland

Results and Discussion

We estimated 930.51 km² of land area with potential HNV status in uplands, which further categorised in to six different levels of intensification (Fig. 2). Highest coverage was observed in level 3 while least in level 2.

This indicates that most of the upland areas tend to have good HNV potential.

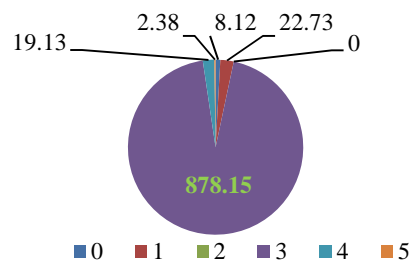


Fig. 2. HNV status in uplands, where 0 stands for least and 5 for maximum potential for HNV (values in km²)

The slope observed using SRTM elevation data varied between 0-63 degrees, while only 7.6 km² as flat land. Highest HNV potential was observed between 0-10 degree slope, which gradually decreased with increasing slope (Fig. 3).

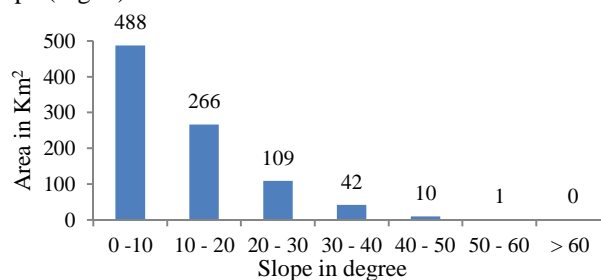


Fig. 3. Distribution of HNV areas at different slopes

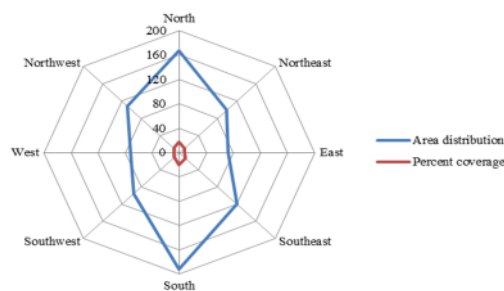


Fig. 4. HNV area distribution at different aspects

Southern aspect was observed with 202.5 Km² area, which contributes 21% of the total HNV land present in uplands, followed by Northern aspect (18%), while least in East and West aspects (Fig. 4).

Conclusions

Upland possesses major part of HNV farmlands in Ireland, characterised with different degrees of slope and aspects. Such commonage farmlands (as most of the HNV uplands are under commonage practice) exhibits more HNV potential than of flat lands especially at gentle slopes with South and North aspects.

Acknowledgments

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First year growth from an alley coppice land use system in Ireland

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Introduction

Approximately 93% of the energy used for electricity generation in Ireland is fossil-fuel based (Connolly et al., 2011). Renewable energy systems from woody crops could help redress this ecological imbalance. Combining a wide spaced tree crop with a short rotation coppice in the lower canopy can increase overall biomass accumulation and deliver timber, biomass and environmental benefits, including: reduced net greenhouse gas emissions, improved soil and water quality, expanded wildlife habitats, increased land use diversity, and revitalise rural economies (Heller et al., 2003). Combining timber production and biomass crops (alley coppice) has been recently reviewed (Morhart et al., 2014); however, the potential of alley coppice in Ireland is unknown.

The objective of this present study is to examine and quantify the main interactions and competitiveness of a willow biomass crop in the first year, with an established poplar tree crop and to provide knowledge on the potential feasibility of such a system in Ireland.

Materials and Methods

A field trial was established near Loughgall, Co. Armagh (54°23'N, 6° 36'W; 45m a.s.l.) on a Brown Earth soil (pH 6.4 0-30cm) consisting of poplar (*Populus* spp.) trees under-planted with willow (*Salix* spp.) trees. Poplars (15 years old) were 5m apart within tree rows with alleys of 14m wide between tree rows, orientated East-West. Willow was planted as the biomass intercrop in 5 double rows across the alleys, 0.75m apart with spacing between double rows of 1.5m within main plots and all cultivars established successfully to commercial standards. Site mean annual air temperature was 10.2°C; mean annual precipitation, 894mm. The experimental design was a randomised split split plot design in 4 blocks with 4 Poplar cultivars (Hoogvorst, Trichobel, Beaupré and Gibecq), 7 sub-plots (6 monoculture willow cultivars, Tora, Olaf, Terra Nova, Endeavour, Beagle, Resolution and 1 mixed-cultivar willow treatment simulating a commercial mixture), and planted in 5 positions as sub-sub plots. Willow was established using dormant 20cm long unrooted willow cuttings (spring 2013). Measurements were made on plants across the alley transect to avoid any edge effects. Mean willow height and stem diameter at root collar were recorded in August on samples at varying distances from the poplar trees (Fig. 1 & 2). The data was analysed by analysis of variance (ANOVA) using Genstat in a manner appropriate for a split split plot design to determine significance values among treatments. Contrasts were used to test the effect of distance to nearest poplar on plant position.

Results and Discussion

There was no significant three-way interaction between poplar, willow and plant position in willow height in August 2014. The linear effect of distance to nearest poplar interacted with willow to give a highly significant plant position by willow interaction ($P < 0.01$) (Fig. 1). The interaction between poplar and plant position was very highly significant ($P < 0.001$) (Fig. 2).

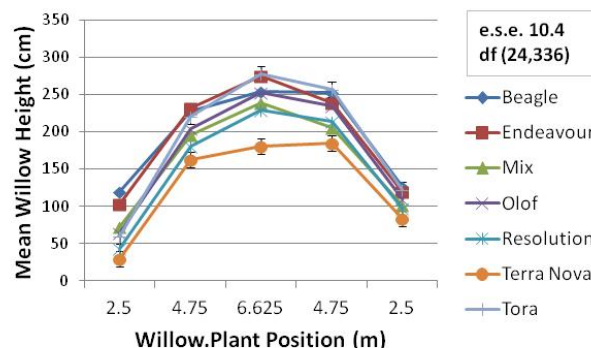


Fig. 1. Mean willow height in relation to willow by plant position. Error bars represent s.e.

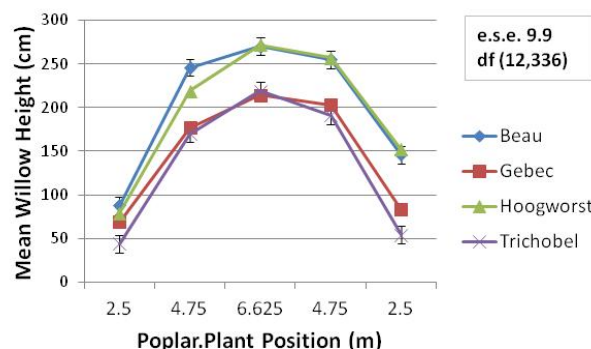


Fig. 2. Mean willow height in relation to poplar by plant position. Error bars represent s.e.

Conclusions

After one year's growth, preliminary results from one site showed that willow height was significantly reduced due to the proximity of the poplar trees, and that this effect depended on both the willow cultivar and the poplar cultivar. Plant position can negatively affect growth and ultimately yield via competition from the (over-story) tree crop along the interface. Plant distance from the tree-line and spacing/density of willow could be manipulated to maximise crop yield.

Acknowledgements

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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 data 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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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 were detected on BTA 18 of which the 57.4-58.4 Mb interval exhibited the strongest SNP associations ($p < 2.5 \times 10^{-8}$). The strongest SNP association ($p = 6.3 \times 10^{-10}$; Bonferroni $p = 5.7 \times 10^{-4}$) was a downstream intergenic variant located ~3Kb from the KLK14 gene. Sixteen gene/gene-products across BTA18 contained SNPs with a p -value $< 2.5 \times 10^{-8}$; 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; $p = 8.9 \times 10^{-10}$; Bonferroni $p = 8.2 \times 10^{-4}$). 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.

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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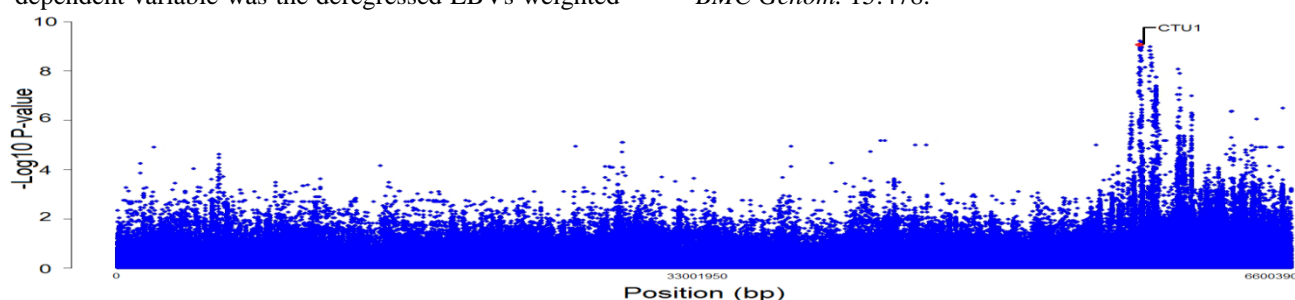


Fig. 1. Association results for direct calving difficulty on BTA 18 using imputed sequence data.

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 $\geq 95\%$ 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.

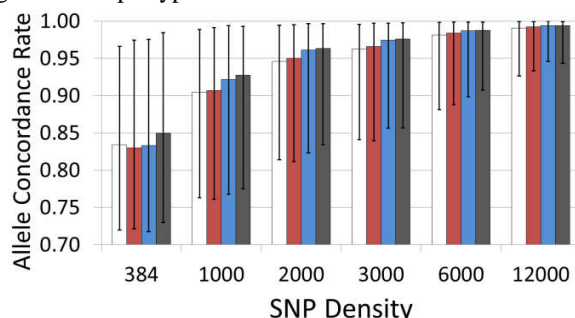


Fig. 1. Mean allele concordance rate (range represented as standard error bars) in dairy, across varying number of SNPs selected randomly (white columns), uniformly (red columns), based on genomic architecture (blue columns) or by the block method (grey columns).

Conclusion

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

Acknowledgements

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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) kg² to 1548.20 (83.12) kg² 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).

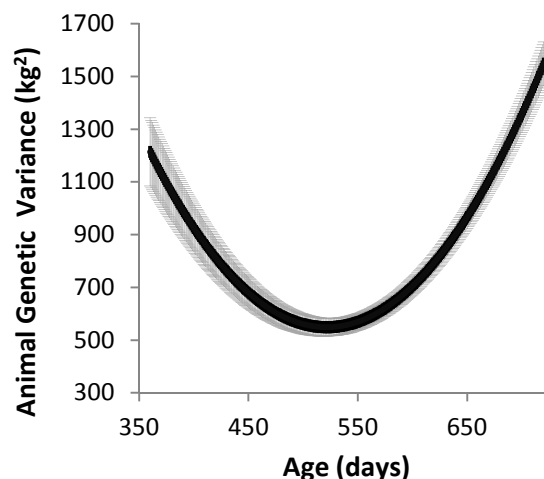


Fig. 1: Estimated animal genetic variances (\bullet) \pm one standard error (error bars) of carcass weight at each age at slaughter.

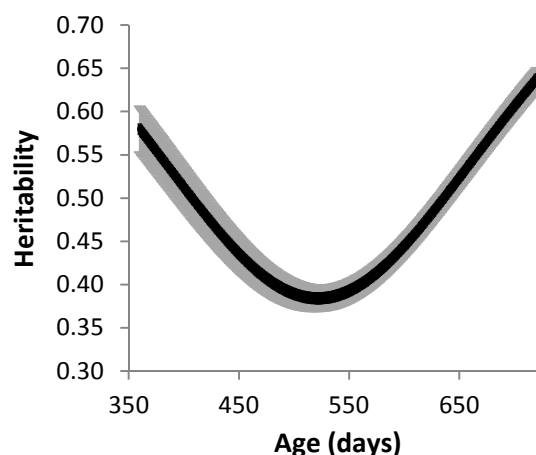


Fig. 2: Heritability estimates (\bullet) \pm one standard error (error bars) of carcass weight at each age at slaughter.

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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Genetic (co)variances of Gompertz growth function parameters in pigs

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Introduction

The economic importance of the weight-age relationship of an animal has long been established. Studies have shown that the Gompertz growth function parameters are heritable (Koivula *et al.*, 2008) and therefore could be incorporated into a breeding program to alter the shape of an animal's growth. The objective of the present study was to estimate the genetic (co)variance of the Gompertz growth function parameters in Finnish Yorkshire and Landrace boars, gilts, and barrows.

Materials and Methods

A total of 61,715 live weight records from 12,768 animals, between the years 2006 and 2012, inclusive, were obtained from the Finnish pig breeding company Figen Oy. All animals were on trial in the Längelmäki central test station in Finland. Quality control of the data has been described in detail elsewhere (Coyne *et al.*, 2015). The final dataset consisted of 51,893 live weight records from 10,201 animals. The Gompertz growth function applied to the individual animal live-weight data is described as:

$$Y_t = A \exp(-B \exp^{-kt})$$

where the dependent variable (Y_t) represents the observed weight of the animal at t days of age, A represents the asymptotic mature weight of the animal as its age approaches infinity; B represents the logarithm of the ratio of mature weight to birth weight; and k represents the maturing rate defining the ratio of maximum growth rate to mature weight. The growth function was fitted initially to live weight data for each animal separately as a fixed effects model and progressively built up to a mixed model. The predicted parameter estimates A , B and k were obtained for each animal and limits were imposed in order to maintain biological sense. The models were compared on the accuracy (R^2), defined here as the square of the correlation between the actual and predicted weights, and root mean square error (RMSE). Genetic (co)variance components for the parameters A , B , and k estimated in the fixed effects model and mixed model were quantified using a linear mixed model in ASReml (Gilmour *et al.*, 2012). Contemporary group, defined as start date on test by gender, was included as a fixed effect in all variance component models. A direct additive genetic effect of the animal, maternal genetic effect of the dam as well as a within litter and across litter dam permanent environmental effect were tested as random effects. The log likelihood ratio test between the nested models was used to determine the significance of the contribution of each random term (i.e. dam, dam litter effect and dam permanent environmental effect) to the fit of the data. Heritability estimates (h^2) were calculated for each growth function parameter.

Results and Discussion

Heritability estimates for the parameters from the fixed effects and mixed model Gompertz function are summarized in Tables 1 and 2, respectively. The direct heritability for parameters A and k for both approaches were relatively similar. Direct heritability for the B parameter for both the fixed and mixed models was moderate and was identical to the direct heritability estimates for parameter A for the mixed models ($h^2 = 0.38$) and were lower, for both the A and B parameters, than previous published estimates for pigs (Koivula *et al.*, 2008). A significant maternal heritability ($P < 0.05$) was detected for all three parameters of the Gompertz function. Maternal repeatability was also significant for all parameters.

Table 1. Direct heritability (h^2_d), maternal heritability (h^2_m), and maternal repeatability (R_m) for the parameters A , B and k in the fixed effects Gompertz model (SE in parentheses)

Parameter	h^2_d	h^2_m	R_m
A	0.14 (0.03)	0.03 (0.01)	0.09 (0.01)
B	0.46 (0.05)	0.15 (0.03)	0.18 (0.02)
k	0.20 (0.03)	0.03 (0.01)	0.09 (0.01)

Table 2. Direct heritability (h^2_d), maternal heritability (h^2_m), and maternal repeatability (R_m) for the parameters A , B and k in the Gompertz mixed model (SE in parentheses)

Parameter	h^2_d	h^2_m	R_m
A	0.38 (0.05)	0.37 (0.03)	0.42 (0.02)
B	0.38 (0.05)	0.37 (0.03)	0.42 (0.02)
k	0.34 (0.04)	0.02 (0.01)	0.19 (0.02)

Strong negative genetic correlations existed between parameter A and the function parameters k (-0.92) and B (-0.72). The phenotypic correlations between the function parameter values (i.e., A , B and k) in the present study were weaker than those reported from other studies in pigs (Koivula *et al.*, 2008). This might be due to the fact that the prevailing breeding goal may be selecting for faster growing animals with heavier mature weights; selecting for both characteristics could weaken the strength of the correlation between the growth curve parameters.

Conclusions

Ample genetic variation exists in parameters A , B and k of the Gompertz function. Knowledge of these genetic components is required to facilitate the incorporation of such functions into pig breeding programs.

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A comparison of the whole blood mRNA transcriptome between Holstein–Friesian and Jersey calves, preceding and succeeding gradual weaning

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Introduction

Holstein-Friesian (H-F) and Jersey (J) are the two most predominant dairy sire breeds used in Ireland (AIM, 2013). Our group has previously reported breed differences in leukocyte relative gene expression, between H-F and J calves during the peri-weaning period (Johnston, *et al.*, 2014). The objectives of the present study were to use RNA-Seq technology to examine the effect of (i) breed and (ii) gradual weaning on the whole blood mRNA transcriptome of artificially reared H-F and J calves.

Material and Methods

Eight H-F and eight J bull calves with a mean \pm s.d. age (days (d)) and bodyweight of 23 \pm 7 d, 46 \pm 6 kg and 37 \pm 8 d, 34 \pm 5 kg, respectively, were group housed on sawdust bedded floored pens from d -56 to d 8 of the study (weaning occurred on d 0). Calves were individually fed using an electronic feeding system (Forster-Technik SA 2000, Engen, Germany). The pre-weaning, weaning and post-weaning periods were defined as d -56 to d -14, d -13 to d 0 (milk feeding ceased), and d 1 to d 8, respectively. During the pre-weaning period, calves were offered 6 litres (L) milk replacer and *ad libitum* concentrate. All calves were offered approximately 400 g straw daily, from a rack within the group pen, throughout the study period. Calves were weaned when consuming 1 kg of concentrate daily for three consecutive days. During the weaning phase, milk replacer was gradually reduced from 6 L to 0 L over a 14 d period (d -13 to d 0). Straw and concentrate allocations were not changed during or after gradual weaning. Throughout the trial period, calves were weighed weekly. Relative to weaning, on d -14, d 1, and d 8, blood samples were collected via jugular venepuncture into Tempus Blood RNA Tubes for subsequent differential messenger RNA (mRNA) gene expression analysis. Total RNA was extracted from whole blood using the Tempus Spin RNA Isolation Reagent Kit. Quantity and quality of the extracted RNA was checked with a Nanodrop spectrophotometer and an Agilent 2100 Bioanalyser, respectively. Samples had an RNA Integrity Number (RIN) of 9.6 (\pm 0.29). Forty-eight individual libraries were prepared from a starting material of 1000 ng RNA using the Illumina TruSeq RNA Sample Preparation Kit v2. Two μ L of a 1/400 dilution of ERCC RNA Spike-In Mix 1 were added to each sample at the beginning of library preparation. Libraries were validated with an Agilent 2100 Bioanalyser, then pooled and sent to Clinical Genomics (Canada), for RNA sequencing on an Illumina HiSeq 2500 with four libraries per lane. Forty million 76 bp paired end reads were sequenced per library. Raw sequence reads were assessed for quality using FastQC. Reads were aligned to the bovine

genome UMD3.1 using the STAR aligner. Read counts were generated using htseq-count. Differential gene expression was determined using EdgeR. Pathway analysis was performed within GOSep using Kyoto encyclopaedia of genes and genomes (KEGG), on statistically significant ($P < 0.05$) differentially expressed genes (DEGs), with a false discovery rate (FDR) of 10% and a fold change of ≥ 1.5 . A 10% FDR cutoff was implemented on the results of the pathway analysis using Bioconductor's qvalue package.

Results and Discussion

Breed affected gene expression ($P < 0.05$; $FDR < 0.1$). There were 550 DEGs between H-F and J on d -14. Additionally, there were 490 DEGs between H-F and J on d 1, and there were 411 DEGs between H-F and J on d 8. Nine KEGG pathways were represented significantly more than by random chance (over-represented), among the DEGs between the two breeds (H-F versus J) on d -14 ($P < 0.01$; $Q \leq 0.1$). Five KEGG pathways were over-represented on d 1 and five KEGG pathways were over-represented on d 8 ($P < 0.01$; $Q \leq 0.1$). Two KEGG pathways, the cytokine-cytokine receptor interaction pathway (KEGG I.D. = bta04060) and the neuroactive ligand-receptor interaction pathway (KEGG I.D. = bta04080), were over-represented between H-F and J at each time-point (d) ($P < 0.01$; $Q \leq 0.1$) (Table 1). Gradual weaning had no effect on gene expression within breed ($P > 0.05$; $FDR < 0.1$).

Table 1. Over-represented KEGG pathways between H-F and J at three different time points.

Pathway	d -14	d 1	d 8
Cytokine-cytokine receptor interaction (bta04060)	***	**	***
Neuroactive ligand-receptor interaction (bta04080)	**	**	***

** $P < 0.01$, *** $P < 0.001$

Conclusions

Signalling pathways were over-represented between H-F and J calves at three different time points. These results suggest differences in immune responses and cell signalling activity between the two breeds. Knowledge of breed-specific immune responses could enable improved health management practices which could be better tailored towards the specific disease sensitivities of particular breeds of interest enabling the development of cost effective breed targeted prophylactic and therapeutic veterinary interventions. Furthermore, the results suggest that gradual weaning does not induce a systemic immune response in either breed of dairy calf as no differentially expressed genes were detected between time-points by RNA-Seq analysis.

Acknowledgements

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Illumina MiSeq amplicon sequencing shows a large decrease uncharacterised highly abundant putative Succinivibrionaceae species and an increase in methanogens in feed-restricted cattle

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Introduction

Knowledge of the rumen microbiome is central to ruminant livestock based production systems in terms of cost, health, quality of product and environmental pollution, particularly methane emissions. However, because it is currently not possible to culture the majority of the thousands of species that comprise the rumen microbiome, it remains poorly understood. Recently there has been a rapid increase in the capability of next generation sequencing (NGS) of 16S rRNA genes that has enabled identification and quantification of species in complex microbial populations such as the rumen microbiome. We used NGS amplicon sequencing to examine the effect of feed restriction and subsequent re-feeding on the rumen microbiome of beef cattle on a high concentrate diet.

Material and Methods

Rumen samples were derived from a compensatory growth model that was previously described (Keogh *et al.*, 2012). In brief, a group of 60 Holstein-Friesian bulls (479 ±15 day old) was divided into two groups of 30 animals. One group was offered an *ad libitum* diet (group A) and the other group was subjected to a restricted diet (group R). Both groups received a 70% concentrate and 30% grass silage diet. Group R animals were fed to grow at 0.6 kg/day for 125 days and animals on the *ad libitum* diet were predicted to grow in excess of 1.5 kg per day. At 125 days, 15 animals from each group (R and A) were slaughtered and rumen contents were collected. The 15 remaining group R (renamed RA) and group A (renamed AA) animals were then offered the same diet on an *ad libitum* basis for a further 55 days, after which they were slaughtered and their rumen contents were collected. Amplicon libraries (110) were generated by PCR amplification of the hypervariable (V4) region of the 16S rRNA gene in bacteria and archaea from 20 ng of rumen DNA extracted from either the solid (S) or liquid (L) fractions of rumen contents from 55 individual bulls from the four treatment groups R, A, RA and AA. PCR amplification was performed with barcoded 16S Illumina adapter fusion 515F/806R rcbc primers. The 110 libraries were designated according to rumen fraction and treatment group as follows: SR (n=14), SA (n=13), SRA (n=15), SAA (n=13), LR (n=14), LA (n=13), LRA (n=15) and LAA (n=13). Sequencing was conducted on the Illumina MiSeq and 240,000-260,000 merged reads were generated per library. QIIME analysis was conducted to combine sequence reads that shared 97% identity into operational taxonomic units (OTUs). OTUs were assigned, based on their sequence similarity, to the closest taxonomic identities on the 'Greengenes' data base. Taxonomic assignments with a

minimum of 80% sequence identity were accepted. A Welch's t-test was used to compare Log-transformed relative abundances of OTUs.

Results and Discussion

Sixty five percent of the OTUs were significantly different (FDR<0.05) between groups R and A, whereas there were no significant differences between groups RA and AA. Of particular interest was a 1.7-fold (solid) and 2.4-fold (liquid) (FDR<0.001) increase of methanogenic archaea in group R and a 452-fold (solid) and 87-fold (liquid) (FDR<1 x 10⁻⁸) decrease in group R of a highly abundant OTU (designated OTU3004) which was assigned to an uncharacterised putative member of the bacterial family Succinivibrionaceae (Fig 1). High abundance in group RA indicates that re-feeding led to a recovery of OTU3004. Succinivibrionaceae utilise hydrogen to produce succinate which is rapidly converted to propionate in the rumen. Unlike acetate, propionate production in the rumen does not yield methane and methane emissions are positively associated with acetate:propionate (A:P) ratio (Russell and Hespell 1981). Percentage relative abundance of OTU3004 showed a negative Spearman correlation ($\rho = -0.69$, $P = <1 \times 10^{-20}$) with ruminal A:P in the rumen liquid fraction. This suggests that OTU3004 may be negatively associated with methane and so should be isolated and characterised.

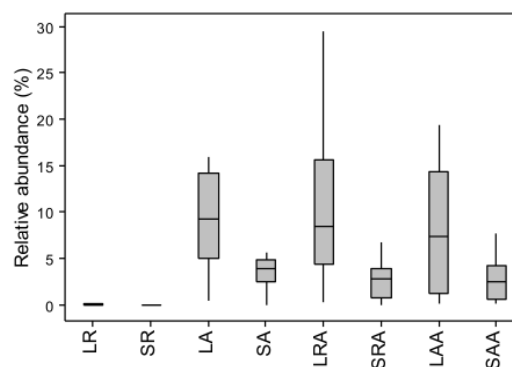


Fig. 1. Relative abundance (%) of putative Succinivibrionaceae OTU3004 in rumen samples. LR=Liquid Restricted, SR=Solid Restricted, LA=Liquid *Ad lib*, SA=Solid *Ad lib*, SRA=Solid Restricted/*Ad lib*, SAA=Solid *Ad lib*/*Ad lib* (n=13), LRA=Liquid Restricted/*Ad lib* and LAA=Liquid *Ad lib*/*Ad lib*. Box and whisker plot shows median, quartiles and maximum and minimum values.

Conclusions

A period of feed restriction in cattle led to an increase in relative abundance of methanogens and a near elimination of an uncharacterised putative Succinivibrionaceae species.

Acknowledgements

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Comparison of sheep breeding objectives in New Zealand and Ireland

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Introduction

Breeding objectives underpin the direction, extent, and economic implications of genetic selection in livestock populations. The definition of breeding objectives may differ between countries and production systems however objective comparisons of alternative indexes may inform producers how livestock selected through specific breeding objectives are likely to perform in alternative systems. The objective of this study was to calculate correlations between national sheep selection indexes in New Zealand and Ireland. Results from this study will help to determine the suitability of New Zealand genetics to Irish production systems.

Material and Methods

Two national sheep breeding objectives exist in New Zealand; the Dual Purpose Overall index (Dual_{NZ}) and the Terminal Sire Overall index (Term_{NZ}). Similarly two breeding objectives are published for the national sheep evaluations in Ireland, the Replacement (Dual_{IRE}) and Terminal (Term_{IRE}) indexes. Across both countries similar traits are recorded in the national breeding objectives and these traits can be categorised into the five broad groups: reproduction, ewe weight, lamb survival, growth and meat traits. Other traits that are unique to a national breeding objective include faecal egg count, ewe fleece weight and facial eczema in New Zealand, and lambing ease in Ireland. To calculate the index correlation and the response to selection for individual traits, selection index methodology was used as described by Santos *et al.* (2015). For comparison, the economic weights of the New Zealand indexes were converted into Euro (€), at conversion rate of 0.6344. The correlation ($r_{x,y}$) between two indexes (X and Y) was calculated as:

$$r_{x,y} = \frac{\mathbf{a}_x' \mathbf{G}_{xy}^* \mathbf{a}_y}{\sqrt{\mathbf{a}_x' \mathbf{G}_x^* \mathbf{a}_x \cdot \mathbf{a}_y' \mathbf{G}_y^* \mathbf{a}_y}}$$

where, \mathbf{G}_{xy}^* is the genetic variance–covariance matrix (\mathbf{G}) between breeding objective traits in indexes X and Y adjusted for accuracy of the respective genetic evaluations, \mathbf{G}_x^* and \mathbf{G}_y^* are matrices of accuracy adjusted genetic variance-covariances within indexes X and Y , respectively, and \mathbf{a}_x and \mathbf{a}_y are vectors of trait economic weights used in the respective indexes, X and Y .

The prediction of response to selection (R_{xi}) in trait i from selection on the index X was calculated as:

$$R_{xi} = i \cdot \frac{\mathbf{b}_x' \mathbf{G}_{xi}^*}{\sqrt{\mathbf{b}_x' \mathbf{G}_x^* \mathbf{a}_x}}$$

where, i is the assumed selection intensity (assumed here to be 1 so that all results are per unit of selection intensity), \mathbf{G}_{xi}^* is the column vector of \mathbf{G}_x^* relating to trait i , \mathbf{a} denotes a vector of economic weights and \mathbf{b}_x is

the column vector of selection coefficients of index x , calculated as:

$$\mathbf{b}_x = \mathbf{P}_x^{*-1} \mathbf{G}_x^* \mathbf{a}$$

where, \mathbf{P}_x^* is the accuracy adjusted phenotypic variance–covariance matrix. The genetic and phenotypic covariance matrixes within and between countries were calculated based on the pooled correlations for international estimates, similar to the approach described by Koots *et al.* (1994).

Results and Discussion

Moderate to strong correlations were calculated between the indexes both within and between countries (Table 1). The strongest correlation was recorded between the Dual_{IRE} and Dual_{NZ} indexes (0.86). A moderate correlation was calculated between both terminal indexes. Weaker correlations were calculated between the terminal and dual indexes across both countries.

Table 1. Correlations calculated within and between breeding objectives in New Zealand and Ireland.

	Term _{IRE}	Dual _{IRE}	Term _{NZ}
Dual _{IRE}	0.67	-	-
Term _{NZ}	0.66	0.48	-
Dual _{NZ}	0.52	0.86	0.68

The expected annual economic responses to selection between comparable traits in New Zealand and Ireland were of a similar direction for most traits, but in general greater economic responses were recorded in the New Zealand breeding objectives compared to the Irish breeding objectives. The differences in the economic response between countries can be attributed to the higher trait accuracies and genetic variance recorded for the New Zealand population. The greatest economic response in the Dual_{IRE} index was recorded for days to slaughter (€ 0.11) and ewe mature weight (€ 0.10). In New Zealand, the greatest response to selection on the Dual_{NZ} was calculated for carcass weight (€ 0.72). For the terminal indexes, the greatest economic response in the Term_{NZ} index was on lean yield (€ 0.48); in the Term_{IRE} the greatest economic response to selection was on days to slaughter (€ 0.25). The total economic response from selection on both dual indexes was € 1.16 and € 0.27 for the Dual_{NZ} and Dual_{IRE} indexes, respectively. For the terminal indexes greater economic responses were also recorded in the Term_{NZ} (€ 1.07) compared to the Term_{IRE} (€ 0.28).

Conclusions

Results of this study indicate that selection indexes in Ireland and New Zealand are moderate to strongly correlated. Moreover, trait responses to selection on the indexes are in a similar direction, but of different magnitudes. Future research should be conducted to determine the extent of $G \times E$ between the populations.

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Genomic breed prediction in Irish dairy and beef cattle

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Introduction

Genomic breed prediction may be of interest in commercial mating programmes, especially within crossbreeding schemes. Verifying the genomic distance between groups could be useful to maximise the production potential of offspring by exploiting the most diverse breed groups with good combining ability, while simultaneously benefiting from heterosis. The objective of this study was to determine the genomic distance between the major cattle breeds in Ireland.

Materials and Methods

Illumina high-density genotypes (777,962 SNPs) were available on 4,623 purebred bulls (430 Angus, 298 Belgian Blue, 893 Charolais, 174 Friesian, 327 Hereford, 1087 Holstein, 75 Jersey, 943 Limousin, 33 Montbéliarde, and 363 Simmental). Only purebred animals with a recorded breed fraction of $\geq 96.875\%$ based on pedigree were considered; the exception was the Holstein-Friesian when animal “breed” was based on the recorded major breed proportion. The pedigree of all animals was traced back to founder animals. Animals with a genotype call rate ≥ 0.95 were retained. Mendelian inconsistencies were used to validate animal identification through parentage assessment but also to discard autosomal SNPs that did not adhere to Mendelian inheritance. After edits a total of 624,179 SNPs remained for the 4,623 animals. PCA was carried out using the smartpca program from the EIGENSOFT package on all genotypes (Price *et al.*, 2006). The population structure of the breeds was investigated using Admixture 1.23 software (Alexander *et al.*, 2009). The genetic differentiation among populations was calculated using the F_{st} statistic and used to generate a polygenetic tree using the APE package in R software (Paradis *et al.*, 2004).

Results and Discussion

The first two principal components were successful in separating out breed clusters based on the genotypic data ($p < 0.001$) (Fig. 1). Holstein and Friesian clusters were in close proximity depicting the close relatedness between these dairy black and white breeds. This can be expected as the Holstein originated from the crossing of white animals within Friesian populations. The French breeds (Montbéliard, Limousin, and Charolais) were grouped closely, suggesting that the location of origin is central in determining relatedness (Gautier *et al.*, 2010). Similarly, Angus and Hereford clusters highlight the close ancestry from which both breeds originated (the British Isles), and appeared quite distinctive from the other breed groups. The genetic differentiation between breeds as measured by F_{st} was lesser for breed pairs closely clustered on the PCA plot. For example, breeds closely related (e.g., Holstein-Friesian and Belgian Blue) had a low F_{st} value ($F_{st} = 0.067$) whereas the genetic differentiation was high between the Jersey and

Hereford ($F_{st} = 0.165$). The between population F_{st} values ranged between 0.049 (Limousin and Charolais) and 0.165 (Jersey and Hereford). The Jersey was the most divergent breed (F_{st} between 0.12 and 0.17) and had the longest branch (Fig 2). For the purposes of dairy crossbreeding, the Jersey and Montbéliard would be considered genetically diverse from the Holstein and Friesian breeds and their crosses, which are themselves, quite similar. Therefore, knowing the genomic distance between breeds may facilitate the exploitation of greater heterosis leading to increased performance.

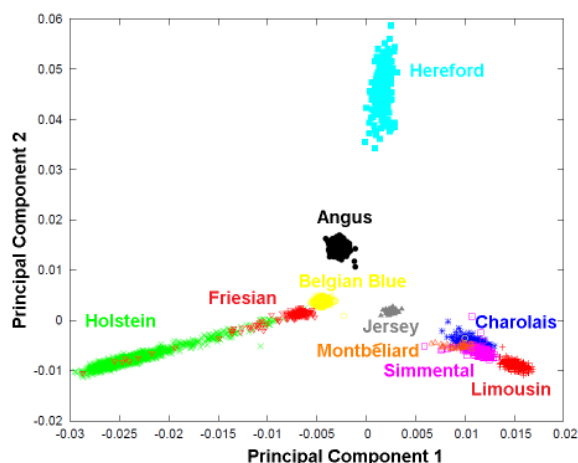


Fig. 1. Principal component analysis of the purebred bulls distributed across the first two principal components.

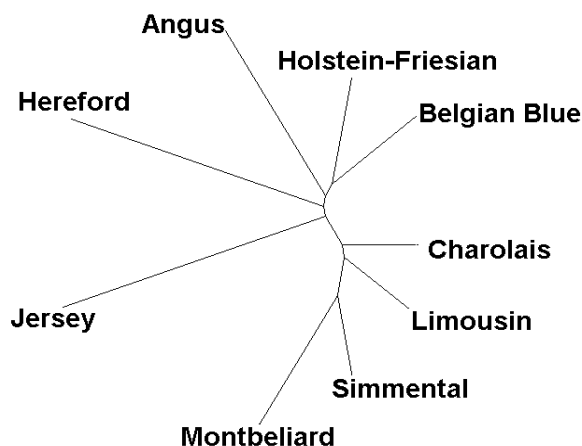


Fig. 2. Polygenetic tree between breeds as estimated by the correlations between F_{st} values for Irish cattle.

Conclusions

Identification of the genomic relationships between cattle breeds can provide information relating to expected heterosis from a resulting crossbreeding strategy.

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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.

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

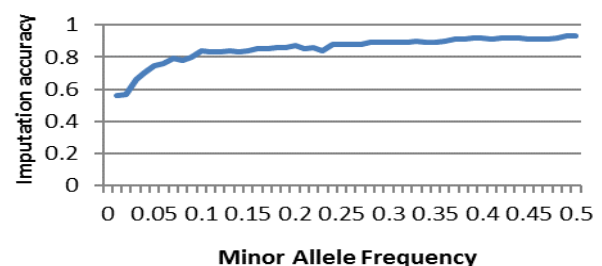


Fig 1. Imputation accuracy vs minor allele frequency

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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High accuracy of imputation from the Irish custom bovine genotype panel to higher density genotypes

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Introduction

Genomic selection exploits medium to high density genotypes (Berry *et al.*, 2009). The cost of acquiring high density genotypes hinders widespread uptake of genomic selection in commercial cattle populations. A lower density, lower cost, custom bovine single nucleotide polymorphism (SNP) genotype panel (International Dairy & Beef panel; IDB panel) was developed for Ireland in 2012 (Berry *et al.*, 2013); a large proportion of these SNPs were chosen to maximise the accuracy of imputation to higher density in both dairy and beef cattle. The objective of the present study was to quantify the accuracy of imputation from the IDB lower density panel to medium and high density genotype panels.

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 33,648 individuals. In total, 14,840 autosomal SNPs were common to both panels. All individuals had a genotype call rate of $\geq 90\%$ and parentage was verified for all animals using the genomic information. Four higher density genotype panels were generated from the complete Illumina high density panel; all panels included the 14,840 SNPs common to both the IDB panel and the Illumina high density panel. The panels investigated were: 1) representative of the Illumina Bovine50 Beadchip which in the present study was based on autosomal SNPs common to the Illumina high density genotype panel and the Bovine50 Beadchip (50K; 51,487 SNPs), 2) all autosomal SNPs on the Illumina high density genotype panel (HD_{FULL}; 735,239 SNPs), 3) only SNPs segregating on the Illumina high density panel in the population under investigation (HD_{SEG}; 691,978 SNPs), and 4) only SNPs on the Illumina high density panel that passed the following quality controls (HD_{QC}; 613,089 SNPs); SNP call rate ($>95\%$), mendelian inheritance consistencies between parent-offspring pairs, and SNP clustering quality. Every one-hundredth SNP on the IDB panel was masked. This was iterated ten times with the masked SNP staggered by ten SNPs for each iteration. Family-based and population-wide imputation was undertaken using FImpute for the entire genome simultaneously. Accuracy of imputation was based on 1) the correlation between the imputed genotype of the masked SNPs and the actual genotype, and 2) allele concordance rate.

Results and Discussion

Imputation on a 64-bit Intel dual quad core processor with 288 Gb RAM took 8.84 hours, 36.95 hours, 35.05 hours, and 35.08 hours for imputation to the 50K, HD_{FULL}, HD_{SEG}, HD_{QC}, respectively. There was therefore little time saving in the imputation process itself from the elimination of monomorphic or SNPs of poor quality in the imputation process. Across the entire dataset (i.e., >40 million genotypes), the correlation between imputed and actual genotypes across all iterations was 0.9493, 0.9466, 0.9467 and 0.9491, for the 50K, HD_{FULL}, HD_{SEG} and HD_{QC}, respectively; the respective allele concordance rate was 0.9737, 0.9725, 0.9725 and 0.9737. Therefore, high accuracy of imputation was achievable from the IDB genotype panel to the higher density panel and little difference existed between the panels in accuracy. Allele concordance rate per individual was on average 0.9732 for imputation to the 50K and varied from 0.5384 to 1.000. Imputation accuracy per individual varied by the extent of the ancestry of the individual included in the reference population for the generation of the haplotype phases (Fig. 1). The accuracy of imputation was lower for animals whose major breed component was not represented in the higher density genotype panels; such breeds included Piedmontese, Saler, Parthenaise, Aubrac, and Blonde d'Aquitaine.

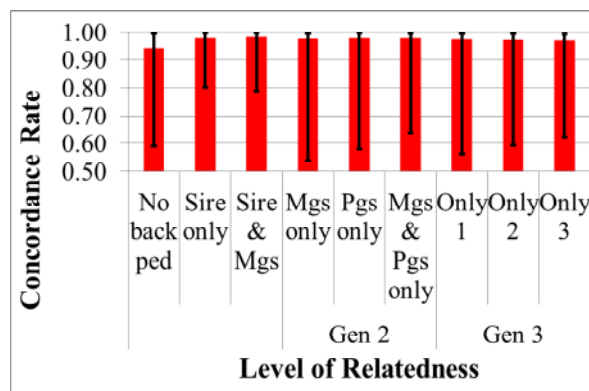


Fig. 1. Mean and range (represented by error bars) in the allele concordance rate from IDB to 50K genotype density with different levels of pedigree genotyped on the 50K genotype panel.

Conclusions

The accuracy of SNP imputation from the IDB genotype panel to higher density was high and sufficiently accurate for use in whole-genome enabled predictions of genetic merit. Higher density genotypes on minority breeds should be procured to increase the poorer accuracy of imputation in these breeds.

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Association between polymorphisms in the *Stearoyl coA Desaturase* and *Retinoic Acid Orphan Receptor C* genes and milk and carcass quality traits in Holstein-Friesian cows

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Introduction

Interest in beef production from the dairy herd has increased in recent years. For meat quality traits such as intramuscular fat, inclusion of genetic markers on industry-relevant single nucleotide polymorphism (SNP) platforms offers opportunities to genetically select for improved eating quality. SNP with important roles in fat metabolism may however also have pleiotropic effects on parameters related to milk and carcass fat quality and quantity. SNP in *Stearoyl coA Desaturase* (SCD1) and *Retinoic Orphan Receptor C* (RORC) genes have been previously associated with fat content and composition in beef (Barendse *et al.*, 2010; Taniguchi *et al.*, 2004) and in milk for SCD1 (Conte *et al.*, 2010). The aim of this study was to examine these SNP for their association with milk composition and carcass traits in Irish Holstein-Friesian cows.

Materials and Methods

SNP in the RORC (g.3290T > G) and SCD1 (g.878T > C) genes were added to the research component of the custom SNP chip for cattle breeding called the International Dairy and Beef chip (IDB; (Mullen *et al.*, 2013)). Genotypes and phenotypes were obtained from the Irish Cattle and Breeding Federation (ICBF). A total of 3310 Holstein-Friesian cows with SNP call rates \geq 90% were available for analysis. In this study, a subset of nine phenotypic traits related to milk and carcass composition were analysed (Table 1). Phenotypes (expressed as parental transmitted averages) were deregressed and parental contributions removed following Garrick, Taylor & Fernando (2009). The association between the SNP and performance were individually quantified using mixed models (EMMAX, (Kang *et al.*, 2010)) accounting for relationships between animals using a genomic relationship matrix. P values were adjusted using a Bonferroni correction.

Results

Call rates in SNP genotyping were greater than 99% for both SNP. Minor allele frequencies were 0.33 for the SCD1 SNP and 0.28 for the RORC SNP. The RORC SNP departed from conditions of Hardy-Weinberg equilibrium ($P < 0.05$). Associations with milk fat % and milk fat yield (kg) were observed for the SCD1 SNP (adj $P < 0.01$) and a nominal association with carcass weight (kg) was observed for the RORC SNP ($P < 0.05$, Table 1).

Table 1. Association analysis (nominal P-values) between SNP in the SCD and RORC genes and milk and carcass composition traits in 3,310 dairy cows

Trait	SCD1	RORC
	<i>P</i> -value	<i>P</i> -value
Milk yield	0.41	0.34
Milk protein %	0.29	0.50
Milk protein yield	0.65	0.85
Milk fat %	0.00001	0.62
Milk fat yield	0.0008	0.35
Carcass weight (CWT)	0.23	0.04
Carcass conformation	0.42	0.42
Carcass fat	0.19	0.43
Body condition score	0.81	0.09

The SCD1 SNP explained approximately 0.5% of the phenotypic variance within the population for milk fat %. A smaller effect for carcass weight was observed for the RORC SNP (Table 2).

Table 2. Allelic substitution effect

	SCD1 (C)	SCD1 (C)	RORC (G)
	Fat (%)	Fat (kg)	CWT (kg)
Effect (s.e.)	0.032(0.007)	1.51(0.45)	-6.91(3.46)
%	0.58	0.35	0.18

#: percentage phenotypic variance explained

The SCD1 allele (C) previously associated with higher intramuscular fat (Reardon *et al.*, 2010) was also associated with higher milk fat content. Selection for improved meat quality in terms of intramuscular fat content based on the minor allele frequencies at this SNP could also enhance milk quality lending a multifactorial benefit to selection based on SCD1.

Conclusions

A significant effect on milk fat content was observed for SCD1. No effect of RORC on milk quality was observed but a nominal association with carcass weight was present. Further work could focus on associations of SCD1 with milk fatty acid profiles.

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Association analysis of SNPs in Calpain and Calpastatin genes with production traits in Holstein-Friesian cows

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Introduction

Beef tenderness is widely considered to be the most important beef quality trait. It is not possible to assess tenderness pre-mortem so inclusion of genetic polymorphisms associated with tenderness on SNP platforms is a potentially useful approach to permit breeders to begin to incorporate tenderness into selection programmes. While several SNP in the calpain (*CAPN1*) and calpastatin (*CAST*) genes have been associated with tenderness in numerous populations, little research has been done on assessing their pleiotropic effects on production traits. The aim of this study was therefore to examine SNP in Calpain and Calpastatin genes previously associated with beef tenderness for their association with production traits in Holstein-Friesian cows.

Materials and Methods

Three SNP in each of the calpain (*CAPN1_316*, *CAPN1_530*, *CAPN1_4751*) and Calpastatin (*CAST_282*, *CAST_2959*, *CAST_2870*) genes (Ribeca *et al.*, 2013) were added to the research component of the custom SNP chip for cattle breeding called the International Dairy and Beef chip (IDB; (Mullen *et al.*, 2013)). In addition, all six mutations have been validated on the IDB using known carrier DNA. Genotypes and phenotypes were obtained from the Irish Cattle and Breeding Federation (ICBF). A total of 3310 Holstein-Friesian cows with call rates $\geq 90\%$ were available for analysis. In this study, 20 phenotypic traits were analysed. Phenotypes (expressed as PTA's) were deregressed and parental contributions removed following (Garrick *et al.*, 2009). The association between the SNP and performance were individually quantified using mixed models (EMMAX, (Kang *et al.*, 2010)) accounting for relationships between animals using a genomic relationship matrix.

Results and Discussion

Call rates in SNP genotyping were greater than 99% for all SNP except *CAST_282* ($>91\%$). Allele frequencies at *CAST_282* and *CAST_2870* loci only, departed from conditions of Hardy-Weinberg equilibrium. No significant associations with any production trait were observed for *CAPN_316*, or the *CAST* SNPs. A nominally significant effect on protein percentage in milk was observed for two Calpain SNP (4751 and 530, Table 1). Calpain 1 is responsible for protein turnover *in vivo* (Cruzen *et al.*, 2013) which could provide a putative biological rationale for this effect.

Table 1. Significant associations (effect sizes and nominal *P* values) between SNP in the *CAPN1* gene and milk traits in 3310 dairy cows.

SNP (Allele)	Trait	Effect (s.e)	%	<i>P</i>
<i>CAPN1_4751</i> (T)	Protein (%)	0.06 (0.03)	0.10	0.04
<i>CAPN1_530</i> (G)	Protein (%)	0.07 (0.03)	0.10	0.03

P: P-value; %: % phenotypic variance

The *CAPN1* SNPs explained approximately 0.1% of the phenotypic variance within the population for milk protein %. The *CAPN1_4751* allele (T) previously associated with tougher beef (White *et al.*, 2005) was associated with higher milk protein content.

Conclusions

No significant impact on the 20 production traits examined were observed for *CAPN1_316*, or *CAST* polymorphisms. A small nominally significant, effect on protein percentage in milk was observed for two calpain SNP. While on the whole this analysis suggests selection for calpain and calpastatin SNPs (associated with improved meat quality in terms of tenderness) in dairy cattle would not result in any deleterious large effects on other production traits there was some evidence for a small negative effect in milk solid content. Further analysis using larger sample sizes would be required to validate these findings.

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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.

Acknowledgments

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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)

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 examination 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 2 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.

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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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)

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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The Irish Soil Information System

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Introduction

The Irish Soil Information System project was established in 2008, following a comprehensive inventory of Irish soil data compiled by Daly and Fealy (2007) which highlighted that soil data coverage of Ireland was incomplete in both detail and extent. The project was funded under the Environmental Protection Agency STRIVE Research Programme 2007-2013 and co-funded by Teagasc. It was led by Teagasc with the participation of researchers from Cranfield University (UK) and University College Dublin. The overall objective of the Irish Soil Information System project was to conduct a programme of structured research into the national distribution of soil types and construct a soil map, at 1:250,000 scale, which would identify and describe the soils according to a harmonised national legend.

Development of the Irish Soil Information System

The Irish Soil Information System project has utilised existing data and maps from the previous National Soil Survey (NSS) conducted by An Foras Talúntais (forerunner organisation to Teagasc). The NSS produced: mapping at 1:126,720 scale for 44% of the country; a General Soil Map of Ireland and a National Peatland map, both at 1:575,000 scale and other miscellaneous large scale mapping of experimental farms. In addition, more recent map products have been included such as the Indicative Soil and Subsoil mapping (Fealy et al., 2009) with national coverage using GIS and remote sensing techniques. Comparison of soil information at European scale has led to the requirement for the harmonisation and coordination of soil data across Europe and, in light of the demands for soil protection on a regional basis within member states, there is a growing need to support policy with a harmonised soil information system. The European Soil Bureau Network (ESBN) Technical Working Group dealing with Soil Monitoring and Harmonisation recommended a soil map of Europe at a scale of 1:250,000 as an economically feasible intermediate scale that can identify specific problems at regional scale (Montanarella and Jones, 1999).

The project adopted a combined methodology of utilising novel predicted mapping techniques in tandem with traditional soil survey applications at a national scale. Building upon the detailed work carried out by the An Foras Talúntais (AFT) survey (known as *Terra Cognita*), the Irish Soil Information System project generated soil-landscape models at a generalised scale of 1:250,000 for the counties of Carlow, Clare, Kildare, Laois, Leitrim, Limerick, Meath, Offaly, Tipperary South, Waterford, Westmeath, Wexford, West Cork, West Mayo and West Donegal. These soil-landscape models (also referred to as soilscape) were used as the baseline data for statistical models (random forests, Bayesian belief networks and neural networks) to

predict soil map units in counties where there was no map available (referred to as *Terra Incognita*). To validate the methodology, this work was supported by a 2.5 year field survey, in which 11,000 locations were evaluated for soil type, using an auger bore survey approach (Simo et al., 2014). These data were used to check the predicted soil mapping units (associations) for counties: Cavan, Dublin, East Cork, East Donegal, East Mayo, Galway, Kerry, Kilkenny, Louth, Monaghan, Roscommon, Sligo, Tipperary South and Wicklow, where a detailed soil survey map was not available. Where new soil information was generated, due to previously unknown combinations of soil-landscape units, profile pits were selected at representative locations across the country. These 225 pits were described and sampled in detail and were used to generate a new soil classification system for the country (Fig. 2).

The final product is a unique combination of new and traditional methodologies and soils data from both the AFT and the Irish Soil Information System project. The final, soil association map of Ireland (Fig. 1) consists of 58 associations (excluding areas of alluvium, peat, urban, rock or marsh) that are made up from 213 soil series. Associated representative profile information is available in the online soil information system. Details of the project can be found at (<http://gis.teagasc.ie/soils>). Creamer *et al.* (2014) provides a full summary of this project and there are 17 technical reports available for download from <http://erc.epa.ie/safer/>

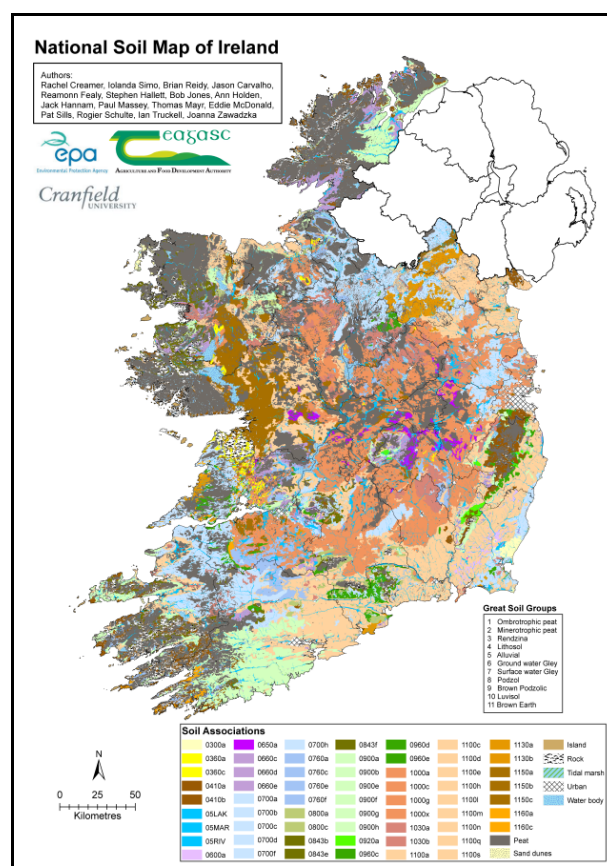


Fig. 1. Irish Soil Map (3rd Edition)

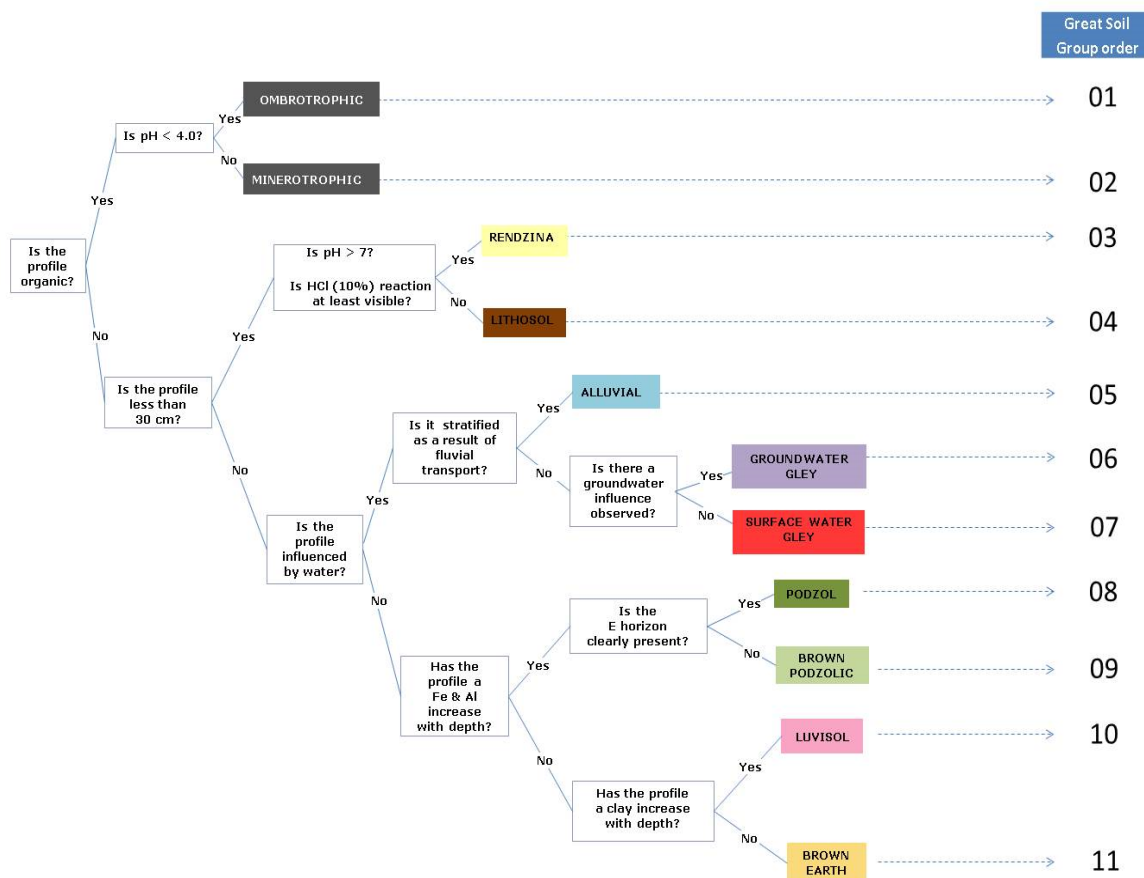


Fig. 2. Irish Soil Classification System – Identification of Great Soil Groups, 2014.

Conclusion

A key component of this project has been the development of a soil and land information system and associated public web site. This system was designed to hold the complete set of information deriving both from the field programme and modelling activity, as well as the previously existing legacy soils information available for Ireland. Drawing on this information system, the web site is designed to hold and disseminate this information online both in cartographic and tabular form to stakeholders. Prior to this development, there was no harmonised computerised system in place to hold and manipulate national Irish soils data. The information system therefore addresses the pressing need and requirement for a publicly-accessible, integrated IT framework based upon contemporary informatics standards to serve the many and varied stakeholders having an interest in soils information in Ireland.

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