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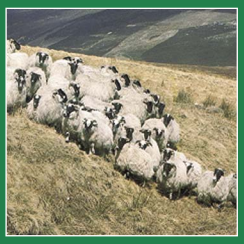


Advances in Animal Biosciences

Science with Impact

Proceedings of the British Society of Animal Science
in association with AVTRW, CFER and EBLEX

advances in animal biosciences

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Advances in Animal Biosciences

Aims and Scope

Advances in Animal Biosciences is an associated publication to the journal *animal*. It aims to publish high-quality conference, symposium and workshop proceedings about animal-related aspects of the life sciences with emphasis on farmed and other managed animals. These can be in the form of a book of abstracts, summaries or complete papers. The format will highlight the title of the meeting and organisations involved but the publications will have the added advantage of forming a series under *Advances in Animal Biosciences*.

Subject areas can include aspects of Breeding and Genetics, Nutrition, Physiology and Functional Biology of Systems, Behaviour, Health and Welfare, Livestock Farming Systems, Human Health and Product Quality.

However, due to the integrative nature of biological systems, monographs and conference proceedings dealing with the translation of basic and strategic science into the whole animal and farming system and the impact on Productivity, Product Quality, Food Security, the Environment, Climate Change and Humans will be particularly welcome.

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The Animal Consortium together with Cambridge University Press offers conference organisers a package that enables publication of high-quality conference, symposium and workshop proceedings about animal-related aspects of the life sciences with emphasis on farmed and other managed animals.

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Proceedings

of the British Society of Animal Science
in association with AVTRW, CFER and EBLEX

2015

Advances in Animal Biosciences

This book is part of a series which is a companion to the journal ANIMAL

The Proceedings of the British Society of Animal Science constitute summaries of papers presented at the Society's Annual Conference, *Science with Impact* held in Chester, UK, 14-15 April 2015.

The meeting was organised in association with the AVTRW, CFER and EBLEX.

The summaries have been edited. Views expressed in all contributions are those of the authors and not those of the BSAS.

This publication contains all the summaries that were available at the time of going to press.

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Producing the UK's first carcase trait Estimated Breeding Values (EBVs) using national abattoir data

K Moore, F Pearston, T Pritchard, E Wall, M Coffey
SRUC, Scotland's Rural College, Edinburgh, UK
Email:kirsty.moore@sruc.ac.uk

Implications Carcase trait EBVs produced from national abattoir data, for traits of direct economic importance to commercial breeders, will enable the beef industry to increase the rates of genetic improvement for carcase traits. Furthermore it will help to link the different sectors of the beef industry as they will all be using the same trait definitions from breeder to finisher to abattoir.

Introduction Farmers are paid for carcases using the EUROP system; however, pedigree animals are selected based on ultrasound muscle and fat depth. This reduces genetic progress as the traits are different reducing the efficiency of selection. In addition, the lack of clear signals between pedigree and commercial farmers often make it difficult for farmers to select the most appropriate sires. The aim of this study was to produce EBVs for the abattoir carcase traits providing tools to enable the industry to make genetic improvement for carcase traits of importance.

Material and methods Using the software MiX99, EBVs were produced for carcase weight and visually assessed EUROP fat and conformation class (converted to a numeric scale where higher values for both traits indicate more muscular and fatter carcases) using statistical models and genetic parameters previously developed (unpublished results; Pritchard *et al*, 2013). The animal models were adjusted for age and genetic parameters were moderately heritable with moderate positive genetic correlations between weight and conformation and moderate negative genetic correlations between fat and the other traits. Nearly 4 million abattoir records were available and matched to the BCMS database to obtain further information about the fixed effects and movement information. These data were reduced to just over half a million records from nearly 40,000 sires from 31 different breeds after data edits. The data edits applied removed records of non-prime slaughter animals (this accounted for the greatest loss of records), were incomplete (i.e. recent records not yet included in the BCMS data snapshot) or in error. A three generation pedigree was built and EBVs produced for approximately 1.4 million animals.

Results The first ever UK EBVs for abattoir carcase traits are shown in Table 1. As these EBVs have not been re-based the average EBVs are near 0, with some differences due to differences in breed. Within different breed subsets, the EBVs were shown to be normally distributed (results not shown) with a trend for those animals with the higher EBVs also being those with higher phenotypic values for the traits of interest. Figure 1 shows the average EBVs for high accuracy sires for individual breeds within breed types. It can be seen that for carcase weight, the continental breeds had the higher EBVs and the dairy breeds the lowest.

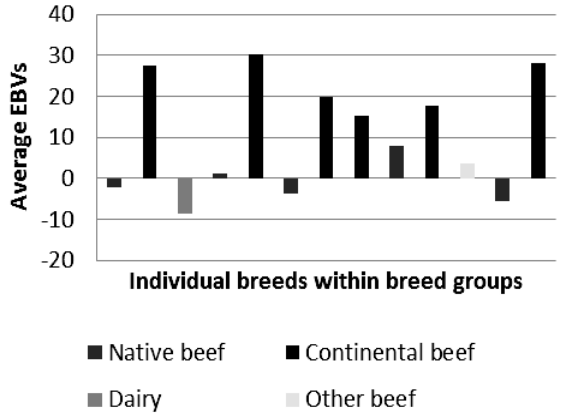

Figure 1 Average carcase weight EBVs of high accuracy sires within breed and breed type

Table 1 Summary of across-breed EBVs (reliability in brackets) for abattoir carcase traits (n=1,423,070)

Trait	Average	Std	Range
Dead weight (kg)	0.96 (0.26)	13.9	-56.6 to 76.8
Conformation (score1)	0.02 (0.18)	4.4	-9.7 to 11.9
Fat (score[1])	0.08 (0.25)	1.63	-10.9 to 10.1

[1] numerical score from 3 to 45 where higher values indicate carcases with more muscle and/or more fat

Conclusion These EBVs are the first of their kind in the UK and can be used to assist both pedigree and commercial farmers to produce animals that better meet market specification contributing to a more profitable and efficient beef industry.

Acknowledgements We would like to acknowledge the abattoirs (ABP, Stoddarts, Dovecote Park, MacIntosh, Morrisons and Dunbia), the Rural payments Agency's British Cattle Movement Service (BCMS), and EGENES for supplying the data. Funding was received from AHDB (EBLEX and DairyCo divisions) and Hybu Cig Cymru (HCC).

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Estimation of genetic parameters for Video Image Analysis (VIA) carcass traits

J Nani, M Coffey, K Moore
SRUC, Scotland's Rural College, Edinburgh, UK
Email:kirsty.moore@sruc.ac.uk

Implications VIA provides an objective way to measure carcass traits. Genetic evaluation of VIA carcass traits will bring better opportunities for genetic selection, providing many benefits for the beef industry including processors and retailers, breeders and farmers.

Introduction The UK pedigree beef cattle sector's breeding program for carcass traits is based on Estimated Breeding Values (EBV) for live weight and ultrasound scans (proxies for conformation and fat) from a limited number of performance recorded live animals (Moore *et al*, 2014). The carcass trait genetic evaluations can be improved by utilising imaging technologies such as Video Image Analysis (VIA) to routinely collect data on the slaughter population. VIA machines can be placed into the abattoir's processing chain, allowing for carcass traits to be routinely collected with a relatively high throughput, and the information provided can be used as phenotypes for the genetic evaluations (Pabiou *et al*, 2011). The aim of this study was to estimate genetic parameters of routinely collected VIA data to facilitate its use in genetic evaluations.

Material and methods 111,394 records were collected from two abattoirs for animals slaughtered between 2012 and 2014. These records included all animals slaughtered during this time, including older cull cows. After edits, 17,765 records were kept from one abattoir as the second abattoir had only recently installed the machinery. The carcass traits considered were: carcass weight, conformation and fat (converted to a numeric scale (3-45) with higher values indicating carcasses of high conformation and/or fat), and seven VIA primal cut yields: Topside, Silverside, Knuckle, Rump, Striploin, Fillet and Flank. All animals were progeny of purebred sires. The most common breeds represented were Charolais (24.9%), Limousin (18.3%), Simmental (18.7%), Aberdeen Angus (17.7%), and Holstein Friesian (10.7%). Genetic parameters were estimated using restricted maximum likelihood (REML) as implemented in ASReml (Gilmour *et al*. 2006) using an animal model that included an adjustment for age, sex and birth-herd-season. Also heterosis and recombination effects were included in the model.

Table 1 Heritability (h^2) and phenotypic variance (σ^2_p) estimates for carcass traits

trait	h^2	σ^2_p
Conformation	0.44 (0.03)	12.94 (0.17)
Fat	0.31 (0.03)	19.66 (0.25)
Carcass Weight (Kg)	0.43 (0.03)	849.56 (11.20)
Striploin (Kg)	0.41 (0.03)	0.57 (0.01)
Fillet (Kg)	0.42 (0.03)	0.11 (0.00)
Pc Striploin (%)	0.28 (0.03)	0.01 (0.00)
Pc Fillet (%)	0.22 (0.03)	0.00 (0.00)
Retail yield (%)	0.23 (0.03)	0.16 (0.00)

Results Heritability and phenotypic variance estimates for each trait are presented in Table 1. Moderate to strong heritabilities were estimated for Conformation, Carcass Weight, Striploin and Fillet ranging from 0.41 to 0.44. High phenotypic variance estimate was obtained for Carcass Weight due to a wide range of beef and dairy breeds present in this population. A moderate heritability was estimated for Fat (0.31). While still heritable, when the traits were expressed as a percentage of net weight (and thus now also adjusted for carcass weight) the heritabilities were lower: 0.28 for Pc Striploin, 0.22 for Pc Fillet and 0.23 for Retail yield (the sum of 7 VIA yields expressed as percentage of carcass weight). Not only was the heritability lower, but the phenotypic variation for the traits expressed as percentages were also lower.

Conclusion The results of this study showed that there was moderate to large heritability and genetic variability for the VIA carcass traits for this British commercial population. Therefore, using VIA carcass traits, breeding values can be estimated using real carcass data rather than proxy measurements. This evidence suggests that VIA carcass traits are suitable for genetic evaluation allowing for increased genetic gain for carcass traits more closely related to value received by farmers.

Acknowledgements The authors acknowledge their project partners ABP and BLCS, Rural payments Agency's British Cattle Movement Service (BCMS) for supplying data. Funding was received from Innovate UK and BBSRC.

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Genetic parameters for conformation traits in dairy goats

S Mucha, A McLaren, R Mrode, M Coffey, J Conington
SRUC, Scotland's Rural College, Edinburgh, UK
Email:sebastian.mucha@sruc.ac.uk

Implications These estimates of genetic parameters are a first step before their inclusion into comprehensive selection indices for dairy goats. Genetic antagonisms exist between a number of conformation traits and milk yield, indicating that it is essential for conformation scoring to be included in future dairy goat breeding programmes.

Introduction Improving the functional fitness of dairy goats, such as animal mobility and structural correctness, is important for the improvement of animal health if genetic selection for increased productivity is actively pursued. The aim of this work is to quantify genetic and phenotypic properties of udder, teat, legs and feet scores with milk yield in UK dairy goats.

Material and methods The data set comprised 2,429 conformation records (udder, legs, and feet) and 126,262 milk yield records on 2,429 first lactation mixed breed and age dairy goats, scored in 2013. The pedigree file contained 30,139 individuals. In total 10 conformation traits were scored on a linear scale (1-9) by one scorer. The scoring system was similar to that developed by the French dairy goat breeders' association CAPGENES and used by Manfredi *et al*. (2001) and Rupp *et al*. (2011). Covariance components were estimated with the AI-REML algorithm in the DMU package (Madsen and Jensen 2008) with a random regression model for milk yield (Mucha *et al*. 2014) and the following model for the conformation traits:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}$$

where: **y** - vector of observations for the analysed conformation score; **b** - vector of fixed effects: farm, lactation stage, and birth year; **a** - vector of random additive animal effects; **e** - vector of random residuals. **X** and **Z** - incidence matrices.

Results Heritability estimates for the conformation traits, ranged from 0.02 to 0.45. The genetic and phenotypic correlations estimated between all conformation traits along with trait explanation are shown in Table 1. The highest genetic correlation was between UF and TS (0.96) and the lowest between FF and BF (0.004). The standard errors associated with the genetic correlations were relatively high, being between 0.02 and 0.79. The phenotypic correlations ranged from 0 to 0.39. Genetic correlations estimated between milk yield and udder and teat conformation traits were negative, ranging from -0.60 to -0.20, and from -0.50 to -0.20, respectively. Genetic correlations with feet and leg conformation were between -0.30 and 0.30.

Table 1 Heritabilities (diagonal), genetic and phenotypic correlations (lower and upper diagonal) of conformation traits

Trait	UF	UD	UA	TS	TA	TP	FL	BL	FF	BF
Udder Furrow (UF)	**0.11**	0.27	0.10	0.24	-0.16	-0.30	0.00	0.03	-0.04	0.01
Udder Depth (UD	0.74	**0.45**	0.37	0.16	0.20	0.16	-0.01	0.12	0.00	0.01
Udder Attachment (UA)	0.66	0.60	**0.27**	-0.002	0.14	0.19	0.03	0.06	0.05	-0.05
Teat Shape (TS)	0.96	0.15	0.21	**0.10**	-0.11	-0.08	0.00	0.03	-0.03	0.02
Teat Angle (TA)	-0.33	0.25	0.12	-0.33	**0.24**	0.38	-0.02	0.13	0.03	0.02
Teat Placement (TP)	-0.31	0.09	0.07	-0.20	0.60	**0.36**	-0.01	0.05	0.04	-0.03
Front Legs (FL)	-0.09	0.42	0.58	0.39	0.19	0.62	**0.02**	0.07	0.39	0.01
Back Legs (BL)	0.57	0.39	0.42	0.43	0.48	0.15	-0.06	**0.11**	0.09	0.35
Front Feet Set (FF)	-0.13	0.11	0.36	-0.04	0.19	0.06	0.61	0.28	**0.08**	0.20
Back Feet Set (BF)	-0.08	-0.30	0.12	-0.23	0.67	0.07	0.27	0.11	0.00	**0.05**

Conclusion Udder and teat conformation traits were low to moderately heritable with those associated with feet and legs less heritable. The genetic correlations between the conformation traits and milk yield indicate that breeding programmes for dairy goats should include conformation scores, so that selection for productivity is not accompanied by deterioration in functional fitness.

Acknowledgements The authors gratefully acknowledge the Technology Strategy Board for funding this research and the cooperation of the participating farms. We acknowledge contribution of Marta Rus who performed conformation scoring.

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Genetic parameters of serum Ca, P, Mg and K concentration in Holstein dairy cows

V Tsiamadis[1], A Kougioumtzis[1], N Panousis[1], M Kritsepi-Konstantinou[1], G Banos[1,2], G E Valergakis[1]
[1]Faculty of Veterinary Medicine, Aristotle University, Thessaloniki, Greece, [2]Scotland's Rural College/Roslin Institute, Edinburgh, Scotland, UK
Email:etsiamad@vet.auth.gr

Implications The results can contribute towards defining a breeding strategy for enhancing (sub)clinical hypocalcaemia resistance in dairy cows.

Introduction Hypocalcaemia is the most important macromineral disorder that affects transition dairy cows and is related to many early-lactation health disorders (Goff, 2008). Prevention has been attempted mainly with acidifiers for transition rations and calcium drenches after calving. So far, genetic studies have focused on the genetic parameters of clinical hypocalcaemia. Our objective was to estimate genetic parameters of Ca and other related macromineral (P, Mg, K) serum concentration in Holstein dairy cows and to investigate the correlation between serum Ca concentrations/changes and disease incidence after parturition.

Materials and methods The study included 1,021 Holstein dairy cows (1–4+ lactations) in 9 herds in Northern Greece. Clinical examination and blood sampling was carried out at 1st, 2nd, 4th and 8th DIM. Milk fever (MF), mastitis, metritis, retained foetal membranes (RFM) and displaced abomasum (LDA, RDA) were recorded during the same time. Ca and Mg serum concentration was determined with atomic absorption spectrophotometry (AAS Perkin Elmer A 100), while for P and K with a biochemical (Vitalab Flexor E) and electrolyte analyser (Roche 9180). Total number of repeated records summed to 4,060. Subclinical hypocalcaemia/hypophosphatemia was defined as Ca/P serum concentrations below 8.3 and 4.2 mg/dL, respectively. Each trait (Ca, P, Mg, K serum concentration and respective changes from DIM 1 to 8, and postpartum health disorders) was analysed with a univariate random regression model, including the fixed effects of herd, year-season of calving, parity, age at calving and DIM, and the random regressions on DIM from calving associated with the animal additive genetic effect. All pedigree available was included in the analysis bringing the total number of animals to 4,262. Estimates of (co)variance components from this model were used to calculate heritabilities for each trait. Correlations between Ca, P, Mg and K serum concentration/changes and health disorders were estimated with bivariate analysis using the same model. The ASREML software was used for all statistical analyses (Gilmour *et al*., 2006).

Table 1 Significant (P<0.05) phenotypic correlations between serum Ca, P, Mg and K concentration/changes and health traits; Ns=non-significant

	MF	Mastitis	Metritis	RFM	LDA
Ca	-0.32	Ns	-0.18	-0.14	-0.15
P	Ns	0.12	Ns	Ns	Ns
Mg	Ns	Ns	-0.15	-0.10	-0.07
K	-0.11	Ns	-0.13	-0.14	Ns
Change Ca 1-8	Ns	Ns	-0.07	-0.10	Ns
Change Ca 1-4	0.07	Ns	-0.09	-0.08	Ns
Change P 1-8	Ns	Ns	Ns	0.07	Ns
Change P 1-4	0.06	Ns	Ns	Ns	Ns
Change Mg 1-8	Ns	Ns	-0.07	-0.06	-0.11

Results Mean serum Ca, P, Mg and K concentration (±s.e.m.) was 8.92±0.018 mg/dL, 5.21±0.020 mg/dL, 2.24±0.006 mg/dL, and 4.58±0.009 mmol/L, respectively. Daily heritability estimates for serum concentration ranged from 0.23 to 0.32 (Ca), 0.30 to 0.43 (P), 0.20 to 0.39 (Mg) and 0.15 to 0.23 (K) and were all statistically significant (P<0.05). Daily heritability estimates for subclinical hypocalcaemia and hypophosphatemia were 0.13 – 0.25 and 0.18 – 0.33, respectively. Regarding concentration changes, only Mg change between DIM 1 and 8 had a significant (P<0.05) heritability of 0.18. Postpartum health disorders that had significant daily heritabilities (P<0.05) were mastitis (0.15 – 0.41), LDA (0.19 – 0.31) and MF (0.07 – 0.11). No significant genetic correlations between serum Ca, P, Mg and K concentration or changes and health traits were found; significant (P<0.05) phenotypic correlations between serum Ca, P, Mg and K concentrations/changes and health traits are shown in Table 1.

Conclusion Serum concentrations of Ca, P, Mg and K, at the first critical days after parturition, are heritable. Selection against (sub) clinical hypocalcaemia may be achieved using these biochemical traits. All but three phenotypic correlations are minor (except Ca/MF) and negative (desirable), however, between P serum concentration and mastitis and Change Ca 1-4/P 1-4 and MF -although small- are positive (undesirable). Preventive measures (management/nutrition) establishing normal serum macromineral concentrations must apply during the close up period in order to avoid major health problems.

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Genetic parameters for enteric methane from dairy cows measured using Laser Methane Detector

S Smith[1], M Coffey[1], M Chagunda[2], S Ross[3], S Denholm[1], E Wall[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]SRUC, Scotland's Rural College, Dumfries, UK, [3]Singapore University of Technology and Design, Singapore
Email:stephanie.smith@sruc.ac.uk

Implications Calculating the genetic parameters and heritability of methane production in dairy cows will help determine the potential to select for less methane production as part of broader breeding goals.

Introduction Ruminants release enteric methane primarily via eructation as a by-product of digestion and may account for up to 6% of gross energy intake (de Haas *et al*., 2011). Such inefficiency in feed utilisation and the role of methane as a greenhouse gas means there is a focus on mitigation of methane emission from ruminants. Understanding the genetics of methane production is hindered by the difficulty of collecting data on sufficient numbers of animals. Results from the Laser Methane Detector (LMD) have shown strong correlation with results from the respiratory chambers (r = 0.80; Chagunda and Yan, 2011) whilst allowing methane production to be recorded without disturbing cow activity. Improving the amount of data on methane emissions from dairy cattle could allow selection for lower emitters and more efficient feeders via genetic improvement (Wall *et al*., 2010). This study examines the feasibility of using data on individual animal methane production sampled using a LMD to estimate genetic parameters for the methane emissions (ppm-m).

Material and methods The Holstein-Friesians cows in this study were from the Langhill selection experiment housed at SRUC Dairy Research & Innovation Centre, subject to a long term experiment of 2 diets X selection lines. The LMD was used to take 2 recordings every second for approx. 5 minutes after midday milking. In this study, an average of 500 records was taken for each of 207 Holstein Friesian cows on approx. each of 3 recording periods from 2010, 2011 and 2014. Average methane measurements were calculated for 780 animal-testdates once values lower than 1 standard deviation from the mean were removed and within 450 days in milk. Average methane measures were log transformed and modelled in a univariate model which included week in milk with a 2nd order polynomial, season of calving, feed group, genetic group and the interaction between feed and genetic group as fixed effects and random effect of animal using a pedigree. A bivariate model was also constructed on the same dataset to estimate the correlation between methane and the concurrent daily dry matter intake (DMI, data for 571/780 methane testdates). Analyses used ASReml 3.0 (Gilmour *et al*., 2009).

Results Despite the small size of the dataset, univariate modelling estimated the heritability of enteric methane in this study at 0.041 (±0.028, P=0.13) and diet type was consistently a significant variable in explaining this. The bivariate model between enteric methane and DMI intake showed a strong positive correlation (±0.48, P =0.16) and a significant phenotypic correlation (0.098) (Table 1). The heritabilities reduced slightly in the bivariate analysis (methane=0.038 and DMI=0.22).

Table 1 Heritabilties (h^2) and correlations (phenotypic, r_p; residual, r_e; genetic, r_a) for models (standard error in brackets and significant effects in bold). Model No. 1 is the univariate and model 2 the bivariate.

No.	Variable	h2	p-value	r_p	p-value	r_r	p-value	r_a	p-value
1	Methane	0.041 (0.028)	0.13						
2	Methane	0.038 (0.027)	0.15	0.098 (0.045)	0.037	0.063 (0.048)	0.169	0.479 (0.359)	0.164
	DMI	0.220 (0.056)	**<0.001**						

Conclusion Results suggest that enteric methane production is heritable and positively correlated with DMI (Pickering *et al*., 2014), whilst more continuous data is required to confirm its significance. This highlights the potential to include this in selection indices and also the importance of feed composition in effecting emissions. Due to its ease and mobility the LMD will enable data collection from commercial farms with accuracies similar to respiratory chambers.

Acknowledgements With thanks to the staff at Crichton Dairy farm and Ian Archibald for managing the appropriate databases with long term funding from the Scottish Government (RESAS) Strategic Research Programme 2011-16. SS is funded from BBSRC/Innovate UK. The 2014 methane data were collected as part of the OptiMir (InterReg) project.

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Genetic analysis of circulating mineral concentrations in milk and serum of dairy cows

S J Denholm[1], A A Sneddon[2], A Bagnall[1], T N McNeilly[3], M C Mitchell[3], D J Roberts[1], G C Russell[3], E Wall[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]The Rowett Institute of Nutrition and Health, Aberdeen, UK, [3]Moredun Research Institute, Penicuik, UK
Email:scott.denholm@sruc.ac.uk

Implications Estimating the heritabilities of, and associations between, levels of circulating minerals in milk and serum will help determine if healthy dairy products are associated with healthy cows. Importantly, results will be used to discuss whether human nutrient intake can be improved through selection and breeding.

Introduction Minerals, such as zinc (Zn), copper (Cu), magnesium (Mg), calcium (Ca), iron (Fe) and selenium (Se), are vital components in the diet of humans. These micronutrients are required in order to maintain normal body function and remain healthy, however, there is a concern that sizable proportions of the human population do not meet the mineral Reference Nutrient Intake (RNI) values, i.e., the amount of nutrient required to prevent deficiency (Givens *et al*., 2014). Dairy products can contribute substantially to the intake of micronutrients and manipulation of minerals in livestock has been demonstrated. There is, however, a lack of knowledge concerning the heritability of micronutrients at present (Rooke *et al*., 2010). Further, the circulating levels of these elements in the blood of dairy cows could relate to the fitness of the animal given their role in various physiological/immunological systems. Here we aim to estimate genetic parameters of mineral concentrations in milk and serum and the correlation between them.

Material and methods The study was performed on the Langhill selection lines of Holstein-Friesian dairy cows (n=330) housed at the SRUC Dairy Research Centre. The cows are involved in a long-term selection experiment (genetic line x feeding system, Roberts and March, 2013). Milk samples were collected on 5 occasions between Jun 2012 and Jul 2014 (summer and winter) with 1 serum sampling point (Aug 2013). Milk and serum samples were microwave digested in nitric acid and then analysed using ICP-MS (Inductively-coupled plasma mass spectrometry). For Iodine only, samples were digested at 90'C in TMAH (Tetramethylammonium hydroxide). Data were analysed using a mixed linear animal model with year by season of calving interaction, diet group, genetic group, lactation number by age at calving interaction and lactation week as fixed effects. Cow was fitted as a random effect. Genetic parameters and correlations were obtained by univariate and bivariate analyses respectively. Analyses were carried out using ASReml version 3 (Gilmour *et al*., 2009).

Table 1 Heritability estimates (with standard errors) of trace element concentration in milk and serum

Element	h^2 milk	h^2 serum	Element	h^2 milk	h^2 serum
Na	0.09 (0.05)[a]	0.43 (0.42)[b]	Co	0.12 (0.19)[c]	-
Mg	0.12 (0.05)*	-	Ni	0.03 (0.07)[d]	na
P	0.10 (0.05)*	-	Cu	-	0.16 (0.39)[d]
K	0.09 (0.05)[a]	-	Zn	0.06 (0.04)[b]	0.16 (0.40)[d]
Ca	0.10 (0.05)*	-	Se	0.05 (0.04)[b]	0.53 (0.40)[b]
Cr	0.00 (0.04)[d]	0.04 (0.36)[d]	Cd	-	0.09 (0.36)[d]
Mn	0.03 (0.04)[c]	-	V	0.65 (1.14)[c]	na

* P<0.05; a P≤0.1; b P≤0.2; c P≤0.3; d P≤0.4; - not estimable; na not available

Results Fe, Mo, Hg, Pb and I were not estimable or not available. Table 1 shows that many of the estimates of heritability were non estimable or did not reach significance There are, however, some interesting and informative results. Heritability estimates were obtained for 6 elements (in serum), although none were significant. The suggestive heritability of Na and Se in serum was 0.43 and 0.53 respectively. In milk, heritabilities were obtained for 12 out of 19 elements, with three being statistically significant. The heritability of Mg, P and Ca was estimated to be 0.12, 0.10 and 0.10, respectively.

Conclusion The results above highlight the limited power in the size of the data for undertaking an in-depth genetic study. Of those elements that showed significant estimates of heritability, dairy products are important sources of P, Ca (both 60% of RNI) and Mg (10% of RNI) in the diet (Kliem & Givens, 2011). Importantly, Mg and Ca are increasingly significant factors in bone development, especially in children (Givens *et al*., 2014), thus, selecting for higher levels of these and other elements in milk may assist consumers in meeting the relevant RNIs.

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061

Young bull genetic growth profile for carcass weight

T M Englishby[1,2], R D Evans[3], G Banos[1], M P Coffey[1], K L Moore[1], D P Berry[2]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]Teagasc, Fermoy, Cork, Ireland, [3]Irish Cattle Breeding Federation, Bandon, Cork, Ireland
Email:tanya.englishby@sruc.ac.uk

Implications 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.

Introduction Livestock mature at different rates depending on their genetic merit. 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.

Material 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 sire 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 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 modelled 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 The average (standard deviation in parentheses) carcass weight and age at slaughter across the data was 366.8 (68.8) kg and 586.9 (85.6) days, respectively. A linear random polynomial regression was fitted. Animal genetic variance components functions for carcass weight followed a parabolic shape with greater variances at the very young and very old ages (Fig. 1). The genetic variance in carcass weight (standard error in parentheses) ranged from 549.05 (33.47) kg^2 to 1548.20 (83.12) kg^2 indicating that sufficient genetic variation exists for selection on this trait. The heritability (standard error in parentheses) of carcass weight was least (i.e., 0.38; se=0.01) at 520 days of age and greatest (0.64; se=0.01) at 720 days of age (Fig. 2).

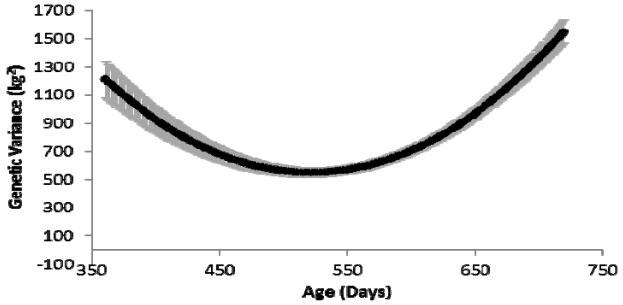

Figure 1 Estimated animal genetic variances (•) ± one standard error (error bars) of carcass weight at each age at slaughter.

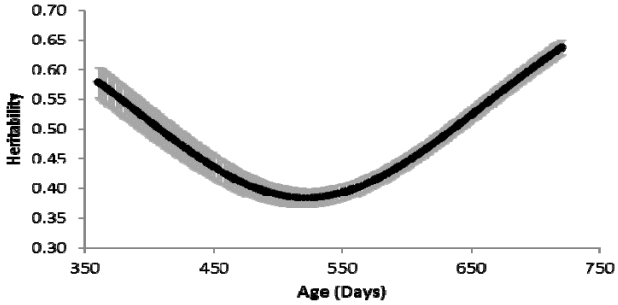

Figure 2 Heritability estimates (•) ± one standard error (error bars) of carcass weight at each age at slaughter.

Conclusion 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.

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Variation and genetic profile of milk fatty acid indices in dairy sheep

G Banos[1,2], S Symaiou[3], O Tzamaloukas[3], D Miltiadou[3]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]School of Veterinary Medicine, Aristotle University of Thessaloniki, Greece, [3]Department of Agricultural Sciences, Biotechnology and Food Science, Cyprus University of Technology, Limassol, Cyprus
Email:georgios.banos@sruc.ac.uk

Implications To improve lipid fraction in ovine milk and products thereby enhancing their nutritive value.

Introduction The fatty acid (FA) composition of ovine milk, which is rich in fat, is important to human health since consumption of saturated FA (SFA) may increase risk of cardiovascular disease, while consumption of other lipids such as the conjugated linoleic acid or total polyunsaturated FA (PUFA) contributes to the prevention of atherosclerosis, osteoporosis, or cancer (WHO, 2002). Genetic variation is known to affect bovine milk FA content (Stoop *et al.*, 2008) but such knowledge in sheep is very limited. The objectives of this study were to (i) estimate genetic and phenotypic variation and parameters for ovine milk FA unsaturation indices (ii) identify genetic variants at candidate genes putatively affecting the ovine milk FA content, and (iii) assess the effects of polymorphisms in candidate genes on milk FA.

Material and methods A dataset was developed comprising 429 dairy sheep of the Chios breed raised in four flocks in Cyprus. All animals were milking ewes in their 1st to 7th lactation that had lambed in 2012-2013. Each ewe had an average of 1.5 records with information on the concentration of 37 FA from which seven indices were constructed: total SFA, short-chain FA (SCFA), medium-chain FA (MCFA), long-chain FA (LCFA), mono-unsaturated FA (MUFA), PUFA and total unsaturated FA (UFA). The entire coding region, the 5' and 3' UTRs, of the genes *DGAT1*, *SCD*, *ACAA2* and *LIPG* was initially sequenced in 50 of these sheep to identify polymorphisms. *DGAT1* and *SCD* were found to be monomorphic whereas *ACAA2* and *LIPG* were polymorphic in this population. Subsequently, all 429 animals were genotyped for a total of eight single nucleotide polymorphisms (SNP) at three polymorphic exons: one SNP in *ACAA2* exon 10, one in *LIPG* exon 1 and six in *LIGP* exon 10, all located on chromosome 23. Trait variation and the effect of each genomic position on each trait were assessed with a mixed model including the fixed effects of flock, year and season of lambing, age of ewe at lambing, lactation number and stage of lactation as well as the random effect of animal. Both genotype and SNP effects were tested, separately, with this model. Bonferroni correction for multiple testing was applied post-analysis. Statistical analyses were conducted with ASReml (Gilmour *et al.*, 2009).

Results Between animal variation was evident ($P<0.05$) for all FA indices and most specific FA, suggesting the presence of inherent differences amongst individual animals. The ratio of animal to phenotypic variance ranged from 0.28 to 0.64 ($P<0.05$) for the FA indices, the highest pertaining to PUFA. This ratio for specific FA ranged from 0.07 to 0.94 (highest for C17:1. None of the FA indices was statistically significantly affected by the studied loci. On the contrary, locus effects ($P<0.05$) were found on specific FA and are summarised in Table 1 (marginal solutions expressed as % of total fat in milk).

Table 1 Significant ($P<0.05$) locus effects on specific fatty acids

Fatty acid	Locus	MAF[1]	Effect[2]	Size[3]
C5:0 (Valeric acid)	ACAA2 exon 10	0.47 (C)	SNP additive (C>T)	0.03
C14:1 (Myristoleic acid)	LIPG exon 10	0.08 (C)	Genotype dominance (CC>AA=AC)	0.64*
C16:1 (Palmitoleic acid)	ACAA2 exon 10	0.47 (C)	Genotype dominance (TT=CT>CC)	1.25
	LIPG exon 10	0.08 (C)	Genotype overdominance (AC>AA>CC)	1.30
C17:1 (Heptadecenoic acid)	LIPG exon 1	0.02 (A)	SNP additive (A>C)	0.47*
C18:2n6c (α Linoleic acid)	LIPG exon 10	0.08 (C)	Genotype dominance (AA=AC>CC)	0.25

[1]Minor allele frequency (base in parentheses); [2]Description of the effect; [3]Marginal effect of genotype with highest value (% of total fat in milk); *Significant after Bonferroni correction

Conclusion Individual animals exhibited significant variation in specific milk FA and FA indices, suggesting that classical selective breeding can be used to improve these traits. The three genes examined affected some of the traits of interest meaning that molecular information may be added to the breeding schemes for more effective management and improvement of specific milk fatty acid concentration.

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063

Reading the leaves: sheep parchment as a 1,000 year genetic resource

M J Collins[1], S Fiddyment[1], C Webb[1], T P O'Connor[1], D Bradley[2], M Teasdale[2], S Doherty[1], A Curtis[3], J Vnoucek[1], S Hall[4], J Finch[1]
[1]University of York, UK, [2]Trinity College Dublin, Ireland, [3]Norfolk Record Office, UK, [4]Livestock Diversity Ltd, Lincoln, UK
Email:matthew.collins@york.ac.uk

Implications England has a very rich record of sheep genetics over the last millennium in the form of archival parchment which could be used to enhance our understanding of sheep improvement.

Introduction Eileen Power wrote in The wool trade in English medieval history (1941) "The story of English sheep-farming is hidden in a great mass of documents for the most part unpublished. But it has left many visible marks up and down the country, easier to read than dusty records. Where it has left least mark, however, is upon our present-day sheep, for what we might have learned about breeds and their locations has been blurred by the meddling of scientific breeders of modern times. Bakewell may have his meed of praise from the economist, but to the historian he is an arch-iconoclast who defaced an irreplaceable collection of walking documents. We should have preferred the old originals to the New Leicesters. As it is, all we can say about medieval breeds is largely a matter of inference and conjecture." Using next generation sequencing parchment we aim to recover the genetics of these lost 'walking documents'.

Material and methods Sampling has been crowd-sourced to the archives - to whom extraction kits have been sent. Each parchment sample is first subject to peptide mass fingerprinting (ZooMS, van Doorn 2014) to establish species (~1,000 samples), sub samples are screened for DNA using MiSeq (~100 samples) of which approximately 20% are targeted for whole genome analysis, these sample being selected based upon the age of the sample, its provenance and yield of ovine DNA.

Results Parchment was a common medium for legal documents until the widespread availability of typewriters displaced legal scribes at the beginning of the 20thC. Unlike modern parchment, (which is typically made from goat or calf), of approximately 1,000 English legal documents that we have analysed (spanning the last millennium), peptide mass fingerprints (by MALDI-TOF mass spectrometry) reveals that all bar one are made from sheep-skin. The causes and timing of the development of British sheep breeds is debated, as is the extent to which improvers such as Robert Bakewell (1725–1795) of Dishley Grange, Leicester were true innovators (in-and-in breeding) or merely the lauded champions of a much more gradual process of breed development. Our initial findings suggest a rapid transition in Yorkshire, 'improved' animals are forming York parchment contemporaneous with the foundation of the Dishley Society (1789, Wykes 2004), displacing earlier Highland/Scandinavian type animals (Teasdale *et al*. 2015).

Conclusion Parchment offers tremendous scope for documenting the loss of genetic diversity in sheep breeds, the transition from a wool to meat economy and the genetic response to starvation and disease. It is important to better document the genetics of today's rare breeds and contrast these with the animals that were pre-adapted for different economic and environmental forces which shaped last 1,000 years of animal husbandry

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Estimation of genomic breeding values in a multi-breed context

A Brown[1], G Banos[1,2], M Coffey[1], J Woolliams[2], R Mrode[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]The Roslin Institute and R(D)SVS, University of Edinburgh, UK
Email:alex.brown@sruc.ac.uk

Implications To enhance genomic evaluations across different breeds and facilitate genomic selection programmes.

Introduction Genomic evaluations are now routinely published for a number of dairy cattle breeds worldwide. The UK has so far published commercial genomic breeding values (GEBVs) for Holstein cattle, & plans to release a Friesian evaluation in the near future. However, success usually relies on a large reference population, & there are few Friesian animals with genotype data available for inclusion in a single breed genomic evaluation. There has been a reasonable degree of crossbreeding between Holstein and Friesian cattle in the UK, to the point where there is a high degree of relatedness between the two breeds (Brown *et al*. 2014) & the breeds are collectively known as 'Holstein Friesian' cattle. As it may therefore be possible to use Holstein cattle in a Friesian genomic evaluation, this study aims to compare two different methods for the estimation of GEBVs in a multi-breed dairy cattle population.

Material and methods The dataset comprised de-regressed proofs (DRPs) for milk yield & somatic cell count (SCC) for 18,356 Holstein (H, n=6,986), Friesian (F, n=10,549) & Holstein Friesian cross (X, n=821) bulls. Of these, 4,765 were genotyped using Illumina 50k bovine or Illumina BovineHD (770k) SNP chips (using SNPs common to those on the 50k chip). 43,121 markers were used for analysis after sample quality control. Conventional (GBLUP) & single-step (ssGBLUP) methods were used & compared for GEBV estimation. The BLUPF90 software package (Misztal *et al*., 2002) was used to fit the following mixed model: $\mathbf{y = Xb + Za + e}$; where **y** is a vector of DRPs, **b** is a vector of fixed effects for overall mean & breed, **a** & **e** are vectors of random animal & residual effects, & **X** & **Z** are respective incidence matrices. Variances of **a** & **e** were assumed $N(0,\sigma^2_a\mathbf{G})$ & $N(0,\sigma^2_e\mathbf{I})$, where **G** is the genomic relationship matrix (VanRaden, 2008). For ssGBLUP analysis, the **G** matrix was substituted with the **H** matrix, which was constructed by combining **G** with the numerator relationship matrix **A**, allowing the use of reference animals with phenotype but no genotype. GEBVs were calculated using 3 reference populations, (i) H only reference, (ii) reference containing H & F animals, & (iii) the full reference (H, F & X animals). Each of these was used to predict accuracies in 3 validation populations containing (a) H, F & X, (b) H only & (c) F only. Number of animals per breed can be seen in Table 1. In all cases the accuracy of evaluation was calculated as the correlation between DRPs & GEBVs. Relationship matrices based on pedigree data (**A**) & SNP data (**G**) were calculated for all genotyped animals & principal component analysis was performed on each matrix to look at population structure.

Table 1 Number of animals in each reference and validation population broken down by breed and trait of interest

		Reference populations			Validation populations		
		H	F	X	H	F	X
Milk	Genotyped	2,370	62	37	1,964	42	7
	Ungenotyped	2,262	10,443	777	0	0	0
SCC	Genotyped	2,593	12	33	1,999	18	4
	Ungenotyped	2,364	573	84	0	0	0

Results GEBV accuracy for Friesians only ranged from 0.08 to 0.21 for GBLUP, & from 0.05 to 0.38 for ssGBLUP depending on trait & reference population composition. Accuracies based on the full reference population are shown in Table 2. ssGBLUP accuracies for SCC were either equal to or higher than GBLUP accuracies in all cases. Accuracies from ssGBLUP for milk yield were lower than or equal to GBLUP accuracies in all cases, due to different distribution of milk yield DRPs for Friesians compared to Holsteins.

Table 2 Accuracy of evaluation for milk yield and SCC using the full reference population

	Full validation population		Holstein validation population		Friesian validation population	
	GBLUP	ssGBLUP	GBLUP	ssGBLUP	GBLUP	ssGBLUP
Milk yield	0.67	0.36	0.60	0.48	0.09	0.16
SCC	0.59	0.60	0.59	0.59	0.21	0.38

Conclusion ssGBLUP can be used to increase accuracy of predictions for breeds with a small number of genotyped animals. Traits with bi-modal distributions due to differences in breeds may need to make use of a bivariate model.

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Genomic-based optimum contributions with antagonistic fitness and productivity traits

E Sanchez-Molano[1], R Pong-Wong[1], G Banos[2,3]
[1]The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, UK, [2]SRUC, Scotland's Rural College, Edinburgh, UK, [3]School of Veterinary Medicine, Aristotle University of Thessaloniki, Greece
Email:enrique.sanchez-molano@roslin.ed.ac.uk

Implications The results of this study show that an increase in productivity can be obtained while still maintaining fitness levels by controlling the level of inbreeding in conservation and animal genetic improvement programmes.

Introduction Genetic selection for productivity traits in cattle in the last decades has led to a decrease in fitness (which includes ability to reproduce and health and robustness traits) caused by the antagonistic correlation with productivity. The use of optimum contributions (Meuwissen, 1997) could be combined with genomic-based index selection to select both production and fitness while constraining the rate of inbreeding and the impact of inbreeding depression. The aim of this simulation study was to assess these strategies both from conservation (emphasis on inbreeding and fitness) and selection (emphasis on productivity) perspectives.

Material and methods A population of 1,000 animals (equal sex ratio) was managed for 20 generations under a genomic-based optimum contributions scheme. The genome of each animal consisted of 20 chromosomes (140 cM each) with 64,000 bi-allelic single nucleotide polymorphisms (SNPs) evenly distributed. From these SNPs, 10,000 SNPs were selected as markers to compute genomic inbreeding and 1,000 per trait (productivity and fitness) were chosen as functional genes, allowing for a -0.5 genetic correlation among traits. Mutation rate was 2.2×10^{-5} per nucleotide and recombination was simulated from the Haldane mapping function. Genomic selection was based on normally distributed genomic breeding values with a selection index accounting for different combinations of productivity/fitness (50%/50%, 75%/25% and 100%/0%). Two management strategies were tested: i) Maximise genetic gain for a given rate of inbreeding (MG strategy), ii) Minimise the rate of inbreeding for a given rate of genetic gain (MI strategy). Constraints were applied to either both sexes or sires only. Inbreeding depression was simulated as a 5% phenotypic reduction in fitness per 10% increase in genomic inbreeding as differences were expected between pedigree and genomic rates of inbreeding due to selection (Sonesson *et al*., 2012), and a 50% fitness threshold was considered as minimum for an animal to be able to mate.

Results An MG strategy for both sexes constraining the rate of genomic inbreeding to 0.01 per generation provided similar rates of genetic gain and genomic inbreeding to those obtained with a truncation selection scheme of the best 10% animals. However, when reducing the constraint to 0.005, the impact of inbreeding depression on fitness was reduced by 40-60% (Figure 1A) and only slightly smaller rates of genetic gain were yielded for both traits. Comparing MG for both sexes with sires only, a reduction in genetic gain for productivity (20-24%) and fitness (4-11%) was observed when traits were equally weighted, but when productivity was emphasised on, considering sires only led to higher fitness that including both sexes. From a conservation perspective (MI strategy), the use of low constraints for genetic gain in productivity provided a rate of inbreeding similar to that in the absence of selection, but still allowing for a noteworthy increase in genetic gain for productivity and fitness (Figure 1B), and reducing also the impact of inbreeding depression. Divergence in the rates of pedigree and genomic inbreeding was observed in all scenarios, being specially pronounced in the MI strategies.

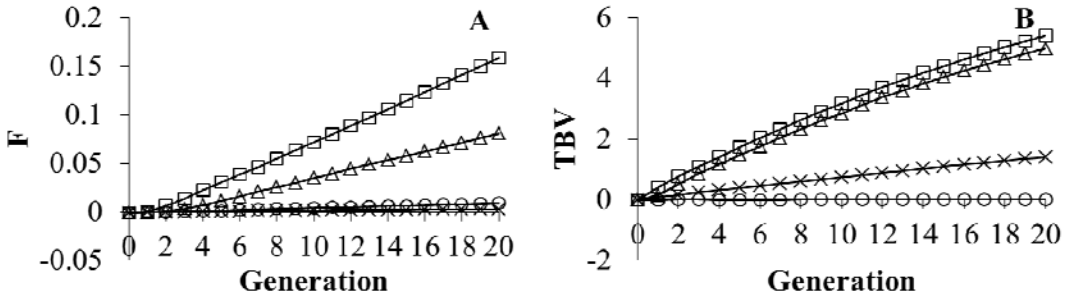

Figure 1 Genomic inbreeding (A) and productivity genetic gain (B) for MG (Δ), MI (x), truncation (□) and absence of selection (○) schemes.

Conclusion Genomic-based optimum contribution strategies are recommended both from conservation and selection perspectives, controlling fitness and inbreeding depression while allowing genetic gain in productivity.

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066

A robust assay for the measurement of telomere length in dairy cattle

L Seeker[1], B Holland[2], A Psifidi[3], G Banos[1,3], D Nussey[2]
[1]Animal and Veterinary Sciences, SRUC, Scotland's Rural College, Edinburgh, UK, [2]Institute of Evolutionary Biology, University of Edinburgh, UK, [3]Roslin Institute, University of Edinburgh, UK
Email:georgios.banos@sruc.ac.uk

Implications An assay for measurement of telomere length was developed and will be used in a large-scale longitudinal study on telomere length dynamics in association with cattle longevity and other functional traits.

Introduction Telomeres are the ends of chromosomes consisting of repetitive TTAGGG nucleotides and associated proteins. Several cross-sectional studies in different species including cattle have shown that telomeres shorten with age but length may vary within age groups (Brown *et al.*, 2012). A few longitudinal studies, mostly on wild bird populations (Heidinger *et al*. 2012), support the hypothesis that individuals born with long telomeres are more likely to live longer, indicating that telomere length might be a useful predictive marker for longevity. However, high throughput methods for measuring telomere length, necessary for large-scale longitudinal studies, are not standardised across species. The objective of this study was to develop a high throughput method for measuring telomere length, optimised for cattle, with a view of implementing this method in a large-scale study of telomeres as predictors of longevity.

Material and methods Whole blood samples were taken from 58 Holstein cattle at the Royal Crichton Farm in Dumfries (Scotland) and stored at -40°C. The age of the donor animals ranged from 0 to 2287 days. Leukocyte DNA was extracted using a salting out method (Gentra Puregene kit, Quiagen). DNA yield and purity were measured on a Nanodrop1000 and DNA integrity was checked by running all samples on a 0.5% agarose gel. Telomere length was measured using a qPCR protocol based on the method of (Cawthon 2002), where the ratio of telomere measurement to a reference gene measurement was proportional to the average relative telomere length (RTL) of the individual. Telomeres were amplified with tel 1b (CGG TTT GTT TGG GTT TGG GTT TGG GTT TGG GTT TGG GTT) and tel 2b (GGC TTG CCT TAC CCT TAC CCT TAC CCT TAC CCT TAC CCT) primers, and the reference gene with ovine B2M primers (Primerdesign). The qPCR was performed on a LightCycler 480 (Roche). A Freedom Evo robot by TECAN loaded a 384 well plate on which all samples, a calibrator DNA, the negative control and a reference DNA standard dilution curve (1:5 dilutions) were run in triplicates. The software LinRegPCR (Ruijter *et al*. 2009) was used for baseline correction and intra plate quality control. The repeatability of the qPCR assay was assessed by running the same plate four times on two different days.

Results The qPCR protocol produced highly repeatable results. Correlations of RTL measurements between plates were greater than 0.88 (Figure 1). The reaction efficiencies were high when calculated using standard DNA dilution curves (1.9-2.0, where 2 is the ideal efficiency indicating that DNA doubles with every thermal cycle) and were similar between reactions. Well-specific efficiencies calculated with LinRegPCR were very similar within and between reactions (1.86-1.87 for B2M and 1.85-1.87 for telomere reaction) and all efficiencies were within 5% of the across plate efficiency. All samples except one (0.4%) across the four plates passed successfully the LinRegPCR quality control. The coefficient of variation within triplicates was less than 5%, further attesting to the robustness of the method. Mean RTL was highly variable between individuals (39% shorter to 61% longer than the reference sample), implying trait amenability to selection. The method developed was equally applicable across all ages and telomere lengths of the donor samples.

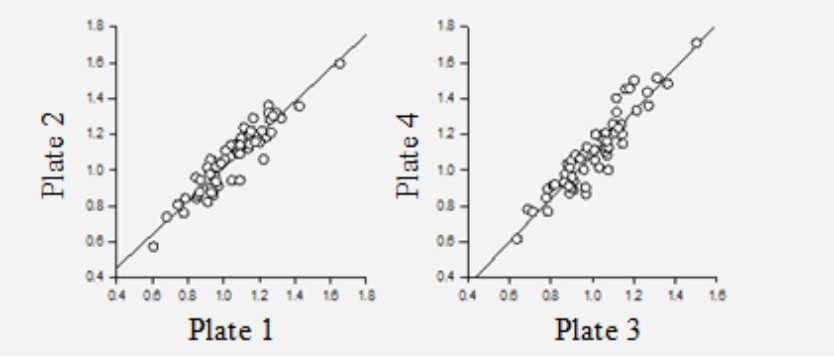

Figure 1 RTL correlation between plate 1 and 2 resp. plate 3 and 4

Conclusion A robust, high-throughput method for telomere length measurement in dairy cattle was developed, which will now be implemented to a large-scale longitudinal study on the association between telomere lengths and animal longevity.

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067

The problem with the chi-squared test in genome-wide association studies to detect a new autosomal recessive genetic disease

G E Pollott
RVC, London, UK
Email:gpollott@rvc.ac.uk

Implications When searching for the site of a mutation causing a recent autosomal recessive genetic disease the chi-squared test has a limited set of scenarios where it is useful.

Introduction One of the ways to detect the site of a new mutation giving rise to autosomal recessive genetic disease is to use a chi-squared test. This can be applied using a genotypic or recessive model. In the former, a 3x2 table of genotype (say AA, AT, TT) by case/control is analysed with 2 degrees of freedom whereas in the latter a 2x2 table (AA+AT,TT) is used with one degree of freedom. In this paper a genotypic model was explored to demonstrate the limited scenarios in which this is a feasible solution to finding the mutation.

Material and methods The Lavender Foal Syndrome (LFS) dataset of Brooks *et al*. (2010) was analysed in PLINK (Purcell *et al*., 2007) using the genotypic model and Fisher's Exact Test on 36,000 SNP genotyped with the Equine SNP50 chip. This dataset comprised 6 cases, all dying from LFS within the first few days of life, and 30 controls, some of which were the parents of the affected foals. The results of Brooks *et al*. (2010) were replicated and used as a model to investigate at what allele frequencies the results would have appeared significant.

Results The results of Brooks *et al*. (2010) were replicated using the chi-squared test in PLINK on a 3-by-2 genotype-by-disease status table using Fisher's exact test excluding SNP with a MAF < 0.05 and a missingness > 0.5. Brooks *et al*. (2010) identified "14 highly significant SNPs encompassed a region spanning 10.5 Mb (ECA1:129,228,091 to 139,718,117)." They also found 4 unique haplotypes in the 6 cases in this region. Within these 4 haplotypes there was one block of 27 SNP which was homozygous in all cases. Subsequent candidate-gene sequencing in this region by Brooks *et al*. (2010) finally discovered the causal mutation to be a single base change located at base position 138,235,715, in the MYO5A gene. Interestingly the causal mutation was located between two SNP, one was monomorphic in both cases and controls and the other had 35 homozygous identical genotypes and one heterozygote in controls. Not surprisingly they did not appear as significant in the chi-squared tests. Also the SNP with the lowest P value (BIEC2-58164 at base position 133,508,742) was not in the identified region and would not have been considered significant if the Bonferroni correction had been applied (-logP = 5.85 equivalent to P = 0.05 after correction).

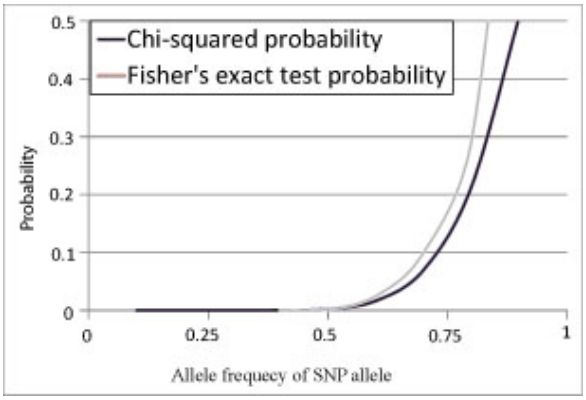

Figure 1 Chi-squared and Fisher's Exact Test probabilities for a range of allele frequencies of the SNP associated with the mutation in controls using values from the LFS dataset.

Figure 1 shows the results of calculating the chi-squared values for 6 cases and 30 controls at different allele frequencies of the allele associated with the mutation. This demonstrates that the probability of finding a significant SNP site linked to the new mutation would only occur when the allele frequency of the disease-associated allele was <0.65 in controls. Since the mutation is more likely to be associated with a major allele, by chance, then the chi-squared test will only be effective in a small number of situations. These include the scenario where the mutation occurs in a monomorphic region of the genome. It has been shown that tests utilising runs of homozygosity are more likely to be successful than the chi-squared test at locating the site of a recent autosomal recessive mutation (Pollott, 2013).

Conclusion The often-used chi-squared test is only effective where SNP allele frequencies specific characteristics and not in the case of an allele with a major allele frequency.

Acknowledgements Prof. Samantha Brooks and colleagues at Cornell are gratefully acknowledged for the use of their data.

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068

A meta-analysis for bovine tuberculosis resistance in dairy cattle

S Tsairidou[1], J A Woolliams[1], A R Allen[2], R A Skuce[2,3], S H McBride[2], R Pong-Wong[1], O Matika[1], E K Finlay[4], D P Berry[5], D G Bradley[4], S W J McDowell[2], E J Glass[1], S C Bishop[1]
[1]The Roslin Institute and RDVS, University of Edinburgh, UK, [2]Agri-Food and Biosciences Institute, Belfast, UK, [3]School of Biological Sciences, Queen's University Belfast, UK, [4]Department of Genetics, Trinity College Dublin, Ireland, [5]Teagasc, Moorepark, Fermoy, County Cork, Ireland
Email:smaragda.tsairidou@roslin.ed.ac.uk

Implications These results add insight into the design of a complementary approach for the control of bovine Tuberculosis (bTB), i.e. breeding for increased resistance. The feasibility of genomic prediction for bTB resistance and potential implementation in breeding programmes are investigated.

Introduction Bovine Tuberculosis has been one of the most persistent animal health problems in the UK (Allen *et al*. 2010). bTB control traditionally relies on diagnosis through the tuberculin skin test and abattoir carcass inspection. However, limitations in the sensitivity of these methods have prevented successful eradication. Previous studies have demonstrated the presence of heritable genetic variation underlying the control of bTB resistance (Finlay *et al*. 2012; Bermingham *et al*. 2014; Tsairidou *et al*. 2014). Our hypothesis is that selection of individuals with increased resistance to bTB may offer a complementary strategy to control bTB. The aim of this study was to conduct a meta-analysis combining populations of distantly related individuals, genotyped with SNP arrays, to identify specific loci or genomic regions underlying bTB resistance.

Material and methods Two populations were combined in a meta-analysis: the first population comprised 1,151 female Holstein-Friesians, confirmed bTB cases or controls, from herds in Northern Ireland, genotyped with the Illumina high-density Bead Chip; the second population comprised 287 Holstein bulls from the Republic of Ireland, genotyped with the Illumina Bovine50 SNP chip. Standardised phenotypes pre-corrected for non-genetic effects were used for population 1 and standardised de-regressed EBVs were used for population 2. Regional Heritability Mapping (RHM) methodology was used to identify genomic regions affecting the trait and to obtain heritability estimates for those regions. Chromosomal heritability estimates gave insight into properties of the genomic heritability and the genetic architecture of the trait. The predictive ability of the genomic EBVs was tested by means of cross validation (CV), either through a 5-fold CV on the combined data to obtain an expected accuracy, over 50 replicates, or through across-populations prediction.

Results The genomic heritability estimates obtained for the combined populations were 0.14 (0.05) and 0.19 (0.06), for the full dataset and after removing bulls of lower reliability, respectively. The strongest evidence for association from the RHM was on BTA6, significant at the suggestive level, with the window explaining 2.7% of the phenotypic variance. Chromosomal heritability estimation analyses confirmed results from RHM for BTA6. Further, BTA3, BTA6, and BTA14 were identified to account for most of the observed variation, being significant at the suggestive level. In total 17 chromosomes explained 29% of the phenotypic variance. Several candidate genes reside within the genomic region identified. The proportion of variance explained by each chromosome was not significantly related to its length (p-value: 0.6) indicating that bTB resistance is a moderately polygenic trait (Figure 1). The average prediction accuracy obtained for the combined populations was 0.33 for the full dataset and 0.34 after removing the low reliability bulls. Across-population prediction resulted in reduced accuracy.

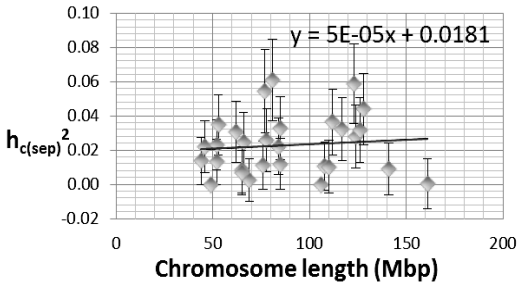

Figure 1 Regression of chromosome-specific h^2 on chromosome length**.**

Conclusion BTB resistance was found to be moderately polygenic with a few major chromosomes collectively controlling the trait, suggesting the presence of clusters of causal variants spread over several chromosomal regions. Regional heritability mapping and chromosomal heritability approaches suggested a region on BTA6 putatively associated with bTB resistance. This result was not observed when the two populations had been analysed separately. Combining only distantly related populations is a challenging procedure, with the joint populations behaving differently than when analysed separately. The cross validation conducted in this meta-analysis has confirmed the feasibility of genomic selection for bTB resistance in cattle, and combining populations only distantly related was found to have only little impact on prediction accuracy. However, drawing robust inferences from predictions across populations would require larger datasets.

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069

Genomics and metagenomics applied to animal health and food security

M Watson
The Roslin Institute, R(D)SVS, University of Edinburgh, Easter Bush, Midlothian EH25 9RG, UK
Email:mick.watson@roslin.ed.ac.uk

A UN FAO report on the issue of "Food Security" forecasts that global food production will need to increase by over 40% by 2030 and by over 70% by 2050. The objectives of research in farm animals must be to increase yield, disease resistance, food production, food safety and quality and to decrease infections, water use, energy use, the environmental impact and the chance of zoonoses. Genomics technologies are becoming increasingly critical in the pursuit of these goals, and second and third generation sequencing technologies have fuelled a revolution in biological research. I will present results from a range of collaborative research projects that demonstrate the power of sequencing technologuies, including the structure and function of small RNAs in farm animal disease, insights from bacterial genomics, de novo genome sequencing of small and large viruses and the use of metagenomics to investigate the rumen gut microbiome, with impacts in novel enzyme discovery, methane emissions and food production.

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Using label-free quantitative proteomics and untargeted metabolomics to study bovine mastitis

MAV Mudaliar[1,2], FC Thomas[2], M McLaughlin[3], R Burchmore[1,4], D Wilson[7], P Herzyk[1,5], PD Eckersall[2,3], RN Zadoks[2,6]
[1]Glasgow Polyomics, University of Glasgow, UK, [2]Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, UK, [3]School of Veterinary Medicine, University of Glasgow, UK, [4]Institute of Infection, Immunity and Inflammation, University of Glasgow, UK, [5]Institute of Molecular Cell and Systems Biology, University of Glasgow, UK, [6]Moredun Research Institute, Edinburgh, UK, [7]Humanities Advanced Technology and Information Institute, University of Glasgow, UK
E*mail:manikhandan.mudaliar@glasgow.ac.uk*

Implications The appearance of both host and pathogen factors in milk during an infectious mastitis can influence dairy production and animal welfare, but makes milk a natural substrate to study host-pathogen interactions and to identify biomarkers for mastitis.

Introduction Bovine mastitis or inflammation of the udder is an important disease affecting production in dairy cattle. Recent improvements in mass-spectrometry-based high-throughput proteomic and metabolomic technologies have enabled characterization of the bovine milk proteome (Eckersall *et al*. 2012) and metabolome. We present a novel approach to assess quantitative changes in the proteome and metabolome in bovine milk during the course of a *Streptococcus uberis* infection.

Material and methods Milk samples for this study were collected from an intra-mammary challenge experiment with a putatively host-adapted strain of *Streptococcus uberis* (Tassi *et al*. 2013). Briefly, six clinically healthy Holstein cows with no history of clinical mastitis were intramammarily challenged with *S. uberis*. Milk samples were collected at various intervals, and samples from six selected time points (0, 36, 42, 57, 81 & 312 hours post-challenge) were used to generate quantitative label-free proteomic data and metabolomic data. For proteomics, the milk samples were centrifuged at 150,000g to deplete caseins; whey proteins were precipitated, re-suspended at a defined concentration and digested with trypsin. MS/MS data acquisition was performed using an Orbitrap Elite mass spectrometer coupled with Dionex UltiMate 3000 RSLCnano in-line HPLC using reversed-phase liquid chromatography with a 120-minute elution gradient. Peptide identifications, protein assignments and label-free quantifications were performed using MaxQuant software coupled with Andromeda search engine using UniProt *Bos taurus* and *S. uberis* reference proteomes. Perseus software was used for performing data transformation, principal component analysis, differential expression analysis using ANOVA and generating plots. For metabolomics, metabolites were extracted in a 1:3 mixture of chloroform and methanol. LC-MS analysis was performed in both negative and positive ionisation modes using an Exactive mass spectrometer coupled with a Dionex UltiMate 3000 RSLCnano in-line HPLC. The separation of metabolites was performed using a ZIC-pHILIC column with a 25-minute elution gradient. The metabolomics data was analysed using Ideom and R software.

Results LC-MS/MS proteomics data was generated from all 36 samples (6 cows x 6 time points). The quality of the raw data was examined by generating total ion current chromatograms and base peak chromatograms. The dataset showed overall consistency and data from all the samples were used in down-stream analysis. We identified and quantified 2,339 peptides in the dataset and assigned them to 483 proteins (with at least one unique peptide). Similarly, we determined 3,828 peaks from both the positive and the negative ionisation modes in the metabolomics data, and from that 740 metabolites were identified and quantified. Principal component analysis (PCA) and hierarchical clustering analysis were performed on both the proteomics and metabolomics datasets. PCA showed most of the samples clustered corresponding to their time points. Overall, the clusters were separated on principal component 1, which had captured the highest proportion of variance in the dataset. The samples at time point 81 hours were the farthest away from the samples at time point 0 hours suggesting the point of largest change in proteome/metabolome during the time course, even though most cows had cleared the infection at that point. Clusters that were formed by the samples at time points 0 hours and 312 hours located close together suggesting a return to the pre-infection and pre-inflammation state. ANOVA test was performed to find the proteins/metabolites that were differentially expressed by a fold change greater than 2 combined with a false discovery rate adjusted *P* value less than 0.05 between time point 0 hours and the rest of the time points. The highest number of differentially expressed proteins (158 in number) were in the 0 hours vs 81 hours contrast, while 0 hours vs 312 hours showed the lowest number (44 proteins). A similar trend was observed in the differentially expressed metabolites.

Conclusion The study showed high concordance between milk proteome and metabolome at global expression levels. We identified many proteins and metabolites that change during the time course in response to the infection, particularly in the acute phase response signalling pathway and proteins involved in antimicrobial activity (e.g. cathelicidin). Using proteomics and metabolomics we identified the dynamics of host-pathogen interactions in bovine mastitis and candidate biomarkers.

Acknowledgements The authors gratefully acknowledge material support from Glasgow Polyomics.

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071

The measurement of chicken acute phase proteins using a quantitative proteomic approach

E L O'Reilly[1], P D Eckersall[1], G Mazzucchelli[2], E De Pauw[2]
[1]University of Glasgow, UK, [2]University of Liège, Belgium
Email:emilymoo90@hotmail.com

Implications Selected reaction monitoring (SRM) was used to measure Serum amyloid A in chickens, a low abundant yet major acute phase protein in chickens. C-reactive protein was not identified in any of the samples and is an unlikely responder during the chicken acute phase response. Using SRM enables proteins that other modalities have failed to identify and measure to be successfully targeted.

Introduction The characterisation and measurement of acute phase proteins (APPs) in chickens is a challenging area owing to the limited availability of specific antisera and in some cases very low abundance in serum. This study established a method, using selected reaction monitoring (SRM), to measure known APPs serum amyloid A (SAA), C-reactive protein (CRP), ovotransferrin (OVT), transthyretin (TTN) and apolipoprotein A-1 (Apo-A1) in chickens.

Material and methods Serum concentrations of the established APP □$_1$-acid glycoprotein (AGP) was used to pool samples into three acute phase groups: highly acute phase serum (AGP ≥1000μg/ml – n=3), acute phase serum (AGP= 700-1000μg/ml – n=4) and non-acute phase serum (AGP ≤300μg/ml – n=4). Selected APPs were identified using an initial shotgun (SG) analysis. Low molecular weight proteins (<30 kDa) were enriched using Protein Discovery GelFree® 8100 Fractional system (10% cartridge). For CRP, highly acute phase and acute phase serum was added to four mini-columns containing immobilised p-aminophenyl phosphoyl choline gel (Thermo Scientific 20307) and the elutions collected and concentrated. The low molecular weight fractions (<30 kDa) and the phosphoyl column eluates, together with whole serum, pooled into the three acute phase groups underwent sample preparation and trypsin digestion, as described in Collodoro, *et al*., (2012). The peptides were applied over 2D nano UPLC system (RP x RP, nano Acquity, Waters) coupled to a Q-Exactive Hybrid Quadrupole–Orbitrap mass spectrometer (Thermo Scientific) with a top 12 data dependant acquisition method (Thermo Scientific). The Q-Exactive-Orbitrap Mass spectrometer then performed MS/MS spectra analysis, and comparisons were made to the *Gallus gallus* protein database (Uniprot) using Sequest (Thermo Scientific) and Mascot (Matrix Science). A quantitative targeted method was established by identifying acute phase proteins within the SG results and characterising suitably quantotypic peptides from each target protein. Once peptides were identified and validated the nano UPLC - Q-Exactive was used in the targeted mode (single ion monitoring SIM/targeted MS2). Data was assimilated and analysed using Skyline software and the peptide intensities (the sum of all the fragment ions of that peptide) were used to determine the intensities of each APP in each sample. For each APP, three peptide intensities were used and one way ANOVA and t-tests (Microsoft Excel, 2010) were used to compare the peptide intensity for each selected peptide across the three sample groups and identify significant differences.

Results C-reactive protein was not identified during SG analysis of the whole serum or enriched samples. Enriching the lower molecular weight proteins resulted in the identification of a higher number of lower molecular weight proteins and increased the number of SAA peptides identified. All three SAA peptides were only identified in the highly acute phase group. No SAA peptides were identified in the non-acute phase group and a single peptide was identified in one sample of the acute phase group only. Ovotransferrin behaved as a positive APP with significantly higher intensities in highly acute phase group compared to the acute phase and control groups in two of the three peptides. For TTN two of the three peptides behaved as negative APP. Apolipoprotein A-1, a negative APP, showed highly significant differences in all three peptides, with Apo-A1 peptides in the highly acute phase group being significantly lower than both the acute and non- acute phase groups.

Conclusion SAA is a major APP in chickens having been conclusively identified in the highly acute phase serum. Despite the role of CRP as a major APP in mammalian species, CRP was not identified in any sample, suggesting that CRP is not an APP in chickens or that serum concentrations are lower than the limit of detection of this system. Ovotransferrin is a moderate APP in chickens and the results of this investigation corresponds to previous work undertaken. Both Apo-A1 and TTN are known negative APPs and the results for Apo-A1 demonstrate that this APP acts in a negative fashion in the chicken. This study highlights the usefulness of a targeted and quantifiable proteomic approach to measuring biomarkers in farm animals.

Acknowledgements BBSRC

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072

Physico-chemical study and anti-parasitic properties of aqueous *Cissus ruspolii* and *Adenia sp.* extracts

K Tolossa[1,2], S C Fry[2], S Athanasiadou[1], G J Loake[2], J G M Houdijk[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]Institute of Molecular Plant Sciences, University of Edinburgh, UK
Email:ketema_tolossa@yahoo.com

Implications Physico-chemical study of active plant extracts combined with egg hatch inhibition (EHI) activity can indicate the nature of the active constituents and assist the choice of appropriate methods for their purification.

Introduction With regard to the physico-chemical study of aqueous extracts in the egg hatch inhibition (EHI) assay, it is important to devise the method of separation, to choose appropriate purification techniques and to understand the conditions under which the processes would be carried out without affecting the active constituents responsible for the targeted activity. The objectives of this study were to assess: (i) the nature (such as molecular size, heat-stability and polarity) of active constituents of aqueous extracts, and (ii) how the EHI activities of the extracts are affected by these physico-chemical parameters. The three physico-chemical techniques employed in this study were membrane dialysis (Tierney *et al.* 2013), thermal stability testing (Builders *et al.* 2010) and solvent partitioning (Tierney *et al.* 2013).

Material and methods We characterized the active principle(s) of aqueous extracts of *Cissus ruspolii and Adenia* sp. physico-chemically via three approaches; generated products were examined for EHI activity using *Teladorsagia circumcincta* eggs (Coles *et al.* 1992). 1) Membrane dialysis**:** a volume of 10 mL of 10 mg/mL aqueous extract per plant was dialysed in 12–14-kDa molecular weight cut-off dialysis tubing. The sac was immersed in 50 mL external de-ionized water at 4 °C with continuous stirring for 24 h, then the external solution was collected and freeze dried (external). The sac was transferred into a beaker containing 1 L of deionised water and dialyzed for another 24 h under the same conditions; then the sac contents were recovered and freeze dried (sac content). 2) Heat stability**:** three aqueous extracts (2 mL per plant) were heated at 100 °C for 0, 10 or 60 min, cooled and bio-assayed. 3) Solvent partitioning**:** aqueous extracts (2 mL per plant) were shaken with 2 mL of butan-1-ol or ethyl acetate, and then centrifuged at 4000 rpm for 10 min. The upper (organic) and lower (aqueous) phases were dried in a SpeedVac and reconstituted in de-ionized water. EHI activity of the resulting products was analysed via factorial ANOVA, which included the two plant species and the number of product types generated within each approach used.

Results After dialysis, the external solutions (small molecules) of both plant samples showed significantly greater EHI activities than the sac contents (large molecules) ($P<0.001$; Figure 1a). This effect was stronger for *C. ruspolii* than for *Adenia* sp. ($P<0.001$). EHI activities similarly decreased with increased heating time for both plants ($P<0.001$; Figure 1b). Active principles of aqueous extracts of *C. ruspolii* and *Adenia* sp. partitioned very similarly partly into lower-polarity solvents (ethyl acetate or butan-1-ol) but the majority was found in the water phase ($P<0.001$; Figure 1c).

Conclusion The outcome of this physico-chemical study supports the view that major active component(s) responsible for the EHI activities observed from *C. ruspolii* and *Adenia* sp. are water-soluble, small, highly polar, slightly heat-labile molecules.

Acknowledgements We gratefully acknowledge funding from BBSRC/DFID/SG and SRUC's International Engagement Strategy.

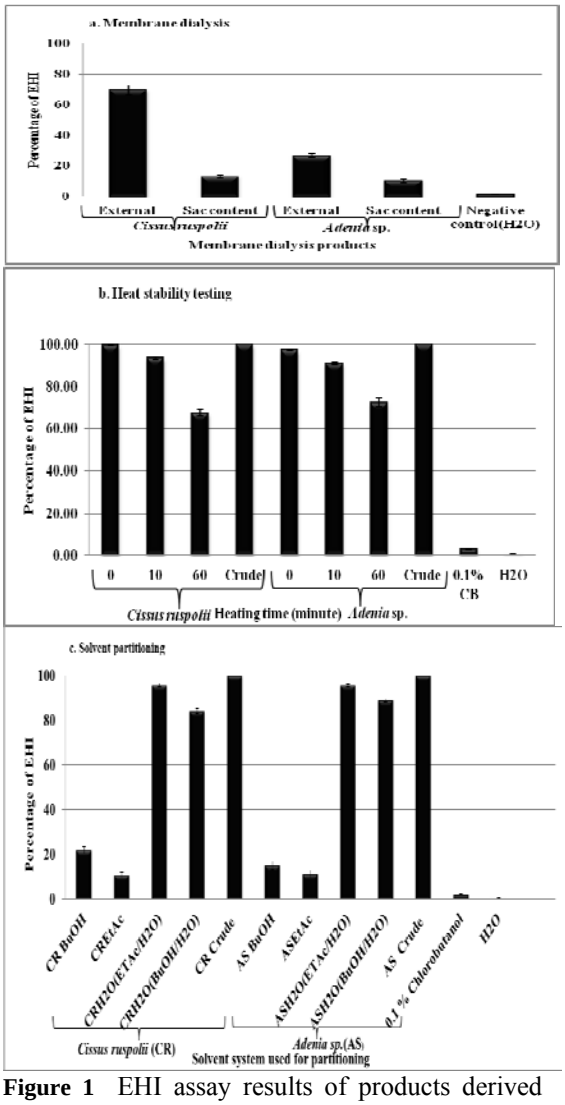

Figure 1 EHI assay results of products derived from (a) membrane dialysis, (b) heat stability testing, and (c) and solvent partitioning

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073

Validation of acaricidal activity of medicinal plants*: in vitro* and *in vivo* studies

S Athanasiadou[1], E Debela[2], A Tolera[2], K Tolossa[1,2], S T G Burgess[3], S Terry[1], J G M Houdijk[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]Hawassa University, Ethiopia, [3]Moredun Research Institute, Midlothian, UK
Email:spiridoula.athanasiadou@sruc.ac.uk

Implications *In vitro* assays allow high throughput screening but *in vivo* validation of the acaricidal activity of plant extracts is necessary prior to their use in animals.

Introduction Medicinal plants play an important role for parasite control in developing countries, and are of growing interest in developed countries where drug resistance increasingly hinders chemoprophylaxis. However, scientific evidence on plant efficacy is scarce, which hampers establishing phytomedicine as a reliable parasite control strategy. Here, we present *in vitro* screening and *in vivo* validation of medicinal properties of plants originating from Ethiopia, against the ovine mite *Psoroptes ovis.*

Material and methods The selection of plants for the *in vitro* screening was based on a recent ethno-botanical survey (Tolossa *et al*., 2013), whereas for the *in vivo* experiment was based on the *in vitro* screening. Mite immersion tests (n=3) were adapted from Borges *et al*. (2003). In total 90 extracts were tested *in vitro* from 30 plants (five of which are routinely used by traditional healers against ecto-parasites). Dried plant matter was extracted by three solvents, MeOH, 70% MEOH and H_2O. Forty, four-month old sheep were either infested with 50-100 *Psoroptes ovis* mites between the withers (n=30) or remained the un-infected controls (n=10). Once lesions reached 10cm^2 size (3 weeks post infestation) sheep were treated locally with either (n=10): i) MeOH extract of *Premna schimperi* ii) MeOH extract of *Commiphora erthrea* or iii) water (control). The extracts were used at a 5% concentration (0.5g of plant extract in 10 ml water) and each sheep received 2-3 ml of extract once per day for 7 days rubbed gently into the lesion. Lesion size development was measured weekly. Weekly blood samples were analysed for Acute Phase Proteins (APP) as markers of inflammation. *In vitro* data were analysed by t-test and *in vivo* data by one way ANOVA.

Results Acaricidal activity was confirmed for at least one extract of 4 out of the 5 plants routinely used by traditional healers (Fig 1a); efficacy varied between 55-80% and mortality was significantly higher than in controls. Furthermore, extracts from 3 plants that have not been previously associated with activity against ecto-parasites showed *in vitro* efficacy between 50 and 80% (Fig 1b). Sheep treated with the *P. schimperi* extract showed smaller (P<0.05) lesion size at PM (74 cm^2) whereas those treated with *C. erthrea* extract showed similar (P>0.1) lesion size (160 cm^2) with the infected controls treated with water (138 cm^2). *P. schimperi* treated sheep had lower mite recovery compared to that of other sheep (13 vs 22 mites per strip), although this was not statistically significant. From the second day of the application of treatment, sheep treated with the extracts showed reduced discomfort and scratching compared to controls, although this was not quantified. APP levels were similar in infected and non-infected animals, throughout the course of the infection (Fig 2).

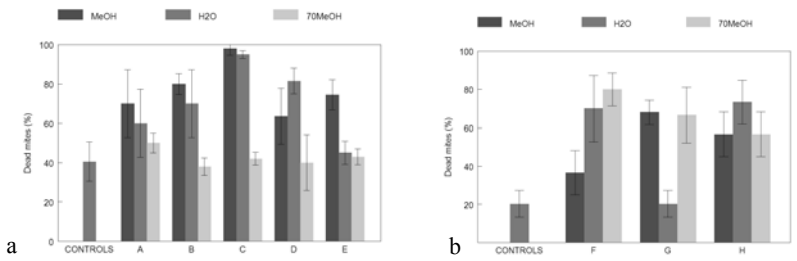

Figure 1 % mortality of mites following immersion tests in plant extracts.
a)A: *D. angustifolia,* B: *C. erthrea,* C: *P. schimperi,* D: *C. aurea,* E: Taflila,
b)F: *A. anthelmintica,* G: *Artemisia* spp, H: *B. rotundifolia*

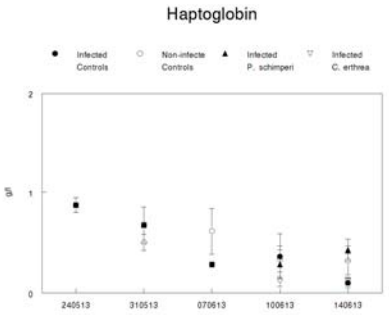

Figure 2 Haptoglobin levels in serum

Conclusion Both extracts tested reduced scratching and discomfort associated with the development of the lesions. MeOH extract of *P. schimper* tested *in vivo*, resulted in significant reduction in lesion size and the number of mites recovered at the end of the trial, an effect which was supportive of the *in vitro* screening. The outcome of the testing of the second extract did not confirm the *in vitro* testing, highlighting the importance of *in vivo* validation.

Acknowledgements The authors gratefully acknowledge funding from the DFID/BBSRC/SG CIDLID program (BB/H009299/1).

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Geographical distribution and hosts of ixodid ticks of livestock in Oman

P A Bobade[1], S A Al-Riyami[1], R M Al-Busaidi[1], Z A Korra[2], Y A Al-Shehhi[1], H Heyne[3], A Latif[3]
[1]Sultan Qaboos University, Al-Khod, Muscat, Oman, [2]Veterinary Hospital, Salalah, Oman, [3]ARC Onderstepoort Veterinary Institute, Onderstepoort, Pretoria, South Africa
Email:ekisbly@yahoo.com.sg

Implications The livestock population of Oman are infested by ixodid ticks of economic importance. There is a need for effective control of these ticks to prevent economic losses caused by the diseases which they transmit.

Introduction Oman has a livestock population of 3,235,777 which is made up of 2,085,206 goats; 548,231 sheep; 359,507 cattle and 242,833 camels (Oman Ministry of Agriculture and Fisheries 2014). This number of animals is insufficient to meet the demands for meat, milk and other livestock products by the country's human population of 3,314,000 (WHO 2014). This has resulted in considerable importation of live animals, meat, milk and other livestock products. In order to reduce this dependence on importation, the country needs to boost its livestock production. One of the important keys for this is the control of animal diseases. Tick-borne diseases are well known causes of morbidity and mortality in livestock. This on-going study is being carried out to determine the prevalent tick vectors of livestock diseases in Oman.

Material and methods Between 2007 and 2011, with the informed consent of the owners, ticks were collected off 248 goats, 107 sheep, 36 cattle and 47 camels at 29 locations in the northern and southern parts of Oman. The geographic coordinates of each location where ticks were collected were recorded at the time of tick collection and later mapped. At each location, at least 10 animal hosts of a particular species with visible tick infestation were selected for tick collection. Where there were less than 10 infested animals, all the infested animals were selected. The ticks collected from each animal were preserved in bottles containing 70% ethanol and each bottle was labelled with a strip of paper on which was recorded the animal's details, date of collection and the location. The ticks were later identified morphologically and counted, using a stereoscopic microscope.

Results A total of 3,480 adults, nymphs and larvae of ticks were collected off all the animals. This number was made up of 1,504 collected off the goats, 462 off sheep, 870 off cattle and 644 off camels. All the ticks were hard ticks (Family Ixodidae) and belonged to 12 species, namely: *Amblyomma* (*A.*) *variegatum*, *Hyalomma (H.) anatolicum*, *H. dromedarii*, *H. excavatum*, *H. impeltatum*, *H. marginatum*, *H. rufipes*, *H. scupense* (= *H. detritum*), *Rhipicephalus* (*Boophilus*) *annulatus*, *Rhipicephalus* (*Boophilus*) *decoloratus*, *Rhipicephalus (R.) camicasi*, and *R. leporis*. The most prevalent and numerous tick species was *R. camicasi* and it was found at locations in both the northern and southern parts of the country. The other tick species that were found at locations in both the northern and southern parts of the country were *H. anatolicum*, *H. dromedarii*, *H. excavatum*, *H. marginatum*, *H. rufipes*, and *H. scupense*. Three tick species, namely *A. variegatum*, *R. annulatus* and *H. impeltatum* were found only in the southern part while *R. decoloratus* and *R. leporis* were found in the extreme northern part of the country (Musandam region). Only three of the 12 tick species found in this study infested one type of host species; *R. annulatus* being found on cattle while *R. decoloratus*, and *R. leporis* were found on goats. The other nine tick species infested more than one type of host species. Two species of ticks, *H. anatolicum* and *R. camicasi* were found on all the host species (cattle, sheep, goats and camels); while three species, *A. variegatum*, *H. impeltatum* and *H. rufipes* were found on cattle, goats and camels. *H. excavatum* was found on cattle, sheep and goats; *H. marginatum* on sheep, goats and camel; *H. scupense* on cattle and goats; and *H. dromedarii* on cattle and camels. Concurrent infestation with more than one tick species was found on approximately 68.1% of the camels, 52.8% of the cattle, 12.5% of the goats but not on any sheep.

Conclusion At least nine of the ticks found in this study, namely *A. variegatum*, H. *anatolicum*, *H. dromedarii*, *H. excavatum*, *H. marginatum*, *H. rufipes*, *H. scupense*, *R. annulatus*, and *R. decoloratus* are vectors of pathogens that cause livestock diseases of economic importance such as heartwater, bovine babesiosis, anaplasmosis, and theileriosis; as well as human diseases like Crimean-Congo haemorrhagic fever and African tick bite fever (Jongejan and Uilenberg 2004). If these ticks are not controlled, these diseases may become major causes of morbidity and mortality in the livestock and human populations of Oman.

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Clinical text mining: the cutting edge of computer science meets the coalface of small animal veterinary practice

J Newman[1,4], P-J M Noble[3,1], G Nenadic[4], A D Radford[2], P H Jones[1]
[1]Epidemiology and Population Health, University of Liverpool, UK, [2]Infection Biology, University of Liverpool, UK, [3]School of Veterinary Science, University of Liverpool, UK, [4]School of Computer Science, University of Manchester, UK
Email:njen@liv.ac.uk

Implications Clinical text mining provides the potential to facilitate real-time syndromic surveillance, clinical decision support and risk factor identification, directly from the clinical narrative recorded during a consultation.

Introduction The wide adoption of electronic health records and growing demands for high quality and evidence-based health care are powerful drivers to the development of techniques for natural language processing of the narrative component of the electronic health record.
The Small Animal Veterinary Surveillance Network (SAVSNET) collects data from diagnostic laboratories and veterinary practices in real time, in order to provide surveillance for sentinel markers of disease. The data collected from veterinary practices includes signalment, location, date, clinical free text and the results of a short clinical questionnaire.
Amongst other syndromic and tempero-spatial analyses of the wealth of coded data accumulating within the SAVSNET dataset, natural language processing techniques are being developed to explore and extract information from the veterinary narrative. This permits access to, and analysis of, the host of information previously locked within the large, unconstrained, clinical free text field.
Following clinical and computational identification of patterns of language used to describe specific presentations; it is possible to identify other consultations matching the lexical fingerprint of the syndrome of interest. As a result, clinical text mining has many implications for improving animal health and welfare by facilitation of syndromic surveillance, risk factor identification, identification of management patterns and clinical decision support. We explore a range of instances where natural language processing facilitates information retrieval and analysis from the veterinary clinical text captured within the SAVSNET dataset.

Material and methods By the 30th November 2014 the SAVSNET database contained 423,375 consultations, relating to 165,027 animals, captured in real-time. These data formed the basis of the work described. Additional datasets collated by specialists in the field were utilised as a source of confirmed cases of a syndrome. Identification of the key components of consultations, conferring meaning related to the syndrome or event of interest, first required the pre-processing, or cleaning, of the text; identification of stop-words, acronyms, abbreviations, colloquialisms, mis-spellings and negating terms. Clusters of terms with similar meaning were then identified. It was vital at this stage to recognise those clusters likely to introduce or accentuate bias if included in a syndrome identification algorithm, for example those related to a perceived risk factor or prior knowledge of an outcome. The relative likelihood of each cluster of words occurring within the text of consultations of confirmed cases, as compared to non-cases, was calculated and the efficacy of terms as markers for the syndrome evaluated.
For syndromic surveillance to be undertaken, clinical records were annotated to note the presence or absence of word clusters most strongly associated with the syndrome in question. Sequential adjustments were made to the model formed in Weka, an open source machine learning software workbench, thus identifying the optimum sensitivity and specificity achievable in identifying the syndrome from the veterinary narrative.
A similar strategy is undertaken in identifying management patterns or specific events from the clinical narrative. As an exemplar, terms associated with the administration of a drug can be sought, this is then utilised to ascertain consultations where a drug, or group of drugs, were administered. Using the recorded animal weight, the dose given can be determined and compared to that licensed. As this process is integrated within software scripts, specifically developed by the team for this purpose, hundreds of thousands of consultations can be analysed in seconds.

Results Utilising natural language processing techniques to infer meaning from the veterinary narrative has, to date, resulted in the development of a number of screening tools capable of identifying specific events within the clinical narrative, including euthanasia, vaccination, and administration of specific drugs. In addition, syndromic surveillance tools have been developed to identify consultations that bear the hallmarks of emerging syndromes.

Conclusions Clinical text mining offers the opportunity to maximise information retrieval from electronic health records in small animal and other branches of veterinary practice. Analysis of this information will confer benefits to practising veterinary surgeons, epidemiologists, public health agencies and most importantly animal health and welfare.

Acknowledgements This work is undertaken as a component of a PhD funded and supported as part of the Health e-research Centre (HeRC) Doctoral Training Scheme. SAVSNET is a partnership between the University of Liverpool and the British Small Animal Veterinary Association. Clinical records in the SAVSNET dataset, and confirmed cases of specific syndromes, are contributed by practising veterinary surgeons. Without each of these contributions this work would not be possible.

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Preliminary study of prevalence of rumen fluke in Irish flocks

A M Martinez-Ibeas[1], N Byrne[1], K Lawlor[2], M P Munita[1], G Mulcahy[2], M Sekiya[2]
[1]1ABRD, AGRIC, Teagasc, Moorepark, Fermoy, Cork, Ireland, [2]2 School of Veterinary Medicine UCD, Belfield, Dublin, Ireland
Email:anamaria_mi@hotmail.com

Implications The number of reports of clinical paramphistomosis in cattle has increased in Ireland in recent years. A prevalence study will allow the design of parasite control strategies.

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 has been 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**.**

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. 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 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 of feces (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 Overall, 201 out of the 254 farms (79%) were positive for rumen fluke. The prevalence in different regions ranged from 68% in the South-West to 100% in the Mid-West.

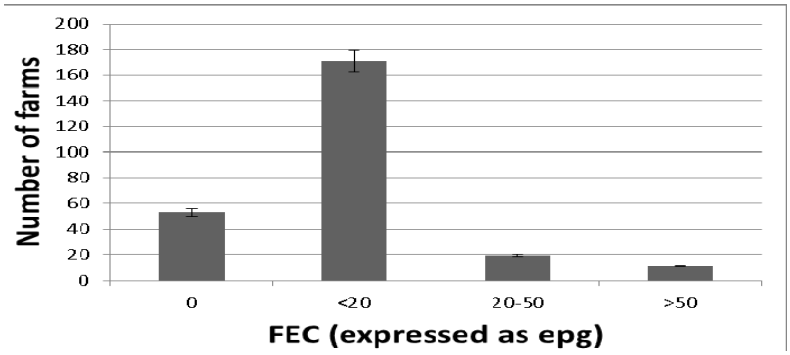

Figure 1 Number of farms with differing FEC status.

Conclusion This study is the first approach to gain knowledge of the rumen fluke prevalence in Irish flocks at a national level. The high proportion of infected farms recorded highlights the need to develop sustainable paraphistome control programmes. Further studies are required to generate a comprehensive epidemiological model of paramphistomosis, including further statistical analysis and identification of the species of rumen fluke present in Ireland. Such studies will provide a basis for the implementation of effective control measures and also allow investigation of production and economic outcomes of rumen fluke infestations

Acknowledgements This study is an output from DAFM RSF funding

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Production performance of lactating dairy cows offered two different commercial fat supplements

R M Kirkland[1], J Flockhart[2]
[1]Volac International Ltd, Orwell, Royston Herts., SG8 5QX, UK, [2]Scotland's Rural College, West Mains Road, Edinburgh, EH9 3JG, UK
Email:richard.kirkland@volac.com

Implications Cows offered a fat supplement based on calcium salts of palm fatty acids produced 1.6 kg additional milk per day compared to those offered an alternative fat supplement at equal energy supply.

Introduction Fat supplements are commonly used to increase the energy density of diets for dairy cows. There are many different fat supplements on the market which differ in source of fat, structure of fat (free fatty acids or triglycerides) and whether they are rumen-active or rumen-protected. The objective of this study was to determine the production effects of two commercial fat supplements when offered to lactating dairy cows.

Material and methods Eighteen early lactation (mean 55 days in milk; range 20 to 93) Holstein-Friesian dairy cows, mean initial milk yield 45.3 kg/d (range 35.5 to 55.8), were split into three treatment groups in a Latin Square design study with 28-d periods. Two 3 x 3 Latin squares were used. Three groups of six cows were established based on similarity of milk production, live weight, days in milk and parity and cows in each group allocated at random to one of six experimental groups. Three of these groups were then assigned to one Latin square template while the other three groups were assigned to the second Latin square template. Two commercial fat supplements were included as treatments within this wider study and data for these treatments were analysed separately for this paper : (1) Megalac® (M) rumen-protected fat (a calcium salt of palm fatty acid distillate; Volac International Ltd) offered at 400 g/cow/d; (2) a '50%' fat product (blended oil / fibre mix) (D) offered at 530 g/cow/d (equivalent to the energy supplied by 400 g of M based on manufacturer's data). The energy supplied by the fat supplements was calculated to supply 12.6 MJ/d based on manufacturer's claimed values. The fat supplements were added to the same basal total mixed ration containing grass silage, dairy concentrate blend, wheat, Soypass® and mineral/vitamin supplement (577, 219, 148, 44 and 10 g/kg DM, respectively), such that the diets offered with the fat supplements had equal energy density. The fat products were supplied unbranded so that the study was carried out 'blind'. The composition of the M and D products was (g/kg fresh weight): fat 840 and 517, crude protein 0 and 17.0, crude fibre 0 and 245, respectively. Fatty acid profiles (g/kg total fatty acids) were: C16:0, 490 and 140; C18:0, 40 and 140; C18:1, 360 and 270; C18:2, 80 and 280; C18:3, 0 and 2; other 30 and 150, for the M and D products, respectively. Cows were offered fresh feed each day and dry matter intake measured for the last seven days of each 28-d feeding period. Milk yield and composition (fat and protein) were measured daily for the last five days in each feeding period and used for statistical analysis. Live weight and condition score of each cow were measured weekly. Data for the two commercial fat supplements were analysed separately by ANOVA (data for the third treatment were not included in the analyses), using GenStat Release 11.1 (PC/Windows).

Results Production data from cows offered the two fat supplements are presented in Table 1. Cows offered the M supplement consumed an additional ($P<0.01$) 0.9 kg DM/d and produced 1.6 kg/d additional ($P<0.05$) milk compared to cows offered the D supplement. Milk composition and milk protein yield were not significantly ($P>0.05$) different between fat supplement groups, but milk fat yield was higher ($P>0.01$) in the M-supplemented cows. Cows offered the M supplement also had higher ($P>0.01$) live weight.

Table 1 Mean production performance of cows offered different fat supplements

Parameter	Fat supplement		SED	Significance
	M	D		
Dry matter intake (kg/d)	20.0	19.1	0.26	**
Milk yield (kg/d)	33.7	32.1	0.57	*
Milk fat (g/kg)	38.8	38.1	0.40	NS
Milk fat (kg/d)	1.30	1.20	0.028	**
Milk protein (g/kg)	30.1	30.6	0.25	NS
Milk protein (kg/d)	1.01	0.97	0.021	NS
Live weight (kg)	629	621	2.1	**
Condition score[#]	1.8	1.8	0.03	NS

[*] $p<0.05$; **$p<0.01$; NS = not significant [#] 5-point scale

Conclusion These data indicate that different fat supplements, when offered at equal energy, can result in contrasting effects on cow performance.

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Is there a 'colour fashion' in British bred sports horses? An investigation into British equestrians preference for horse colours and perception of equine coat colour bias

A Fisker Hansen[1,2], H Randle[2], J Dixon[2,3]
[1]Plymouth University, UK, [2]Duchy College, Callington, UK, [3]Plymouth Marine Laboratory, UK
Email:anna.fiskerhansen@plymouth.ac.uk

Implications Survey results suggest a perceived bias in the British Equestrian Federation (BEF) Futurity according to the colour of the horses. Blocked Coloured and Spotted were the least favourite horse coat colours of the British equestrians.

Introduction Changes in 'fashion preference' of equine coat colours is evident through history, through domestication of the horse and particular with the introduction of modern day studbooks, described by Linderholm and Larson (2013) and Cieslak *et al.* (2007). Anecdotal feedback from participants of the BEF Futurity has suggested a judging bias in the young horse evaluations according to the colour of the horse. The aim of this study was to investigate whether a current preference in horse coat colours exists amongst British equestrians, and furthermore, to investigate British equestrians' perception of equine coat colour bias in sport horse performance evaluations.

Material and methods A 10 question online survey was designed, piloted and distributed though social media (June-September 2014) targeted at British equestrians. Participants (n=65) had a varied background within the equine sector. Questions were a combination of randomised multiple choice with free text options, agreement range questions, and free text opinion. The survey was designed to obtain participants own opinion with minimal suggestion bias. Chi-square tests on survey responses were used to analyse the significance of answers to questions about favourite (n=40) and least favourite (n=37) horse colours. Responses were compared with an expected equal spread of preference responses amongst the 7 horse coat colour groups: Bay, Chestnut, Black, Grey/White, Block Coloured (piebald and skewbald), Spotted (spotted and roan) and Dilutions (palomino, dun, buckskin). Horse coat colours were grouped according to similar phenotypes, and in accordance with horse colour categories of the BEF Futurity data.

Results Although the majority of survey participants indicated a favourite horse colour (n=40/65), an overall preferred coat colour within the sample was not evident (p=0.68). The majority of survey participants also indicated having a least favourite horse colour (n=37/65), with Block Coloured and Spotted being chosen as the least favourite by a significant number of respondents ($p<0.001$). Favourite and least favourite horse coat colours of survey participants can be seen in Figure 1. The majority of survey participants did not think equine sports performance judging was biased according to the colour of the horse, although 45/65 did think dressage could be more susceptible. Most participants (27/45) though the performance evaluation process of the BEF Futurity could be biased according to the colour of the horse, whereas only 14/45 thought the same about the veterinary component.

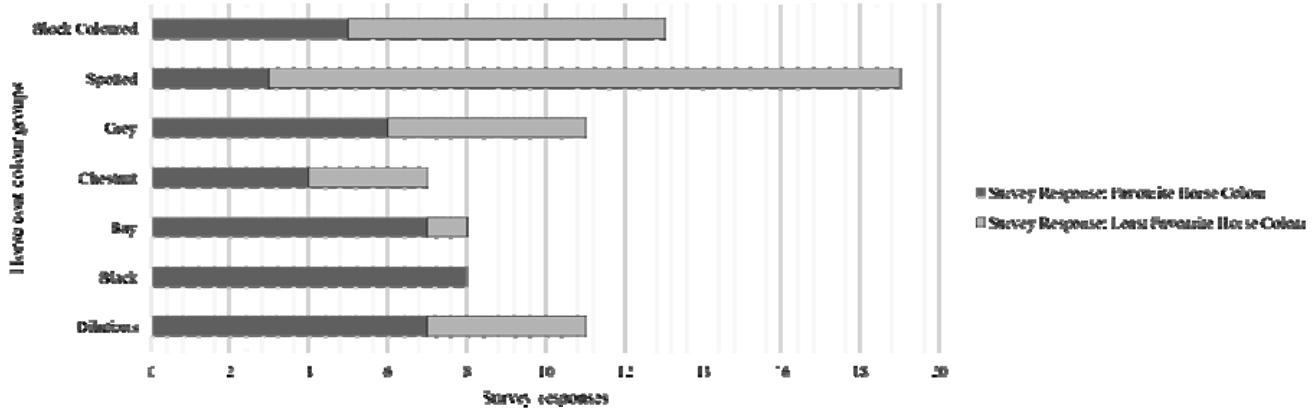

Figure 1 Frequency of the surveyed British equestrians' favourite and least favourite horse colours

Conclusion The majority of survey participants did not think that equine sport performance judging is biased according to the colour of the horse. However, they did think that performance evaluation process of the BEF Futurity is, suggesting a cause for investigation. The significantly lower preference of Spotted and Block Coloured horses, compared to no significance of favoured horse colours, suggest the possibility of a negative bias amongst British Equestrians for these horse coat colours. Further detailed analysis of horse coat colour bias within the BEF Futurity data of the years 2008-2013 will investigate this further.

Acknowledgements The author would like to thank the ESF-CUC for the research programme bursary.

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079

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

M P Munita Corbalan[1], N Byrne[1], K Lawlor[2], A M Martinez Ibeas[1], G Mulcahy[2], M Sekiya[2], R Sayers[1]
[1]ABRD, AGRIC, Teagasc Moorepark, Fermoy. Co. Cork, Ireland, [2]School of Veterinary Medicine, UCD, Belfield, Dublin, Ireland
Email:maria.munitacorbalan@teagasc.ie

Implications Determination of prevalence of *F. hepatica* in Irish sheep flocks is necessary to define efficient control measures in the different regions of the country.

Introduction *Fasciola hepatica* is one of the most important helminth parasites of sheep in temperate climate zones. The presence of the intermediate host (*Galba truncatula*) in these areas determines the presence of the trematode. The importance of this parasite in sheep relates to the fact that it can cause a per-acute syndrome which is fatal as a result of haemorrhage and liver damage. This results in significant economic losses in fluke-infested flocks and it has been estimated that *F. hepatica* results in annuals losses of €90 million across Irish livestock (AHI, 2010).
Temperature and moisture are the most important factors for *F. hepatica* development i.e. a wet environment with temperatures higher than 10^{o}C are required (Borgsteede, 2011). The Irish climate, therefore, provides ideal environmental conditions for *F. hepatica* development at certain times of the year. The aim 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 per county and nationally. Each farmer submitted 20 faecal catch samples from 20 ewes between October and November 2014. Standardised sampling kits were provided to each farmer and samples were submitted by post to the Parasitology Laboratory, School of Veterinary Medicine, UCD for faecal egg counting.

For each flock, 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 through a 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 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 (epg).
Prevalence (proportion of flocks with *F. hepatica* eggs in faecal samples) was calculated nationally and for seven different regions of Ireland.

Table 1 *Fasciola hepatica* prevalence in the different Irish regions

Region	%
Border	54
Midland	48
West	40
Mid-East & Dublin	56
Mid-West	40
South-East	41
South-West	59

Results Overall prevalence of *F. hepatica* in the 254 flocks was 48%. Prevalence varied in different regions from 40% (West & Mid-West) to 59% (South-West) 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). 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 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. Further statistical analysis is required to more fully describe the data presented and allow design of appropriate control protocols.

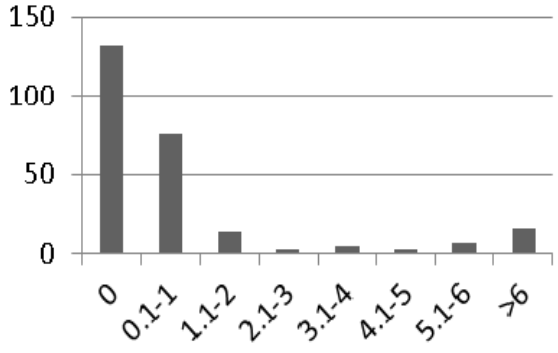

Figure 1 Quantity of farms with different FEC (X: number of farms, Y: FEC)

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.

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080

The effect of low-level laser therapy on the linear motility of chilled boar semen

H Varnes, R Cooke, T Coop
Writtle College, Essex, UK
Email:tracey.coop@writtle.ac.uk

Implications Linear motility of porcine semen is not effected by low level laser therapy *in vitro*

Introduction Low level laser therapy (LLLT) has been found to increase the linear motility of sperm notably the straight line velocity and the linearity coefficient (LIN) (Abdel-Salam *et al.*, 2011; Firestone *et al.*, 2012). The reaction of the cell to LLLT is dependent on the wavelength, power and dose rate of the laser used. Varying wavelengths of 655nm (in dogs), 830nm and 905nm (in humans) have proven successful in improving linear motility (Corral-Baquas *et al.,* 2005; Firestone *et al.*, 2012; Yazdi *et al.,*2013), with differing power and dose rates. However little research has been undertaken on the effects of these parameters in boar semen. The aim of this study was to compare different dose rates on the linear motility of boar semen.

Material and methods Chilled boar semen was divided into 200µl aliquots and incubated at 37°C. Using a 200mW single probe 820nm GaAIAs laser (Omega Laser Systems, Essex, UK) the treatment groups were irradiated for 5 seconds with differing doses (control, 8, 24 and 40 J/cm^2) with a pulse frequency of 2.5Hz. LIN of the spermatozoa in each group was assessed using the computer aided sperm analysis software SpermVision^{TM} immediately after irradiation and at 15, 30 and 45minutes according to manufacturer's guidelines (Minitüb, Germany).

Results No significant differences in LIN were observed between treatment groups over the time period, however after 45 minutes, sperm irradiated with the 40 J/cm^2 dose had higher linear motility (0.44 ± 0.009) than the control (0.41 ± 0.008) (Figure 1).

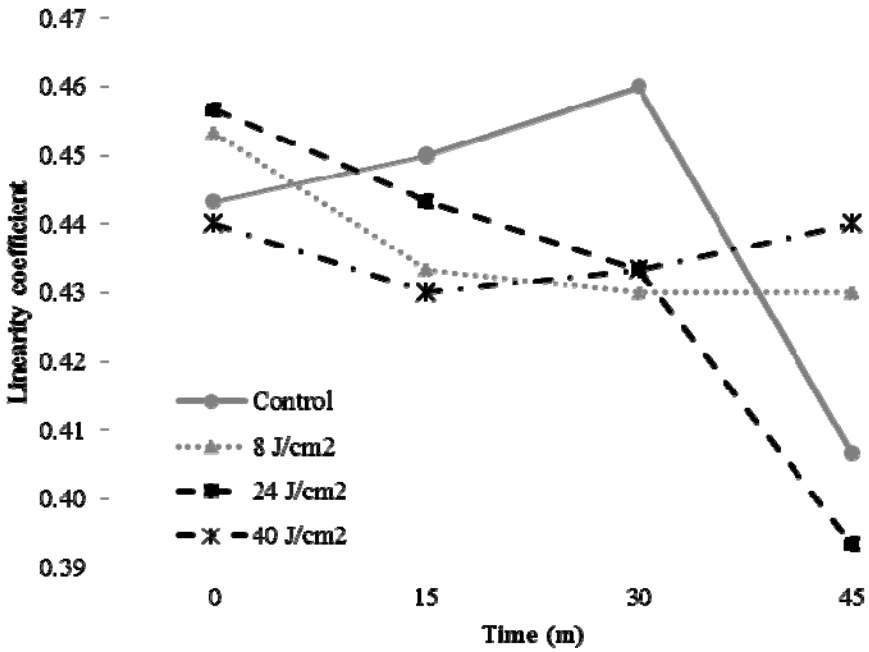

Figure 1 Effect of irradiation on linearity of spermatozoa

Conclusion These results demonstrate that LLLT at a dose of 40 J/cm^2 has the potential to increase linear motility in chilled boar sperm however, the results of this study are comparable to the results seen in research conducted by Firestone *et al.,* (2012) on normozoospermic samples after 30 minutes. Further work into doseage, pulse rate and irradiation time is required to determine if the effect seen in other species can be repeated with porcine semen.

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081

The relationship between lameness and body condition in dairy cattle

G Isaac, R Coffin, K Hunt
Sparsholt College, Hampshire, UK
Email:kerry.hunt@sparsholt.ac.uk

Implications The relationship between lameness and body condition is complex where body condition can be loss due to lameness or the loss of body condition can lead to lameness both causing an effect on the animal's welfare.

Introduction Lameness and high and low body condition are significant problems for dairy cow production and welfare. It was originally though that lame cows lost weight as a consequence of impaired mobility leading to a reduced time spent feeding. However since then it has been shown that cows with low body condition scores (BCS) go on to become lame due to the thinning of the digital cushions in the hoof. This can lead to increased movement of the third phalanx within the hoof horn which causes pressure necrosis and ulceration over the sole causing lameness (Bicalho *et al*., 2009). The aim of the present study was to assess the impact of body condition score (BCS) on the subsequent development of lameness in dairy cows and the inter relationship between BCS and lameness and the demographic factors that affect this relationship.

Material and methods The experiment was conducted on the herd of 49 Holstein Friesian (HF) and British Friesian (BF) (18:31) dairy cows. The cows were at various lactation stages and of various ages (μ= 6.45, SE=0.38). The cows were mobility scored and body condition scored (BCS) every two weeks over a three month period between June and September 2013. During these three months the cows were out at pasture 24 h/day and were milked twice daily in a 10 by 10 herringbone parlour. Cows in the last two months of lactation were also at pasture but were not milked twice daily. Cows in the milking herd were mobility scored whist walking across the yard after evening milking. This route was part of the cow's daily routine whilst heading out to pasture. The group of non-milking cows were mobility scored along a tack between two adjoining fields where they were grazing. The surface area of the yard and track was flat with a hard non-slip surface and was adequately lit. These parameters were put in place to allow the assessment to be accurate and consistence. The overall gait was assessed using a four point numerical rating system created by DairyCo. Cows were classifies as normal, imperfect locomotion, lame and severely lame. Cows that were deemed as lame were generally treated for lameness within 2-3 days of diagnosis. BCS was carried out while the cows were in cubical stalls, using a 5-score key with 0.25-unit intervals. The BCS was based on examination of the transverse processes of the lumbar vertebrae, ligaments of the pelvis, the ribs and surrounding fat created by DairyCo for farmers. Data was analysed by splitting the data set into groups dependent on body condition score and mobility score. Cows with a BCS of <2.5 were classed as having low BCS, BCS between 2.5 and 3.5 were classed as ideal and BCS >3.5 were classed as high BCS. Cows were classed as lame if they had a mobility score of either 2 or 3 and non-lame cows had mobility scores of either 0 or 1. Average BCS and mobility scores were used to assess the relationship of body condition and lameness using correlation analysis. Age, lactation stage and breed were statistically assessed using General Linear Modelling (GLM) to see what affect they have on the relationship between body condition and lameness

Results Low BCS was associated with an increased mobility score (P=0.044). A scatter plot of the relationship can be seen in figure 1. Age (P = 0.014), breed (P = 0.011) and lactation stage (P = 0.005) all had a significant effect on the relationship between body condition and lameness.

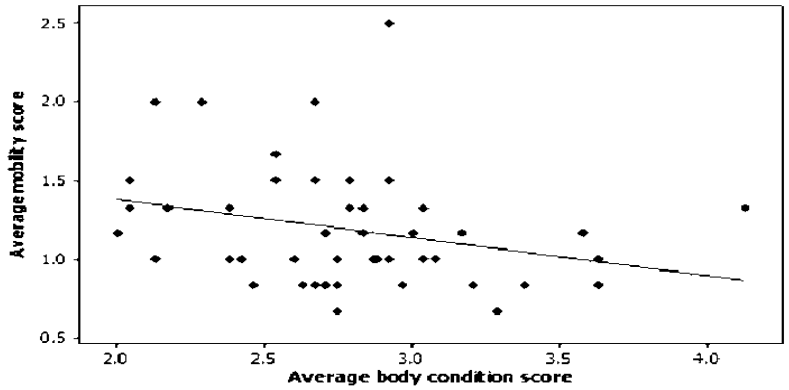

Figure 1 Scatterplot of the differences of body condition score vs. mobility score.

Conclusion When body condition decreases it has a significant effect and causes increased lameness. Given the increase risk in cows with a decreasing BCS of becoming lame it would be beneficial to maintain BCS of cows and prevent them from falling below three. Age, breed and lactation stage appear to have an effect on the relationship between lameness and body condition and merits further investigation over a longer period of time.

Acknowledgements The authors gratefully acknowledges Cornish View dairy farm.

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082

Practice-based veterinary research: fostering links between clinicians and academics

I Nanjiani
Westpoint Veterinary Group, West Sussex, UK
Email:ian.nanjiani@westpointfarmvets.co.uk

Increasing use of computerised recording systems in veterinary practices and farms give today's vets access to volumes of data we could only have dreamed of a decade ago. Turning this information into knowledge that can benefit clients and their owners is another matter, and the skills, resources and infrastructure to achieve this are not always available in veterinary practice. University hospitals and clinics have the benefit of accessible epidemiologists, statisticians, social scientists, an internal ethical review framework supported by Home Office Licences, legal support for informed client consent and interns and students needing projects can supply labour, and time allocated to write-ups and publications. Veterinary practices? Well you know the answer to that one…..

So why even consider conducting research in veterinary practice? Well, for a variety of reasons: practice offers a veterinary window on the "real world" of high first opinion case loads (compared to predominately referral populations in university hospitals), with variety in breeds, clinical presentations and disease, and on the livestock side of practice, access to farms with varying management and production systems, with sophisticated production data systems in "real-world" environment. Well designed studies in such populations are routinely conducted as part of the pharmaceutical registration process where randomised controlled trials "in the field environment" are required to generate field safety and efficacy data, and studies all the way down the evidence pyramid of case-control studies and case reports contribute to the evidence-base on which we aspire to stand as a profession. We have a highly skilled profession, with many enrolled in structured professional development programmes needing research projects, so how can we make the best use of this valuable resource?
Collaboration between academics and practitioners seems an obvious way forward. If the scientific and infrastructural support of the academic centres can be paired with the skill base, client base and case-load of busy practices, then we support a robust, "research-based" mentality in our profession, answering real research questions in the real world. Academics can have access to animal populations they could not access previously, practitioners can have access to design advice and support to ensure their investigations are conducted ethically and robustly, and ultimately the animals under our care benefit from an increased evidence base of robust science. What are we waiting for?

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083

Statistical exploration of Faecal Egg Count Reduction Test methods when investigating anthelmintic efficacy in cattle

J Love[1], L A Kelly[1], C Robertson[1], M A Taylor[3], I Nanjiana[2]
[1]University of Strathclyde, Glasgow, UK, [2]Westpoint Veterinary Group, London, UK, [3]VParST Ltd, E Riding of Yorkshire, UK
Email:johnathan.love@strath.ac.uk

Implications The results of this work could lead to changes in current practices and guidelines for the investigation and classification of the efficacy of anthelmintic treatments in cattle.

Introduction For many years, the animal health industry has advocated the use of anthelmintic treatments to control parasitic nematode infections in livestock. Over the past thirty years, however, the use of such treatments has been increasingly under threat due to parasite populations becoming resistant to products in use. In order to determine treatment efficacy, and thus classify populations of worms as resistant or not, worm control experts have relied on the use of the "Faecal Egg Count Reduction Test" (FECRT); based on World Association for Advancement in Veterinary Parasitology (WAAVP) guidelines (Coles *et al,* 1992, 2006). These guidelines make recommendations on both test performance and statistical analysis and data interpretation in an effort to quantify levels of resistance present at the farm level. Whilst aimed primarily at sheep, the guidelines are also used for FECRT in cattle. However, due to differences in levels of faecal egg outputs between sheep and cattle and the limits of detection in faecal egg count (FEC) methods; the guidelines applied to cattle have come under much review. A collaborative project involving the authors has been set up in which one of the aims is to evaluate a range of analytical and statistical methods on extensive field data collected over 3 grazing seasons in which cattle were screened, treated and monitored for parasitic nematode infections using several FEC methods and sensitivities.

Material and methods Parasitological field studies were carried out over 3 grazing seasons from 2012-2014, on first year grazing calves on farms across England (Defra funded project VM0503). In these studies groups of cattle were monitored by routine FEC methods until they reached the recommended group mean threshold of 150 eggs per gram (epg) of faeces, at which point an FECRT was conducted to determine anthelmintic efficacy of the product(s) used. Various permutations of the studies were conducted, which were based on the numbers of animals on farm, the products used , and whether some farms, had both one or more treatment groups and negative control groups. This led to the production of large datasets on cattle nematode burdens, responses to treatment with different anthelmintic products and classes, and preliminary analyses and interpretations of anthelmintic efficacy and resistance. Since then, statisticians from the Department of Mathematics and Statistics, University of Strathclyde have been exploring both the data and the statistical methodologies in greater depth. Differing and appropriate statistical techniques are being investigated and will be presented for consideration to future working groups on anthelmintic resistance. The work is being analysed as part of a PhD programme, supported by the Engineering and Physical Sciences Research Council and Defra. As a result, this investigation presents the use of large datasets in veterinary research and the synergy between veterinarians, parasitological field experts and academics.

Results This investigation shows that the current recommended methods of comparing pre and post treatment faecal egg counts to untreated controls may not always be robust enough in the presence of over dispersion associated both between group, and within individual animal variability. Alternative approaches based upon Poisson Regression and Bayesian Models will be illustrated and compared to current methods and the advantages and disadvantages of all approaches illustrated. These newer methods should give clear indications when the recommended methods are not as strictly valid, and should also result in more robust confidence interval calculations.

Conclusion The work highlighted in this abstract aims to emphasise the valuable collaboration and synergy between students, academics and field experts, and how this can benefit research - particularly in the veterinary and parasitological fields - of current and topical issues.

Acknowledgements The authors gratefully acknowledge funding from the Engineering and Physical Sciences Research Council and Defra.

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084

Prevalence and herd-level risk factors for *Fasciola* spp and other trematode infections in cattle in Kwara State, North-Central Nigeria

N Elelu[1], A G Ambali[2], G C Coles[1], M C Eisler[1]
[1]University of Bristol, UK, [2]University of Ilorin, Kwara State, Nigeria
Email:nusirat.elelu@bristol.ac.uk

Implications The burden of *Fasciola* infection was found to be higher than in previous abattoir surveys, highlighting the importance of the parasite in Kwara State, Nigeria. Risk factors were identified that could be helpful in formulating control strategies.

Introduction Trematode infections of livestock are of global veterinary and public health importance and cause serious economic losses. Fasciolosis caused by *Fasciola gigantica* is estimated to cause an annual loss in cattle of up to US$ 840M in Africa (Spithill *et al*., 1999). Approximately 165 million cattle are likely to be infected with *Schistosoma* spp worldwide (De Bont *et al* 1994). The majority of data on the burden of *Fasciola* infection in Nigeria are based on abattoir surveys and there are few data on herd level risk factors. This study investigated the prevalence and herd level risk factors of trematode infections in cattle in Edu local government area, Kwara State, Nigeria.

Material and methods A cross sectional survey using a two-stage study design was carried out to investigate cattle within households. A total of 65 households were sampled from 11 villages. Two questionnaires were administered for household-level and individual cattle-level data. Faecal samples were obtained from the cattle, coprological analyses were carried out using the commercially available Fluke Finder® and trematode eggs identified microscopically. Cattle body condition scores were evaluated using a nine point scale (Nicholson and Butterworth, 1986). All locations were geo-referenced using a handheld GPS. Statistical analysis were carried out using Microsoft excel® and SPSS® version 21. Spatial analysis was also carried out using QGIS® software version 2.4.

Results Of 686 faecal samples analysed, 514 (74.9%), 110 (16.1%), 50 (7.3%) and 8 (1.2%) were positive for *Fasciola,* paramphistomes, *Dicrocoelium* and *Schistosoma* infections respectively. *Fasciola* had higher prevalence in adult cattle (77.3%) than those under 2 years of age (62.5%). One hundred (14.6%), 40 (5.8%) and 5 (0.7%) of the animals studied had a co-infections of *Fasciola* with paramphistome, *Dicrocoelium* and *Schistosoma* respectively. Male cattle had significantly higher body condition scores than females (P=0.001). Cattle in herd size greater than 100 were less likely to have *Fasciola* infections than those of smaller herds (odds ratio [OR] 0.28; 95% confidence interval [CI]: 0.14-0.58). While adult cattle (≥2 years) were more likely to be infected (OR 1.94; CI: 1.19-3.16) than younger cattle. Cattle belonging to household heads aged between 40-59 years were more likely to be infected with paramphistomes (OR 1.95; CI: 1.02-3.74) than those belonging to other age groups, while those belonging to the Zabaruma ethnic group were less likely infected (OR 0.05; CI: 0.01-0.22) than the Fulani or Zimbabwean farmers. Cattle in herds size greater than 100 were more likely to be infected with *Dicrocoelium* than those in smaller herds (OR 6.98; CI: 2.94-16.6), while those with body condition score greater than 7 were less likely to be infected (OR 0.01; CI: 0.03-0.49). Distribution maps of the prevalence of the various trematodes could be useful for investigation of possible associations between prevalence and intermediate snail host habitats such as watercourses.

Conclusion This study revealed a very high prevalence of *Fasciola* infection (74.9%) in Kwara state. This is considerably higher than the 22.5% prevalence rate reported in a previous abattoir study in the state capital (Adewole 2010). Risk factors identified in surveys such as this including herd size, cattle age and body condition score could assist in tailoring control strategies for various trematode infections to particular groups of farmers and cattle.

Acknowledgements University of Bristol, UK and University of Ilorin, Nigeria are thanked for providing support and enabling the research. We are also grateful to the staff of the Kwara State Ministry of Agriculture and the participating farmers.

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085

An investigation into the proportion of Schmallenberg virus affected lambs born into flocks where Schmallenberg virus has previously been diagnosed

S Young[1], I Nanjiani[1], P Williams[2]
[1]Westpoint Veterinary Group, West Sussex, UK, [2]MSD Animal Health, South East, UK
Email:shona.young@westpointfarmvets.co.uk

Implications The results of this project could help determine the impact of Schmallenberg virus (SBV) on farms which were known to have been exposed previously. It also demonstrates the value of collecting lambing data for monitoring flock performance.

Introduction The main aim and objective of the research was to investigate the proportion of SBV affected lambs born in flocks where SBV exposure has been previously confirmed. The flocks involved had been screened serologically under a separate project (Nanjiani *et al* 2013), to determine seropositivity rates which ranged from 4-83% across the 6 farms. A proportion of the flock had birth outcomes recorded at lambing time.

Material and methods 6 farms were selected to be involved in the project, all of which had SBV affected lambs born in 2012. Flock infection was confirmed by SBV serology as part of a separate study, and each farm had to have at least 200 breeding ewes. The aim was to follow a group of at least 200 ewes and record their individual lambing data. Farms had to be willing to comply with keeping accurate lambing records, and willing to submit lamb carcases for *post mortems*. All farmers were met on farm prior to the start of the project to clarify requirements and identify which group of sheep to record.
Data was collected from all ewes at lambing in a pre- selected group. Ideally both replacements and adult ewes were to be included. Data requested included ewe ID, litter size, number of lambs born dead, number of lambs dying within the first week of life, signs of SBV and whether the ewe was a replacement or not. This data was checked throughout lambing by either a technician or vet to ensure compliance. Suitable lambs to submit for *post mortem* examination included aborted lambs, lambs with clinical signs of SBV and lambs which were born dead, or died within the first week of life.

Results 2 farms had lambs born with possible SBV signs from 2 litters, and 1 deformed lamb born. All were negative for SBV antibodies and the deformed lamb was also negative on PCR. One farm had one lamb with possible SBV signs, which was negative on diagnostics. One deformed lamb was born which was not submitted for *post mortem* due to adverse weather conditions.
The other 4 farms had no lambs with clinical signs of SBV, and all diagnostics carried out for SBV antibody on foetal fluids were negative except for one lamb. This lamb died at 24 hours old and had suckled, so the antibody could have been maternally derived; its littermate died at birth and was SBV antibody negative. The dam was antibody negative when sampled in December, but was not re-tested.
Lambing percentage between the 6 farms ranged from to 114% to 228%. Mortality rate in the first week of life ranged from 2.2% to 17.1%. For the 2 farms which supplied weaning data, mortality rate between 7 days old and weaning was 24.1% and 16.8%. Enzootic abortion was diagnosed on aborted lambs on one farm. Toxoplasmosis was diagnosed in one lamb on one other farm.

Conclusion In all 6 of our farms, only 2 deformed lambs and 3 with possible SBV signs were born. All SBV diagnostics carried out were negative except for 1 lamb which was SBV antibody positive. We cannot rule out that SBV has been involved on these farms and may indeed have caused early embryonic loss, resulting in the small litter sizes seen on some farms. Without the use of paired serology at this time of pregnancy, we cannot rule out its involvement at this stage of gestation. However, as all of our diagnostics, with the exception of one antibody titre, were negative it is proposed that SBV had no or very little impact on lambs born into flocks previously affected with SBV.
Recording flock performance at lambing, proved valuable on each farm, identifying performance, and consequently highlighting areas responsible for either low lamb numbers or high lamb deaths. Specific action plans and targeted improvements to increase flock productivity on each of these farms can consequently be developed.

Acknowledgements Erin Caswell, Peter Aitken and Andre Baptista, members of the Westpoint Veterinary Group sheep working group for their help with data collection. Thanks to MSD Ruminant Research Bursary for funding.

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086

Prevalence of *Trypanosome* species in Nigerian breeds of sheep in Abeokuta and its environs using polymerase chain reaction

I K Oyewusi, M I Takeet, A O Talabi, J A Oyewusi, O O Adeleye, E B Otesile
Federal University of Agriculture, Abeokuta, Ogun State, Nigeria
Email:gbengamcf@yahoo.co.uk

Implications PCR is a more sensitive and precise diagnostic technique in the diagnosis of trypanosomiasis than the haematocrit centrifugation technique (HCT) and wet blood film.

Introduction Among domestic ruminants, sheep have been observed to be the least susceptible to natural trypanosomiasis and fewer in-depth studies have been conducted on sheep compared to cattle and goats (Osaer *et al*., 1994). There has been a dearth of knowledge on the use of PCR as a diagnostic tool for trypanosomiasis in Nigeria

Material and methods About 5ml of blood was collected from the jugular vein of 243 sheep consisting of 97 West African Dwarf, 60 Yankassa, 62 Ouda, 19 Balami and 5 Crossbreeds of Nigerian breeds of sheep into tubes containing di-potassium ethylene di-amine tetra acetic acid (K_2EDTA) as anticoagulant. The detection of typanosomes was first carried out by haematocrit centrifugation method and by wet blood film (Murray *et al*., 1977). For the molecular detection, DNA was extracted from the blood using Quick-gDNA™ Mini-Prep as described by the manufacturer. PCR primers were selected for optimization based on previously published work (Takeet *et al.,* 2013). These primers were optimized with DNA extracted from the blood of cattle that were parasitologically positive for *T. vivax, T. congolense, and T. brucei* which led to final selection of seven primer sets for this study. PCR amplification was performed in 20 µl final reaction volume containing equivalent of 20 ng of genomic DNA 10mM Tris-HCl, pH 8.3, 1.5mM $MgCl_2$, 50 µM KCl, 200 µM each of dNTPs, 40ng of each of the primers and 1 unit of Taq DNA polymerase (Bioneer, Inc. Alamada CA USA). The reactions were placed in a MJ MINI™ Personal Thermocycler model PTC-1148 (Biorad, Hercules, CA, USA). The reaction conditions were followed as described by (Takeet *et al.*, 2013). The data were summarized using descriptive statistics.

Results None of the 243 samples was positive for *Trypanosoma* sp. using the HCT and wet blood film. Of the 243 samples, 35.4% were positive for *Trypanosoma* sp. by PCR, 33.7% of these positive samples were mixed trypanosomes infection while the remaining 66.3% were single trypanosome infection. The results of the PCR assays are presented in Table 1.
The breed specific prevalence were WAD (25.8%), Yankassa (36.7%), Ouda (43.5%), Balami (47.4%) and Crossbreeds (60%). The prevalence of *Trypanosoma* species/sub-species recorded were *T. vivax* (23.05%), *T. congolense* Savannah (13.38%), *T. congolense* Forest (7.82%), *T. congolense* Kilifi (0%), *T. brucei brucei* (4.53%), *T. brucei gambiense* (0%) and *T. brucei rhodesiense* (0%).

Table 1 Species prevalence of trypanosomes in Nigerian breeds of sheep

Breed	Number (percentage) positive of species/subspecies of trypanosomes						
	T. vivax	*T. congolense*			*T. brucei*		
		Savannah	Forest	Kilifi	*brucei*	*gambiense*	*rhodesiense*
WAD	11(11.34)	2(2.06)	10(10.31)	Nil	7(7.22)	Nil	Nil
Yankassa	14(23.33)	12(20)	2(3.33)	Nil	2(3.33)	Nil	Nil
Ouda	22(35.48)	12(19.35)	5(8.06)	Nil	1(1.61)	Nil	Nil
Balami	7(36.84)	5(26.32)	2(10.53)	Nil	Nil	Nil	Nil
Crossbred	2(40)	2(40)	Nil	Nil	1(20)	Nil	Nil
Total	56(23.05)	33(13.38)	19(7.82)	Nil	11(4.53)	Nil	Nil

Conclusion: The finding underscores the higher sensitivity of PCR technique compared to HCT and wet blood film. The higher overall prevalence (35.4%) of trypanosomiasis in sheep in the study area implies the endemicity of the disease with potential reservoir host to other livestock particularly a serious threat to cattle production.

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Schmallenberg virus in a sero-endemic region: surveillance using individual blood and bulk tank milk samples

Á B Collins[1,2], A Hallinan[4], J Grant[3], D Barrett[5], M Doherty[2], J F Mee[1]
[1]Teagasc, Animal and Bioscience Research Department, Moorepark Research Centre, Fermoy, Co. Cork, Ireland, [2]Faculty of Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland, [3]Teagasc, Applied Physics and Statistics, Kinsealy Research Centre, Malahide Road, Dublin 17, Ireland, [4]Brucellosis Testing Laboratory, Department of Agriculture (DAFM), Food and the Marine (DAFM), Model Farm Road, Bishopstown, Cork, Ireland, [5]Sligo Regional Veterinary Laboratory, DAFM, , Doonally, Co. Sligo, Ireland *Email:aine.collins@teagasc.ie*

Implications The within-herd and between-herd seroprevalence of Schmallenberg virus (SBV) varied widely in this sero-endemic region. Bulk milk tank (BMT) samples are moderately predictive of within-herd SBV seroprevalence.

Introduction 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 relationship between BMT and blood ELISA results is also unknown. The objectives of this work were to determine the SBV seroprevalence in a seroendemic region and to determine the relationship between blood and bulk milk ELISA results for SBV.

Material 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 14 March and 5 April 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 Animal-level seroprevalence was 61.1%. Seronegative animals (38.0%) were predominantly replacement heifers (97.4%). Within-herd seroprevalence ranged widely (8.3% to 97.5%) 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) suggesting seropositive animals can be present in herds with negative BMT values. A large population of seronegative animals, principally less than 2 years old, were identified. This suggests 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. A positive relationship was found between the mean herd seroprevalence and the level of SBV antibodies in bulk tank milk. Blood and milk ELISA results were closely 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 (81.02 and 81.45), 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.

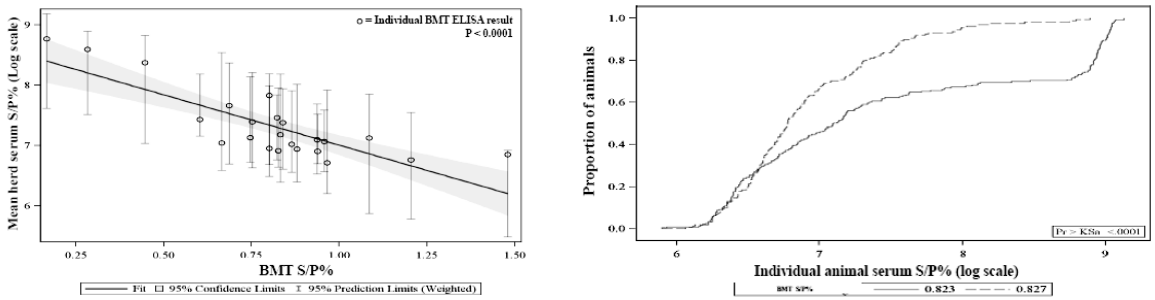

Figure 1 Relationship between herd mean serology and BMT results (left) and between individual animal serology and BMT results (right)

Conclusion There was wide variation in between-herd and within-herd SBV seroprevalence in this seroendemic region. The moderate-high correlations between mean herd serum and BMT ELISA results (r = 0.75-0.85) suggest BMT-ELISA results are a moderate predictor 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.

Acknowledgements This research is funded by the Teagasc core programme and the Walsh Fellowship Scheme.

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Longitudinal study of a Johne's disease control programme on an Irish dairy herd

A E Kennedy[1,2], N Byrne[1], J O Mahony[2], R G Sayers[1]
[1]Teagasc, AGRIC, Fermoy, Cork, Ireland, [2]Cork Institute of Technology, Cork, Ireland
Email:aideen.kennedy@teagasc.ie

Implications Test and cull programmes for JD may prove more effective in Ireland than elsewhere.

Introduction Infection with *Mycobacterium avium* subspecies *paratuberculosis* (MAP) causes Johne's disease (JD). Clinical JD is characterised by diarrhoea and progressive cachexia, which ultimately results in death. The reported impact of JD on on-farm profitability and animal health has led to interest in the control of MAP at farm level. Animal Health Ireland (AHI) recently launched a pilot control programme for JD in Ireland with ELISA testing forming an integral part of the scheme. While faecal culture is considered the gold standard test for MAP, ELISA testing is still the method of choice for epidemiological studies and herd-based diagnosis (Gilardoni *et al*., 2012). With this in mind the aim of this study was to report the results of a control programme on an Irish dairy herd involving serial ELISA testing.

Material and methods A 139 cow, spring calving, dairy herd was recruited to the study. Prior to study commencement no clinical case of JD was ever identified. A sampling protocol was implemented in May 2012 involving monthly collection of blood and milk samples for MAP ELISA testing. Serum (S) and milk (M) samples were tested in a commercial laboratory using the ID Screen Paratuberculosis Indirect Screening Test (ID Vet, Montpellier, France). Faecal samples were collected from consistently ELISA positive cows and tested by microbial culture and PCR. Animals considered highly suspect on the basis of ELISA or faecal culture/ PCR were culled and subjected to complete pathological examination (PE).

Results A maximum of 10% of the herd tested MAP positive (this excludes the 3 month period post TB testing where studies show an increase in MAP ELISA positives). A total of ten animals yielded PCR positive results. Veterinary examination did not yield any clinical signs of JD in these animals. A decision was taken to isolate and cull the cow repeatedly recording the highest ELISA S/P% ratio (M&S) and PCR results. On PE severe gross changes consistent with JD were identified (July 2013). In winter 2013 a further 10 cows, with similar S/P% ELISA positive results (M&S) and number of positive tests, as the JD positive cow, were selected for culling and in depth PE. Of these, 4 had previously tested PCR positive although at a lower level than the JD positive cow. All cows were JD negative on PE. Any remaining ELISA positive cows were calved in isolation and returned to the milking herd following calving. Within two months of return to the herd, all remaining previously positive cows (n=5) recorded negative results on ELISA (M&S). Whole herd ELISA negative results (M&S) have been obtained during monthly samplings in 2014. A number of international studies report that 'test and cull' programmes are largely ineffective in eradicating JD from a herd (Kudahl *et al*., 2007). Prior to commencement of this study no management practices were implemented on farm to minimise JD, indicating that results from the current study are based on culling practices alone.

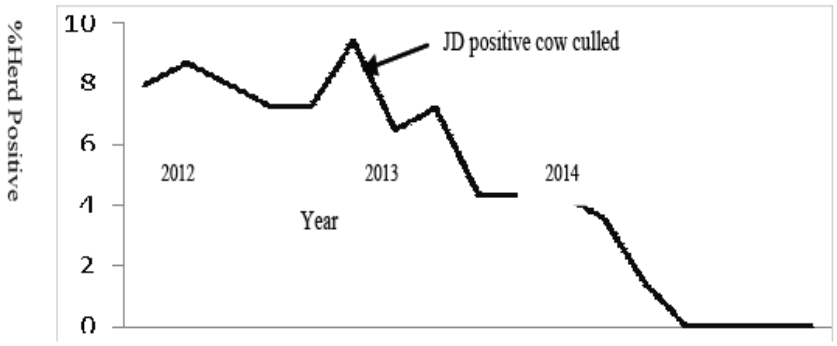

Figure 1 Proportion of herd ELISA positive over a 3 year period.

Conclusion Based on the results of the current study, 'test and cull' programmes based on ELISA and PCR may prove more effective in Irish herds than internationally reported. Further investigation is required to determine if this approach is applicable to other herds and, if so, why this is the case in Ireland.

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Cost-benefit simulation analysis of vaccination against contagious agalactia of dairy sheep in Greece

G E Valergakis, S A Termatzidou, A I Gelasakis, G Arsenos
Aristotle University, School of Veterinary Medicine, Thessaloniki, Greece
Email:geval@vet.auth.gr

Implications Farmers must be able to make informed decisions regarding the cost and benefits of preventive veterinary practices, in this case, vaccination against contagious agalactia of dairy sheep.

Introduction Contagious agalactia (CA) is a common disease of dairy sheep and goats in southern Europe (Sargison 2008, Scott 2010). It results in substantial financial burden due to high milk losses which is the main source of income in dairy sheep and goat production systems. Moreover, CA is associated with high morbidity and mortality rates. The losses are not limited to the year of infection; CA has carryover effects the following year, e.g. delayed reproduction, abortions and smaller flock size due to mortality/culling. Vaccination against the dominant pathogen *Mycoplasma agalactiae* is not common practice among sheep farmers, despite the fact that the disease is endemic in Greece and considering that vaccination is proven effective. The aim here was to estimate the financial losses of CA in relation to vaccination costs.

Material and methods A simulation was undertaken considering published data and clinical experience. The factors in the model were the level of milk production (kg/ewe/year; 5 classes: 150, 200, 250, 300, 350 kg), morbidity rate (from 20% to 50%, 7 classes with 5% increments), treatment rate (2 classes, either morbid ewes only or all flock ewes), mortality/culling (50/50) rate (from 5% to 25%; 5 classes with 5% increments) and milk losses (from 10% to 50%, 9 classes with 5% increments). The latter are representative of the situation in practice because CA can appear either early or late in the milking season. Losses were calculated as follows: a) treatment costs (average ewe: 60kg BW), 2.7 €/ewe (long-acting oxytetracycline, i.m., 20mg/kg BW once and tylosine, i.m., 10mg/kg BW for 3 days), b) mortality/culling costs, 165 €/replacement ewe (60 € for a 2-month grade ewe-lamb, 90 € feed costs plus 30 € for other expenses until first lambing at 14th month of age, minus 30 €/cull ewe) and, c) milk losses, 0.7 €/kg (milk price 0.97€/kg, concentrate price 0.39€/kg, 0.7 kg of concentrates/kg of milk). A 20% increase was added to total losses to account for the decreased production the year following the outbreak. The 5x7x2x5x9 factorial arrangement of the variables resulted in 3,150 scenarios. The effects of variables on losses were estimated with analysis of variance (SPSS 21.0). All factors were fitted as fixed effects in the model. The vaccination schedule included primo-vaccination (twice) of flock replacements (25%) and 6-month boosters for the breeding flock, resulting in a total of 2.5 vaccine doses/ewe/year (1.75€/ewe/year).

Results Mean losses/ewe (min-max) were 69.9€ (23.2-115.7), 82.5€ (27.4-136.7), 95.1€ (31.6-157.7), 107.8€ (35.8-178.7), and 120.4€ (40.0-199.7), for ewes producing 150, 200, 250, 300 and 350 kg of milk/year, respectively (Figure 1). Vaccination costs would break-even with CA losses if flocks were infected once in 40, 47, 54, 61 and 69 years, for the 5 milk production classes, respectively. On average, milk losses, mortality/culling and treatment costs represented 66.4%, 31.3% and 2.3% of the total, respectively. Statistically significant effects on losses (P<0.001) are shown in Table 1. Morbidity had no effect, due to confounding with treatment rates.

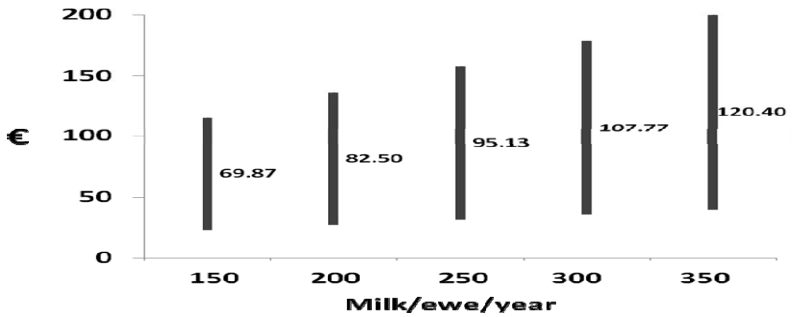

Figure 1 Losses (€) due to CA based on milk production level

Table 1 Factors affecting losses from CA and corresponding adjusted Wald statistic (F)

Factor	F
Milk production per ewe	4,212.000
Treatment rate	2,600.265
Mortality/culling rate	4,875.000
Milk loss	8.604
R^2 0.955	

Conclusion Financial losses from CA can be very high and vaccination is an efficient and low cost practice to avoid them. Veterinarians must consider the epidemiology of CA and communicate the risk for each flock to the farmers.

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090

The consequences of protein supplementation during gestation on performance and immune parameters in mammals

A Masuda[1], J E Allen[2], J G M Houdijk[1], S Athanasiadou[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]Institution of Infection and Immunology, University of Edinburgh, UK
Email:aya.masuda@sruc.ac.uk

Implications Protein supplementation leads to improved physiological and immunological status in pregnant animals.

Introduction Animals experience dramatic changes in their physiological and immunological status throughout gestation associated with a need to maintain the growth of their foetus. Livestock animals are often feed-restricted at these times, and highly likely to allocate their scarce nutrients to maintain reproductive effort rather than to immune function (Barger, 1993; Coop and Kyriazakis, 1999). Here, we tested the hypothesis that host growth performance and immune responses during late pregnancy are sensitive to dietary protein level.

Material and methods Second parity female Sprague Dawley rats were given a primary infection of 1600 *Nippostrongylus brasiliensis* 3rd stage larvae subcutaneously 14 days prior to mating. Once mating was confirmed (day 0) all rats were fed a diet with 200g crude protein (CP) per kg dry matter (DM) *ad libitum* until day 10. Then, rats went under restricted feeding with diets containing either 60 (L, n=6), or 200 (H, n=7) g CP per kg DM until day 20. Restricted feeding was achieved by giving the same amount as mean DM intake between day 5 and day 10. Dam weight and food intake were recorded daily; on day 20, rats were killed by CO_2 asphyxiation. Litter weight and numbers were recorded. Spleen, mesenteric lymph nodes (MLN) and small intestine were removed for gene expression analysis, and serum for determining immunoglobulin (Ig) levels. Candidate genes for gene expression analysis included Type 1 immunity related molecules; IFN-γ, TNF-α, ICAM-1, and iNOS, Type 2 immunity related molecules; IL-13, PPAR-γ, Arginase 1, 12/15 Lipoxygenase, and Goblet cell related molecules; Relm β, MUC 2 and Tff3. Live weight and food intake were analysed through repeated measures ANOVA, using initial body weight and average food intake from day 5 to 10 as covariates respectively. Diet effects on dam organ, foetus weight and all immune responses (Ig and mRNA level) during gestation were analysed by one-way ANOVA. Log transformations were performed to stabilise the variance where necessary before statistical analysis. All statistical analyses were carried out using GenStat 15th edition. $P<0.05$ was considered significant.

Results There was a significant diet × time interaction on both DM intake ($P=0.003$) and dam weight ($P=0.005$) over gestation period. L rats had smaller DM intake and weight gain compared to H rats (Figure 1). Liver weight was significantly heavier in H animals (5.031 % body mass) compared to L (3.675 % body mass, SED 0.205, $P<0.001$). Individual foetus weight was significantly heavier in H (3.689g) animals compared to L (3.116g, SED 0.129, $P=0.001$). Spleen weight and serum Ig levels were not affected by gestation diet. Expression of intestinal ICAM-1 was significantly higher in L rats ($P<0.05$). In spleen, 12/15 Lipoxygenase, Arginase 1, PPAR-γ and IFN-γ mRNA levels were significantly higher in H rats ($P<0.05$).

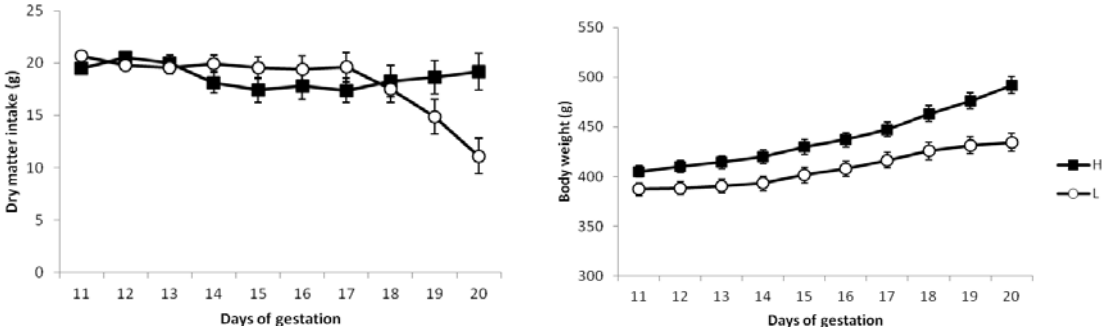

Figure 1 DM intake (left) and dam weight (right) during gestation.

Conclusion Maternal performances, as evaluated by dam and foetus parameters, and immune responses measured in the spleen and small intestine were affected by dietary protein level. High protein intake during gestation improved maternal performances and created an immunological environment biased towards a Type 2 immunity, which promotes effective expulsion of nematode parasites (Anthony *et al*., 2007).

Acknowledgements The authors would like to acknowledge the funding from SRUC and Japanese Student Services Organization.

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Early host responses to *Clostridium perfringens* in two commercial breeds as measured *in situ*

KM Russell[1], P Kaiser[2], NH Sparks[1], V Parreira[3], JF Prescott[3], MA Mitchell[1], RE Clutton[2], T Kanellos[4], S Athanasiadou[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]The Roslin Institute and R(D)SVS, University of Edinburgh, UK, [3]Department of Pathobiology OVC, University of Guelph, Ontario, Canada, [4]Zoetis, Paris, France
Email:kay.russell@sruc.ac.uk

Implications Immune responses of broilers of two commercial breeds may be subverted by strains of *C. perfringens* containing the *netB* virulence gene. This could have implications for future preventative treatments such as vaccine candidates and nutritional supplements.

Introduction Necrotic Enteritis (NE) is a disease which impacts on health and welfare of broilers. Antibiotics are commonly used as a treatment which increases production costs to the industry. The NetB toxin produced by *C. perfringens* is one of the main virulence factors contributing to disease pathogenesis. Host responses are not well characterised, but gross pathology and antibody levels appear to differ between commercially available breeds (Jang *et. al* 2013). Here, we used a previously developed *in situ* model (Russell *et.al* 2014) to characterise host responses from two commercial breeds when exposed to virulent and avirulent *C. perfringens* strains.

Material and methods Cobb and Hubbard broilers (n=10/breed) were anaesthetised and three, *in situ*, isolated loops were created in the duodenum (Athanasiadou *et. al* 2011). Loops contained one of: i) Control preparation (bacterial culture media alone), ii) bacterial culture from a wild type virulent *C. perfringens* strain (CP1) or iii) bacterial culture of the *netB*-mutant avirulent strain (CP1M). Four hours post infusion the loops were removed and processed for histological examination, immunohistology and gene expression analysis. Antibodies for macrophages/monocytes (KUL01) and γδ T cells (TCR1) were used on cryosections to quantify the area occupied by immune cell types in the different treatments. The expression of genes related to pro-inflammatory responses (IL-6, IFNγ, IL-1β), disease pathogenesis (FAS) and antigen presentation (B-LA) were measured. A two-way ANOVA was carried out on log-transformed data to determine statistical differences between the two breeds (Cobb and Hubbard) and the three loop treatments (Control, CP1 and CP1M).

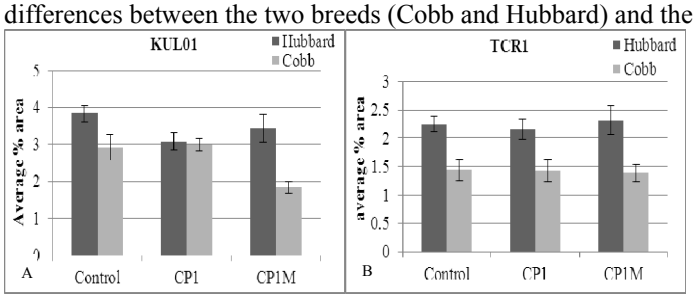

Figure 1 Average % area identified by ImageJ on cryosections.

Table 1 Average gene expression for each loop treatment. Different letters within row indicate significant differences in expression between loop treatments.

		Loop treatment		
Gene	Transformation	Control	CP1	CP1M
FAS	Log10	-0.96[a]	-1.60[b]	-1.25[c]
B-LA	N/A	7.86[a]	6.80[a]	14.52[b]
IL-1β	Log10	1.48[a]	1.23[b]	1.82[c]
IL-6	Log10	-1.07[a]	-1.24[b]	-0.86[c]
IFNγ	Log10	-1.85[a]	-1.09[b]	-1.36[c]

Results The area positive for the KUL01 marker was greater in Hubbard broilers compared with Cobb ($p=0.0072$). The positive area for the same marker was smaller in the CP1 and CP1M loops compared with the control ($p=0.0053$). There is also a significant interaction, where the positive area for KUL01 was smaller in the CP1M loop in Cobb broilers compared to the other treatments. Hubbard birds showed greater area positive for TCR1 compared to Cobb birds ($p<0.001$); (Figure 1A & B).
mRNA expression of IL-6, IFNγ, IL-1β was increased in CP1M loops compared with control loops. CP1 reduced IL-6 and IL-1β mRNA expression compared to control loops but increased IFNγ expression. B-LA was increased in CP1M loops compared with control and CP1 loops. Reduced FAS mRNA expression was detected in CP1 and CP1M loops compared with control loops.

Conclusion Increased positive areas for both KUL01 and TCR1 stained sections were observed in Hubbard broilers indicating differences between these two commercial breeds may influence the size and number of macrophages and γδ T cells present in the duodenum prior to any challenge. As the two *C. perfringens* strains only differ in their ability to express NetB toxin, increased levels of IFNγ in CP1 treated loops may indicate that this effect could be mediated by NetB specifically. The lower mRNA levels of IL-6, IL-1β and B-LA in loops containing the wild type in comparison to the mutant strain may indicate a mechanism for the *netB* virulence factor to subvert the immune response.

Acknowledgements The authors gratefully acknowledge the funding from the BBSRC and Zoetis for this work.

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092

In vitro screening of anti-parasitic properties of four Ethiopian medicinal plant extracts

K Tolossa[1,2], S C Fry[2], S Athanasiadou[1], G J Loake[2], J G M Houdijk[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]Institute of Molecular Plant Sciences, University of Edinburgh, UK
Email:ketema_tolossa@yahoo.com

Implications The *in vitro* egg hatch inhibition (EHI) assay results support the view that the four plants tested have anti-parasitic properties, and informed us *Adenia* sp. and *Cissus ruspolii* would be the most promising plants for further phytochemical studies.

Introduction Many smallholder farmers and pastoralists rely on their indigenous knowledge, practices and locally available plants for the management of parasitic infections both in humans and livestock (Tolossa *et al*. 2013; Tekle, 2014). In this study, we conducted *in vitro* EHI assays of four Ethiopian medicinal plant crude extracts using a standard anthelmintic evaluation method (Coles *et al*, 1992) on *Teladorsagia circumcincta* eggs to validate the claimed activity and to choose the most promising medicinal plant(s) for further phytochemical studies.

Material and methods Four plants were selected during an ethno-medicinal study in South-Western Ethiopia (Tolossa *et al*. 2013). Powdered plant materials of *Adenia* sp., *Cissus ruspolii*, *Euphorbia* sp. and *Ipomoea eriocarpa* were extracted by maceration, under continuous stirring, using four solvent systems (acetone, methanol (MeOH), 70% MeOH and de-ionized water) for 72 hours at room temperature. The supernatants were filtered using four layers of Miracloth, centrifuged, dried by rotary evaporator (organic extracts) or freeze dryer (aqueous extract), weighed, and then stored at -20^{o}C pending analysis. *T. circumcinicta* eggs were obtained from donor sheep faeces using saturated salt flotation technique. The EHI assays were done by incubating the parasite egg suspension with plant extracts using 24-well culture plates at 25^{o}C and 90% RH. Incubation was stopped by Lugol's reagent after 48 h. The total numbers of unhatched eggs and hatched first-stage larvae were counted microscopically. Data were expressed as fractions and arcsin transformed prior to 4×4×3 factorial analysis to examine the effect of plant, solvent, concentration and their interactions, and are reported as back-transformed means.

Results We observed a highly significant three-way interaction between plant, solvent and concentration ($P<0.001$; Figure 1), indicating that the EHI increased with increasing extract dose, although these increases differed in magnitude between the plant solvent combinations used. At a 10 mg/mL concentration, 70% MeOH extracts (*C. ruspolii*) and aqueous extracts (*C. ruspolii* and *Adenia* sp.) inhibited egg hatching by 100%. *Euphorbia* extracts in all solvent systems, at each tested concentration, showed less than 30 percent EHI activity. For *I. eriocarpa*, only the 70% MeOH extract at 10 mg/mL showed greater than 70% EHI (Figure 1).

Conclusion Our data support the view that the four plants tested have anti-parasitic properties. Since the 70% MeOH and aqueous extracts of *Adenia* sp. and *C. ruspolii* showed better EHI activities at each tested concentration than the other two plants, they have been selected for further phytochemical studies.

Acknowledgements We gratefully acknowledge funding from BBSRC/DFID/SG and SRUC's International Engagement Strategy. Sokratis Ptochos for training me in parasitological techniques.

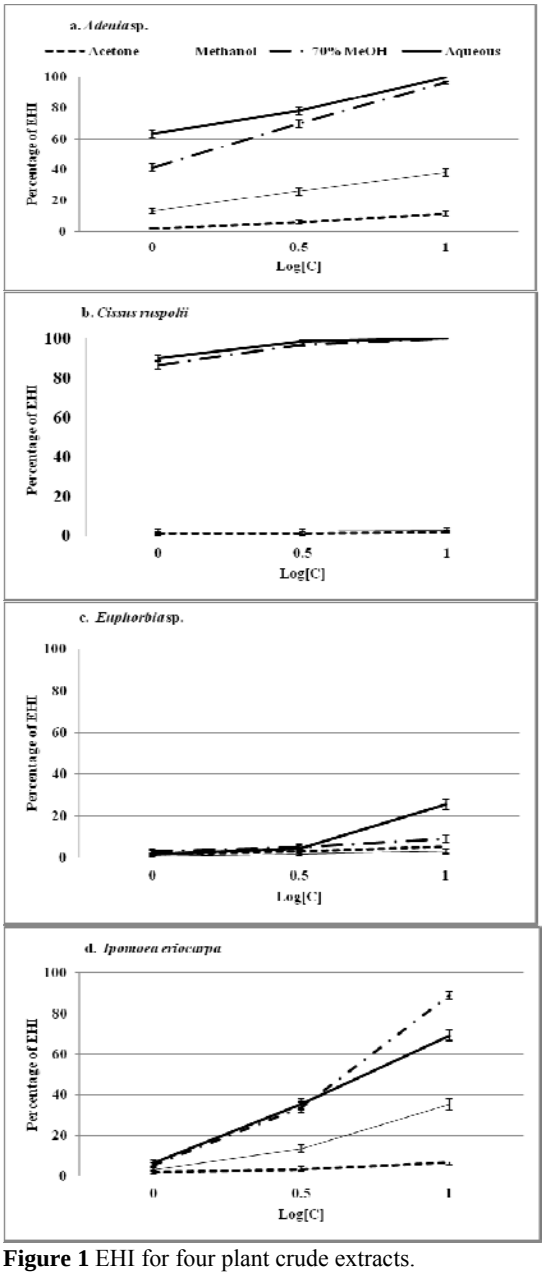

Figure 1 EHI for four plant crude extracts.

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Intestinal adhesion and faecal shedding of enterotoxigenic *Escherichia coli* in experimentally challenged weaned pigs

J Pollock[1,2], D L Gally[2], R Tiwari[3], M R Hutchings[1], J G M Houdijk[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]Roslin Institute, The University of Edinburgh, UK, [3]Zoetis, Kalamazoo, Michigan, USA
Email:jolinda.pollock@sruc.ac.uk

Implications Prolonged ileal adhesion and faecal shedding following a single enterotoxigenic *Escherichia coli* (ETEC) challenge in weaned pigs strengthens a model to assess nutritional sensitivity of post-weaning colibacillosis (PWC).

Introduction The weaning transition period in pigs is linked with increased vulnerability to enteric disorders, such as PWC. This is primarily caused by ETEC strains that express F4 fimbriae, which act by adhesion to F4-specific receptors which are present in the small intestine. Although single and trickle ETEC infection models have been developed (Houdijk *et al*., 2005; Athanasiadou *et al*., 2010), these have not confirmed ETEC colonisation in the small intestine. Therefore, the aim of this study was to assess ETEC adhesion and shedding in experimentally challenged weaned pigs.

Material and methods Twenty-one newly weaned piglets (7 from 3 litters) were selected. At weaning (day 0), one piglet from each litter was subjected to post-mortem to provide baseline samples. The remaining 18 piglets were housed in 3 challenge treatment pens (5 pigs/pen) and 1 control treatment pen (3 pigs/pen) and were fed a commercial weaner pig diet *ad libitum*. Challenged pigs were orally administered with 3 ml phosphate buffered saline (PBS) containing 8×10^8 cfu of nalidixic acid (nal)-resistant ETEC F4 on day 2; control pigs received 3 ml PBS only. Further post-mortems were carried out post-challenge on days 4, 6 and 8 (one animal from each challenged pen, balancing for litter origin), and day 11 (all remaining challenged and control pigs). Rectal faecal samples were collected daily from each pig. Pen faeces scores were taken daily on a scale from 1 (solid) to 4 (severe diarrhoea). At post-mortem, the last 25 cm of the ileum was excised, emptied and ligated into 5 segments before placing into PBS prior to culture. Faeces, ileal digesta and homogenised ileal segments were prepared for plating onto nal-enriched MacConkey agar. Presence of ETEC F4 was confirmed by PCR via amplification of the major F4 fimbrial subunit (FaeG) by randomly selecting a suspect bacterial colony from each sample analysed, taken from an appropriate serial dilution plate. Descriptive statistics are used to present the data obtained.

Results All pigs tested negative for ETEC F4 in the faeces on day 1 (Figure 1a). In addition, ETEC F4 was not detected in the faeces, digesta or on the intestinal tissue of control animals throughout the experiment. Post-challenge, ETEC F4 was detected in the faeces of a variable proportion of challenged pigs (Figure 1a), gradually increasing to day 7, when 100% of challenged pigs still present tested positive. On day 6, ETEC F4 was isolated from all pigs at post-mortem in the faeces, digesta and ileal tissue samples (Figure 1b). However, on day 8, none of the pigs sampled tested positive for ETEC F4 in the ileum, whilst only one pig tested positive for ETEC F4 in the faeces. After day 8, ETEC F4 was no longer detected in any faecal, digesta or tissue samples. Mean faecal scores temporarily increased for the challenged pens only (Figure 1c).

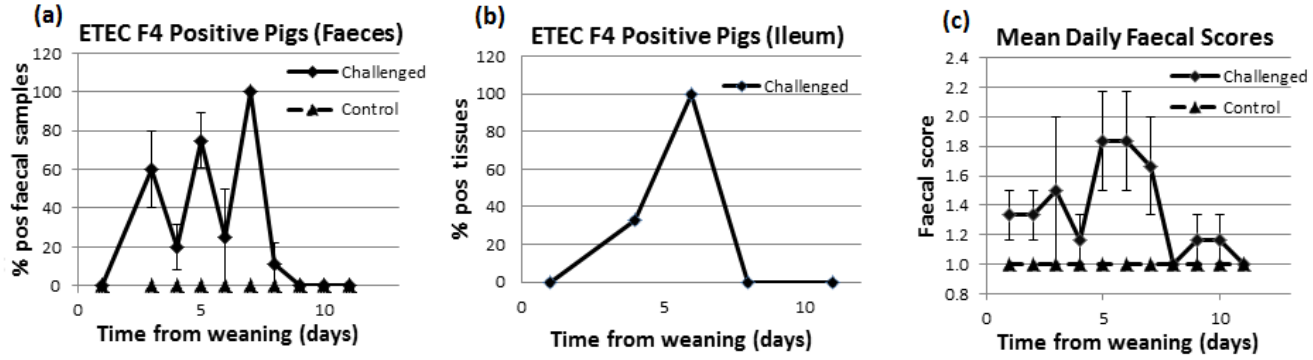

Figure 1 Percentage of pigs testing positive via FaeG-specific PCR in (a) faeces and (b) ileal tissue, and the (c) mean daily faecal scores (per pen) over the trial duration. Pigs were challenged with ETEC F4 on day 2 post weaning.

Conclusion This study has highlighted that this single-dose infection model results in intestinal adhesion and faecal shedding up to 4 and 5 days post-challenge, respectively. As a result, this model will be taken forward for further work studying gut microbiota shifts in response to dietary manipulation and ETEC F4 challenge.

Acknowledgements The authors greatly acknowledge BBSRC and Zoetis for sponsorship of this PhD project.

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Bio-assay guided fractionation of crude aqueous extracts of *Cissus ruspolii* and *Adenia* sp.

K Tolossa[1,2], S C Fry[2], S Athanasiadou[1], G J Loake[2], J G M Houdijk[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]Institute of Molecular Plant Sciences, University of Edinburgh, UK
Email:ketema_tolossa@yahoo.com

Implications Fractionation of active crude extracts into discrete fractions followed by bioassays of their egg hatch inhibition (EHI) activities help to quickly home in on those fractions containing active anti-parasitic compound(s).

Introduction Prior to applying purification techniques to isolate individual active compounds from bio-active plant extracts, separation into discrete fractions with similar properties is required (Atawodi *et al*, 2011). Gel-permeation chromatography is one such technique that exploits the molecules' ability to move through gel pores of clearly defined sizes. Here, we used the gel-permeation chromatography to assess EHI of discrete, bio-active *Cissus ruspolii* and *Adenia* sp. aqueous fractions.

Material and methods Powdered root samples (50 g each) of *C. ruspolii* and *Adenia* sp. were macerated separately in 1L of de-ionized water containing 0.05% (w/v) chlorobutanol (CB) to inhibit microbial growth. Macerated samples were stirred continuously at room temperature for 72 h. The supernatants were filtered through Miracloth, specifically designed for quick filtration of gelatinous materials. *Adenia* sp. and *C. ruspolii* filtrates were centrifuged at 4000 rpm for 10 min (Eppendorf 5810R centrifuge) and 17000 rpm for 30 minute (Dupont SA-600 centrifuge), respectively. Clear supernatants were pooled by plant and stored at –20°C in 50 ml aliquots. A 10 ml aliquot was freeze dried to assess yields. 3.5-ml of the clarified extract was passed through a glass column containing 70 ml bed volume of Bio-Gel P-2, eluted with de-ionized water. Fifty-five 4-ml fractions were collected. The column used for *Adenia* sp. extract fractionation was washed with de-ionized water for 24 h before its use for *C. ruspolii* extract fractionation. All fractions were assayed for their EHI properties using *Teladorsagia circumcincta* eggs (Coles *et al.* 1992). A small portion of each Bio-Gel fraction was analysed by thin-layer chromatography (TLC) in BuOH:HOAc:H_2O (4:1:1 by volume) and separated spots were examined under UV-light and after staining with molybdate, thymol in sulphuric acid, ninhydrin and iodine vapour. Variation between EHI activities of different fractions for each plant was analysed via ANOVA, using fraction as factors.

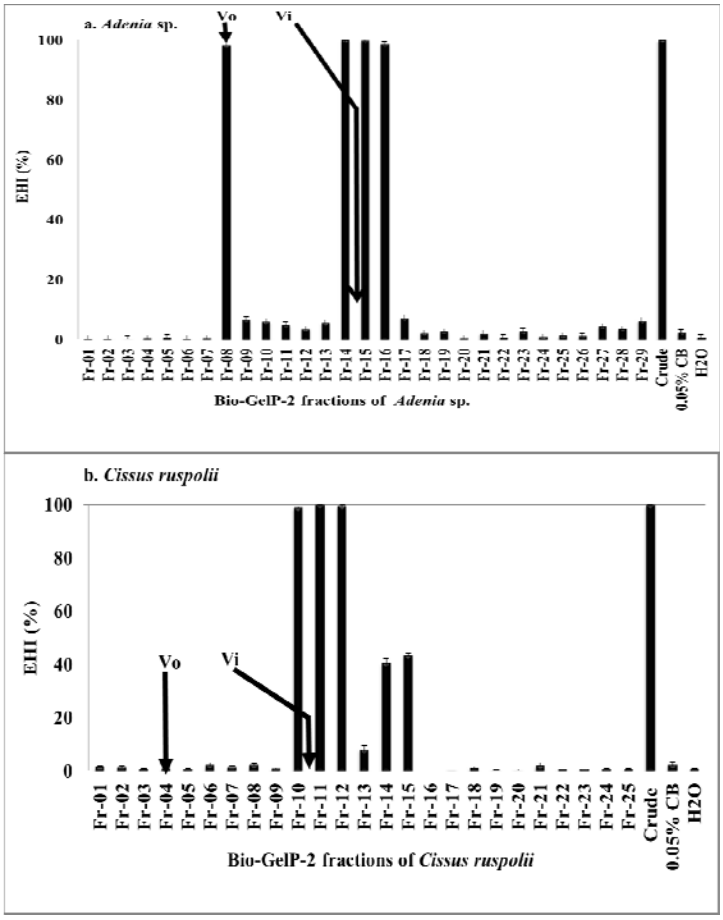

Figure 1 EHI assay results of Bio-GelP-2 aqueous fractions of *Adenia* sp. (a) and *C. ruspolii* (b)

Results Figure 1 shows that fractions differed remarkably in EHI activities ($P<0.001$), suggesting that *Adenia* sp. and *C. ruspolii* active constituents were located in fractions 8 and 14-16 (Fig 1a), and fractions 10-12, 14 and 15(Fig 1b), respectively. The TLCs demonstrated that the majority of the solutes eluted earlier than the principal peak of EHI activity (data not shown). The TLCs also indicated the void and included fractions (V_0 and V_i respectively, as indicated in Figure 1).

Conclusion The EHI assay results of active fractions indicated that active compounds would be isolated from the relatively late-eluting active fractions of both plants, containing low total solutes as seen by TLC, and thus partially purified.

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Characterisation of a novel vaccine delivery system for livestock

R K McLean[1,2], A R Wood[1], J C Hope[2], G Entrican[1], D J Griffiths[1]
[1]Moredun Research Institute, Edinburgh, UK, [2]The Roslin Institute and Royal (Dick) School of Veterinary Studies, Edinburgh, UK
Email:rebecca.mclean@moredun.ac.uk

Implications Healthy animals perform better than those that are diseased; therefore there are significant benefits from preventing disease on farm by investigating new vaccine delivery systems - bringing food security for future generations.

Introduction Recently, viral vectors have risen to prominence as candidates for generating immune responses. Of these viral candidates, lentiviruses are attractive as they have the ability to transduce non-dividing antigen presenting cells. For example, lentiviral vectors have been shown to produce an antigen mediated immune response in mice, providing long term, sterile protection against Malaria[1]. The use of ovine lentiviruses as vaccine vectors will be investigated and characterised in this project.

Material and methods Transformed human embryonic kidney (293T) cells were transfected with four plasmids which encode the various vector components for the production of lentiviral vectors. Vectors produced so far contain an eGFP reporter cassette to facilitate measurement of infectivity by flow cytometry.
Self-inactivating (SIN) vectors have been produced to decrease the probability of the generation of replication-competent virus[2]. To produce a SIN vector, viral enhancers and promoter sequences were deleted by Gibson Cloning leaving expression of transgenes controlled by an internal promoter.
Integrase deficient lentiviral vectors were produced by introducing point mutations by PCR on the D,D-35-E motif within the integrase protein to reduce insertional oncogenesis[3].

Results Stable expression of antigens is important to a successful vaccine, therefore the stability of ovine lentiviral transduction was evaluated over a 4 week period with eGFP-positive cells measured at 24 hours, 48 hours, 72 hours, 1 week and weekly from there onwards until 4 weeks post transduction. 50% of cells remained eGFP-positive after 4 weeks in rapidly dividing cells suggesting a sustained, stable transduction.
Ovine lentivirus vectors have the ability to infect a wide range of cell types from different species with similar efficiency to the well characterised murine leukaemia virus (MLV) vector (Table 1).

Table 1 Cell line susceptibility to ovine lentivirus vectors

Cell Line	Species	Ovine Lentivirus Vector (IU/ml)	MLV Vector (IU/ml)
CRFK	Cat	4.9×10^5	1.9×10^6
FLSk	Sheep	2.1×10^5	5.1×10^5
TIGEF	Goat	3.2×10^5	4.1×10^5
MLE-15	Mouse	1.0×10^6	4.5×10^6
208F	Rat	1.2×10^5	5.9×10^5
BOMAC	Cow	8.7×10^4	1.9×10^5
HEK293	Human	1.0×10^6	1.2×10^6

Self-inactivating vectors with non-active LTRs retain the ability to express transgenes *in vitro*.
Integration deficient vectors appear to have to correct phenotype as eGFP-positive cells decreased over time in dividing cells.

Conclusion We have created a novel, self-inactivating, integration deficient ovine lentiviral vector which retains the ability to express transgenes *in vitro*. Future studies will investigate ovine lentiviral vectors mechanisms of immune response *in vitro* and study their efficiency to deliver appropriate immunity *in vivo*.

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The effect of human isolated probiotic bacteria in preventing *Campylobacter jejuni* colonization of poultry

N Corcionivoschi[1,2], A Cean[2], L Stef[2], R Madden[1]
[1]Agri-Food and Biosciences Institute, Belfast, UK, [2]Banat's University of Agricultural Sciences and Veterinary Medicine, King Michael I of Romania, Timisoara, Romania
Email:nicolae.corcionivoschi@afbini.gov.uk

Implications *Campylobacter jejuni*, a Gram-negative bacterium, was classified as the leading cause of bacterial gastroenteritis in the Western world. Any attempt made toward reducing colonization in poultry can potentially reduce the incidence of campylobacteriosis in humans.

Introduction Poultry (ducks, turkeys, and chickens) can rapidly become colonized with *Campylobacter*, and in general, each broiler cycle starts with a negative flock (Wagenaar *et al*., 2006). The aim of our study was to investigate the potential of four new human isolated probiotic strains to reduce *C. jejuni* invasion of chicken primary cells, *in vitro*, and to limit its presence, *in vivo*, in farmed broilers.

Material and methods In order to investigate the effect of probiotics inclusion in the feed a total of 280 chicken broilers (ROSS 308) were allocated randomly in 7 groups. Each group had five replicate floor pens with eight chicks per pen. The feeding program included the starter (0–10 days), grower (11–35 days), and finisher diets (36–42 days). Mixed-gender chicks were allowed *ad libitum* access to feed and water during the experiment (Table 1).

Table 1

Lot 0	Lot 1	Lot 2	Lot 3	Lot 4	Lot 5	Lot 6
The moment of probiotics administration in feed						
Control	0-42 days	O-42 days	35-42 days	35-42 days	0-42 days	35-42 days
Probiotic strains included						
-	*L. paracasei* CMGB 18 *L. rhamnosus* CMGB 34	*L. paracasei* CMGB 18 *L. rhamnosus* CMGB 34 L. lactis CMGB 31 L. lactis CMGB 32	*L. paracasei* CMGB 18 *L. rhamnosus* CMGB 34	*L. paracasei* CMGB 18 *L. rhamnosus* CMGB 34 *L. lactis* CMGB 31 *L. lactis* CMGB 32	*L. paracasei* CMGB 18 *L. rhamnosus* CMGB 34	*L. paracasei* CMGB 18 *L. rhamnosus* CMGB 34 L. lactis CMGB 31 L. lactis CMGB 32

Results Our results show that the probiotic strains (*Lactobacillus paracasei J.R, L. rhamnosus 15b, L. lactis Y, and L. lactis FOa*) had a significant effect on *C. jejuni* invasion of chicken primary cells, with the strongest inhibitory effect detected when a combination of four was administered. Combinations of two probiotics reduced the internalization of *C. jejuni* from 10^4 CFU/well to 10^3 CFU/well. Combinations of four probiotic strains had a dramatic effect on invasion (10^2 CFU/well) compared to the control. The differences in invasion were significant ($p < 0.05$) compared to an invasion assay performed in the absence of probiotics. The inclusion of probiotics in the diets of the experimental groups L3, L4, and L6 in the last week of growth had a significant negative effect on the pathogen load in the faeces. The effects on the pathogen presence in the cecal and duodenal content or in the mucosa were similar to when they were introduced in their diets at the beginning of the growth period. The inclusion of probiotics in the diet induced modifications in the thickness and structure of the intestinal mucosa with a proven negative effect on the number of campylobacters found in the intestinal compartments of the experimental broilers.

Conclusion We conclude that these four new probiotic strains are able to reduce the ability of *C. jejuni* to invade, *in vitro*, and to colonize broilers intestinal compartments, *in vivo*. These probiotics are now proven to be effective even when introduced in broiler's feed 7 days before slaughter, which makes them cost-effective for the producers.

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Gonadal and extra-gonadal sperm reserves of West African Dwarf rams treated with FSH/LH

M A Oguike[1], U N Egu[2], J Ezea[1]
[1]Michael Okpara University of Agriculture Umudike, Umuahia, Abia State, Nigeria, [2]Abia State University Umuahia Campus, Umuahia, Abia State, Nigeria
Email:maoguike2000@gmail.com

Implications Exogenous gonadotropins induced a high rate of daily sperm production and a greater percentage of cauda sperm reserve, indicating that cauda epididymis is the major site for sperm reserve.

Introduction The development of numerous reproductive techniques has given livestock farmers' extensive control of the reproductive processes of farm animals. However, the use of these techniques by resource–poor farmers in developing countries has been limited. Preparations of hormones are expensive and the hormones often deteriorate due to inadequate storage and handling. Pergonal® (Ferring Laboratories) which is an FSH and LH preparations, in the ratio 1:1 (Dixon and Hopkins, 1996), is cheap, does not require cold storage and is readily available. Follicle stimulating hormone (FSH)and luteinizing hormone (LH) are involved in the formation of spermatozoa, and sperm features are among the determinants of fertility. The objective of the study was to investigate the effect of Pergonal® on reproductive parameters of West African Dwarf (WAD) rams managed by most Nigerian resource-poor farmers.

Material and methods A completely randomized design study was conducted in the Sheep Unit of Michael Okpara University of Agriculture Umudike, Nigeria, Research Farm. Twenty four WAD rams aged 2 years and weighing 10-11.5 kg, were fed 2kg /ram/day of a concentrate diet supplemented with forage. The rams were randomly allocated to one of three treatments (n=8): (T1) daily injections with saline (control); (T2) daily injections of19.26IU/3 days of FSH and 19.26IU/3 days LH, (T3), daily injections of39.00IU/3 days of FSH and 39.00IU/3 days LH. Injections were made intramuscularly into the hind limbs. Water was given *ad libitum*. After 65 days of treatment (to allow for the duration of seminiferous epithelium cycle), 4 rams from each group were slaughtered and testicles and epididymes were incised for estimation of gonadal and extra-gonadal sperm reserve, following homogenized count using haemocytometer. Daily sperm production was determined by dividing gonadal sperm reserve with time divisor 3.66 corresponding with the semimiferous epithelial cycle of the ram. .Data collected were subjected to ANOVA, significant means separated using LSD

Results The results of the experiment, presented in the Table 1 show significantly higher sperm reserves of the gonads, caput and cauda sections of the epididymis following treatment.

Table 1 Gonadal and extra-gonadal sperm reserves of West African Dwarf rams treated with Pergonal®

Variables	**Treatments**			
	T1	T2	T3	LSD
Daily sperm production ($X10^{9)}$	0.31	0.71	0.89	0.63
Daily sperm production/gram testis ($X10^{9}$)	0.01	0.02	0.01	0.01
Gonadal sperm reserve ($X10^{9}$)	1.12^{a}	2.59^{b}	3.26^{c}	0.30
Caput sperm reserve ($X10^{8}$)	0.71^{a}	6.98^{b}	13.91^{c}	0.45
Corpus sperm reserve($X10^{8}$)	4.34	8.50	11.97	0.48
Cauda sperm reserve ($X10^{8}$)	8.98^{a}	18.66^{b}	24.24^{c}	0.14
Vas deferens sperm reserve ($X10^{8}$)	7.54	10.32	7.13	0.17
Percentage epididymal distribution of the rams used in the study				
Caput 18.57 (%)	Corpus 21.33 (%)		Cauda 60.10 (%)	

^{abc}means with different superscripts are significantly different ($P<0.05$).

Conclusion Pergonal® induced a higherlevel of gonadal sperm reserve, as well asa higher cauda sperm reserve, compared to the other sections of the epididymis.

Acknowledgements We are indebted to Michael Okpara University of Agriculture, Umudike for providing technical support for the study.

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Evaluation of performance and haematological parameters of West African Dwarf goats fed selected browse species based diets

O Akinyode, O O Adeleye, O Akinfenwa, A B J Aina
Federal University of Agriculture, Abeokuta, Ogun State, Nigeria
Email:gbengamcf@yahoo.co.uk

Implications The high cost of conventional feed, including inadequate forage, especially during the dry season, has been a recurring problem in the tropical environment. We have formulated an alternative feed combination from locally available ingredients for west African dwarf goats without having an adverse effect on goat health and performance.

Introduction Ruminants are majorly faced with scarcity of feed supply and low pasture quality in the humid region of West Africa during dry season when natural vegetation is of low nutritive value (Aye, 2007). The inclusion of forage in a concentrate ration has been suggested by Adeloye, (1998) to improve the growth performance and health of WAD goats.

Material and methods Twelve yearling WAD goats (mean weight 9kg), which had been quarantined and vaccinated for two months, were assigned to one of 3 treatments in groups of 4. Treatment 1 (T1) consisted of (g/kg DM) Gmelina (300), cassava peels (400), wheat offal (280), bone meal (10) and salt (10). In the other treatments, Gmelina was replaced by 300g/kg Leucaena (T2) or Gliricidia (T3). The browse plants had been sun-dried and chopped for even mixing and to reduce the effect of anti-nutritional elements such as tannin. The goats were given experimental diets for three months. At the end of the study blood samples were taken by jugular venupuncture in tubes containing EDTA anticoagulant for haematological and serological studies. Chest girth and body length were also taken. Data obtained were subjected to analysis of variance (ANOVA) in a completely randomised design (CRD) using Minitab (version 16) software and TUKEY test to compare the means.

Results The diets had no significant influence ($P>0.05$) on the performance of the goats. Likewise, the haematological and serological parameters shows no significant differences ($p>0.05$) except for the monocytes count which was highest in goats fed Gliricidia and lowest in goats fed Leucaena ($p<0.05$).

Table 1 Means of growth performance and linear body measurement of WAD goats fed selected browse species diets

Parameters	T1	T2	T3	SEM
Initial weight(kg)	7.82	7.50	7.75	0.817
Final weight(kg)	11.18	10.71	10.43	1.233
Weight gain(g/d)	53.3	50.8	42.5	0.05
Feed intake(g/d)	317	295	308	0.13
Body length(cm)	66.2	65.5	65.4	0.57
Chest girth(cm)	51.9	51.4	52.3	0.66
Height at wither(cm)	42.0[a]	40.9 [a]	40.0 [b]	0.41
FCR	5.95	5.81	7.25	3.257

Table 2 Haematological and serological parameters

Parameter	T1	T2	T3	SEM	P-value	Standard values
Packed Cell Volume (%)	36.3	31.0	30.7	1.81	0.16	22-28
Red Blood Cell ($x10^{12}$/l)	13.4	10.4	10.2	1.29	0.24	8-18
White Blood Cell ($x10^{9}$/l)	18.9	18.8	21.7	2.86	0.86	4-13
Monocyte (%)	1.3[ab]	0.0[b]	1.7[a]	0.50	0.03	0-4
Protein (g/l)	61.2	60.5	65.9	4.09	0.79	61-75
Urea (mg/dl)	24.9	27.6	27.7	2.61	0.63	13-26
Creatine (mg/dl)	1.3	1.4	1.27	0.15	0.06	0.7-1.5

Means in the same row with different superscripts are significantly different .Standard values were obtained from Merck's Veterinary Manual (9^{th} Edition), 2008.

Conclusion: This study showed that the *Gmelina*, *Gliricidia* and *Leucaena* can be included and substituted in concentrate rations for West African Dwarf goats without an adverse effect on their growth and health status.

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In vitro gas production of *Pennisetum purpureum* varieties fertilized with animal manures

S O Badaru, V O A Ojo, A O Ogunsakin, A O Ajayi, O O Adelusi, O S Onifade
Federal University of Agriculture, Abeokuta, Ogun State, Nigeria
Email:seunayo11@gmail.com

Implications Application of manures are necessary, especially to sustain herbage production. Therefore, high quantity and quality herbage can be produced from application of manure.

Introduction Fertilizing pastures with organic manure improves grass yield, is readily available and, cheap to obtain compared to inorganic fertilizer. Also the application of organic manure has no negative effect on the grass (Olson and Papworth, 2000). The present study compared the nutritive value, measured *in vitro*, of four varieties of *Pennisetum purpureum* that had been fertilized with four manure types in South Western Nigeria.

Material and methods An area of (53m×11m) was divided into individual plots $2m^2$ after land clearing and was sown with *Pennisetum purpureum* stem. The soil contained total N (0.15%), organic C (1.31%) and available P (32.87mg/ kg).The experiment was a factorial arrangement (replicated 3 times) of 4×4 with. four manure types (swine, 10.16; cattle (22g); poultry, 7.92 (kg/plot) and control) on the main plot and four *Pennisetum purpureum* varieties (Local, S 13, S 15 and Purple) on the sub-plot. Forage subsamples were harvested after 12 weeks of growth, oven dried and *in vitro* gas production of the samples were determined for 48 hours following the procedure of Menke and Steingass (1988). Post incubation parameters were calculated using the procedure of Getachew *et al*. (2004). The data obtained were analysed as a two-way analysis of variance using the SPSS 20 statistical package.

Results Grasses fertilized with swine manure produced highest value for methane (4.67ml) while control (unfertilized) had lowest value of 3.58ml. Control (unfertilized) produced highest CO_2 (11.12ml) while those fertilized with swine manure had lowest value of CO_2 (7.63ml). *In vitro* organic matter digestibility, metabolizable energy and SCFA had the highest values (12.84%, 4.39 MJ/kg and 0.30 µmol respectively) in those fertilized with poultry manure. Manure did not affect organic matter digestibility (OMD) (P>0.05) in all grasses. The Purple variety had highest ME (4.54 MJ/kg) and SCFA (0.33µmol). Effects of variety on *in vitro* post incubation parameters of *P.purpureum* were significant (P<0.05).

Table 1 Effects of manure and season on *in vitro* dry matter digestibility and post incubation parameter of *Pennisetum purpureum* varieties

Parameter		CH_4 (ml)	CO_2 (ml)	IVDMD (%)	ME (MJ/kg)	OMD (g/kg)	SCFA (µmol)
Manure	Swine	4.67^{a}	7.63^{b}	12.12^{c}	3.99^{b}	329..6	0.23^{b}
	Cattle	4.00^{b}	9.92^{a}	12.74^{b}	4.20^{ab}	330.1	0.27^{ab}
	Poultry	3.92^{b}	11.46^{a}	12.84^{a}	4.39^{a}	343.0	0.30^{a}
	Control	3.58^{b}	11.12^{a}	10.90^{d}	4.31^{ab}	337.8	0.29^{ab}
	SEM	0.228	0.742	0.033	0.112	9.37	0.019
Variety	Local	5.00^{a}	8.75^{b}	12.79^{b}	4.18^{b}	342.9^{a}	0.26^{b}
	S 13	2.67^{c}	8.50^{b}	13.13^{a}	3.83^{c}	303.3^{b}	0.20^{c}
	S 15	4.00^{b}	10.88^{a}	10.57^{d}	4.33^{ab}	339.5^{a}	0.29^{ab}
	Purple	4.50^{b}	12.00^{a}	12.11^{c}	4.54^{a}	354.7^{a}	0.33^{a}
	SEM	0.228	0.742	0.033	0.112	9.37	0.019
Manure×Variety significance		P<0.001	P<0.001	P<0.001	P<0.001	P<0.05	P<0.001

Means on the same column with different superscripts are significantly different (P < 0.05).

Conclusion *Pennisetum purpureum* (Purple) fertilized with poultry manure had the highest nutritive value (measured *in vitro*) The use of animal manure to improve the nutritive quality of grasses should be encouraged.

Acknowledgements The authors gratefully appreciate the contributions of the laboratory technologists of the Department of Pasture and Range Management for this project.

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Seasonal variations of mineral content of grasses from natural pasture in South West Nigeria

O Oluwafemi Adeyemi, J Alaba Olufunmilayo, D Peter Aniwe, A Bolanle Temitope
Federal University of Agriculture, Abeokuta, Department of Pasture and Range Management, Abeokuta, Nigeria
Email:femi_okukenu@yahoo.co.uk

Implications Ruminant production during dry season is limited by low productivity of pasture forages, which often contain minerals with concentrations that care too low to meet the minimum requirement for optimal productivity of livestock.

Introduction Natural pasture species are the main source of feed for livestock, and forms the major component of domesticated livestock feed. However, uneven seasonal growth and unavailability pasture during certain times of the year have been considered as the major limitations to constant supply of forages. Even when forage is available they are in limited quantities and cannot maintain the animal feed throughout the year. The low quality of grasses during some period of the year is reflected in low production and reproductive performance, as well as slow growth in ruminants (Kakengi *et al.,* 2001).

Material and methods The experimental sites were selected villages in south west Nigeria which include Afami, Atokun, Iboro, Ile-niku, Ipaya and Oke-rori and the experiment was carried out at the laboratory of the Department of Pasture and Range Management, Federal University of Agriculture, Abeokuta. An area of 100 m^2 was mapped out on the natural pasture along the grazing path of the Fulani cattle in each selected village. The area was sub-divided into five plots of 5mx4m dimension each for effective sampling based on the topography of each area. Thereafter, a 1m^2 quadrat was thrown randomly thrice in each sub-plot. The grass species that dominate the area were harvested and oven dried to constant weight and milled. Macro minerals (Ca, P, K, Mg and Na) and micro minerals (Cu, Zn, Mn and Fe) were analysed according to A.O.A.C. (1995). The study was carried out using complete randomized design (CRD) comprising four seasons (Early rain, Late rain, Early dry and Late dry). Data collected were subjected to one-way analysis of variance and the treatment means were separated using Duncan's multiple range test using the SAS (1999) package.

Results

Table 1 Effects of season on the mineral content (g/kg DM) of grass species found in study areas

Season	P	Ca	Mg	K	Na	Cu	Zn	Fe	Mn
			g/kg				mg/kg		
Early rain	2.7^{a}	3.2^{d}	4.2^{a}	50.5^{a}	1.5^{c}	27.6^{c}	46.2^{b}	411.7^{b}	22.3^{c}
Late rain	2.2^{b}	4.6^{b}	4.0^{b}	33.0^{d}	1.6^{a}	34.8^{a}	41.7^{c}	248.3^{d}	21.0^{d}
Early dry	1.5^{d}	6.6^{a}	4.2^{a}	37.0^{c}	1.5^{b}	29.3^{b}	50.9^{a}	348.3^{c}	43.2^{a}
Late dry	2.0^{c}	4.1^{c}	2.2^{c}	45.2^{b}	1.3^{d}	12.3^{d}	36.3^{d}	705.0^{a}	38.9^{b}
SEM	0.21	0.47	0.23	2.14	0.06	8.04	2.82	38.46	1.92

$^{a, b, c, d}$: Means in same column with different superscripts are significantly ($P<0.05$) different

Conclusion The research revealed that calcium level in grass in the wet season was lower than in the dry season and there is higher level of magnesium, phosphorus as well as potassium in grass in the wet season than in the dry season. The herbage collected during rainy season was in their early boot stage while the one collected in dry season were already wilting. It can therefore be concluded that changes in season have much significant impact on the mineral content in grass species in study areas.

Acknowledgements I would like to thank Prof. (Mrs.) Jolaosho for her help and inspiration for the possibility to conduct this study.

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In vitro gas production of silage made from cultivated pastureland with or without additives from Yewa area of Ogun State, Nigeria

D T Olorunnisola, V O A Ojo, O A Jolaosho, J O Olanite, A O Ogunsakin, O G Ojambati, T E Otaru, A E Adesorioye
Federal University of Agriculture Abeokuta, Ogun State, Nigeria
Email:seunayo11@gmail.com

Implications Ensiling of forage with a combination of molasses and salt resulted in increased nutritive content and digestibility of the silage, which will enhance the performance of animals especially when served as a dry season feed resource.

Introduction Silage production is a forage conservation method which aids dry season feeding and the use of additives serve to increase the nutritional value of silage or improve fermentation so that storage losses are reduced. The determination of *in vitro* gas production provides information on fermentation kinetics of forage consumed by ruminants, which is dependent on the rate of passage and the degradation rate (Mould *et al.*, 2005). This study was conducted to evaluate the *in vitro* gas production of silage from cultivated pastureland with or without additives from Yewa North Local Government of Ogun State, South West Nigeria.

Material and methods The silage materials were collected from Yewa North Local Govt. on cultivated pasture which comprised of *Panicum maximum* and Stylosanthes species. The plants were harvested at 10cm above ground level, 9 months after planting. The experiment was replicated 3 times. They were weighed to obtain fresh weight. The harvested forage samples were divided into four parts, and ensiled as follows; (1) without additive, (2) with molasses at four percent (4%) by weight of material (green matter basis), (3) with salt at 0.5% and (4) with the combination of molasses and salt at 2% molasses and 0.25% salt, respectively, and ensiled in laboratory bottle (960ml) silos. Bottle silos were allowed to ferment for four weeks. After the fermentation, the bottles were opened and samples were taken for analyses. Proximate composition (AOAC, 2002) was analysed. The *in vitro* gas production was determined by the procedure of Menke and Steingass (1988). Data were analysed using one-way analysis of variance.

Results The proximate composition showed that silage ensiled with a combination of molasses and salt had the highest ($P<0.05$) values for dry matter (348.10 g/kg), crude protein (138.90 g/kg) and ether extract (134.20 g/kg). There was a significant difference ($P<0.05$) for gas produced at 3hrs for the additives. Molasses had the highest value (1.13ml/200mgDM) when compared with the other additive levels. At 48hrs, the highest gas volume produced was 15.50ml/200mgDM and the least value was 10.63ml/200mgDM, which are the values for silage with molasses and silage with salt, respectively.

Table 1 The effect of additives on the proximate composition (g/kg), gas production (ml/200 mg DM) and fermentation constants of silage made from cultivated pasture over different incubation times.

	Gas production (ml/200mg DM)				Fermentation constants							
Treatment	DM	CP	EE	Ash	3hrs	6hrs	12hrs	24hrs	36hrs	48hrs	b	c (s)
Control	334.5^{b}	134.1^{b}	114.6^{c}	80.00^{ab}	0.13^{c}	0.88^{b}	2.50^{b}	6.36^{b}	8.75^{b}	10.86^{b}	4.45^{ab}	0.02^{b}
Molasses	326.00^{ab}	136.10^{ab}	121.30^{bc}	79.20^{ab}	1.13^{a}	2.13^{a}	5.13^{a}	11.00^{a}	13.86^{a}	15.50^{a}	4.31^{ab}	0.03^{a}
Salt	343.10^{b}	138.90^{a}	129.60^{ab}	85.80^{a}	0.38^{c}	1.43^{b}	2.50^{b}	5.75^{b}	8.50^{b}	10.63^{b}	6.39^{a}	0.02^{b}
Molasses+salt	348.10^{a}	138.90^{a}	134.20^{a}	75.00^{b}	0.75^{b}	2.00^{a}	4.50^{a}	9.63^{a}	12.50^{a}	13.88^{a}	2.78^{b}	0.03^{a}
S.E.M	6.10	1.92	3.56	2.32	0.15	0.28	0.59	0.89	1.02	1.08	1.53	0.00

$^{a-b}$: Means on the same column with different superscripts are significantly different ($P < 0.05$).

Conclusion Additives had an effect on the proximate composition silage with highest values for dry matter, crude protein, ether extract and ash recorded when molasses was combined with salt. The highest gas was produced with molasses as additive while the highest potential gas was obtained when salt was used as additive.

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Effects of thyme essential oil on abundance of sheep rumen cellulolytic bacteria as determined by real-time polymerase chain reaction

H Jahani-Azizabadi[1], M Danesh Mesgaran[2], A R Vakili[2], K Rezayazdi[3]
[1]Department of Animal Science, Faculty of Agriculture, University of Kurdistan, Sanandaj, Kurdistan, Iran, [2]Dept. Animal Science, Excellence Centre for Animal Science, Faculty of Agriculture, Ferdowsi University of Mashhad, Khorasan Razavi, Iran, [3]Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Tehran, Iran
Email:ho.jahani@uok.ac.ir

Implications The addition of thyme essential oil changed the ruminal cellulolitic bacteria relative abundance.The genus of some cellulolytic bacteria may have increased and others decreased.

Introduction In recent years, researchers have been interested in developing alternatives for antibiotic growth promoters. Many plant extracts and essential oils have been investigated. However, few studies have investigated the effect of essential oils on rumen microbial populations (Benchaar *et al*., 2007; Patra and Yu 2012). The aim of the present study was to determine the effects of thyme essential oils on relative abundance of sheep rumen cellulolytic bacteria (*Fibrobacter succinogenes*, *Ruminococcus albus* and *Ruminococcus flavefaciens*).

Material and methods Six ruminally cannulated sheep were used in a completely randomized design. Dietary treatments were basal diet (50:50, lucerne hay: concentrate) alone (as Control) and basal diet plus 1.3 ml/d/ head of thyme essential oil (extracted by steam distillation of raw thyme). Dietary treatments were fed to sheep (0.6 kg Lucerne hay and 0.6 kg of concentrate) for 5 weeks. On week 5 samples of ruminal fluids were taken using ruminal probes at 4 h after morning feeding and immediately stored in liquid N_2 until used for bacterial quantification by real time PCR. DNA was extracted from the samples using the GeNet Bio® DNA isolation kit (GeNet Bio, N.3000) following the manufacturer's instructions. Cellulolytic rDNA concentrations were measured by real time PCR relative to total bacteria amplification ($\Delta\Delta$Ct). Data are expressed relative to quantification of same bacteria in control (relative fold change) using specific primers (Maeda *et al*., 2003; Zhang *et al*., 2007 and Koike and Kobayashi, 2000). Data were analyzed using the MIXED procedure of SAS and the means compared by the Tukey test ($P < 0.05$). At the end of week 5, daily feed intake and total faecal excreta were weighed and samples of sheep faeces and diet were collected to determine total tract apparent NDF disappearance for the two treatments.

Results The addition of thyme essential oil increased the relative abundance of *Ruminococcus albus* and decreased that of *Ruminococcus flavefaciens*, relative to those of the control ($P<0.05$). In addition, thyme essential oil increased ($P<0.05$) total tract apparent NDF disappearance of basal diet.

Table 1 Effect of thyme essential oil on total tract NDF disappearance and relative quantity[a] of the major species of cellulolytic bacteria of sheep rumen fluid

	Thyme essential oil (ml/ head/day)			
	0.0	1.3	SEM	p-value
Fibrobacter succinogenes	1	3.23	0.69	NS
Ruminococcus albus	1	10.03	0.71	**
Ruminococcus flavefaciens	1	0.052	0.01	**
Total tract apparent NDF disappearance (g/kg)	475	573	25	**

Mean with asterisk in each row were significant relative to the control ($P< 0.05$); [a] fold change relative to the control, ns= not significant

Conclusion The study demonstrated that rumen cellulolytic bacteria do not have similar response to thyme essential oil. The study suggested that essential oils may have resulted in changes in ruminal bacteria diversity and compensation for a decrease in one genus of cellulolytic bacteria with another genus in the same species.

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Effect of enzyme additive on *in vitro* gas production and dry matter degradability of total mixed rations

K O Yusuf, E A Akinyosoye, V O A Ojo, R Y Aderinboye, O A Isah, C F I Onwuka
Federal University of Agriculture, Abeokuta, Ogun State, Nigeria
Email:yomowumi@gmail.com

Implications Exogenous fibrolytic enzyme additive increased fibre degradation *in vitro*. The highest *in vitro* gas production and *in vitro* dry matter digestibility was obtained when enzyme was included at 0.6g/kg TMR.

Introduction Adequate feeding of ruminants in the dry season is usually a challenge to farmers in Nigeria. Hence, the feeding of crop residues and agro-industrial by-products which are high in fibre become rampant among farmers. The primary objective of using feed enzyme is to enhance availability of nutrients that are locked within cell wall components. Digestion of plant cell walls in fibrolytic feeds by ruminants is possible mainly due to the enzymes produced by ruminal bacteria, protozoa and fungi. Exogenous enzymes are added to stimulate rumen digestive microorganisms' activities. The aim of this study was to determine the efficiency of an exogenous fibrolytic enzyme containing cellulase, xylanase and beta glucanase in increasing fibre degradation *in vitro*.

Material and methods A total mixed rations (TMR) were formulated with 4 levels of enzyme (ROXAZYME G2, containing cellulase, xylanase and beta glucanase added at 0.0, 0.2, 0.4 and 0.6g/kg TMR). The ingredient composition of the TMR (g/kg)was: maize stover 320: maize 100, wheat offal 250, soyabean meal 100, palmkernel cake 200, bone meal 20, salt 5, premix 5. Rumen fluid was obtained from four West African Dwarf goats by suction tube and bulked together into a vacuum flask prior to the early morning feeding of the goats. The rumen fluid was sieved through a four-layered cheese cloth to remove solid residues. Incubation of the samples was carried out as described by Menke and Steingass (1988). Four blanks containing 30ml of inoculums were included. Gas production was recorded at 6, 12, 18, 24, 30, 36, 42 and 48h with six replicate syringes incubated per treatment from the start of incubations. At the end of the incubation period 4ml NaOH (10M) was introduced to three syringes each from the same treatment to estimate methane production. The mean volume of gas from blank was deducted from the volume of gas produced to determine the net gas production. Syringe contents were centrifuged (2300 rpm) and the precipitates were washed with warm water was and dried at 65^{o}C. The weights of the dried residues were recorded. The percentage dry matter degradability (DMD) was calculated as (DM of sample incubated – DM of residues)/DM of sample incubated × 100. Metabolizable energy (ME) and organic matter digestibility (OMD) were estimated (Menke and Steingass, 1988; ME = 2.20 + 0.136GV + 0.057CP + 0.0029CF, OMD = 14.88 + 0.889GV + 0.45CP + 0.651 XA) and short chain fatty acid (SCFA) was calculated (Getachew *et al*., 1998; SCFA = 0.0239GV – 0.0601),where GV, CP, CF, and XA are net gas production (ml/200mg DM), crude protein, crude fibre and ash of the incubated samples, respectively. Data were subjected to one way analysis of variance in a completely randomized design.

Results Gas production increased as incubation progressed and was significantly (P<0.05) highest at 0.6g/kg and lowest at 0.0g/kg enzyme inclusion level (Table1). All other parameters measured followed the same trend.

Table 1 Effect of enzyme additive on *in vitro* gas production (ml/200mg DM)

	Hours of incubation								Post incubation parameters				
Enzyme level)g/kg TMR	6	12	18	24	30	36	42	48	ME	OMD	SCFA	CH_4	DMD
0.0	3.7	5.4^{c}	8.4^{c}	10.6^{c}	12.3^{c}	13.6^{c}	14.1^{c}	14.8^{c}	5.4^{c}	35.0^{c}	0.3^{c}	37.0^{b}	42.3^{b}
0.2	4.5	7.6^{bc}	16.4^{c}	21.1^{bc}	26.6^{bc}	31.6^{b}	34.3^{b}	37.3^{b}	8.4^{b}	55.0^{b}	0.8^{b}	46.6^{a}	48.3^{b}
0.4	5.2	14.9^{b}	26.9^{b}	33.8^{b}	39.1^{b}	42.8^{b}	46.3^{b}	48.6^{b}	9.9^{b}	65.0^{b}	1.1^{b}	48.5^{a}	60.3^{a}
0.6	6	25.4^{a}	46.4^{a}	48.3^{a}	54.8^{a}	59.8^{a}	63.1^{a}	66.3^{a}	12.4^{a}	80.8^{a}	1.5^{a}	54.8^{a}	67.3^{a}
SEM	0.46	2.33	3.49	4.12	4.57	4.88	5.2	5.42	0.74	4.82	0.^{13}	2.07	2.73

Means in the same column having different superscripts are significantly different(P<0.05,)
Units: CH_4 (ml/200mg DM);IVDMD (%);ME (MJ/kg DM);OMD (%), SCFA (µmolar)**.**

Conclusion *In vitro* gas production, as well as the post incubation parameters were increased by enzyme inclusion and highest at the 0.6g/kg inclusion level. This implied that to improve the nutritive value of fibrous feed enzyme additive containing cellulose, xylanase and beta glucanase could be added at 0.6g/kg feed.

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Effect of grasshopper meal diets on performance of broiler chickens

O Daudu, T Yusuf, T Olugbemi, O Odegbile
Ahmadu Bello University, Zaria, Kaduna, Nigeria
Email:remidaudu@yahoo.com

Implications Grasshopper meal can be included in the diet of chickens in areas where it is readily available.

Introduction With global demand for livestock products expected to more than double between 2000 and 2050 (from 229 million tonnes to 465 million tonnes), meeting this demand will require innovative solutions (FAO, 2013). The opportunity for insects to help meet rising demand in meat products (FAO, 2013) and replace other protein sources is enormous. By feeding insects to chickens, the use of antibiotics in the poultry industry which may lead to human infection with drug-resistant bacterial strains may be diminished (FAO, 2013).

Material and methods A total of one hundred and fifty three day old Cobb broiler chicks were used for the starter phase which lasted four weeks. The chicks were randomly allotted to three treatments with three replicates comprising seventeen chicks in a completely randomized design (CRD). Grass hopper meal was included in the diets at three levels (0, 50 and 100g/kg). Crude protein and ME are (24% and 2840kcal/kg) and 21% and 2960kcal/kg) respectively for starter and finisher phases. Other ingredients in the diets included maize, groundnut cake, soyabean cake, bone meal, common salt, methionine, lysine and vitamin premix. For the finisher phase, a total of 144 broiler chicken aged 28 days were fed the broiler finisher diet for 28 days. Sundried grasshopper used for the experiment was purchased from the market. The birds were weighed at the beginning of the experiment and weekly thereafter. Values for feed consumption, weight gain, feed to gain ratio and mortality were calculated. All data obtained were subjected to analysis of variance test using the SAS (2002) general linear model procedure and treatment means were compared using Duncan Multiple Range Test.

Results Table 1 shows that at the starter phase, the initial body weight, final body weight, body weight gain, daily weight gain, daily feed intake and feed conversion ratio were not significantly (P>0.05) different. Mortality of 5.9% was recorded in all the treatments, *post mortem* report showed that the mortalities recorded was not due to experimental diets. Table 2 shows that at the finisher phase, the initial body weight, final body weight, body weight gain, daily weight gain, feed conversion ratios were not significantly (P>0.05) different. The total feed intake decreased as the level of grasshopper increased probably due the fibrous nature of the exoskeleton made of chitin (FAO, 2013).

Table 1 Performance of broiler chicken fed graded levels of grasshopper meal Diets

	Levels of grasshopper meal (g/kg)				
Parameters	0	50	100	SEM	P value
Starter Phase					
Initial body weight (g/bird)	50.0	50.0	50.0	0.0	0.12
Daily feed intake (g/b/d)	35.23	35.08	35.02	0.03	0.36
Final body weight (g/bird)	614.58	620.92	620.83	7.57	0.12
Daily weight gain (g/day)	20.16	20.39	20.38	0.17	0.86
Feed conversion ratio	1.75	1.72	1.71	0.01	0.71
Cost/kg feed (₦/Kg)	84.22^{a}	90.88^{b}	101.70^{c}	2.57	0.00
Finisher Phase					
Initial body weight (g/bird)	614.58	620.92	620.83	4.78	0.86
Daily feed intake (g/b/d)	140.06^{b}	139.92^{b}	136.17^{a}	0.34	0.01
Final body weight (g/bird)	1566.67	1616.67	1750.0	38.59	0.14
Weight Gain (g/bird/day)	34.0	35.56	40.33	1.37	0.14
Feed conversion ratio	4.42	4.22	3.59	0.17	0.11
Cost/kg feed (₦/Kg)	80.65^{a}	87.45^{b}	95.66^{c}	2.19	0.001
Mortality (%)	5.88	5.88	5.88	0.10	0.11

^{abc} Means within row with different superscript differ significantly (P<0.05)

Conclusion Grasshopper meal can be included as a protein source in the diet of broiler chickens up to 100g/kg in areas where it is cheap and readily available without adverse effect on performance

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Evaluation of liquid co-product feeds in ruminant diets using a mechanistic whole cow simulation model: Biopara-Milk

V Ambriz-Vilchis[1], R Fawcett[1], A Masri[1], N Robertson[1,2], P Holder[3]
[1]Bioparametrics Ltd, Edinburgh, UK, [2]The Glenside Group Ltd, Livingston, UK, [3]E D & F Man Liquid Products, Liverpool, UK
Email:v.ambriz-vilchis@sms.ed.ac.uk

Implications Simulation exercises with mathematical models can aid in the research, development and evaluation of novel feed ingredients used in the feeding of livestock, by providing theoretical evidence of the impact of the inclusion of such ingredients on performance and its environmental impact

Introduction The use of novel ingredients in ruminant diets starts with feed evaluation. The *in vitro gas* production technique (Menke and Steingass, 1988) enables the study of the nutritive value of feedstuffs e.g. it provides useful data on fermentation kinetics of both soluble and insoluble fractions of carbohydrates. The data obtained can then be used to formulate rations for livestock. Mathematical models of ruminant nutrition have been employed for over four decades and have stimulated improvements in feeding cattle. Mathematical modelling is a way to test different feeding strategies before putting into place feeding trials on-farm. Biopara-Milk is a whole cow dynamic mechanistic simulation model driven by the parameters measured via IVGPT able to predict performance, rumen pH and methane emissions from dairy and beef (Ambriz-Vilchis *et al* 2014a,b). The model is an independent evaluation of the complete diet formulated, predicting dry matter intake of any ration combination, allowing for interactions between ingredients and finally predicting performance. The aim of the present study was to evaluate the performance of molasses based liquid products and syrup co-product feeds to feed high yielding dairy cows using a simulation model Biopara-Milk.

Material and methods A simulation exercise was developed to evaluate the inclusion of four by-products used in the dairy industry: two molasses formulated products from ED&F Man Ltd (ReguMaize44) and two commercially available liquid co-product syrups (Ethanol Distillery spent wash (EthDSW) and Pot Ale syrup (PAS)) as part of total mixed rations (TMR) compared to a control diet including molasses. The TMR were formulated to feed high yielding dairy cows. Data required as input for Biopara-Milk was used to simulate feeding a 650kg Holstein dairy cow, 2.5 BCS 12 week of lactation producing 45 kg/d milk and 4% butterfat and 3.3% protein content. The TMR rations developed were forage based (Grass silage, grass silage plus maize silage, and grass silage plus whole-crop cereal silage) with commonly used feedstuffs (Rapeseed meal, Soya Hipro, Barley, wheat, Molasses, Bread by product, Brewers grains). The simulation exercise included a detailed description of the chemical composition and degradation kinetics characteristic of each of the ingredients. Predicted milk yield, daily ME and MP supply of the control diets and treatment diets were analysed by two way ANOVA using MINITAB 16.

Results Three different sets of diets were formulated (Grass, Grass and Maize and Grass and Wholecrop) to achieve 50kg milk d. No statistically significant differences were observed between the diets by type of basal forage (P= 0.47). Statistically significant differences (P <0.05) were observed between the control diet and the different treatments. However a marginal improvement was obtained with ReguMaize 44. This might be due to the higher and more stable pH predicted by Biopara-Milk and also to the higher ME level obtained from the diets containing this product.

	Diet composition						Predicted supply		
Treatment (Grass diets)	DM %	CP (%DM)	NDF (%DM)	uNDF (%DM)	Quick CHO (%DM)	Slow CHO (%DM)	ME (Mj/d)	MP (g/d)	MY (kg/d)
Control	39.2	17.4	34	12.5	18.5	34.8	322	2462	45.0
ReguMaize 44	38.5	18.1	35	13	15.5	36.1	312	2515	44.2
PAS	38.1	18.2	34	12.8	15.0	35.5	307	2500	43.5
EthDSW	38.9	17.7	34	12.9	15.1	37.5	308	2503	43.9

Conclusion Mathematical models can aid research, development and evaluation of novel feed ingredients, helping the decision making process by providing theoretical evidence of the impact of the inclusion of such ingredients i.e. performance. Liquid by products are a good alternative source of energy to feed ruminants and their use should be tested with on-farm trials.

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Trends in efficiency of compound feed use by dairy cows in Great Britain

M Wilkinson[1], J Allen[2]
[1]University of Nottingham, UK, [2]Kite Consulting LLP, Staffordshire, UK
Email:j.mike.wilkinson@gmail.com

Implications Increased milk production per cow between 1990 and 2013 was associated with greater compound feed production per cow with no increase in efficiency of conversion of compound to milk. The trends were not driven by the ratio of milk price to compound price.

Introduction The ratio of compound and blend feed production per cow to milk yield per cow is an indirect estimate of greenhouse gas emissions intensity (DEFRA, 2014a). Efficiency of conversion of feed into milk is also a major indicator of economic efficiency since average feed cost per litre on dairy farms in Great Britain comprised 0.76 of total variable costs in 2012/13 (DairyCo, 2014). Trends in milk production and compound feed production were examined in relation to trends in milk and concentrate price to test the hypothesis that changes were driven by the ratio of milk price to compound price.

Material and methods Statistics were obtained for total annual production in Great Britain by animal feed mills of dairy compounds and blends, excluding raw material feeds used directly on dairy farms, together with statistics for annual number of dairy cows and milk production (DEFRA, 2014b). Data were also collated for mean annual wholesale farm gate price of milk including bonuses paid to producers (DEFRA, 2014c) together with Kite Consulting data for the mean retail price of compounds and blends. All data were for 1990 to 2013 inclusive, scaled to 1990 to show relative trends over the period.

Results

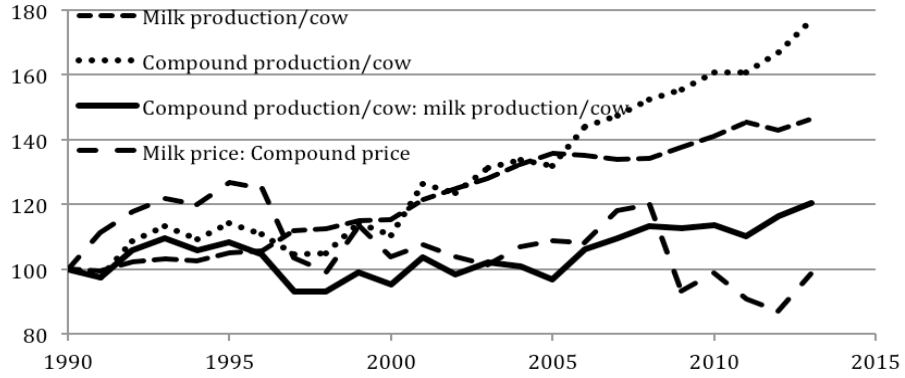

Figure 1 Annual milk and compound feed production and ratio of milk price to compound price (1990 =100).

Trends in milk and compound feed production per cow from 1990 to 2013 and in ratios of compound to milk production and milk to compound feed price relative to 1990 are in Figure 1. Both compound production per cow and milk yield per cow increased substantially over the period, with the increase in compound production being relatively greater than that in milk production since 2005. This trend indicates that higher milk output per cow was achieved from increased concentrate feeding and not through greater utilisation of home-produced forage. Relative change in ratio of compound production to milk production per cow was small until 2005, with an upward trend thereafter, indicating no overall improvement in efficiency of conversion of compound feed to milk. Further, raw material feeds purchased for direct use on farms probably also increased over the period. Ratio of milk price to compound feed price increased from 1990 to 1995, then decreased to 1998, stabilised to 2007 and decreased from 2008 to 2012.

Conclusion Changes in ratio of compound production to milk production per cow were not driven by the ratio of milk price to compound price. On the contrary, between 2008 and 2012 increases in the ratio of compound production to milk production coincided with decreases in the ratio of milk price to compound price.

Acknowledgement We thank DEFRA staff for provision of statistical data.

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Seasonal variability in the relationship between fatty acid and chlorophyll content of perennial ryegrass (*lolium perenne*)

S A Morgan, S A Huws, J K S Tweed, N D Scollan
IBERS, Aberystwyth University, UK
Email:sgm8@aber.ac.uk

Implications Enhancing the fatty acid (FA) content and/or composition of forage is currently receiving a great deal of interest due to potential applications in human nutrition, animal feed and biofuel sectors.

Introduction Enriching the FA profile of forage opens up the potential to: (1) increase energy provision to ruminants, (2) improve FA profile of ruminant products, and (3) develop non-seed biomass oil crops. The majority of plant FAs are contained within thylakoid membranes of chloroplasts, and consequently a positive correlation exists between FAs and chlorophyll (Chl) (Dierking *et al*., 2010). A previous study has demonstrated this relationship via *in vivo* Chl determination (hand-held Chl meter, Morgan *et al*., 2013). The present study aimed to examine how the relationship between FA and Chl changes over a growing season, using an *in vivo* and an *in vitro* technique to determine Chl content.

Material and methods Twenty four genotypes, differing in FA content, were selected from two populations of perennial ryegrass with four replicates of each, set out as spaced plants in a randomised block design under field conditions. Plants were harvested at ~28d intervals from early June to late September 2013. *In vivo* Chl content was measured one day prior to harvesting using a portable Chl meter, *SPAD*-502Plus (Konica Minolta, Japan). Twenty healthy leaves were randomly selected and measured at the mid-section of each leaf, with the average of these twenty measurements recorded. *In vitro* Chl content was determined using an acetone extraction procedure followed by spectrophotometric analysis at A_{663} and A_{645}. Total Chl concentration (mg/l) was calculated using Arnon (1949) then converted to mg Chl/mg DM. FA data was derived as described by Morgan *et al* (2013). Data were analysed via Genstat (16th edition; VSN International Ltd, Hemel Hempstead, UK) using Spearman's rank correlation and linear regression.

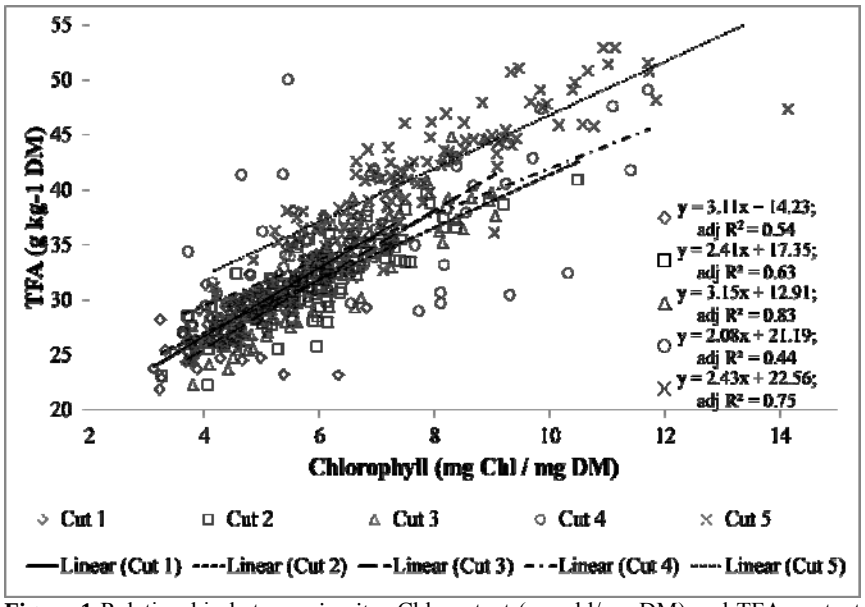

Figure 1 Relationship between *in vitro* Chl content (mg chl/mg DM) and TFA content (g kg^{-1} DM) of perennial ryegrass at 5 different cuts during one growing season.

Results Positive correlations were found at every cut for *in vitro* Chl vs. TFA content (P<0.001; Figure 1). Correlations between *in vivo* Chl vs. TFA content were also positive but only significant at Cut 2, 4 and 5 (P<0.001; Table 1). *In vitro* Chl vs. TFA content had consistently higher R^2 values, averaging at 0.64 across cuts compared to 0.14 for *in vivo* Chl vs. TFA content.

Table 1 Coefficients of determination (R^2) for *in vivo* and *in vitro* Chl vs. TFA content

Cut	Chl vs. TFA		*SPAD* vs. TFA	
	R^2	P	R^2	P
1	0.54	***	0.00	NS
2	0.63	***	0.14	***
3	0.83	***	0.01	NS
4	0.44	***	0.20	***
5	0.75	***	0.37	***

NS – Not significant; *** P<0.001

Conclusion Overall, there was minimal difference between Cuts in terms of the relationship between *in vitro* and *in vivo* Chl vs. TFA content. However the strength of the *in vivo* Chl vs. TFA relationship was much weaker and more variable. Further analysis of the lipid composition of these plants is warranted to investigate whether the genotypic difference in FA content is due to additional chloroplastic membrane in the higher FA genotypes.

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Evaluating the fermentable characteristics of molasses formulated feeds and liquid co-product syrups using *in vitro* gas production technique

V Ambriz-Vilchis[1], R Fawcett[1], A Masri[1], N Robertson[1,2], P Holder[3]
[1]Bioparametrics Ltd., Edinburgh, UK, [2]The Glenside Group Ltd., Livingston, UK, [3]E D & F Man Liquid Products UK Ltd, Liverpool, UK
Email:v.ambriz-vilchis@sms.ed.ac.uk

Implications The *In vitro* gas production technique is widely used in animal nutrition and feed evaluation. The characterisation of novel ingredients facilitates assessment of their suitability for inclusion in ruminant diets.

Introduction The use of novel ingredients in ruminant diets starts with feed evaluation. The *in vitro* gas production technique (IVGPT) (Menke and Steingass, 1988) has been widely used in animal nutrition for feed evaluation and to study the kinetics of microbial fermentation process in the digestive tract. The IVGPT is objective evidence of the rate of fermentation of feedstuffs. Gas volume data obtained from sample fermentation is then transformed, using mathematical modelling, into dynamic degradation parameters for both quickly and slowly fermentation fractions of protein and carbohydrate contained in feeds and forages. Two molasses formulated products from ED&F Man Ltd (ReguMaize 44 and ReguMix) and two commercially available liquid co-product syrups (Ethanol Distiller spent wash (EthDSW) and Pot Ale syrup (PAS)) that have been used as sources of energy and protein in ruminant diets were tested. The objective of this study was to evaluate the gas production profile and fractions of the protein quick (QCP) and slow (SCP), and carbohydrate quick (QCHO) and slow (SCHO) along with the rate of fractions and lag times of the examined products.

Material and methods Samples were incubated in gas tight syringes containing rumen liquor and buffer solutions (Menke and Steingas., 1998) in triplicates for CP and duplicates for CHO. The CP objective weight of each sample was set to meet the target of 79mg N/litre in each syringe whereas 200mg DM was sufficient in CHO fermentation syringes. Cumulative gas production then measured at 30 min intervals up to 3 hours, then every 1 hour up to 6 hours, followed by every 2 hours up to 12 hours and finally every 4 hours up to 48 hours. While protein gas curves were corrected only for blank samples, carbohydrate gas curves were corrected for blanks and nitrogen fermentation. CP and CHO gas curves were fitted to the model: Total degraded substrate = (Quick prop)*(1-exp (-Quick rate (-h) *t(h)))+ (Slow prop))*(1-exp (-Slow rate (-h) *(t (h) – lag (h)))) (Palmer, 2006).

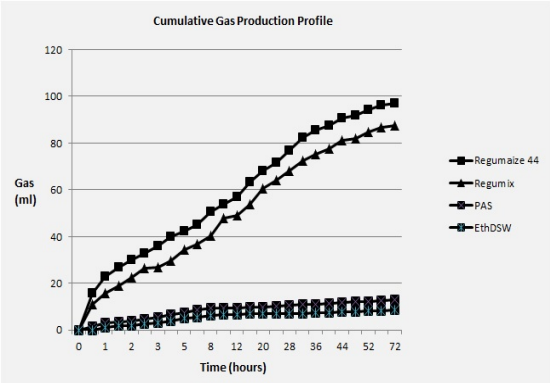

Figure 1 Cumulative gas production profile of ReguMaize 44, ReguMix , EthDSW and PAS

Results

Figure 1 shows the cumulative gas production profile of ReguMaize 44, ReguMix , EthDSW and PAS.
The cumulative gas production for ReuMaize 44 and ReguMix across 72 hours was higher than the other liquid co-products syrups. The significant exert of gas in molasses formulated feeds works as an evidence of how fermentable these products are, and hence the rumen utilisation.
Table 1 shows the protein and carbohydrate degradation parameters of ReguMaize 44 and EthDSW obtained by IVGPT

Table 1 Protein and carbohydrate parameters (fraction, rate and lag time) of ReguMaize 44 and EthDSW

Ingredient	QCP (propCP)	QCP rate/h	SCP (propCP)	SCP rate/h	Lag t	QCHO (prop DM)	QCHO rate/h	SCHO (prop DM)	SCHO rate/h	Lag t
ReguMaize 44	0.98	0.229	0	0	0	0.42	1.041	0.26	0.041	2.5
EthDSW	0.96	0.333	0	0	0	0.06	0.345	0.10	0.014	3

ReguMaize 44 and EthDSW had QCP fraction but no SCP fraction. No variation on QCP as proportion of CP content was observed. However, ReguMaize44 had significantly greater QCHO and at faster rate/h when compared to EthDSW. At a shorter lag time, ReguMaize 44 had higher SCHO than EthDSW.

Conclusion The study confirmed the importance of evaluating the CP and CHO fermentation fractions of feed and forage as a base for later utilisation as ingredients of ruminant diets. The present study showed that not all liquid co-products have the same profile of degradation parameters when evaluated by IVGPT, hence, would not have the same nutritive values.

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Evaluation of fertiliser treatment and harvesting age on proximate composition of *Arachis pintoi*

S A Adeoye[1], J A Olanite[1], V O A Ojo[1], O S Onifade[1], F O Oke[2], R O Folarin[1], A A Ogunsusi[1], O M Bada[1]
[1]Federal University of Agriculture, Abeokuta, Ogun State, Nigeria, [2]Federal University Dutse, Jigawa, Nigeria
Email:wescoye@gmail.com

Implications Establishment of *Arachis pintoi* is considered very low, appropriate management, combined with forage production strategies, such as fertilisation, can assist in the rapid establishment and productivity of the forage legume.

Introduction Forage legumes play a major role in improving pasture production and animal performance (Adeoye *et al*., 2011). *A. pintoi* is used in grazing systems for both beef and dairy cattle and has been recognised as a legume with high intake potential, defoliation and trampling tolerance (Argel, 1995). Although little attention has been gained by the legume in Nigeria, the plant grows well in soils low in P although some P fertilizer is advisable for soils extremely low in P. The present study thus aimed at evaluating effects of fertilizer and harvesting time on the proximate composition of *A. pintoi*.

Material and methods A total area of 693 m^2 was mapped out and was divided into 30 plots, each of 4 m x 3m, located on latitude 7º12' 33.6" N and longitude 3º25' 37.2" E. The soil available P, 32.05 mg/kg, total, nitrogen, 0.19 %, organic Carbon, 2.54. The study was laid out in a 5 x 2 factorial experiment in a randomized complete block design. The two factors were: Murate of Potash fertiliser, M. O. P. (60 %) at 0, 100, 150, 200 and 250 kg/ha and harvesting age at 8 and 12 weeks. There were 10 treatments, replicated three times which were randomly allocated to the plots. The plots were spaced by 1m, and the replicates by 2m apart. The seeds of *Arachis pintoi* cv. Amarillo were planted at 1 seed per hole spaced at 0.5m apart. The fertilizer was applied four weeks after planting. Proximate compositions were determined according to the procedure of AOAC (2000). All data collected were subjected to the analysis of variance with the use of SAS (2003).

Results
Dry matter, crude protein and ash contents were significantly ($P < 0.05$) higher on the plots that received 200 kg/ha M. O. P than other plots. Crude fibre and nitrogen free extract recorded highest in 100 kg/ha and 150 kg/ha plots respectively. Harvesting at 8 weeks was better than at 12 weeks in terms of crude protein, ash and nitrogen free extract (Table 1).

Table 1 Main effects of fertiliser and harvesting age on proximate composition (%) of *A. pintoi*

Murate of Potash (kg/ha)	DM	EE	CP	CF	ASH	NFE
0	20.21^{b}	2.69^{a}	13.11^{b}	33.29^{b}	5.90^{b}	37.25^{d}
100	21.90^{ab}	1.93^{c}	13.96^{ab}	40.29^{a}	6.56^{ab}	42.53^{c}
150	23.97^{a}	2.33^{b}	12.29^{c}	28.06^{c}	8.14^{a}	51.42^{a}
200	24.15^{a}	1.83^{c}	14.64^{a}	29.00^{c}	8.38^{a}	46.40^{b}
250	20.25^{b}	1.99^{c}	14.22^{ab}	26.37^{d}	7.20^{ab}	50.21^{a}
SEM	0.51	0.24	0.02	1.04	0.89	0.16
Age (Week After Planting)						
8	18.51^{b}	2.22	14.60^{a}	29.39^{b}	8.69^{a}	45.19^{a}
12	23.42^{a}	2.00	13.17^{b}	32.77^{a}	5.57^{b}	46.27^{a}
SEM	0.28	0.11	0.19	0.8	0.42	0.42

DM: dry matter, EE: Ether extract, CP: crude protein, CF: crude fibre, NFE: nitrogen free extract

Conclusion From the results of this study, 200 or 150 kg/ha M. O. P. fertilizer treatment could be recommended for enhanced production of forage peanut, *Arachis pintoi*. Harvesting at 8 weeks also maintained higher CP, Ash and NFE contents, while DM and CF were favoured by 12 week-harvest.

Acknowledgements The authors acknowledge the assistance Mr. John Idehen, Principal Technologist, Department of Pasture and Range Management, Federal University of Agriculture, Abeokuta, Ogun State, Nigeria.

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Growth parameters of *Arachis pintoi* as affected by fertiliser treatment

S A Adeoye[1], J A Olanite[1], V O A Ojo[1], A O Taiwo[2], A Adetona[1], S O Ogundele[1]
[1]Federal University of Agriculture, Abeokuta, Ogun State, Nigeria, [2]University of Ibadan, Oyo, Nigeria
Email:wescoye@gmail.com

Implications *A. pintoi* is a perennial with low stoloniferous growth (Rodrigues *et al*., 2006). Efforts should be made to aid the establishment through organic and/or inorganic fertilizer application.

Introduction Several species of *Arachis* have potential to be incorporated into forage systems. *Arachis glabrata* (*Rhizomatous*), *A. pintoi* and *A. repens* (stoloniferous) are the most collected and evaluated when it comes to forage yield (Valls and Simpson, 1994; Valls and Pizarro, 1994). They are the most promising, since they produce large amounts of high quality forage and they present morphological feature that confer better adaptation to grazing and harvest (Valls and Simpson, 1994; Valls and Pizarro, 1994). The objective of this research was to determine the growth performance as affected by N. P. K. fertilizer treatment.

Material and methods A total area of 390 m^2 was mapped out and was divided into 15 plots, each of 4 m x 3m, located on latitude 7º12' 33.6" N and longitude 3º25' 37.2" E. The soil available P, 32.05 mg/kg, total, nitrogen, 0.19 %, organic Carbon, 2.54. The study was laid out in a completely randomized design. There were 5 treatments, replicated three times which were randomly allocated to the plots. The treatments were N. P. K. (20-10-10) at 0, 100, 150, 200 and 250 kg/ha. The plots were spaced by 1m, and the replicates by 2 m apart. The seeds of *Arachis pintoi* cv. Amarillo were planted at 1 seed per hole spaced at 0.5m x 0.5m. The fertilizer was applied four weeks after planting. Data collection was done 16 weeks after planting the legume. All data collected were subjected to the analysis of variance with the use of SAS (2003).

Results The values of all but one of the growth parameters – plant height – were significantly ($P < 0.05$) higher for the *A. pintoi* that received 250 kg/ha N. P. K (20-10-10) fertiliser, however, the values were either not significantly ($P > 0.05$) different from, or next in performance to the values recorded for the 150 kg/ha fertiliser treatments. The plant height was highest ($P < 0.05$) for the 150 kg/ha fertiliser treatment (Table 1).

Table1 Effect of N. P. K. fertiliser on growth parameters *A. pintoi*

N. P. K (kg/ha)	Ground cover	Leaf length	Leaf width	Plant height	Number of primary branches	Leaf
	← (cm) →				← number/plant →	
0 (Control)	60.33^{e}	3.71^{b}	2.43^{b}	6.37^{d}	13.67^{d}	402.43^{d}
100	68.57^{c}	3.95^{ab}	2.57^{b}	7.97^{c}	16.07^{b}	710.30^{b}
150	85.00^{a}	4.33^{a}	2.73^{ab}	13.17^{a}	17.82^{a}	841.57^{a}
200	73.74^{d}	4.01^{ab}	2.63^{b}	7.93^{c}	15.19^{c}	579.67^{c}
250	88.37^{a}	4.37^{a}	3.00^{a}	11.30^{b}	18.17^{a}	853.63^{a}
SEM	1.08	0.06	0.04	0.41	0.48	10.63

$^{a-e}$ means on the same column with different superscripts are significantly ($P < 0.05$) different

Conclusion Treating *A. pintoi* treated with 150 kg/ha N. P. K. (20-10-10) fertiliser gave a comparable results with 250 kg/ha fertiliser treatment in terms of ground cover, leaf length and width, number of primary branches per plant, and number of leaf per plant.

Acknowledgements The authors acknowledge the assistance Prof. Onifade O. S. of the Department of Pasture and Range Management, Federal University of Agriculture, Abeokuta, Ogun State, Nigeria for providing the seeds used for planting.

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Predicting grass digestible and metabolisable energy contents from chemical composition

S Stergiadis[1], M Allen[2], X J Chen[3], D Wills[1], T Yan[1]
[1]Agri-Food and Biosciences Institute, Sustainable Agri-Food Sciences Division, Agriculture Branch, Hillsborough, County Down, UK, [2]Agri-Food and Biosciences Institute, Finance and Corporate Affairs Division, Biometrics and Information Systems Branch, Belfast, County Antrim, UK, [3]Lanzhou University, State Key Laboratory of Grassland Agro-Ecosystems, College of Pastoral Agriculture Science and Technology, Lanzhou, China
Email:sokratis.stergiadis@afbini.gov.uk

Implications The current study demonstrates a quick and easy means of assessment of fresh grass energy concentrations from its chemical composition, suitable for grazing cattle.

Introduction Grass is the cheapest source of animal feed; hence, dairy and beef production is mostly practiced under pasture-based diets in a number of regions that are suitable for long grazing seasons and high grass production per hectare, such as parts of the UK, Ireland and New Zealand. However, grass nutritive quality, primarily defined by grass metabolisable energy (ME) contents, is predicted either from long-standing equations (Givens *et al*. 1990) or relationships that have been developed from studies using sheep on conserved forage diets (Thomas, 2004). The objective of the current study was therefore to develop prediction equations of grass energy concentrations, which are promptly and routinely available at farm level, using grass nutrient contents as predictors.

Material and methods Data were collected from a series of digestibility studies using non-pregnant dry cows fed fresh grass at maintenance energy level. Grass was harvested from eight ryegrass swards (two primary growth, three first regrowth and three second regrowth) in 2007 and 2008, representing early to late maturity, and two primary growth early maturity swards in 2009. Two groups of four cows were offered solely fresh cut grass from each sward and daily measurements over 6 weeks were performed. The first group (weeks 1-3) and second group (weeks 4-6) of cows were used to assess early and late maturity grass respectively. As a result of the diverse swards used, grass nutritive value varied greatly. Mean grass digestible energy (DE) and ME concentrations were 14.5 and 12.0 MJ/kg dry matter (DM), ranging 11.8-16.7 MJ/kg DM and 9.0-14.1 MJ/kg DM, respectively. Averaged 3-day records of energy contents (n = 464, response variables) and grass chemical composition (n = 116, explanatory variables) were used in a residual maximum likelihood analysis (VSN International, 2013) to develop prediction equations. A combination of the random effects of cow, field, year, harvest date, fertiliser input, maturity stage, and grass variety was removed for each predicted variable.

Results For the prediction of grass DE (Eq. 1a-1c), using grass gross energy (GE), ether extract (EE), acid detergent fibre (ADF), neutral detergent fibre (NDF) and ash contents as predictors maximised r^2. Excluding EE, NDF and ash slightly reduced r^2 but substituting GE, EE, NDF and ash with grass nitrogen (N) content considerably reduced the explained variation. Explained variation for ME (Eq. 2a-2c) was not as high as for DE. The highest r^2 was observed when grass N, EE, ADF and ash were used. Replacing N, EE and ash with GE, marginally reduced r^2 but a further decrease was observed when grass EE, ADF and ash were substituted with water soluble carbohydrates (WSC).

Table 1 Prediction of DE and ME contents in fresh grass using grass chemical composition parameters, assessed with non-pregnant dry cows fed at maintenance level (subscript parentheses represent standard errors)

Equations[1]	r^2	Eq.
$DE = 0.904_{(2.439)} + 0.904_{(0.125)}\,GE + 29.2_{(6.7)}\,EE - 3.465_{(1.992)}\,NDF - 6.290_{(2.045)}\,ADF - 5.599_{(3.166)}\,Ash$	0.71	(1a)
$DE = -5.647_{(2.017)} + 1.264_{(0.100)}\,GE - 11.1_{(1.2)}\,ADF$	0.70	(1b)
$DE = 5.357_{(4.131)} + 154.7_{(31.4)}\,N - 2055.0_{(622.3)}\,N^2 + 34.6_{(16.5)}\,NDF - 41.8_{(16.4)}\,NDF^2$	0.64	(1c)
$ME = 15.0_{(0.6)} - 38.9_{(10.8)}\,N + 34.7_{(7.3)}\,EE - 10.1_{(1.4)}\,ADF - 8.070_{(3.390)}\,Ash$	0.49	(2a)
$ME = -122.6_{(38.9)} + 14.5_{(4.3)}\,GE - 0.398_{(0.119)}\,GE^2 + 30.5_{(12.5)}\,ADF - 71.4_{(22.5)}\,ADF^2$	0.48	(2b)
$ME = 9.613_{(0.732)} + 263.0_{(37.3)}\,N - 4941.0_{(756.4)}\,N^2 - 16.0_{(6.4)}\,WSC + 61.4_{(18.0)}\,WSC^2$	0.45	(2c)

[1] Units: MJ/kg DM for grass DE, GE and ME; kg/kg DM for grass EE, NDF, ADF, N and WSC

Conclusion Concentrations of DE in fresh grass may be efficiently predicted from grass nutrient contents. Predictions of grass ME contents showed lower r^2 indicating that other explanatory variables, highly likely related to nutrient digestibility, may be required for the improvement of the equations. Equations developed in the present study can be used in a wide range of pastures due to the high variation of the quality of grass used.

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Chemical evaluation of selected Nigerian matured forages for their use in ruminant diets

O J Bolaji, A S Chaudhry, J Dolfing
Newcastle University, UK
Email:o.j.bolaji@newcastle.ac.uk

Implications Mature grasses may require nutritional improvement by biological treatments with or without legume supplementation before their feeding to ruminants for sustained animal production.

Introduction Many types of tropical forages including grasses and legumes are limited in quantity and quality due to drastic effects of season and maturity. While some Nigerian grasses have been found promising due to their persistence, hardiness and tolerance to dry seasons, their use for ruminants is restricted due to their variable nutritive values. Although the grasses are supplemented with legumes to compensate for their nutrient deficiency, their chemical analysis is needed routinely to develop strategies to optimise their use in ruminant diets. This paper investigated the chemical composition of selected Nigerian forages to ascertain their potential use in ruminant diets.

Material and methods Replicated (n=4) samples of four grasses (*Pennisetum purpureum* =PP, *Brachiaria decumbens* =BD, *Andropogon gayanus* = AG, *Panicum maximum* = PM), and two legumes (*Leucaena leucocephala* =LL, and *Gliricidia sepium* = GS) were collected randomly from four different sub-plots of an experimental field at the Federal University of Agriculture, Abeokuta (FUNAAB), in March during the end of dry season. The forage samples were then bulked for each forage from each sub-plot, chopped, dried at 55^{o}C and transported to Newcastle University. The samples were re-dried at 55^{0}C for 48 h and ground through a 1 mm screen. Sub-samples of each forage were then analysed in triplicate for dry matter (DM), ether extract, ash, crude protein, neutral detergent fibre, acid detergent fibre, acid detergent lignin, minerals, total phenolics, total tannins and condensed tannin contents by using standard methods. The data were then statistically analysed by using one way analysis of variance in Minitab16 software to compare the selected forages for differences in each nutrient at $P<0.05$. Tukey's *post hoc* test was used to compare means of different forages at $P<0.05$.

Results The forages were significantly different for most components as shown in the following Table ($P<0.05$). The legumes contained lower NDF but higher CP, secondary metabolites, calcium and magnesium contents than the grasses. The grasses contained variable amounts of CP which was highest in AG and lowest in BD

Composition	PP	BD	AG	PM	LL	GS	SEM	P-value <
Proximate and Fibre fractions (g/kg DM)								
Dry matter (g /kg)	950.7	952.0	950.5	897.0	954.8	946.4	4.95	0.0001
Crude protein	65.6	59.0	117.3	61.5	255.0	215.0	19.07	0.0001
Ash	134.0	75.8	84.5	119.4	91.8	116.2	5.07	0.0001
Organic matter	851.1	894.1	880.7	779.0	861.6	835.2	9.18	0.0001
Ether extract	13.0	10.9	15.2	9.2	57.8	27.5	4.12	0.0001
Neutral detergent fibre	659.3	714.0	665.2	704.0	385.7	421.1	32.94	0.0001
Acid detergent fibre	468.6	508.5	502.4	468.7	333.2	389.9	15.53	0.0001
Acid detergent lignin	68.6	72.78	90.5	120.3	254.0	164.5	15.81	0.0001
Secondary Metabolites (g /kg DM)								
Total phenolics	9.8	8.7	24.4	6.6	114.0	28.7	9.12	0.0001
Total tannins	6.2	3.1	21.0	2.0	90.8	20.4	7.49	0.0001
Condensed tannins	3.7	5.7	11.9	5.1	61.9	27.93	5.20	0.0001
Selected Minerals (mg /kg DM)								
Calcium	238.1	192.1	156.7	135.6	834.9	724.7	69.60	0.0001
Potassium	244.2	301.0	347.1	172.5	257.0	296.0	18.90	0.200
Magnesium	130.2	113.9	76.4	75.5	155.5	268.3	15.98	0.0001

Conclusion The grasses contained low CP but high fibre contents and so cannot be used alone for ruminant growth and production. Although, the legumes contained greater CP, they had high secondary metabolites. Further research is planned to investigate if the nutritive value of these grasses could be enhanced compared with a quality grass by using fungal treatment with or without a forage legume to improve ruminant production during the dry season.

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Bioeconomic modelling of six yearling to beef finishing systems

P Crosson[1], P O'Kiely[1], E McGeough[2]
[1]Teagasc, Grange, Dunsany, Co. Meath., Ireland, [2]University of Manitoba, Winnipeg, MB R3T 2N2, Canada
Email:paul.crosson@teagasc.ie

Implications Based on two animal production studies and prevailing prices, the economic ranking, from most to least profitable, of finishing diets for yearling to beef production systems were; maize silage (MS) grass silage (GS), *ad libitum* concentrates (ALC) and whole-crop wheat silage (WCW).

Introduction Beef production in many parts of northern Europe traditionally utilises grass silage as the main finishing feedstuff. However, variability in ensilability and digestibility of grass silage has led to increased interest in whole-crop or grain silages and high grain diets for finishing cattle. The effects on animal performance of offering such feeds to finishing cattle were assessed by McGeough *et al.* (2010a and b). This present study quantified the economic efficiency of yearling to beef finishing production systems based on grass silage, grain silages and *ad libitum* concentrates.

Material and methods To evaluate technical and financial performance, the Grange Beef Systems Model (Crosson *et al.*, 2009) was used. 134 steers were purchased at 12 mo of age at the start of their second season of grazing, and finished at 24 mo of age. Following 240 d grazing, animals were housed in a slatted floor facility for a finishing period of 120 d and offered 1 of 6 different diets (Table 1; McGeough *et al.*, 2010a and b). Silage-based diets were supplemented with concentrates (3 kg fresh weight/animal) to meet the animals' protein requirements. The sixth scenario, an ALC-based diet (McGeough *et al.*, 2010b) was included to permit comparison with a high energy, low forage diet. The total farmed area was 40 ha for each scenario, which encompassed both grazed grass requirements and land for finishing feed production.

Table 1. Feed intake and animal performance data for six yearling to beef finishing systems.

	Systems[1]					
	GS	MS I	MS II	WCW I	WCW II	ALC
DMI relative to live weight (g/kg)	15.05	18.23	18.36	18.22	17.72	16.95
Live weight gain (g/d)	929	1208	1298	1103	1043	1335
Carcass gain (g/d)	664	844	887	765	757	915
Killout rate (g/kg)	546	548	547	548	553	552
Conformation score (1-5)	2.93	2.75	3.08	3.23	2.8	3.27
Fat score (1-5)	3.18	3.42	3.42	3.28	3.13	3.47

[1]GS = Grass silage; MS I & II = Maize silage, harvest date 13 September (MS I) and 23 October (MS II); WCW I & II = Whole-crop wheat silage, grain to straw plus chaff ratio 31:69 (WCW I) and 47: 53 (WCW II); ALC = Ad libitum concentrates

Table 2. Feed budget, beef output and economics of six yearling to beef finishing systems.

	Systems[1]					
	GS	MS I	MS II	WCW I	WCW II	ALC
GS, MS or WCW consumed (t	108	144	149	143	136	21
Concentrate consumed (t DM)	42	42	42	42	42	159
Total feed consumed (t DM)[2]	373	409	414	408	401	403
Beef carcass output (kg/ha)[3]	628	696	714	671	667	731
Gross output (€/ha)	2,008	2,244	2,320	2,155	2,104	2,565
Gross margin (€/ha)	1,110	1,142	1,200	884	863	1,036
Net margin (€/ha)	581	608	665	351	330	508

[1]Systems as per Table 1. [2]Includes 223 t DM pasture. [3]Beef output = beef sold - beef

Results MSII and WCWI had the highest silage consumption, and correspondingly highest profitability, within the respective MS and WCW systems. Net beef output was greatest for ALC and lowest for GS. Gross output value followed net beef output and thus, was highest for ALC and lowest for GS with the grain silage systems intermediate. Gross and net margins were highest for the MS systems and lowest for the WCW systems. Within each of the grain silage systems there were modest differences in profitability. GS was more profitable than WCW or ALC systems.

Conclusion Maize silage production systems were the most profitable of the 6 yearling to beef finishing systems modelled, largely driven by high crop yields and high levels of animal performance. Grass silage-based finishing systems can also be relatively profitable when compared to whole-crop wheat and ad-libitum concentrate production systems.

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Effects of storage on the nutritive quality of grass-legume mixtures in South-western Nigeria

V O A Ojo, I G Nukasi, A O Jolaosho, O M Arigbede, J O Olanite, P A Dele, S A Adeoye, O B Ogunbote, A O Ogunsakin
Federal University of Agriculture, Abeokuta, Ogun State, Nigeria
Email:ojolubunmi@yahoo.com

Implications For sustainable ruminant animal production, feeding of grass legume mixtures will improve overall pasture productivity and can serve as control for the problem of bloat which is usually associated with sole legume feeding.

Introduction Grass-legume mixtures provide superior nutrient balance and produce higher forage yields (Ojo *et al*., 2013). Tropical Kudzu (*Pueraria phaseoloides*) is an abundant leguminous plant in the humid-tropics. It is used as a cover-crop to prevent soil erosion and has high nutritional quality. This research was carried out to evaluate the effects of forage mixtures and duration of storage after drying on the nutritive quality of *Pueraria phaseoloides* and *Pennisetum purpureum*.

Material and methods *Pueraria phaseoloides* was harvested at the vegetative stage while *Pennisetum purpureum* was harvested at 8 weeks after planting at 15cm above ground level on a sandy-loam soil in the derived savannah area of Nigeria with 1037 mm annual precipitation in October, 2012 and conserved as hay. The experiment was a randomised block design with forage proportion of 100% grass or legume: grass-legume mixture of 25%:75%, 50%:50% and 75%:25% and storage duration of 30, 60 and 90 days in three replicates. Proximate composition contents were analysed according to the standard methods of AOAC (2000), Neutral detergent fibre according to Van Soest *et al*. (1991), *in vitro* gas production test was done according to Menke and Steingass (1988) while post incubation parameters was according to Getachew *et al*. (2004).

Results The CP contents were significantly (P<0.05) different and ranged from 80.1 in 100% *P.purpureum* hay to 150.5 g/kg DM in 100% *P. phaseoloides* hay, while 30 days of storage duration had higher CP over other duration. 100% legume hay produced most gas at 48h of incubation with the least gas volume recorded for 100% grass. Short chain fatty acid had values ranging from 0.11 in 100% *P. purpureum* hay to 0.2485 µmol in *P. phaseoloides* 25%: *P. purpureum* 75% hay.

Table 1 Effect of forage proportion and storage duration on the proximate composition (g/kg DM) and *in vitro* gas post incubation parameters of *Pueraria phaseoloides* and *Pennisetum purpureum* hay

	Dry Matter	Crude Protein	Ether Extract	Ash	NDF	GV ml/200mgDM	SCFA µmol	ME MJ/kg	OMD g/kg DM
Effect of forage proportion									
PPH25%:PPR 75%	941.6^{a}	89.3^{c}	71.6^{c}	90.0^{b}	553.3^{b}	28.33^{b}	0.24^{a}	3.98	359.4
PPH50%:PPR 50%	878.3^{b}	90.7^{c}	88.3^{a}	103.3^{a}	576.6^{b}	25.00^{c}	0.18^{ab}	3.62	345.8
PPH75%:PPR 25%	931.6^{a}	106.3^{b}	78.3^{b}	85.0^{b}	573.3^{b}	25.00^{c}	0.16^{ab}	3.53	334.9
PPH 100%	866.6^{b}	150.5^{a}	91.6^{a}	91.9^{b}	501.2^{c}	31.00^{a}	0.22^{a}	3.85	366.9
PPR 100%	886.6^{b}	80.1^{d}	58.3^{d}	71.6^{c}	613.3^{a}	18.67^{d}	0.11^{b}	4.84	322.4
SEM	0.77	0.58	0.28	0.28	0.98	1.00	0.02	0.17	0.84
Effect of Storage time (Days)									
30	904.8^{ab}	96.4^{a}	92.2^{a}	87.2^{a}	552.8	28.78^{a}	0.29^{a}	4.28	360.7
60	922.2^{a}	96.1^{a}	76.1^{b}	73.3^{b}	565.7	22.89^{b}	0.18^{b}	3.61	360.9
90	880.7^{b}	81.6^{b}	61.6^{c}	62.2^{c}	567.8	24.11^{b}	0.24^{ab}	3.97	344.5
SEM	6.80	1.70	3.90	3.20	4.90	0.89	0.02	0.22	1.02

$^{a-d}$:Means in the same column with different superscripts are significantly (p<0.05) different; GV-gas volume at 24hours; PPH- *Pueraria phaseoloides*, PPR- *Pennisetum purpureum*, NDF- Neutral detergent fibre

Conclusion From this result, it can be concluded that hay baled at different proportions of grass and legume mixtures at 30 days of storage duration had better quality than the sole grass in terms of chemical composition and digestibility. Reduction in ash contents of hay could be due to microbial uptake as storage period increased.

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E-learning and assessment systems for maths and statistics

B Foster, C Perfect
Newcastle University, UK
Email:bill.foster@ncl.ac.uk

Implications Demonstrating and reviewing the increasingly widespread use of electronic methods in the teaching, learning and practising of important numerical and statistical techniques and their applications.

Introduction There is increasing availability of on-line information on and practice in numerical and statistical skills for a wide variety of disciplines. The aim of this talk is to review the present state in terms of relevant materials which are freely available and which offer staff, students and practitioners easy access to good quality help and guidance.

Material and methods Animal Science and the School of Maths and Stats at Newcastle University have worked on two projects looking at the use of on-line assessment and learning for undergraduate students in Animal Science and related disciplines. The first, funded by VETNET, reviewed and obtained information from UK colleges and universities on those numerical and statistical topics perceived as critical for, in particular, early stage students.
http://www.mas.ncl.ac.uk/~nwhf1/numeracy/vetnet/survey1.html
Following this, e-assessment diagnostic and practice tests were introduced. The second project, funded by QUILT at Newcastle University built an on-line support wiki for first year students which incorporated the information from the first project and also feedback from final year students. This wiki was created by undergraduate students over a period of 6 weeks and the first phase finished in 2014.
All of the tools and systems used are freely available and open access.

Results The support wiki can be viewed at http://mathsupport.mas.ncl.ac.uk/wiki/Animal_Science.
It incorporates content, examples, on-line practice and assessment with feedback
A variety of on-line and electronic tools were used with no difficulty by the students, under minimal supervision. In particular the videos created by the students were an important part of the teaching material.

Conclusion The success of the wiki project demonstrates that there are excellent freely available tools which can be used to create materials for the support of vitally important skills in numeracy, mathematic and statistics. The purpose of the talk and subsequent paper is to review these tools, in particular e-assessment, and how they can be accessed and used.

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A survey of the study methods used by students of the biological sciences

B T Wolf
Aberystwyth University, UK
Email:btw@aber.ac.uk

Implications Educators need to consider the implementation of formal training in study techniques during transition from school to university and the inclusion of spaced retrieval practice in curriculum design.

Introduction A considerable body of research has demonstrated the poor utility of rereading as a study technique and the benefits of distributed retrieval practice as a means of boosting long-term memory (Dunlosky *et al*, 2013). This survey was conducted to identify the revision methods used during first year studies by students of pure and applied biological sciences.

Material and methods This voluntary survey was conducted with 384 second year students at the Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, between October 5th and October 27th, 2013. The survey was preliminary to a course in research methods in which the theme of study was 'which is the best study method to use when learning course materials?', and results were used to inform activities designed to foster skills in scientific reading and literature review. The survey was delivered through the BlackBoard virtual learning environment and consisted of nine questions, the first being free response to identify, in order of importance, the study techniques that students used. Remaining questions were selected from the surveys of Karpicke, Butler and Roediger (2009) and Kornell and Bjork (2007). Students were randomly allocated to two groups of 192 and took versions of the survey that differed in the wording of one question (see Table 1).

Results Of a possible 192 students per survey group, 174 and 155 attempts were recorded, with 137 and 125 completed submissions for survey versions A and B respectively. The question 'Would you say you study the way you do because a teacher/lecturer (or teachers/lecturers) taught you to study this way?' gave 30: 70% Yes: No responses. When asked 'Do you typically read material more than once during study?' 21.6% reported rereading whole texts, 55.2% reread marked sections and 23.2% would not usually reread. Only 19% of respondents chose to test themselves when there was no option to reread the notes i.e. recognised the benefits of the test effect (Table 1), which is in close agreement with 22% recognising that self testing was a better route to learning (Table 2). A high proportion recognised the diagnostic benefits of self testing, but 17.6% rarely used self-testing as a study technique (Table 2).

Table 1 Percentage responses to the question: Imagine that you are reading lecture notes for an upcoming exam. After you have read the lecture notes one time, would you rather:

	Survey A	Survey B
Number	137	125
Restudy your entire lecture notes or certain parts of them	59.1	39.2
Try to recall material from the lecture notes (without the possibility of restudying the notes)	19.0	
Try to recall material from the lecture notes (with the possibility of restudying the notes)		36.0
Use some other study technique	21.9	24.0

Table 2 Percentage responses to the question: If you quiz yourself while you are studying, why do you do so? (N = 262)

Response	%
I learn more that way than I would through rereading	21.1
To figure out how well I have learned the material that I am studying	55.9
I find quizzing more enjoyable than rereading	5.4
I usually do not quiz myself	17.6

Conclusion These results are similar to those found in a range of universities in the USA and indicate that a high proportion of students do not use study techniques that they have been taught, rely heavily on rereading during study and have poor understanding of the benefits of self-testing as a learning tool.

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The use of the 'Muddiest Point' technique as an in-class evaluation method

M R F Lee[1,2]
[1]University of Bristol, School of Veterinary Science, Langford, Somerset, UK, [2]Rothamsted Research, North Wyke, Devon, UK
Email:michaelrf.lee@bristol.ac.uk

Implications The muddiest point highlighted some key areas which the students were having problems with so early intervention could be developed to improve understanding.

Introduction The issue to be addressed was to gauge the level of knowledge and understanding of the class throughout the course and improve communication between the lecturer and student. This would allow early intervention in areas which were not clear to maximise understanding and improve the course content for future sessions.

Material and methods The Muddiest Point is one of the simplest and least threatening evaluation technique. It was first developed in 1989 by Frederick Mosteller. The method was used for a BSc level 2 Biochemistry module with 35 registered students on the module. The technique follows five simple steps during each lecture developed from the scheme given by Carlson, (2010):

- At the start of the lecture hand out Post-it® notes and ask the students to leave them blank until the end of the lecture.
- At the end of the lecture ask the students to write down on the Post-it® the answer to the question – 'What part of today's lecture was not clear in your mind and could be described as the Muddiest Point?'
- Ask the students to stick them to the desk at the front of lecture anonymously
- Read through all the comments and format the response to the Muddiest point, with three strategies:
    - Answer the questions at start of next class to all points
    - Prepare a handout to clarify the issue if between 10-25% of students raise the issue or it is a re-raised Muddiest point
    - Revise course to have a major revision session on the area if >25% of students raise the issue or if the issue has been raised more than twice over the course
- Ask the students after the lecture if today's Muddiest point has been understood and if not to re-submit it as a Muddiest point at the end of the lecture.

Results The first assessment was the extent that the students used the Muddiest point, which started off modestly (5 per lecture) and rose to around 20 per lecture (mainly on the same topic) as the students got used to the system. Each lecture started with going over the Muddiest points from the previous lecture in-class or with the production of a hand-out, which occurred on three occasions where more than 25% of the class did not fully understand an area. These areas were picked up in an end of course quiz and were answered very well showing that the intervention was successful. To help evaluate the class feedback a questionnaire was given to the students at the end of the module to reflect on the Muddiest Point. The questionnaire was developed based on the models given by Cohen *et al*. (2000). The students were told beforehand that these would be completely anonymous and the reason behind the Muddiest Point was explained. A ratings Likert scale question (1 strongly agree – 5 – strongly disagree) as described by Fowler (1995) was adopted to develop quantitative data at the same time as offering sensitivity and differentiation. All students were required to complete the questionnaire. With a score of 3 being the cut off as neither agree or disagree all the responses had a positive score of <3. Average scores of between 1 and 2 were received for 'Helped solve and seek areas of knowledge', 'improved staff / student interaction', 'highlighted areas of weakness' and was 'a good way to re-cap'. These were all key reasons for the intervention. Areas which scored higher scores (>2) and so were less in agreement were 'showed my current level of knowledge' and 'improved the enjoyment of the course' which were minor aims of the intervention. The question 'highlighted the course demands and outline' received a score close to neutral of 2.5, which was not surprising as this was not the role of the intervention.

Conclusion Key outcomes of the intervention were that students were able to ensure they understood key areas and concepts. Feedback from the students showed they used the Muddiest point to solve and seek areas of knowledge and to highlight areas of weakness. The lecturer was made aware of the level of students in the class and could tailor lectures and assignments accordingly. In addition the student / lecturer interaction and engagement was improved in comparison to years when the Muddiest point intervention was not used.

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Instant expert: development and evaluation of an intelligent, interactive 3D computer game for teaching visual lameness assessment skills through deliberate practice

S D Starke[1], G C Miles[2], S B Channon[2], S A May[2]
[1]University of Birmingham, West Midlands, UK, [2]The Royal Veterinary College, Hatfield, Hertfordshire, UK
Email:s.d.starke@bham.ac.uk

Implications An intelligent, adaptive and feedback-driven computer game based on 3D animations of lame horses allowed novices to systematically practice and improve equine lameness assessment skills up to expert level within hours.

Introduction Lameness is the most common reason why horses are referred to a veterinarian. Worryingly, studies into the validity and repeatability of assessor opinion on the lameness status often report inadequate performance on the side of the veterinarian (Keegan 2007). Lameness assessment poses a particular challenge for novices such as horse owners, students and often new graduates and early career veterinarians. However, at present, there is no option to systematically practice, improve and validate visual assessment skills against a "gold standard". Hence, the danger is that individuals are unable to determine reliably mild and even moderate gait abnormalities due to the lack of practice and feedback. It has previously been highlighted that individuals may in fact 'get stuck' repeating an approach that is consistently incorrect (Waxman *et al*. 2008). The objective of this project was to develop and test a feedback-driven computational lameness teaching game using a deliberate practice / perceptual learning paradigm.

Material and methods This work received approval from the local ethics committee (# 2014 0110H). 3D computer animations of sound and lame horses were developed using a near-photorealistic horse model. The gait cycle of a sound horse was animated using kinematic data recorded from a real horse. Horses presenting with various degrees if fore- and hind limb lameness (movement asymmetry 10 to 70 % in 10 % increments) were then animated based on this 'normal' trot cycle by applying changes to head and pelvis movement patterns according to the published literature. Animations were presented within a game interface. A perceptual learning paradigm based on an 'adaptive staircase' was chosen to facilitate deliberate practice (Ericsson *et al*. 1993). Each point on the staircase corresponded to a 'level' at which participants had to discriminate between sound and lame horses and determine the affected limb if lame. Based on performance, participants moved gradually up and down difficulty levels, and were rewarded with points for correct assessments and penalised with point loss and 'stepping back' for incorrect assessment. Two trials were run, both with the chance to win a prize: Trial #1 included 124 visitors to the RVC Open Day 2014 using two games, one for forelimb- and one for hind limb lameness. Trial #2 was carried out as part of the RVC curriculum, where 72 students voluntarily participated in one to four game modules (forelimb, simplified hind limb, complex hind limb and mixed practice lameness). Here, the game parameters 'correct answers per level' and 'number of lives' were increased. Questionnaires evaluated the perceived impact of the game.

Results The developed game is now freely available online at www.lamenesstrainer.com. In trial #1, rapid acquisition of forelimb lameness detection skills was observed: in typically under 10 minutes, 60 % of players were able to correctly assess 30% movement asymmetry while 25 % of players reached or completed the highest level of 10 % movement asymmetry. On the other hand, visitors struggled with hind limb lameness detection, where only one player reached the 10 % asymmetry level, and most visitors (78 %) were 'wiped out' before completing the 40 % asymmetry level. In trial #2, most students completed a module in 20 minutes or less after we changed game parameters. A large number of students was able to correctly identify the presence/absence of lameness and the correct limb to near expert level after a single training session, hind limb lameness again proving more difficult: 20% movement asymmetry was correctly evaluated by 74% of students for forelimb lameness, 60% for simplified hind limb lameness and 44% for realistic hind limb lameness, rising significantly from pre-training levels ($P < 0.05$). Results further showed that students started to mistake normal gait cycles for lame ones especially for hind limb lameness. Questionnaire results indicated a positive uptake of the game and a perceived skill improvement which matched the quantitative game outcomes.

Conclusion Deliberate practice of a complex visual pattern detection task facilitated by an intelligent computer game allowed novices to rapidly acquire skills that otherwise would take a long time to attain. Encouraged by past results for perceptual learning of similar tasks, we hope that skills transfer to real horses, where 'noise' to the movement pattern may increase task difficulty; we are currently in the process of testing this. Results especially for hind limb lameness detection suggest that individual game modules have to be played several times to reach expert level assessment skills.

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3D Modelling of clinical images in veterinary medicine: development of an interactive teaching and learning application

V Mauricio, J Marshall
University of Glasgow, UK
Email:vitoria.mauricio@campus.ul.pt

Implications Virtual reality models of surgical procedures allow veterinary surgeons and students to learn surgical techniques without the use of cadaver materials.

Introduction Veterinary students and equine surgery residents are required to learn complex three-dimensional relationships between anatomical structures as well as specific arthroscopic anatomy in order to develop required arthroscopic surgery skills**.** The aim of this project was to produce an interactive, 3D educational tool to aid veterinary students and equine surgery residents in the visualisation of the equine fetlock joint as seen through an arthroscope.

Material and methods Two metacarpophalangeal (fetlock) joints were obtained from a horse euthanized for reasons unrelated to this study. The right metacarpophalangeal joint was distended with agar and flexed following McIlwraith *et al*.'s (2005) method of preparing the equine fetlock for arthroscopy of the palmar pouch. Computed Tomography (CT) of the right fetlock joint was performed. After the CT data was obtained, a dissection of this cadaveric material was performed and documented. The DICOM dataset of the CT scan of the right equine metacarpophalangeal joint was analysed using ClearCanvas software. The data acquired by imaging an equine fetlock was imported into the software 3D Slicer, and each of the structures of interest was segmented and its surface model generated. The dissections and correspondent documentation aided the study of anatomical structures in support of segmentation, to create accurate 3D anatomical models using MeshLab and 3ds Max software. The models underwent a post-processing stage and a 3D model of an arthroscope was constructed. The complete 3D model of the fetlock was imported into the Unity 3D game engine and the application 'Arthroscopy: The Equine Palmar Fetlock' was developed as a standalone executable application. Once the development of the interactive application reached a functional stage, the left fetlock was defrosted and examined by arthroscopy. A Karl Storz Hopkins II, 4 mm diameter, 30 degree, 18 cm long arthroscope was used. Photographic images of this arthroscopic visualization were collected. Through this procedure, real arthroscopic images were compared with images of the same anatomical structures taken from the 'arthroscopic view' within the interactive application to validate the application as a surgical simulation.

Results A 3D model of the fetlock containing the anatomical structures relevant to arthroscopy was developed (Fig 1). These were represented with great accuracy, as they were extracted from anatomical data. The interactive application allows the user to visualise the arthroscopic anatomy of the equine fetlock from different approaches: 1) exploring the 3D structures freely - zooming, panning, rotating; 2) in an arthroscopic view as the joint is seen during 'real' arthroscopic procedures; and 3) comparing real arthroscopic images with images obtained from the arthroscopic view within this application.

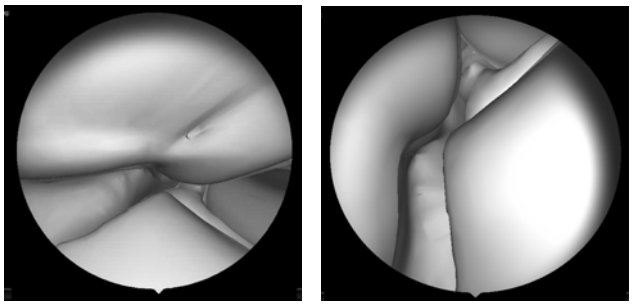

Figure 1 Screenshots displaying the arthroscopy section of the virtual equine arthroscopy application.

Conclusion A realistic interactive training tool for veterinary surgeons and students has been developed. The user is able to virtually explore a realistic equine fetlock joint to learn the relationships between structures during diagnostic arthroscopy. Future development of other surgery simulators and integration into the veterinary curriculum will aid teaching and learning of anatomy, diagnostic imaging and surgery.

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The use of online learning as continuing professional development within animal welfare organisations: A case study with IFAW

L Read[1,4], J MacKay[2], C Milburn[2], F Langford[3]
[1]Kingston Maurward College, Dorset, UK, [2]SRUC, Scotland's Rural College, Edinburgh, UK, [3]International Fund for Animal Welfare, London, UK, [4]University of Edinburgh, UK
Email:lee.read@kmc.ac.uk

Implications Online learning should be an engaging learner experience which facilitates meeting learning objectives.

Introduction Views on animal welfare and ethics differ worldwide, which becomes a problem when international animal welfare organisations want to speak with one, unified voice in their duties. Through developing technologies there are new opportunities to engage and teach people around the world about animal welfare topics, though their usefulness is still being investigated. Previous research using online courses indicates they can be used as a useful supplementary tool which allows for flexible learning (Klupiec *et al*. 2014), though investment in development is required for success (MacKay *et al*. 2014). Articulate has been chosen by the International Fund for Animal Welfare (IFAW) as an online teaching software platform to provide international staff members with continuing professional development. The aim of the online course is to ensure IFAW staff are up to date with the organisation's current values and policies for protecting animals. Usefulness of the online course has been tested based on five key themes; demographics, confidence, attitudes, knowledge, and course feedback.

Material and methods The course was designed in collaboration with IFAW to meet six key learning objectives across five units. The learning objectives were developed so that course users would be able to: 1) recognise IFAW's key principles and approaches; 2) outline IFAW's definition of animal welfare; 3) explain the importance of using ethics **and** science to guide IFAW's principles; 4) outline the arguments for why humanity should be concerned with animal welfare; 5) appreciate that the international history of animal welfare is diverse and complex; and 6) draw on what they have learnt in Topic 1 to answer the end of session quizzes.

Each unit contains three Articulate packages, each one which lasting approximately 20-40 minutes (except the fifth unit which contains only one Articulate package). The titles of the units are: 1) Introduction to Animal Welfare Conservation and Ethics; 2) Understanding views on Animal Welfare; 3) Effective Arguments for Animal Welfare; 4) Animal Welfare and Conservation; 5) Policy and Practice in Animal Welfare. Data was collected using an online questionnaire distributed to 281 IFAW staff hosted by www.surveymonkey.com to compare responses pre- and post- online course completion. We hypothesised that confidence, attitudes and knowledge will improve after completion of the course.

Results Preliminary survey results have been internationally received from 182 IFAW staff. Currently two respondents (1.11%) and 22 respondents (12.22%) are either not very confident or not sure on IFAW's position of animal welfare *respectively.* Comparatively 118 respondents (65.56%) and 38 respondents felt confident or very confident on IFAW's position of animal welfare *respectively.* Currently 124 respondents (70.06%) believe good welfare is good health, 161 respondents (90.69%) believe good welfare is a state of positive mental wellbeing, 164 respondents (92.66%) believe good welfare is a state of positive physical wellbeing, whilst 12 respondents (6.78%) believe good welfare is none of the mentioned points.

Conclusion Preliminary participants suggest the course will be well received due to the interactive and engaging capacity of the online course using Articulate. The preliminary data set indicates an opportunity for the online course to improve confidence levels whilst developing uniformity in belief for what is considered good animal welfare from an IFAW perspective.

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Farm Health Online: Bridging the gap between science and practice for farmers

C Reigate[1], A Bassett[2], S Roderick[1]
[1]Duchy College, Stoke Climsland, Cornwall, UK, [2]Animal Welfare Approved, PO Box 6, Marion, Virginia, USA
Email:claire.reigate@duchy.ac.uk

Implications Farm Health Online (FHO) is a new web-based knowledge hub designed for farmers that promotes high animal welfare and sustainable farming practices by communicating peer reviewed research outcomes in an accessible and easy to use format.

Introduction It is the job of a farmer or stockman, with guidance from their vet, to have procedures and controls in place to ensure that disease is kept to a minimum. There is a plethora of scientific research undertaken to expose aetiological agents, dissecting them to microscopic proportions, mapping their genomes and predicting their fates all using the latest molecular and geometric techniques in order to 'help' farmers prevent certain diseases and conditions proliferating on their farms. But does this science really impact on a farmers' decision? Even if farmers could download published articles, would they have the time to read, translate, comprehend, then incorporate this information into their flock or herd health plans and then put it into practice? Most would not and that is where FHO can help. It is a new portal designed specifically for farmers, vets and advisors to extract the relevant information, convert it into advice (supported visually by novel diagrams, illustrations, images, podcasts and video), validate it with the references, and recommend how it can be implemented into proactive herd health planning on-farm.

Material and methods Based on original material first published as www.organicvet.co.uk (Defra-funded project OF0162) FHO now incorporates the latest web development technologies and communication approaches with more recent published research. The old site contains references from over 3000 cited journal articles, books, published reports and conference proceedings and still receives hundreds of web visits a month from all over the world but as science has moved forward the website has been left behind. Covering the four major livestock species, FHO is composed of three subject areas: Disease Management, Veterinary Questions, and Welfare Promotion. The FHO team are redeveloping, rejuvenating and revising the disease management section which contains over 150 common diseases of cattle, sheep, pigs and poultry with an emphasis on high farm animal welfare standards and good environmental farming practices, which are fundamental to not only organic, but all sustainable livestock production systems. The aim of this section is to enable farmers to understand the different factors influencing risk and to provide information that can be integrated into health planning. Management and practical issues around animal health plans, biosecurity, biocontainment and antibiotic resistance are answered in the Veterinary Questions section. The Welfare Promotion section provides an overview of a range of management and environmental inputs, such as housing, breeding and nutrition as well as providing information that enables promotion of key welfare practices.

The team from Duchy College Rural Business School and Animal Welfare Approved are extracting new results from recent publications, incorporating them into FHO and ensuring that they are reviewed by farmers, vets and industry experts.

Conclusion The importance of disseminating specific agricultural research outputs to farmers is well recognised. However farming is a complex business, with a large number of considerations. This is particularly the case with so-called sustainable systems as there are multiple objectives covering both public and private good. There are also potential conflicts involved. The FHO approach combines ethological thinking, epidemiological knowledge and ecological aims contributing to the development of enhanced communication of science to farmers and advisors.

For science to impact on farmers' decisions, the research findings need to be communicated in context and transformed into straightforward practical information that is readily available. Farming is all-consuming and to follow research developments is understandably not a priority for most, which is why it is our job, as specialists and researchers to sieve though the science and turn it into something useful for the custodians of our countryside.

Acknowledgements This project is a funded by Animal Welfare Approved, an independent non-profit farm certification programme that currently operates in the USA and Canada.

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www.organicvet.co.uk
www.farmhealthonline.com

The role of vet schools in promoting a universal "culture of care" for animals: implications of the (World Organisation for Animal Health) OIE Guidelines and a global survey on criteria for animal welfare education

Titus Alexander
[1]Democracy Matters, Kings Langley/Herts, UK, [2]Crick Centre for Understanding Politics, Sheffield University, UK
Email:titus@democracymatters.info

Implications Vet schools, faculties and continuing professional development need to teach advocacy skills and promote a universal "culture of care" for animals in order to meet the World Organisation for Animal Health (OIE) Guidelines for Day-1 Competencies (2012) for graduating vets. This raises wider questions about the role of advocacy skills training in science education more generally.

Introduction A few countries and companies have adopted a culture of care (NAEAC 2014) for the use of animals in research and testing, but this does not yet extend to all animal production, veterinary practices or vet schools. The OIE Guidelines for Graduating Veterinarians (2012) say that "veterinarians should be the leading advocates for the welfare of all animals" and should be able to "identify animal welfare problems and participate in corrective actions". These Guidelines have been adopted by many national accrediting bodies and vet schools, but they are a long way from being implemented. The America, Canadian and European veterinary associations (AVMA, CVMA and EVA) made a Joint Statement (2011) that "Veterinarians are, and must continually strive to be, the leading advocates for the good welfare of animals in a continually evolving society", but there is little evidence of veterinarians being taught advocacy skills.

Survey and advocacy workshop: A global survey of over 2,600 vets, vet educators and students by the charity World Animal Protection (2014) showed over 80% support for 10 criteria for a whole school framework for improving animal welfare education, ranking intrinsic benefits for animals as the top criteria. The survey and OIE Guidelines informed an introductory workshop on advocacy for vets, which was developed with an international team of vet educators and piloted with vet professors from ten countries, including India, Korea, the Philippines, Peoples' Republic of China, Taiwan, Thailand and Vietnam, in August 2014. The workshop was revised and repeated with groups of undergraduate vets, vet nurses and animal welfare scientists at Bristol Vet School, on 4 October and at Edinburgh University "Dick Vet" at Roslin, on 3 December 2014. The three hour workshop included short presentations on the legal, scientific and professional basis for advocacy for animal welfare, as well as discussion and practical exercises on the following topics:

- The role of vets in animal welfare
- Constraints on vets taking action and how to overcome them
- How to identify and explain problems in animal welfare so that those responsible can take corrective action
- How to address systemic animal welfare issues, particularly in industry
- Where to find information regarding animal welfare regulations and standards
- Advocacy and communication skills

Exercises were designed to both practice advocacy with animal owners or handlers ("Responsible Persons" in terms of the Animal Welfare Act 2006 (HMSO) and to develop a strategy to address a systemic issue in animal welfare.

Results Feedback from this sample of about 50 participants in three different settings was very positive. Many of the international professors were keen to adapt the course for their national circumstances. The response from students was overwhelmingly positive: "I would highly recommend it. It complements our veterinary curriculum quite well." 3rd year vet student, Edinburgh Vet School (Dick Vet) "One of the most useful sessions so far for us at uni" 3rd year vet student, Bristol. When asked to rate the workshop on a scale of 0 – 10, where 10 is Excellent, 70% or more Bristol participants ranked all aspects as 7 or more out of 10, while in Edinburgh all participants rated it 8 or more out of 10.

Conclusion This shows that vet lecturers and students respond positively to a practical skills course to meet the professional commitment for veterinarians to be "the leading advocates for the welfare of animals". Courses like this are needed to meet the OIE Guidelines for Day-1 Competencies for graduating vets and to address animal welfare issues in society.

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Exploring the impact of agricultural science: a project-level assessment of the UK dairy cow fertility index

S Fowler, P Midmore
Aberystwyth University, Wales, UK
Email:suf@aber.ac.uk

Implications More effort invested in evaluating the impact of agricultural science research will enable scientists to set priorities more effectively, monitor and adjust programmes, and increase the value of their activities to society as a whole.

Introduction Research impact evaluations are increasingly important in attracting and focusing scarce resources. However, the process of impact generation is complex, often poorly understood, and there is a need to not only to improve communication of research results to producers, but also to address their needs more effectively (EC, 2011, p. 53). The aim of this study is to outline the changing context of agricultural science research in the UK, and to explore in detail the pathways by which the socio-economic impact of a specific project are achieved.

Material and methods The study uses a mixed methods approach that combines quantitative and qualitative information. To establish the context, an assessment of overall agricultural science effort has been conducted through an expert-led survey, which complements official agriculture RTD statistics. At project level, the case study method is used to investigate how specific knowledge in the form of the UK Fertility Index has been generated and accessed to generate positive linkages with agricultural and rural development, understanding how farm scale, resource endowment and market access have contributed to structural change in agriculture. Using a participatory Programme Theory of change (Douthwaite 2007), an understanding of how the initial science was expected to achieve impacts is contrasted with the views of scientists, knowledge brokers, users of technology and other stakeholders in the dairy value chain. Through participatory workshops, impact pathways have been mapped, social network relationships between funders, researchers, knowledge brokers and other public and private sector actors explored, and spatial and sectorial spillovers analysed. Validation is achieved through triangulation and an active search for disconfirming evidence.

Results Data availability on agricultural science investments is very limited in the UK; where it does exist, series have gaps that make interpretation of overall trends challenging. This contrasts with specific strategic objectives for the sector (BIS, 2013, p. 9), in terms of increasing productivity supported by research, global leadership in agricultural informatics, the development of evidence based metrics for sustainability, and more rapid adoption of innovation across the food and farming supply chain. However, as far as can be ascertained from limited available data, the decline in public sector funding, despite incentives to do so, is not yet being offset by increased private sector activity. This context contributes important concerns in respect of the detailed evaluation exercise of the development, dissemination and uptake of the UK Fertility Index, which has demonstrated its relevance, effectiveness and efficiency. A series of workshops have contributed to the construction of impact pathway maps linking project output, to outcomes, to impact, and identification of networks that show important relationships between actors. This has allowed construction of a revised narrative that explaining how and why the underpinning science resulted in its impacts both anticipated and unanticipated. Production of a coherent narrative allows implicit assumptions to be uncovered and questioned.

Conclusion The change in breeding selection in the dairy industry has emerged from the conjunction of a variety of complex, interacting influences, in which the entrepreneurial behaviour of scientists has played an important part. Information provision, market pressures, finance and the inherited structure of the dairy sector contributed to the set of outcomes that identified a Fertility Index as a tool worth using.

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The sense of feeding fibre to carnivores

G P J Janssens
Ghent University, Merelbeke, Belgium
Email:geert.janssens@ugent.be

Implications Carnivores in zoos or as pets might not receive the proper amount and type of fibre in their diets. Increasing evidence points to the importance of animal fibre and food texture to maintain gastro-intestinal health and beyond.

Introduction For long, dietary fibre has not been considered as a crucial nutrient for feeding carnivores. Yet, numerous studies in cats and dogs have shown beneficial health effects of plant-derived prebiotics through their modulation of intestinal microbial fermentation (e.g. dogs: Verlinden *et al*., 2006; cats: Verbrugghe *et al*., 2009). These prebiotic fibres are not part of their natural diet, but when broadening up the definition of fibre, many components in the natural diet of carnivores do behave as "animal fibre", such as hair, bone, skin, tendons and cartilage (Depauw *et al*., 2012). In zoo practice, diets for the same carnivore species can widely range in type and composition. Although several studies report nutrition-related disorders in captive carnivores, such as obesity, diabetes, gastritis and kidney failure, little effort has been made to identify the nutritional causes for these diseases.

Defining "animal fibre" Although ADF, NDF or TDF analyses have been developed for plant-based diets, these measures are commonly used in cat and dog nutrition. Yet, fibrous components in natural carnivore diets are to a large extent made of protein or other N-containing molecules (e.g. glucosamine), implying that the classical methods for fibre analysis will largely underestimate the actual fibre content of typical carnivore diets, urging for an suitable analytical method to determine animal fibre (Cools *et al*., 2015).

Fibre and satiety Both in domestic species and in captive wild carnivores, the incidence of obesity is worryingly high. Satiation principles in carnivores are insufficiently known, but at least one study points to the effect of plant fibre type to induce satiation in dogs, but the same study also clarified that satiation mechanisms do not seem to match for instance the human situation (Bosch *et al*., 2009). Insoluble fibre can delay gastric emptying in dogs (Pedreira *et al*., 2013), but in general, only anecdotal reports exist on the assumed profound impact of fibrous, texture-rich diets on gastrointestinal passage rate, and eventual concomitant satiety.

Fibre and health More evidence is available on the impact of animal fibre type and intestinal fermentation. Although the fermentative capacity of the carnivore gut will not considerably contribute to the overall energy provision, the role of fermentation in carnivores can still matter for maintaining health and nutrient balance: in cats, propionic acid from fermentation can be used as C3-component in the citric acid cycle, hence saving amino acids from catabolism (Verbrugghe *et al*., 2009). This effect might only be of relevance in clinical situations where amino acid catabolism should be restricted, but studies in captive cheetah have demonstrated that feeding "fibrous" diet such as whole rabbit versus meat alters the fermentation profile, leading to less putrefactant production and less absorption of for instance the nephrotoxic compound indoxyl sulfate (Depauw *et al*., 2013). Feeding carcass instead of meat is associated with reduced gut inflammation in the cheetah (Depauw *et al*., 2014). In addition, a recent global survey on feeding and gastrointestinal health in captive cheetahs revealed that processing diets versus feeding raw increased the odds of developing gastrointestinal problems (Whitehouse-Tedd *et al*., 2015).

A comparative view on fibre demands Even within terrestrial mammals, carnivores range from pack hunters such as the wolf, slaying large preys, to solitary small prey hunters such as domestic cats. Extrapolation from studies in cats and dogs fed commercial diets as "carnivorous model" should therefore be done with caution. For example, Bacteroidetes and Bifidobacteriaceae are largely underrepresented in the faecal microbiota of captive cheetahs when comparing with domestic cats fed processed diets (Becker *et al*., 2014). Studies are ongoing to find body mass or other features that can help explain the differences in dietary fibre appreciation across wild carnivore species.

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Methane production by vertebrate herbivores - a comparative perspective

K Hagen[1], M Kreuzer[2], M Clauss[1]
[1]Clinic for Zoo Animals, Exotic Pets and Wildlife, Vetsuisse Faculty, University of Zurich, Switzerland, [2]ETH Zurich, Institute of Agricultural Sciences, Zürich, Switzerland
Email:katharina.hagen@uzh.ch

Meat production has been estimated to account for up to 6.3% of the greenhouse gas emissions in 2030 (Ellis *et al*. 2007; Fiala 2008). There are two main causative agents named; one is deforestation for grazing (Fiala 2008), the other is the presence of methanogenic microorganisms, which populate the fermentation chambers of the gastrointestinal tract of herbivores (Stevens and Hume 1998; Janssen and Kirs 2008; Liu and Whitman 2008). These microorganisms, members of the domain Archaea, produce methane, mainly by converting H_2 and CO_2, hence acting as a hydrogen sink which means they keep the partial pressure of hydrogen low (Jensen 1996). There are, however, differences in the amount of methane produced from herbage between herbivore species (Crutzen *et al*. 1986; Hackstein and Alen 1996). Ruminants produce the highest amount of CH_4 among mammals in relation to body mass (Franz *et al*. 2010). If this difference was due to the fact that ruminants are foregut fermenters, we would expect that other non-ruminant foregut fermenters, such as macropods (kangaroos) or camelids also produce high levels of methane. The evidence to date suggests that this is not the case for macropods (Kempton *et al*. 1976; von Engelhardt *et al*. 1978; Dellow *et al*. 1988; Madsen and Bertelsen 2012), but suggests similar amounts of methane (per unit of digested fiber) in ruminants and camelids (Dittmann *et al*. 2014). Because camelids also ruminate, this might indicate that some peculiarity of rumination rather than that foregut fermentation is associated with pronounced methane production. One explanation for this is that ruminants have a higher count of Archaea in the major fermentation chamber (Morvan *et al*. 1996), another that the Archaea simply have more time to produce methane, due to a longer digesta retention time in ruminants (Foose 1982; Pearson *et al*. 2006). Another reason could be a higher prevalence of other hydrogen sinks in non-ruminant herbivores (Prins and Lankhorst 1977; Fievez *et al*. 2001). It has been suggested that birds such as ostriches would be an environment-friendly meat source because they do not produce methane at all (Miramontes-Carrillo *et al*. 2008), or only very little (Hackstein and Alen 1996; Fievez *et al*. 2001). However, a recent study contradicts this theory, stating that methane emission is similar between ostriches and non-ruminant mammalian herbivores (Frei *et al*. 2015). The same was claimed for kangaroos, but they fit into the methane range of non-ruminant herbivores as well (Vendl *et al*. 2014). Given the seeming independence of methane production from measurements of digesta passage, more comparative research into the microbiome of the respective species, and the factors determining these microbiomes, is required to understand the variation in methane production observed in vertebrate herbivores.

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Designing diet management software for healthy zoo animals

A L Fidgett[1], M E Edwards[2], L Peterson[3], M Webster[3]
[1]Chester Zoo, UK, [2]California Polytechnic State University, San Luis Obispo, California, USA, [3]Format International, Woking, UK
Email:a.fidgett@chesterzoo.org

Implications Within zoos and aquariums different stakeholders concentrate on different aspects of feeding; some may be mostly concerned with the nutrient content, others with the way food is presented. The physical and behavioral health of animals may be a principal focus and sustainability, efficiency and costs are becoming increasingly significant drivers. All of these aspects require consideration to achieve the shared objective of 'feeding animals well for health, welfare and conservation'.

Introduction Sharing knowledge about best feeding practices can improve global management of living collections, with anecdotal descriptions replaced by meticulous observation, documentation and analysis. Recording and cataloguing feeding practices and the outcome of adjustments, along with the means for systematic retrieval of said records at some later point in time, would represent a significant advance in the evaluation and dissemination of effective feeding practices. Format FAUNA™ has been specifically designed for zoos and aquariums in response to a direct request from the zoo community. Colleagues from EAZA, AZA and ISIS, working alongside Format International, an industrial partner specializing in animal feed formulation software, have developed FAUNA software to allow better audit and prediction of food use and expenditure within zoos, and the collation of best feeding practices between zoos. Feedback has shaped and will continue to shape FAUNA's evolution.

Conclusion Working with an industrial partner specializing in animal feed formulation software (Format International) and colleagues from the global zoo and aquarium community, our vision is a zoo diet management system for all those concerned with feeding zoo animals well, encompassing features associated with feeding, formulation, inventory management and auditing.

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Elephant Milk Composition

A Silva-Fletcher
The Royal Veterinary College, Hatfield, Hertfordshire, UK
Email:asilvafletcher@rvc.ac.uk

Elephants, the largest terrestrial animals make a considerable investment in their offspring. Their gestation and lactation periods are the longest of any mammals. Both the Asian (*Elephas maximus*) and African (*Loxodonta africana*) elephants have pregnancy periods that exceed 660 days and the young are born weighing around 75 – 115 Kg (Shoshani 1992). The young are dependent on mother's milk, initially on colostrum and then on milk for the first 3 - 6 months of their life (Lee and Moss 1986). Lactation can last until the next calf is born and can be up to 2 -8 years (Sheldrick 1990, Welsch 1998). The major constituents of elephant milk are generally similar to other species and consist of lipids, caseins, other major milk proteins, lactose, other oligosaccharides, minerals, vitamins and water (Kunz *et al* 1999, McCullagh and Widdowsan 1970, Peters *et al* 1972). However comparison with other species reveals large differences in the proportions of constituent components (Oftedal and Iverson 1995). Although there is some detailed quantitative analysis to understand the different components of fat, sugar, proteins, minerals and vitamin composition in elephant milk, these are from isolated milk samples and huge variations in relative proportions have been reported. A few studies have attempted to measure compositional change in milk over the duration of the lactation period in parallel with calf's growth (Mainka *et al* 1994, Abbondanza *et al* 2013).

The changes in milk composition over the growth period of the calf show a positive correlation between dry matter, fat, major minerals and gross energy and calf age. The total sugars as measured by lactose and other oligosaccharides are negatively correlated with calf age. The increase in gross energy due to the doubling of total fat (from around 8% to 16%) from 3 to 30 months of lactation (Abbondanza *et al* 2013) is not equated by crude protein and major minerals which remain relatively constant when expressed on per energy unit basis. The reduction in total sugars with an increase in total fat may have biological significance in the growth of a species that nearly triples in weight within the first year of their life.

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Is extracellular vesicle production in milk associated with measures of milk output and quality in dairy cows?

G E Pollott, C Lawson, R Fowkes, K Wilson
The Royal Veterinary College, London, UK
Email:gpollott@rvc.ac.uk

Implications New phenotypes from measuring different factors in milk may be useful future tools. Extracellular vesicle levels in milk are one such possible new phenotype with value in breeding and management programmes.

Introduction Daily milk production in dairy animals is the result of three processes; the number of secretory cells produced up to that point in the lactation, their secretion rate and the number of cells dying through apoptosis (Pollott, 2000). Improved precision in management and selection programmes could be achieved if two of these three processes could be measured. Extracellular vesicle (EV; previously referred to as microparticle) density in cows' milk, a possible indicator of apoptosis, has been shown to be linked with characteristics of lactation curves (Pollott *et al*., 2014). In this study the relationships between the estimated number of EV produced per day and milk production data is explored.

Material and methods Four EV traits were measured on both spun milk (fat removed; SM) and whole milk (WM) from 12 cows measured monthly for 5 months. The four traits were EV stained with Annexin V (AV+), merocyanine 540 (MC+), both dyes (Both+) and the total EV (<1µm; Tot) count. The EV were counted using a Canto II flow cytometer (BD Biosciences, Oxford, UK) as described by Pollott *et al*. (2014). Daily estimates of the 8 daily EV count traits were calculated from the EV density and daily milk yield data. Six of the traits were skewed and so were log transformed ready for analysis. Pearson correlation coefficients were calculated between all EV traits and milk, fat, protein and somatic cell count (SCC) data recorded on the 12 cows. A mixed model was fitted to the 8 EV traits, using ASReml software, to account for the effect of individual cow and either days in milk (DIM) or daily milk yield (DMY) on EV production.

Results No significant correlations ($P > 0.05$) were found between spun milk EV production and any milk trait. All 4 WM EV traits showed significant positive correlations with DIM, and SCC was positively correlated with WMTot and WMMC+. No other significant correlations were found involving WM EV measurements and production traits. Further analysis of the WM traits using mixed models is summarised in Table 1.

Table 1 ANOVA summary from fitting DMY or DIM to 4 EV traits.

	Mixed model fitting DMY and cow				Mixed model fitting DIM and cow			
EV (cells/d)	-logL	DMY (P)	Cow (P)	Residual	-logL	DIM (P)	Cow (P)	Residual
WMTot	-41.9	0.03	0.002	1.38	-42.9	0.008	0.001	1.30
WMBoth (log)	-8.6	0.26	0.28	0.032	-10.7	0.23	0.28	0.30
$WMAV^+$ (log)	16.5	0.04	0.008	0.097	14.7	0.03	0.007	0.095
$WMAV^-$	-22.2	0.02	0.002	0.56	-70.9	0.001	<0.001	0.079

Both DMY and DIM were associated with EV production, with the exception of WNBoth, and they were also influenced by the individual cow. Extracellular vesicle production (AV^-) increased by 1.364 million cells per day and fell by 0.69 million for every extra kg of milk produced. Both $WMAV^+$ and WMTot also showed a positive relationship with increasing DIM and a negative relationship with increased milk yield.

Conclusion Four measures of extracellular vesicle level in milk were found to be related to both days in milk and milk yield such that with advancing lactation they increased in number. If EV production is as a result on apoptosis of secretory cells in the mammary gland then measuring EV production in milk may be a useful tool for improving the accuracy of genetic and management control over milk production.

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Crossbreeding low-input dairy cows in Switzerland with US Brown Swiss: effect on summer milk fatty acid profile

S Stergiadis[1,2], A Bieber[3], E Fransceschin[4], A Isensee[3], M D Eyre[1], V Maurer[3], E Chatzidimitriou[1], G Cozzi[4], B Bapst[5], G Stewart[1], A Gordon[6], G Butler[1], C Leifert[1]
[1]Newcastle University, Nafferton Ecological Farming Group, Stocksfield, Northumberland, UK, [2]Agri-Food and Biosciences Institute, Sustainable Agri-Food Sciences Division, Agriculture Branch, Hillsborough, Co Down, UK, [3]FiBL Research Institute of Organic Agriculture, Department of Livestock Sciences, Frick, Switzerland, [4]University of Padua, Padua, Italy, [5]Qualitas AG, Zug, Switzerland, [6]Agri-Food and Biosciences Institute, Finance & Corporate Affairs Division, Biometrics & Information Systems Branch, Belfast, Co Antrim, UK *Email:sokratis.stergiadis@afbini.gov.uk*

Implications Using Original Braunvieh (OB) crossbred dairy cows in low-input systems may improve milk fatty acid (FA) profile whilst sustaining similar milk yields compared to US Brown Swiss (BS) crosses.

Introduction Crossbreeding is used in low-input dairy systems to improve robustness and fertility of high yielding cows and productivity of low yielding cows thus improving overall farm profitability (Sorensen *et al*. 2003). In Switzerland, Brown Swiss cattle originates from three main populations: (i) OB (pure bred traditional Brown Swiss cows), (ii) BS (developed in US from OB by selecting for milk yield), and (iii) improved Braunvieh (BV, cross between OB and BS). In low-input dairying, higher pasture intakes have increased beneficial (for human health) monounsaturated FA (MUFA), such as vaccenic acid (VA, C18:1 t11) and polyunsaturated FA (PUFA), such as α-linolenic (ALN, C18:3 n-3) and rumenic acid (RA, C18:2 c9t11) in other studies (Stergiadis *et al*., in press). Although the potential effect of crossing high-yielding cows with alternative breeds on milk quality has been highlighted (Stergiadis *et al*. 2012, Stergiadis *et al*. *in press*), studies on the interactions between diet and breed are limited. This study assesses the effect of the proportion of BS genes in crossbred cows on milk FA profile under contrasting pasture intakes.

Material and methods Milk was collected from 865 cows on 38 low-input farms in Switzerland during the grazing season. Animal pedigrees were available from Braunvieh Schweiz (Zug, Switzerland) and animals were categorised into four groups, depending on the contribution of BS genes (BS1, 75-99%, n=670; BS2, 50-74%, n=109; BS3, 25-49%, n=37; BS4, 0-24%, n=47). Questionnaires to record diet, pasture management and husbandry were completed at milk collection. Milk FA profiles were analysed using a Varian CP-SIL 88 fused silica capillary column (100 m x 0.25 mm internal diameter x 0.2 um film thickness) and peak retention times were identified based on external standards. Analysis of variance by linear mixed models used crossbred group (BS1, BS2, BS3, BS4) and estimated grazing intake as a proportion of total dry matter intake (DMI) (GI1, 75-100%; GI2, 50-74%; GI3, 25-49%) as fixed factors and cow as random factor.

Results Cow genotype did not affect milk yield and fat or protein content. Milk from BS2, BS3 and BS4 cows had more PUFA, omega-3 FA (n-3), VA and ALN, less saturated FA (SFA) and higher n-3/omega-6 FA (n-6) ratio than BS1 cows although not always significant (Table 1). Differences may be partly explained by greater pasture intake (from 59% to 76% DMI) with decreasing proportion of BS in the genotype, however, differences were not consistent across all diets. Figure 1 shows higher milk n-3/n-6 ratio in BS3 and BS4 cows than BS1 and BS2 cows but only when pasture intake was high; similar interactions were observed for VA and n-3.

Table 1 Differences between genotypes: relative proportions (%) against BS1.

	BS2	BS3	BS4	P-value
SFA	**-1.4**	-0.6	**-2.4**	*
MUFA	2.2	-0.2	3.6	ns
PUFA	**6.2**	**8.5**	**13.2**	***
n-3	**11.9**	**25.4**	**29.1**	***
n-6	5.6	1.9	6.3	ns
n-3/n-6	5.6	**20.2**	**18.0**	***
VA	6.3	**18.5**	**19.6**	***
RA	5.4	5.4	6.9	ns
ALN	**12.1**	**24.9**	**30.9**	***

Significant to BS1 differences are shown in bold case. ***, P<0.001; *, P<0.05; ns, P≥0.05.

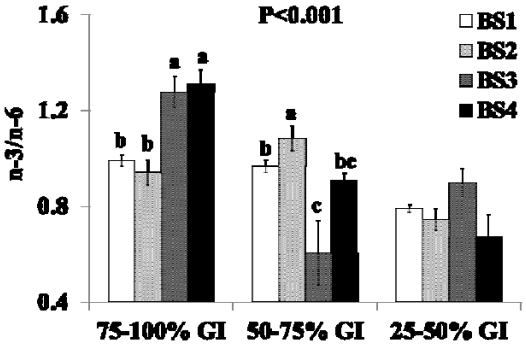

Figure 1 Interactions between genotype (BS1, BS2, BS3, BS4) and grazing intake (GI) on milk n-3/n-6 ratio (means±SE). Bars with different lower case letter within GI differ significantly.

Conclusion Using traditional OB genetics in crossbreeding did not affect milk production in low-input systems while it improved milk FA profile, especially when grazing intake was over 75% DMI.

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The effects of castrating males on lamb performance and meat eating quality attributes

T W J Keady[1], J P Hanrahan[1], V Campos[3], P Allen[2], T Sweeney[3]
[1]Teagasc Animal and Grassland Research and Innovation Centre, Athenry, Co Galway, Ireland, [2]Teagasc Food Research Centre, Ashtown, Dublin, Ireland, [3]School of Veterinary Medicine, University College Dublin, Ireland
Email:tim.keady@teagasc.ie

Implications In systems of prime lamb production in which lambs are slaughtered prior to the end of the grazing season, castrating males has no beneficial effect on meat quality but reduces performance – so why castrate?

Introduction Previous studies have reported that male cattle that are finished as entires (bulls) have heavier carcasses, which have better conformation and lower fat classification than males finished as steers. Traditionally, male lambs in mid-season prime lamb production systems are castrated at birth, due to ease of management in the autumn and the perception of improving the meat eating quality experience of consumers. It is widely acknowledged that present day consumers have an aversion to excess fat on meat. The aim of the current study was to evaluate the effects of rearing males entire on performance and meat eating quality of lambs grazed on pasture as the sole diet and slaughtered at about 6 months of age.

Material and methods Lambs, born in early/mid March, from 43 all male sets of twins (sired by Suffolk rams from Belclare or Belclare x Scottish Blackface dams) were allocated at random to two treatment groups at birth: castration or entire. Within 24 hours of birth, one lamb per set of twins was chosen at random and castrated, using a rubber ring. Post lambing the ewes and their twins were turned out to pasture without concentrate supplementation for the duration of the experiment. The flock was grazed in a rotational grazing system. Lambs were weaned at 100 days. Lambs were grazed as one flock post weaning and were drafted for sale on 30 July, 26 August, 20 September, 23 October, 4 November and 16 December . Ten pairs of twins were slaughtered on 26 September and the *Longissimus thoracis et lumborum* was removed and aged for 10 days at 2 ^{0}C. Samples were then frozen until evaluation, after standard cooking process, by 10 trained assessors for texture (tenderness), juiciness, lamb flavour, abnormal flavour, flavour liking and overall liking.

Table 1 The effect of castration on lamb performance (n=43 pairs of twin lambs)

	Treatment			
	Entire	Castrate	s.e.	sig
Daily gain (g/d)				
- weeks 0 to 5	302	308	9.42	NS
- weeks 5 to 10	286	252	11.0	*
- weeks 10 to 14	208	192	11.5	NS
- weeks 0 to 14	269	257	5.6	*
- weaning to sale	163	153	5.6	NS
- birth to sale	216	206	5.1	*
Final weight	47.1	45.9	0.44	*
Carcass weight	20.1	20.1	0.26	NS
Fat classification	2.68	2.97	0.070	**
Dressing proportion (g/kg)	427	438	5.6	NS

Results The effects of castration on lamb performance are presented in Table 1. Leaving lambs entire increased live-weight gain for weeks 5 to 10, birth to weaning and birth to sale. Entire male lambs had a lower dressing proportion. Carcasses from entire male lambs were leaner than those from castrates. The effect of castration on meat eating quality is presented in Table 2. Meat from entire males had a significantly higher texture score (more tender) than meat from castrates. Castration had no effect on juiciness, lamb flavour, abnormal flavour, flavour liking and overall liking relative to meat from entires.

Table 2 The effects of castration on lamb meat eating quality

Sensory attribute[1]	Treatment			
	Entire	Castrate	s.e.	sig
Tenderness	4.60	4.09	0.120	**
Juiciness	5.16	5.22	0.092	NS
Lamb flavour	4.45	4.55	0.078	NS
Abnormal flavour	2.06	2.13	0.099	NS
Flavour liking	5.23	5.23	0.113	NS
Overall liking	4.99	4.84	0.106	NS

[1]8 point scale; 1 extremely poor, 8 extremely good

Conclusion Relative to castrates entire male lambs grew faster and produced leaner carcasses which resulted in a better meat eating experience due to being more tender.

Effect of muscle weight on crossbred lamb meat eating quality

E M Price[1], J A Roden[1,2], I Richardson[3], N Clelland[4], W Haresign[1], G E Gardner[5], J M Finch[6], N D Scollan[1]
[1]IBERS, Aberystwyth, UK, [2]Innovis Ltd, Aberystwyth, UK, [3]University of Bristol, UK, [4]SRUC, Scotland's Rural College, Edinburgh, UK, [5]Murdoch University, Perth, Australia, [6]Hybu Cig Cymru, Aberystwyth, UK
Email:e_price@hotmail.co.uk

Implications Selecting for muscularity can reduce meat quality in the loin and topside. Further research is needed to understand if the reasons are fat or muscle related.

Introduction Lambs with proportionately greater muscle mass are economically more valuable. However there is evidence that selection for muscling can have detrimental effects on *M.longissimus lumborum* (LL) and *M.semimembranosus,* (SM) eating quality in part due to reduced intramuscular fat (Pannier *et al* 2014; Karamichou *et al*., 2006). This study aims to evaluate phenotypic correlations of LL and SM muscle weight with shear force and sensory traits in crossbred lambs.

Material and methods Crossbred progeny from rams selected for divergent muscle density (differing by 3 SD) were born over a 10 day period. Slaughter lambs were selected on commercial criteria (target carcass weight: 18-21kg and fat class 2-3L). Right lamb LL (lumbar vertebra region) and whole left side LL muscle samples were aged for 7 days *post mortem,* weighed and stored at -20^{o}C. Shear force of the right loin was analysed as described by Price *et al*., (2014). The whole left LL was defrosted, cooked (internal temperature 72°C) and evaluated by a trained sensory panel at the University of Bristol (46 panels, 184 samples). The SM was excised from the right leg, weighed and split into 3 sections, (i) *caudal* - sensory (ii) *medial* - shear force and (iii) *cranial* - fatty acid composition. The SM shear force was evaluated on aged cooked SM (internal temperature of 72°C). SM samples were evaluated for sensory traits using a similar methodology to the LL (36 panels, 144 samples). Data were analysed in GENSTAT 15 using unbalanced ANOVA analysis with sire nested within muscle density and with slaughter weight and sensory panel (for sensory traits) used as covariate and the fixed effects (P<0.2) for sex, dam age (2yr *v*. older), rear type (single/twin/artificially reared), MyoMAX™ status, and slaughter batch. Phenotypic correlations were estimated from residuals of analysis for LL and SM muscle weights and correlated with shear force and trained sensory panel meat eating quality traits.

Results

Table 1 *M.longissmius lumborum (LL) and M. semimenbramosus (SM) tissue weight phenotypic correlations with meat eating quality traits*

	Meat quality trait	LL weight	P-Value	SM weight	P-Value
Shear force	LL shear force	0.02	0.875	0.00	0.964
	LL shear force SD	0.03	0.768	0.06	0.551
	SM shear force	0.01	0.895	**0.20**	**0.035**
	SM shear force SD	**0.23**	**0.019**	**0.25**	**0.008**
LL Sensory	Texture	*-0.18*	*0.067*	**-0.19**	**0.044**
	Juiciness	-0.02	0.859	-0.08	0.405
	Abnormal flavour	0.07	0.440	**0.19**	**0.042**
	Lamb flavour	-0.07	0.483	-0.06	0.519
	Flavour liking	-0.14	0.146	*-0.18*	*0.058*
	Overall liking	*-0.16*	*0.087*	-0.15	0.121
SM sensory	Texture	-0.13	0.195	-0.12	0.224
	Juiciness	0.00	0.979	**0.20**	**0.037**
	Abnormal flavour	-0.04	0.652	*-0.16*	*0.089*
	Lamb flavour	0.13	0.184	0.14	0.138
	Flavour liking	0.06	0.566	**0.21**	**0.029**
	Overall liking	0.05	0.583	0.14	0.154

Bold indicates significance (P<0.05). Italic indicates tendency (P is 0.05 > 0.1) SD – standard deviation

Conclusions LL shear force was not affected by SM or LL muscle weight. SM shear force and variation in shear force values (SD) were tougher for heavier SM. This could be resultant of higher muscled animals having lower fat deposition (Karamichou *et al*., 2006, Pannier *et al.,* 2014). However SM muscle weight had a positive correlation with desirable sensory traits, SM juiciness and SM flavour liking). Heavier SM had an unfavourable effect on LL texture and abnormal flavour. There was a tendency for heavier LL muscles to have lower LL sensory scores for texture and overall liking. Further research is needed on how selection affects muscle metabolism, fat deposition, fat composition and meat quality.

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Shelf life characteristics of meat from indigenous and foreign breeds of dairy ewes in Greece

E Kasapidou[1], P Sitilidis[1], P Mitlianga[1], G Arsenos[2]
[1]Technological Education Institute of Western Macedonia, Department of Agricultural Technology, Division of Agricultural Products Quality Control, Florina, Greece, [2]Aristostle University of Thessaloniki, School of Veterinary Medicine, Department of Animal Husbandry, Thessaloniki, Greece
Email:eleni.kasapidou@hol.gr

Implications Shelf life parameters show no differences between indigenous and foreign breeds in commercially produced dairy ewe meat.

Introduction Sheep farming is a core industry in the rural economies of Mediterranean countries both in terms of employment and overall income. In Greece, traditional indigenous breeds such as Mytilini and Chios have been used for milk production. However, over the last decades a significant number of foreign breeds that were considered superior in terms of milk production, especially the French Lacaune breed, have been imported. Sheep meat in Greece is a secondary objective to milk production in all sheep flocks and is mainly derived from young lambs that are slaughtered after weaning and adult ewes reaching the end of their production life. The notion is that lean meat colour and lipid oxidation are principal shelf life quality characteristics of meat related to freshness and healthiness. The aim of this preliminary study was to evaluate shelf life characteristics of meat from dairy ewes and to assess any differences between breeds.

Material and methods Ewes from two indigenous (Mytilini and Chios) and one foreign breed (Lacaune) from a commercial farm were randomly selected. All animals were fed the same concentrate diet as well as Lucerne hay and wheat straw. After slaughter, individual samples (m. *semimembranosus*) were taken from each animal for muscle colour evaluation and oxidative stability, and aged for 6 days in vacuum at 0˚C. Then each sample was placed in black polystyrene trays, over-wrapped with transparent air-permeable polyethylene film, (a common practice in retail sales) and stored in a non-illuminated refrigerated cabinet at 4°C for 5 days. The later is a representative retail condition of traditional butcher shops in Greece. Lean meat colour was determined daily using CIELAB L*a*b* colour space and oxidative stability was determined as thiobarbituric acid reacting substances (TBARS) after 2 and 5 days of refrigerated storage. Analysis of variance was used to analyse differences between breeds and within the same breed on different storage days.

Results Muscle colour redness and saturation (chroma) values did not differ significantly between breeds. Redness values were greater than 14.8, which is the threshold value for consumer acceptability of aged lamb meat (Khliji *et al*., 2010) on storage day 2 but fell below this value on day 5 in the steaks from all breeds. With regard to colour changes during storage within the same breed, leg steaks from the Lacaune ewes exhibited the greatest stability ($P<0.05$ for both redness and chroma values) whereas there were highly significant changes in the steaks from the Mytilini and Chios ewes ($P<0.01$ for both redness and chroma values in Mytilini and Chios samples). The extent of lipid oxidation was not significantly different between breeds for the same storage day and within the same breed on different storage days. The rate of lipid oxidation was higher in samples from Mytilini and Lacaune ewes in comparison to Chios samples, although the latter had lower initial TBARS values. Overall, lipid oxidation was well below the reported threshold values (>2 mg malonaldehyde/kg muscle) for the detection of rancidity by trained taste panellists in lamb meat (Camo *et al*., 2008).

Table 1 M. *semimembranosus* colour and lipid oxidation changes during refrigerated storage (n=6)

Variable	Breed			s.e.d.	P
	Mytilini	Chios	Lacaune		
Redness (a*) Day 2	15.31	15.23	16.58	0.614	n.s.
Redness (a*) Day 5	12.48	13.33	13.48	0.559	n.s.
Chroma Day 2[1]	15.97	15.93	17.18	0.535	n.s.
Chroma Day 5[1]	13.54	14.17	14.52	0.476	n.s.
TBARS Day 2[2]	0.29	0.60	0.30	0.136	n.s.
TBARS Day 5[2]	1.10	1.19	0.94	0.406	n.s.

[1] $(a^{*2}+b^{*2})^{0.5}$; [2]mg malonaldehyde/kg muscle; n.s. not significant

Conclusion The results showed that both indigenous and foreign dairy breeds can produce meat with acceptable colour and lipid oxidation stability under commercial conditions. Additional research with a greater number of samples is required to estimate the effect of slaughter age on meat quality.

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Metal uptake and liver antioxidants as potential biomarkers of oxidative stress in *Cyprinus carpio* inhabiting river Indus

F Jabeen[1], A S Chaudhry[2], H Raza[1]
[1]GC University Faisalabad, Punjab, Pakistan, [2]Newcastle University, Newcastle Upon Tyne, UK
Email:farjabeen2004@yahoo.co.in

Implications Changes in antioxidant enzyme activity in fish liver can be used as biomarkers of oxidative stress in fish.

Introduction Contamination of river environments by different pollutants is a severe and rising matter. Industrialization and urbanization cause water bodies to take heavy loads of various impurities. Among these impurities, heavy metals are of particular concern due to their broad effects on fish in causing oxidative stress. Fish are relatively more subtle to anthropogenic effluences as they are considered to have a twin role of being on top of the aquatic food chain and their potential use as a bio-indicator of environmental pollution. Many antioxidant enzymes have been proposed as biomarkers of oxidative damage caused by pollutants like heavy metals. The objective of this study was to determine water quality and the usefulness of these enzymes as biomarkers of oxidative stress in *Cyprinus carpio* inhabiting river Indus in Mianwali District of Pakistan to evaluate the impact of environmental pollution.

Material and methods This completely randomised study involved two polluted sites (Shabaz Khel= S2 and Ballo Khel= S3) and a relatively less polluted site (Ghandi=S1 as the control) that were about 30 kilometers apart from each other along a stretch of the River Indus in Mianwali. A total of 81 samples of *Cyprinus carpio* were collected by using nine fish samples of similar size (about 1000g) as replicates from three locations of each site. Replicated water samples were also collected from each of these three sites. The concentration of selected heavy metals (As, Cr, Cu, Mn and Pb) in water and fish samples were analysed by using a Varian Vista-MPX CCD Simultaneous ICP-AES machine (Varian Inc, Australia). Levels of lipid hydroperoxides and activities of enzymatic antioxidants including superoxide dismutase (SOD), catalase (CAT), glutathione-S-transferase (GST) and reduce glutathione (GR) in fish liver were measured by spectrophotometric assays using standard procedures. The data were statistically analysed by using ANOVA in Minitab software version 16 to test the effect of sampling sites on the metals uptake, levels of lipid hydro-peroxide and activities of antioxidant enzymes of fish livers. Tukey's post-hoc test was used to compare the means of different analytes for different sites at $P<0.05$.

Results Table 1 shows that the heavy metal concentrations in river water were within the safe limits except arsenic. However, the heavy metal concentrations in fish tissues were many fold higher than the WHO recommended levels for food fish except Cu in fish muscles. Table 2 shows elevated levels of MDA and liver antioxidants at polluted sites indicating the oxidative stress in fish species ($P<0.05$). The order of heavy metals and antioxidants was S3>S2>S1

Table 1 Mean concentration of heavy metals in fish tissues (mg/kg), river water (mg/l), maximum permissible levels (MPL) of heavy metals in food fish and water suitable for aquatic life according to WHO (2006) and P-values.

	S1			S2			S3			WHO MPL in Fish	WHO MPL in Water	P-Value
	Liver	Muscle	Water	Liver	Muscle	Water	Liver	Muscle	Water			
As	1.83	1.74	0.011	2.66	2.39	0.014	2.76	3.04	0.015	0.1	0.01	0.001
Cr	0.24	1.71	0.001	5.19	3.20	0.001	5.52	4.08	0.002	0.05	0.05	0.001
Cu	41.16	7.11	0.013	76.96	7.19	0.025	81.24	7.86	0.053	30	2	0.001
Mn	3.95	2.33	0.006	6.56	2.47	0.008	10.11	2.55	0.009	0.01	0.5	0.001
Pb	8.14	18.56	0.003	23.49	19.78	0.006	35.57	34.72	0.008	2.0	0.01	0.001

Table 2 Activity of different antioxidant enzymes in liver of *Cyprinus carpio* sampled from the River Indus

Antioxidant Enzymes	S1	S2	S3
TBARS (µM MDA/mg of tissue)	1.64 ± 0.34^{c}	2.21 ± 0.23^{b}	3.29 ± 0.45^{a}
Lipid hydroperoxides (mM/g of tissue)	7.21 ± 0.36^{c}	8.32 ± 0.67^{b}	12.32 ± 1.23^{a}
Reduced glutathione (µM /g of tissue)	28.22 ± 2.23^{a}	29.55 ± 2.12^{a}	29.40 ± 3.28^{a}
Catalase (U/ml of tissue homogenate)	5.56 ± 1.24^{c}	7.75 ± 1.34^{b}	11.53 ± 2.37^{a}
Superoxide dismutase (U/min/mg protein)	0.61 ± 0.03^{c}	0.86 ± 0.04^{b}	0.98 ± 0.05^{a}
Glutathione-S-transferase (nmol CDNB/min/mg/protein)	164.24 ± 24.12^{c}	235.44 ± 22.45^{b}	349.67 ± 35.32^{a}

Conclusion This study suggested that the fish in the study area were living under stressful environment as evident by the alterations in the activities of antioxidant enzymes and elevated levels of heavy metals in fish tissues are cause of a concern.

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Precision calf management for optimal health and welfare

B Earley
Teagasc, Co. Meath, Ireland
Email:bernadette.earley@teagasc.ie

The aim of successful calf rearing is to produce a healthy calf which is capable of optimum performance throughout its life from birth through to finishing. A suitable calf rearing system has the following characteristics; optimal animal performance with minimal disease and morbidity, low cost input and low labour input. To ensure a healthy calf, the aim is to minimise the calf's exposure to disease, and maximise its defence against disease. Calf diarrhoea and calf pneumonia are the main causes of calf mortality. The majority of calf scours are caused by six organisms: viruses such as rotavirus and coronavirus, bacteria such as *E. coli* and *Salmonella sp.,* and protozoa, such as cryptosporidia and coccidia. Vaccination of the dam will help reduce the probability of calf scours but cannot solely be depended upon for prevention. Diarrhoea in calves results in losses of water and electrolytes, such as sodium, bicarbonate, chlorine, and potassium. Calves with diarrhoea can lose 10 to 12% of their body weight in water losses. Depending on the severity of the diarrhoea and dehydration, calves may need to receive oral electrolyte solutions once daily or as many as four times a day. Scientific evidence has accumulated that continued milk feeding does not worsen or prolong the course of diarrhoea, despite a somewhat lowered digestive capacity.

Pneumonia is the major cause of respiratory distress in calves during the first few months of life. It is a multifactorial disease determined by the environment, management, the immune status of the calves and the involvement of primary (viruses), and secondary infections (bacteria), and mycoplasma. Although commercial vaccines are available against viral pathogens such as BPI3V, involved in the pathogenesis of BRD, their efficacy is limited in calves with pre-existing, circulating, and typically maternally-derived, antibodies. As a result, multiple doses of currently available vaccines are required to create protective immunity. Improved vaccines against BRD should ideally: provide long-lasting protection against the associated pathogens; work in animals with pre-existing antibodies; and require the administration of as small a dose as is effective. Nanovaccines are a novel development in the context of protecting farm animals against respiratory or other diseases (Kavanagh *Et al*., 2013a; 2013b; 2014). If such vaccines prove efficacious, as suggested by recent findings, they could result in considerable benefits to the cattle industry globally in terms of improved animal health and welfare. Thus, prophylactic and targeted therapeutic approaches/early diagnosis and intervention is critical.

Information and Computer Technology (ICT) offers a high potential for real time monitoring of animal health in livestock production systems. To apply the high potential of these ICT technologies in livestock production is the core concept of precision livestock farming (PLF). Continuous automated monitoring of livestock results in "early warning systems" that improve the management of individual animal needs at any time. PLF refers to measuring bio responses in animals for monitoring and management within livestock production systems. Traits suitable for the PLF approach include, but are not limited to, animal growth, disease, aspects of animal behaviour, and the physical environment of a livestock building, such as its thermal micro-environment, as well as emissions of gaseous pollutants such as ammonia. Such a tool could provide 24-h monitoring of calf health that is not possible at the moment on farms since the evaluation of animal health is limited only during the time that the owner is present on the farm. Early identification of infected animals could prevent a disease from spreading, resulting in improved animal health and welfare. The use of novel nanotechnology in the context of vaccine delivery could also contribute to state-of-the-art prevention strategies against BRD and other infectious diseases of livestock and potentially make a significant contribution to improving animal health and welfare. Thus PLF in combination with nanovaccine technology will aid disease management, and prevent clinical cases from developing.

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Automatic prediction of parturition in dairy cows using tail-mounted accelerometers

C Michie[2], D Ross[1], C Davison[2], J Konka[2], C Tachtatzis[2], D Bell[1], C-A Duthie[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]University of Strathclyde, Glasgow, UK
Email:dave.ross@sruc.ac.uk

Implications A tail-mounted sensor system which monitors tail raise behaviour can detect the onset of calving in individual dairy cows. This has both welfare and economic implications, by allowing for appropriate interventions where necessary.

Introduction The process of parturition is a significant physiological process for the dairy cow. Pre-partum, during parturition, and immediately post-partum, patterns of behaviour, motion and tail movement depart from those normally expressed (Miedema *et al* 2011). The objective of this study was to investigate the potential of a sensor system which monitors tail movements to predict, the time of parturition.

Material and methods The sensor constituted a tail-mounted, data-logging tri-axial accelerometer which was used to monitor tail raise behaviour (Figure 1 shows typical output). The sensor was mounted externally on the tail of a cow. The data was recorded on to a secure digital memory (SD) card and post-processed to identify the frequency and duration of tail raise activity. A classification algorithm which detected the raising of the tail, was devised by evaluating the difference between the "x" and "z" accelerations, then used to trigger a count of the duration of tail raise activity over a one hour period. The performance of a tail-based sensor to detect the onset of calving was evaluated from 27 pure-bred Holstein multi-parous cows. A 24 hour running average of the hourly tail raise duration was calculated along with the standard deviation. This established a baseline of normal individual cow behaviour for each sensor. A flag was set whenever a tail raise duration for an hourly block was found to deviate from the average value by more than the standard deviation. A prediction model was created that reported that if two successive flags were set, then it was deemed likely that the cow was approaching parturition. If, in addition to the flags, the tail raise duration was found to be greater than 5 minutes, the model reported that parturition had occurred.

Results 25 predictions were True Positive (TP), 1 False Negative (FN) and 1 was False Positive (FP). Out of all TP flagged predictions, 4 were in the period of between 4 and 6 hours pre-partum, 12 in the 2 to 4 hour period, and 9 within 2 hours pre-partum. In all cases, the model continued to flag, following the initial alert, up until the point of parturition. In the case of the False Negative (FN) prediction, the sensor readings were atypical and suggested a sensor fault. The False Positive (FP) showed a high degree of activity for the duration of the time that the sensor was mounted on the tail; this may be indicative of an underlying physiological issue with this cow. Predictions of calving within 6 hours of the parturition point have been made with both a Sensitivity (TP/(TP+FN) and Positive Predictive Value (TP/(TP +FP)) of 0.96

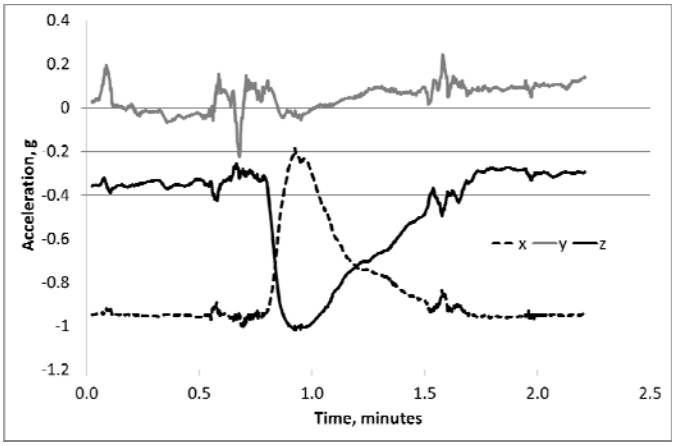

Figure 1 Tail Raise Signature

Conclusion A tail-mounted sensor has been used to identify tail raise activity in individual dairy cattle. Such information is highly valuable to the farming community both for the dairy and the beef sectors, where dystocia has a high welfare and economic effect. The sensors have predicted the onset of calving with a high PPV of 0.96.

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A comparison of the behaviour of lame and non-lame dairy cows using novel local positioning sensors with 3d accelerometers

H Hodges[1], Z Barker[1], J Vasquez-Diosdado[2], E Codling[2], N Bell[3], D Croft[4], J Amory[1]
[1]Writtle College, Chelmsford, UK, [2]University of Essex, Colchester, UK, [3]Royal Veterinary College, London, UK, [4]University of Exeter, UK
Email:jonathan.amory@writtle.ac.uk

Implications Using the differences in behaviour reported here it may be possible to build a predictive model for the early detection of lameness in dairy cattle. The potential earlier treatment of lameness would reduce the severity and duration of cases.

Introduction Automatic measurement of lying and standing behaviour in dairy cows has typically been with leg mounted pedometers. Such technology has been useful in lameness research (Blackie *et al* 2011), but more detailed measurements of behaviour are likely to be beneficial. Feeding and other behaviours has been investigated in lame and non-lame animals using load cells (Palmer *et al*., 2012) and also using accelerometer-based activity monitors (e.g. Nielsen, 2013), but recent technological advances provide new avenues for research. The current study used a neck mounted sensor containing novel local positioning technology with 3D accelerometers to measure the behaviour of lame and non-lame cow

Material and methods Twenty cows from a group of 120 high yielding cows on a commercial dairy farm were fitted with neck mounted oms500 sensors (Omnisense®). All cows in the high yield group were locomotion scored using the DairyCo. Mobility Score and 10 non-lame (score 0) and 10 lame (score 2) cows were selected balanced for yield and parity. Sensor data from four 24 hour periods were collected. Using a 2 minute smoothing window, data from the sensors were classified as high or low activity and in one of four zone types: lying zone, feeding zone, milking zone and loafing zone. A decision tree was applied to the data to allocate the cow to the following behaviours, feeding, lying, loafing in the shed and milking. The proportion of time spent performing these activities between each of the three milking sessions on the farm was determined. After excluding 8% of data due to misclassified behaviours and positional error, activity of lame and non-lame cows was compared using a t-test (Genstat 17). Time since last lying or feeding period before milking and latency to lie or feed after milking was determined for each of the three milking times. These data were non-parametric and analysed using a Mann-Whitney U-test.

Results In the afternoon and overnight the lame cows spent significantly more time lying and less time feeding compared with the non-lame animals (Table 1).
On average over the four days the lame cows lay down for a total of 9.7±0.44 hours compared with 9.4±0.50 hours for the non-lame group (mean ± s.d.; no significant difference). There was a trend (p=0.068) towards lame cows having a shorter interval from their last lying bout to morning milking (Table 2).

Table 1 Proportion of time budget allocated to three behaviours in lame vs non-lame cows (* indicates p<0.05)

Time	Behaviour	Lame	Non-lame	s.e.d
Morning	Lying	0.42	0.38	0.042
	Standing	0.34	0.40	0.050
	Feeding	0.24	0.22	0.031
Afternoon	Lying	0.46	0.31	0.054*
	Standing	0.21	0.21	0.042
	Feeding	0.33	0.48	0.052*
Overnight	Lying	0.45	0.36	0.045*
	Standing	0.27	0.30	0.048
	Feeding	0.28	0.34	0.021*

Table 2 Effect of lameness on time between milking and first or last feeding or lying bout (median and quartiles)

Number of minutes	Morning milking (5am)		Afternoon Milking (1pm)		Night Milking (9pm)	
	Lame	Non-lame	Lame	Non-lame	Lame	Non-lame
Last lying before	7.5 (0,40)	45 (10,120)	23 (13,40)	41 (8,60)	25 (10,60)	43 (10,120)
Last feed before	125 (95,185)	115 (50,155)	48 (25,110)	61 (38,90)	90 (5,175)	75 (0,125)
First lying after	50 (30,80)	68 (35,105)	50 (25,75)	58 (50,80)	50 (25,75)	58 (50,80)
First feed after	8 (0,25)	3 (0,30)	36 (18,53)	0 (0,100)	7.5 (0,15)	40 (20,90)

Conclusion When considering behavioural changes in unhealthy animals, for example in automated disease detection, time of day may be an important factor – if considering the whole day, key differences may be missed. Behaviour around management events such as milking also appears to have value in distinguishing lame/non-lame animals

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Use of an automated calf cough sound detection algorithm for the early detection of bovine respiratory disease

J Vandermeulen[1], C Bahr[1], D Johnston[2], B Earley[2], E Tullo[3], I Fontana[3], M Guarino[3], D Berckmans[1]
[1]KU Leuven, Leuven, Belgium, [2]TEAGASC, Grange, Ireland, [3]Università degli Studi di Milano, Milan, Italy
Email:joris.vandermeulen@biw.kuleuven.be

Implications Early recognition of bovine respiratory disease (BRD), allows earlier treatment intervention. Initial results show that periods with increased coughing can be detected by a cough sound detection system and these correspond with BRD incidences.

Introduction Bovine respiratory disease (BRD) is a multifactorial respiratory disease in cattle which causes major economic and welfare losses. Earlier recognition would reduce the severity of the disease and decrease the associated costs for the farmer. BRD is detected by observation of clinical manifestations of the disease. Diseases can be detected using automated, continuous monitoring of animals with Precision Livestock Farming (PLF) (Berckmans, 2008). The use of an automated cough sound monitor has already been developed in pigs (Van Hirtum *et al*., 2003). However, to date, there has been no published results about the use of this technology in calves (Ferrari *et al*., 2010). The objective of this study was to compare the results of an automated calf cough detection algorithm with respiratory scores of the calves.

Material and methods A total of sixty calves, comprised of Holstein–Friesian and Jersey calves, were housed in three calf houses with 20 calves per house. The calves were housed on sawdust covered floors at Teagasc, Grange Beef Research Centre from the 9th until the 29th of May 2013. Clinical assessments were performed by a trained human observer on all calves at least twice a week. The Wisconsin health scoring criteria were used to create a cumulative respiratory score. A respiratory score, ranging from zero to twelve, was devised from the cumulative score for nasal discharge, eye or ear score (whichever was greatest), cough and rectal temperature. A calf was considered to have BRD if it had a respiratory score of five or greater.
Each calf house was equipped with the hardware of the pig cough monitor (SoundTalks). This consisted of one microphone (C-4 Small Diaphragm Condenser Mic) and a sound Card (MAYA44). The sound was continuously recorded. A calf cough detection algorithm was developed using these recordings and achieved 58% sensitivity, 99% specificity and 76% precision.

Results Figure 1 shows the number of coughs/hour/day in one house. A period with an increase in the detected number of coughs was observed from the 20th until 26th of May from 5:00 to10:00 hours. The increased coughing period shown in grey in Figure 2 corresponds to an increase in the number of calves with a respiratory score greater or equal to five (Figure 2).

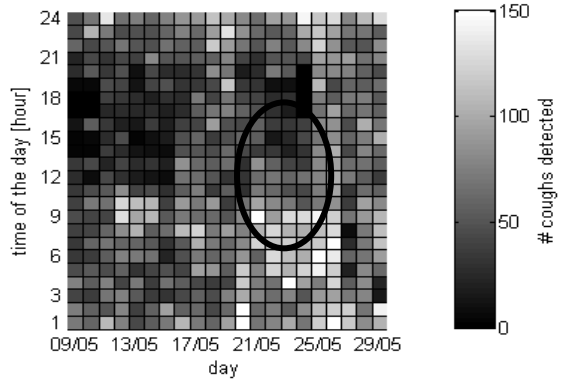

Figure 1 Number of coughs per hour and per day.

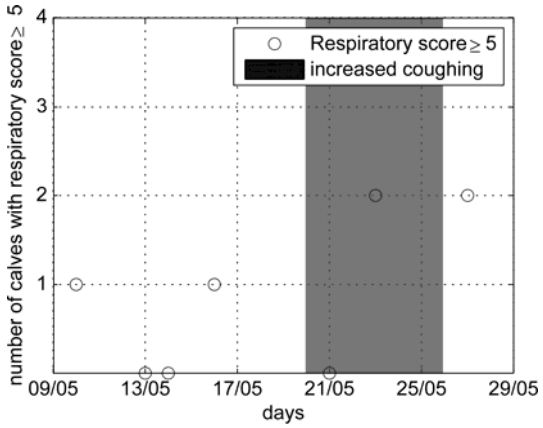

Figure 2 Number of calves with a respiratory score ≥ 5 during a coughing period

Conclusion The number of coughs detected by the algorithm corresponded with the number of calves with high respiratory scores. This demonstrates the possible use of an automated and continuous calf cough sound monitor for the detection of BRD in calves

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The effect of dietary forage proportion on enteric methane emissions of lactating dairy cows

L F Dong[1,2], T Yan[1], C Ferris[1], D McDowell[2]
[1]Agri-Food and Biosciences Institute, Hillsborough, Northern Ireland, UK, [2]University of Ulster, Jordanstown, Northern Ireland, UK
Email:dunlifeng@gmail.com

Implications Manipulation of plane of nutrition is an effective approach to reduce enteric methane (CH_4) output from lactating dairy cows.

Introduction Low input dairy management is widely recognised for the reduced input cost and improved animal health and welfare. However, there are concerns that low milk production under the low input system may increase carbon emission per kg milk yield. The objectives of the present study were to examine the effect of dietary forage proportion (FP) on enteric CH_4 emission rates of lactating dairy cows using a large calorimetric dataset.

Material and methods Data used were collated from 32 calorimetric chamber experiments undertaken at this Institute from 1992 to 2010. The dataset included data derived from lactating dairy cows of pure breed (823 HF and 50 Norwegian) and crossbred (46 Jersey*HF and 16 Norwegian*HF). These cows were either in the 1st (n = 258), 2nd (n = 206) or 3rd lactation or over (n = 466), and at various stages of lactation when housed in chambers, with mean post calving days of 159 for HF, 158 for Norwegian, 179 for Jersey*HF, and 247 for Norwegian*HF. They were offered either forage only diets (n = 66), or a mixture of forage and concentrates (n = 869). Energy metabolism data including enteric CH_4 emissions used in the present study were measured in indirect open-circuit respiration calorimeter chambers. The effects of dietary FP on CH_4 emissions were evaluated using ANOVA by dividing the whole dataset into three sub-datasets according to dietary FP (FP < 50%, 50-99% and 100%, DM basis), with the effects of experiment, animal and dietary factors removed.

Results and Discussion Results are presented in Table 1. There was no significant difference in live weight or body condition score among the three groups. As expected, increasing FP significant decreased DM intake, ME intake and energy corrected milk yield ($P < 0.05$), but significantly increased CH_4 emissions (g/d) ($P < 0.05$). These effects thus led to a greater CH_4 emission rate ($P < 0.05$) for diets with high FP, in terms of CH_4 emission as a proportion of DM intake, or energy corrected milk yield, or CH_4 energy (CH_4-E) output as a proportion of GE intake or DE intake. The ratios of CH_4-E/GE intake with FP groups of 50-99% and 100% were higher than that (0.065) proposed by IPCC (2006) for calculation of enteric CH_4 emissions from dairy cows, indicating using the recommendation of IPCC (2006) could underestimate CH_4 emissions for dairy cows managed under low input systems.

Table 1 Effects of dietary forage proportion on animal performance and enteric methane emissions[1]

	Forage proportion (DM basis)				
	<50%	50-99%	100%	SED	Sig.
Live weight (kg)	555	552	543	7.4	NS
Body condition score	2.57	2.56	2.56	0.159	NS
DM intake (kg/d)	17.9[a]	16.1[b]	14.7[c]	0.35	*
ME intake (kg/d)	240[a]	220[b]	193[c]	14.0	*
Energy-corrected milk yield (kg/d)	22.8[a]	19.8[b]	16.8[c]	0.72	*
CH_4 (g/d)	345[a]	374[b]	381[c]	8.6	*
CH_4/DM intake (g/kg)	21.63[a]	22.67[b]	23.57[c]	0.452	*
CH_4/energy corrected milk yield (g/kg)	15.74[a]	20.26[b]	24.29[c]	0.686	*
CH_4-E/GE intake (MJ/MJ)	0.065[a]	0.068[b]	0.071[c]	0.0014	*
CH_4-E/DE intake (MJ/MJ)	0.087[a]	0.098[b]	0.102[c]	0.0017	*

[1] Within a row, means with a common superscript letter differ significantly ($P < 0.05$); * = $P < 0.05$

Conclusion The present study demonstrated that dairy cows managed under low, rather than high input systems could produce more enteric CH_4 for a given milk production capacity. Using the recommendation of IPCC (2006) for calculation CH_4 emissions could underestimate the carbon footprint for cows managed under low input systems.

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Effects of dietary nitrate or oil concentration on methane (CH_4) and hydrogen (H_2) emissions from beef cattle are basal diet dependant

J A Rooke[1], S Troy[1], C-A Duthie[1], R J Wallace[2], J Hyslop[3], D Ross[1], T Waterhouse[1], R Roehe[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]Rowett Institute for Nutrition and Health, Aberdeen, UK, [3]SAC Consulting, Edinburgh, UK
Email:john.rooke@sruc.ac.uk

Implications The absence of a reduction in methane (CH_4) emissions in response to dietary nitrate or lipid when included in a high concentrate diet highlights the importance of dietary background when considering CH_4 mitigation strategies.

Introduction Worldwide, beef production systems generate 2.9 Mt of CO_2-Eq emissions per year, with methane (CH_4) emissions accounting for 44 % of the total greenhouse gas emissions. The vast majority (97 %) of this CH_4 comes from enteric emissions. Previous studies have shown that adding nitrate or increasing dietary oil concentrations in mixed forage and concentrate diets lowered CH_4 emissions (Leng, 2014; Patra 2013). However there is little information on the effect of these CH_4 mitigation strategies when high concentrate diets are fed. This experiment was designed to investigate the effects of adding nitrate or increasing dietary oil on CH_4 and H_2 emissions from finishing beef cattle fed two contrasting basal diets containing 500 or 920 g concentrate dry matter (DM)/ kg total DM.

Material and methods The experiment had a 2 × 2 × 3 factorial design where the factors were steer genotype (crossbred Charolais or purebred Luing), basal diet (concentrate, Con; mixed, Mix) and CH_4 mitigation treatment (control, C; nitrate, N; lipid, L) giving six nutritional treatments. Main ingredients (g/kg DM basis) for ConC were barley, 739; rapeseed meal, 147; and barley straw, 84; and for MixC were whole crop barley silage, 303; grass silage, 187; barley, 348; and rapeseed meal, 132. Treatments N and L were achieved by replacing rapeseed meal isonitrogenously with Calcinit (Yara, Oslo; 21.5 g calcium nitrate /kg DM) or cold-pressed rape cake (155 g/kg DM), respectively. Diets were fed *ad libitum*. Steers (13 per treatment; live-weight, 696 kg (SE 43)) were offered experimental diets for a minimum of 10 weeks prior to measurement of CH_4 and H_2 emissions using 6 open-circuit respiration chambers (Rooke *et al*. 2014). Steers were assigned to chambers using a randomised block design in 13 weekly periods. Data were available for 75 steers and were analysed using general linear models with fixed effects of breed, basal diet and treatment and random effects of chamber and block.

Results DM intakes (DMI, kg/d) did not differ between treatments (P>0.05). Genotype had no effect on CH_4 emissions but H_2 emissions from Luing steers were lower (P<0.05) than from Charolais steers but there were no interactions between genotype and nutritional treatment. Daily CH_4 outputs (g/d or g/kg DM) were, as observed before, lower on the Con than Mix diet (Table 1). Nitrate and to a lesser extent lipid reduced CH_4 emissions when included in diet Mix but not diet Con. H_2 outputs (g/d or g/kg DM) were greater on diet Mix than Con; inclusion of nitrate increased H_2 outputs and the increase was proportionately greater on diet Mix than Con.

Table 1 Effect of dietary lipid (L) or nitrate (N) on CH_4 and H_2 outputs from steers offered mixed forage:concentrate (M) or high concentrate diets (C), (means with average SED).

Treatment	MixC	MixN	MixL	ConC	ConN	ConL	SED	Diet	Treatment	D x T
CH_4 g/day	242	212	242	149	149	136	15.8	P<0.001	P<0.05	NS
CH_4 g/kg DMI	25.1^{a}	20.6^{b}	23.2^{ab}	14.6	15.4	15.7	1.51	P<0.001	NS	P<0.05
H_2 g/day	0.47^{a}	1.25^{b}	0.60^{a}	0.20	0.34	0.16	0.143	P<0.001	P<0.001	P<0.01
H_2 g/kg DMI	0.048^{a}	0.123^{b}	0.058^{a}	0.019	0.038	0.016	0.0158	P<0.001	P<0.001	P<0.05

Different superscripts ^{ab} indicate differences (P<0.05) between MixC, MixN and MixL. D x T: diet x treatment interaction

Conclusion Methane emissions were substantially lower when the high concentrate diet was fed. Nitrate and lipid treatments inhibited CH_4 production (by 18 and 7%, respectively) with the mixed diet, similar to previous studies (Leng, 2014; Patra 2013), but had no effect with the concentrate diet. H_2 emissions were increased by nitrate irrespective of basal diet.

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A novel method of measuring methane (CH_4) emissions from beef cattle in group housing

S M Troy, C-A Duthie, J J Hyslop, R Roehe, D W Ross, A Waterhouse, J A Rooke
SRUC, Scotland's Rural College, Edinburgh, UK
Email:shane.troy@sruc.ac.uk

Implications This novel method of CH_4 monitoring for individual beef animals can be used to estimate daily CH_4 emissions without removing animals from their normal environment. This hood method can estimate CH_4 yield from large numbers of animals simultaneously, making it a useful tool for investigating CH_4 mitigation strategies.

Introduction Worldwide beef production generates 6% of all human-induced greenhouse gas (GHG) emissions, with CH_4 accounting for 44% of these emissions. Mitigation strategies for beef production are required in order to feed a growing population, without further increasing GHG emissions. Respiration chambers have long been used to measure emissions from individual animals. However, chambers are costly and animals are measured individually which reduces throughput and may alter feeding behaviour. There is strong interest in developing new methods of measuring emissions, which can be deployed without removing animals from regular production systems. The study was designed to measure CH_4 emissions from cattle in commercial group housing, by continuously sampling CH_4 concentration in air samples taken during feeding. Methane emissions from cattle are likely to be highest during feeding as gas is displaced from the rumen by feed ingested.

Material and methods 84 steers, housed under commercial conditions in 6 adjacent group pens, received 1 of 2 basal diets consisting (g/kg, DM basis, forage:concentrate) of either 480:520 (Mix) or 80:920 (Con), respectively. Within each diet, 3 treatments were used: Control (C), nitrate (N) or high lipid (L). Treatments N and L were achieved by replacing rapeseed meal iso-nitrogenously with calcium nitrate (21.5g nitrate/kg DM) or cold-pressed rape cake (155g/kg DM), respectively. Individual animal feed intake was monitored using automatic feed bins (Hoko). To sample CH_4 emissions during feeding a polycarbonate hood was built over each bin. The air below each hood was constantly exhausted (1 m^3/min) by a fan from the top of the hoods. Exhaust air CH_4 concentrations were measured from each hood every 6 min. Hoko bin entry and exit times for each animal were time-matched with gas concentration times for each hood. There was a linear decline in CH_4 concentrations as the wind speed increased (R^2 = 0.44 to 0.55 for each of the 6 treatments). A correction factor was required to correct CH_4 concentrations to 0 wind speed ($CorrCH_4$). The group pen analysis period lasted for 8 weeks. Following this, 75 of the steers were incrementally moved, over a period of 13 weeks, from the group pens to the respiration chambers on the same site. Methane emissions were measured once more using 6 open-circuit chambers (Rooke *et al*. 2014).

Results Mean weekly $CorrCH_4$ for individual animals correlated strongly across all 8 sampling weeks (Fig 1 shows week 1 vs. week 7, R^2 = 0.89). There was also good agreement between individual animal $CorrCH_4$ (averaged over the 8 sampling weeks) and subsequent daily CH_4 production as measured in the respiration chambers, both corrected for dry matter intake (DMI, R^2 = 0.73; P < 0.001; Fig 2). The same dietary and treatment effects were found from data gathered from the hood during group housing and when the animals were subsequently measured individually in the respiration chambers. Nitrate and to a lesser extent L reduced CH_4 emissions when included in diet Mix but not diet Con.

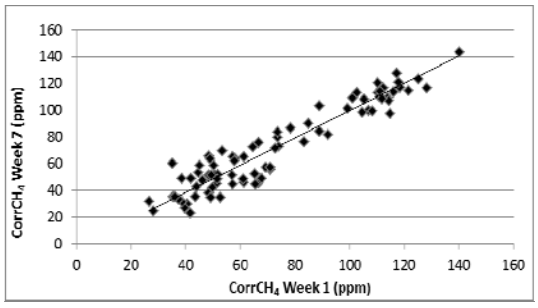

Figure 1 Average weekly $CorrCH_4$ (ppm) values for individual animals on week 1 vs. week 7

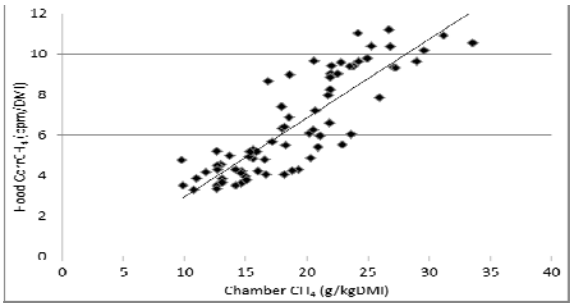

Figure 2 Animal $CorrCH_4$ (ppm/DMI) values measured by hoods compared with chamber CH_4 yield (g/kg DMI)

Conclusion This novel hood measurement system can be used to estimate individual animal CH_4 production and to compare the effects of mitigation strategies on CH_4 production from cattle in a group-housed environment.

Acknowledgements The authors gratefully acknowledge funding from EBLEX, the Scottish Government and by DEFRA and the devolved administrations through the UK Agricultural Greenhouse Gas Inventory Research Platform.

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Methane emissions from sheep receiving dietary mixtures of heather (*Calluna vulgaris*) and grass

R W Mayes[1], F J Perez-Barberia[1,2]
[1]The James Hutton Institute, Aberdeen, UK, [2]Ungulate Research Unit, CRCP Game and Fish Research Centre, Cordoba, Spain
Email:robert.mayes@hutton.ac.uk

Implications Methane emissions from sheep grazing on the hills and uplands of the UK, where heather (*Calluna vulgaris*) may be a significant component of the diet, may be lower than expected from animals receiving grass-only diets.

Introduction Sheep and deer grazing hill and upland pastures may ingest significant quantities of dwarf shrubs, such as heather and bilberry (*Vaccinium myrtillus*), which contain high levels of phenolics and other plant secondary metabolites. Since such compounds are known to affect rumen fermentation (Murray *et al*., 1996), it is possible that methane production (g/kg digestible organic matter intake, DOMI) may differ in animals ingesting heather or bilberry compared with grass diets. This work describes some preliminary studies carried out in which methane production and organic matter digestibility (OMD) was measured in sheep fed a range of freeze-stored mixtures of heather and grass.

Material and methods Three groups of four Scottish Blackface wether sheep (aged 3 years, weighing 50-67kg) received different dietary mixtures of heather (green shoots) and high-quality grass (mainly *Lolium perenne* and *Agrostis capillaris*) (dietary heather proportions: 0.36; 0.57; 0.66). Following a 3-week acclimation period in individual pens the sheep were placed in metabolism cages within open-circuit respiration chambers for 7 days to determine OMD and methane production. Feeds were offered (at predicted maintenance levels) twice each day and dietary refusals and faeces were collected once daily. Linear mixed-effects models were used to relate methane output to DOMI and dietary proportion of heather (both terms and their interaction as fixed effects, and sheep as random effect). Since the interaction was not significant it was removed from the final model. The parameters of the final model were calculated using REML.

Results The proportions of heather in the consumed diet (OM basis) ranged from 0.35 to 0.63 and OM intakes ranged from 0.75 to 1.39kg/d. As expected, OMD declined as the heather proportion increased (OMD= 0.749 – 0.0405 x heather proportion (both intercept and slope $P<0.001$; R^2 =0.765)). Daily methane output was positively related to DOMI ($P<0.001$) and negatively related (P =0.014) to the proportion of heather in the diet (Figure 1). The linear mixed-effect model results are shown in Table 1.

Table 1 Coefficients of fixed effects from model describing relationships between methane output (g/d), DOMI and dietary heather proportion.

	Value	s.e.	t Value	P
Intercept	15.26	1.935	7.89	<0.001
DOMI (kg/d)	12.73	0.116	109.3	<0.001
Heather proportion	-10.95	3.654	-3.00	0.014
R^2	0.834			

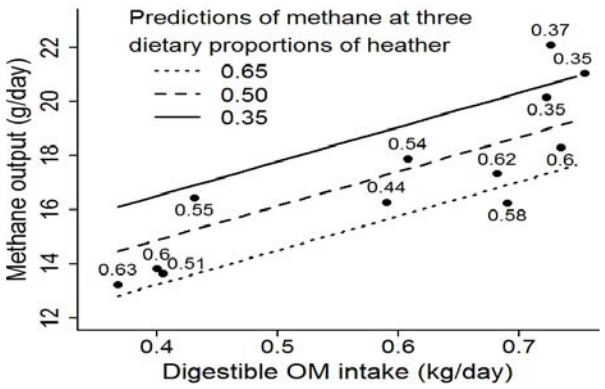

Figure 1 Predictions of methane output against DOMI at three proportions of heather for sheep ingesting heather/grass mixtures. Actual dietary proportions shown next to data points.

Conclusion These studies with sheep offered freeze-stored heather/grass mixtures suggest that the ruminal fermentation of heather OM results in lower methane emissions than those arising from the fermentation of grass OM. Further studies are in progress with sheep and red deer to determine methane outputs from a wider range of heather/grass mixtures and *Vaccinium*/grass diets.

Acknowledgements This work was funded by the Scottish Government's RESAS Strategic Research Programme. The assistance provided by Spanish graduates funded by EU training schemes through CAEB, Confebask, FEUN, FICYT, FGULEN, FUERM and Noviasalcedo is gratefully acknowledged.

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Prediction of methane emissions from lowland lambs using data measured in indirect open-circuit respiration calorimeters

Y G Zhao[1,2], A Aubry[1], R Annett[1], N E O'Connell[2], T Yan[1]
[1]Agri-Food and Biosciences Institute, Hillsborough, UK, [2]Queen's University Belfast, UK
Email:yiguang.zhao@afbini.gov.uk

Implications Feed intake can be used to accurately predict methane (CH_4) emissions from lowland lambs. The present equations provide a practical tool for developing robust CH_4 emission inventories for sheep production systems.

Introduction The IPCC Tier 1 default emission factor was used in UK to estimate enteric CH_4 production for sheep with no consideration of effects of animal and dietary factors (National Atmospheric Emissions Inventory, 2014). There is an urgent need to develop more accurate emission factors specific to growing sheep and representative of the breeds and rearing systems employed in the UK sheep industry. The aim of the present study was to develop prediction equations of CH_4 emissions for lowland lambs.

Material and methods Forty eight lowland lambs were used in a 2 breed (Highlander vs. Texel) × 3 sex (female vs. entire male vs. castrated male) × 2 diet (fresh grass vs. fresh grass plus 0.5 kg/d fresh pelleted concentrates) factorial design study with a single period (23 days). Animals were at approximately 5 months old and 36 ± 5.0 kg live weight (LW) in the commencement of the study and allocated to 2 diet treatments balanced for sex, breed and LW. Fresh grass was harvested daily from the 1st regrowth of perennial ryegrass sward and offered *ad libitum.* Concentrates contained (g/kg fresh basis): 325 barley, 250 beet pulp, 250 soybean meal, 100 maize meal, 30 molaferm, 20 intensive lamb 20 and 25 Vit/Min supplement (V/M 208). The animals were individually housed in pens and fed experimental diets for 19 days before being transferred to individual calorimeter chambers for a further 4 days with feed intake, faecal and urine outputs collected and CH_4, CO_2 and O_2 measured for the final 3 days. Live weight was measured at the beginning of the study and before entering and after leaving the chamber. Grass and concentrate contained (g/kg DM): ash 107 and 60; CP 202 and 210; ADF 257 and 138; NDF 508 and 279; and GE 18.8 and 18.1 (MJ/kg DM), respectively. Data were analysed using the linear and multiple regression techniques with effects of sex, breed and diet removed. The statistical programme used in the present study was Genstat statistical package with a probability level of $P = 0.05$ for significance in relationships.

Results The prediction equations for CH_4 emissions from lowland lambs are presented in Table 1. All relationships were significant ($P < 0.001$) and each predictor had a significant effect on the relationship ($P < 0.001$). The statistical analysis found that DM intake (DMI) and OM intake (OMI) were better predictors for CH_4 emissions than LW ($r^2 = 0.74$ and 0.75 vs. 0.43; SE = 1.69 and 1.71 vs. 2.55). The r^2 value with GE intake (GEI) was higher than with ME intake (MEI) (0.74 vs. 0.67) when used as predictor for CH_4 energy output (CH_4-E). Adding LW to the relationship using DMI marginally increased the r^2 values from 0.74 to 0.76 and reduced the SE values from 1.71 to 1.67.

Table 1 Prediction equations for methane emissions from lowland lambs (n = 48)[1]

Equations		SE	r^2
CH_4 (g/d)	$= 0.389_{(0.0890)}$ LW (kg) + $10.0_{(3.58)}$	2.55	0.43
	$= 17.0_{(1.73)}$ DMI (kg/d) + $4.9_{(2.08)}$	1.71	0.74
	$= 18.4_{(1.85)}$ OMI (kg/d) + $5.4_{(2.01)}$	1.69	0.75
	$= 15.2_{(1.97)}$ DMI (kg/d) + $0.119_{(0.0678)}$ LW (kg) + $2.4_{(2.52)}$	1.67	0.76
CH_4-E (MJ/d)	$= 0.050_{(0.0052)}$ GEI (MJ/d) + $0.28_{(0.116)}$	0.096	0.74
	$= 0.057_{(0.0062)}$ DEI (MJ/d) + $0.41_{(0.107)}$	0.099	0.72
	$= 0.058_{(0.0072)}$ MEI (MJ/d) + $0.53_{(0.108)}$	0.107	0.67

[1]Values in subscript parentheses are SE.

Conclusion DM intake and GE intake are acurate predictors for CH_4 emissions from lowland lambs with relatively high r^2 and low SE values. These equations can be used to predict CH_4 emissions from sheep production systems.

Acknowledgements This work was funded by DEFRA, the Scottish Government, DARD, and the Welsh Government as part of the UK's Agricultural GHG Research Platform project (www.ghgplatform.org.uk).

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Measurement of methane emissions from lactating dairy cows fed diets differing in forage type and neutral detergent fibre concentration using spot sampling or continuous measurement

K J Hammond, D J Humphries, A K Jones, P Kirton, L A Crompton, C K Reynolds
University of Reading, UK
Email:k.j.hammond@reading.ac.uk

Implications Spot sampling (GreenFeed, GF) and continuous (respiration chamber, RC) techniques were equally valid for detecting treatment effects on methane (CH_4) emissions but spot samples need to account for diurnal CH_4 variation.

Introduction Dietary manipulation can be effective for mitigation of CH_4 emissions from dairy cows, and alternative methods to RC are being introduced as a less intrusive way to measure diet effects on CH_4 emission. Replacing grass silage (GS) with maize silage (MS) reduced CH_4 yield (Reynolds *et al*., 2010), and Aguerre *et al*. (2011) found CH_4 yield to be correlated with diet neutral detergent fibre (NDF) concentration. The GF system is a portable sampling tracer gas unit that is used to estimate daily CH_4 emission by extrapolation. Our objective was to compare dietary treatment effects on CH_4 emissions from lactating cows by GF and RC methods in 2 experiments (expts).

Material and methods Dietary treatments for both expts contained 500 g silage/kg dry matter (DM) comprised of 75:25 MS:GS (MS) or 25:75 MS:GS (GS), without or with added NDF (MSNDF and GSNDF) from chopped straw and soy hulls (+47 g NDF/kg diet DM). Cows were milked twice daily and fed *ad lib*, with up to 2 kg of concentrate/d dispensed via a GF unit (expt 1) or added to the ration (expt 2). For expt 1, 40 Holstein Friesian dairy cows (74 days in milk [DIM], body weight [BW] 675 kg, n = 10/treatment), were fed treatment diets for 84 d, with 21 d adaptation to GF, and GF measurements on days 63-84. Expt 2 occurred at the same time as expt 1 and used 4 Holstein Friesian dairy cows (114 DIM, BW 678 kg) in a 4x4 Latin Square design. Periods were 33 d, with 21 d adaptation, and CH_4 measured in RC on days 29-33. Data were analysed by the Mixed Models Procedure of SAS (2011). Each expt tested random effects of cow within treatment and fixed effects of silage (S), NDF, and S x NDF. Expt 2 also included fixed and repeated effects of period.

Results Cows fed MS in expt 1 had a higher ($P<0.001$) dry matter intake (DMI) and milk yield ($P<0.003$), a lower ($P<0.001$) CH_4 yield (g/kg DMI), and visited the GF unit less ($P<0.023$) than cows fed GS. There was a tendency ($P=0.064$) for a higher CH_4 yield with additional NDF for MS, but not GS ($P=0.093$, S x NDF). In expt 2, cows fed MS in RC had a higher DMI ($P<0.011$), produced more ($P<0.004$) milk, and had a lower ($P<0.018$) CH_4 yield compared to GS diets. Additional NDF decreased ($P<0.020$) milk yield, and increased CH_4 yield for MS but not GS diets ($P<0.015$, S x NDF).

Table 1 Dietary treatment effects on CH_4 emissions from lactating dairy cows

	Dietary treatment				SEM	P-value		
	MS	MSNDF	GS	GSNDF		Silage (S)	NDF	S x NDF
Expt 1 GreenFeed								
DMI, kg/d	24.8	24.4	19.3	19.3	0.46	<0.001	0.675	0.632
Milk yield, kg/d	35.6	33.3	30.0	28.0	1.67	0.003	0.207	0.943
CH_4, g/d	410	461	460	460	15.1	0.110	0.109	0.100
CH_4, g/kg DMI	16.5	18.9	24.0	24.1	0.68	<0.001	0.064	0.093
GF visits/d	2.76	2.58	3.35	3.54	0.32	0.023	0.983	0.577
Expt 2 Respiration chamber								
DMI, kg/d	21.7	20.5	18.4	17.0	0.89	0.011	0.205	0.950
Milk yield, kg/d	32.9	30.9	29.5	27.1	1.83	0.004	0.020	0.820
CH_4, g/d	495	472	462	417	26.5	0.097	0.176	0.627
CH_4, g/kg DMI	21.8	23.7	25.5	24.2	0.82	0.018	0.412	0.015

Conclusion Both GF and RC techniques measured a lower CH_4 yield from lactating cows fed MS, compared to GS, but the magnitude of the difference varied between techniques. The number and timing of spot sampling CH_4 measurements through cow GF visitation relative to diurnal patterns of CH_4 emission needs further evaluation.

Acknowledgements This work was funded by Defra, the Scottish Government, DARD, and the Welsh Government as part of the UK's Agricultural GHG Research Platform project (www.ghgplatform.org.uk).

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Life Cycle Assessment of high producing dairy production systems: do functional units matter?

S A Ross[1,3], M G G Chagunda[1], C F E Topp[1], R Ennos[2]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]University of Edinburgh, UK, [3]Singapore University of Technology and Design, Singapore *Email:mizeck.chagunda@sruc.ac.uk*

Implications Interpretation of any results from a Life Cycle Assessment of dairy production systems should be considered in the context of the methods, management practices, and Functional Unit used in order to make an informed appraisal of the information presented.

Introduction A Functional Unit (FU) provides a clearly defined and measurable reference to which input and output data are normalised (IPCC, 2006). This enables the results from Life Cycle Assessment (LCA) of different systems to be treated as functionally equivalent. Although standardised methodology for LCA of dairy production systems has been defined, selection of an appropriate functional unit remains ultimately at the discretion of the individual study. The aim of the present analysis was to examine the effect of different FUs on the relative emissions intensity of different dairy production systems.

Material and methods Analysis was based on data from individual cows in four dairy systems within Scotland's Rural College's (SRUC) long-term Holstein-Friesian genetic and management systems project at DRUC Dairy Research and Innovation Centre, Dumfries. Seven years data (2004-2010) were used, collected from two genetic lines maintained under two feeding regimes. High forage (HF) group had 75% of their ration from home grown crops (grass silage, maize, alkalage) with grazing outdoors when available. Low forage (LF) group were fully housed and were fed a ration of 45% home grown feeds and the remainder sourced from imported concentrates. Select animals (S) represented the top 5% of UK genetic merit, determined by fat and protein content of milk production, while control animals (C) were of UK average genetic merit. This provided four divergent systems: LFS, LFC, HFS, and HFC (Chagunda, 2009). Detail of the four systems, life cycle inventory, specific coefficients employed in analysis, and stochastic sensitivity analysis are described in Ross *et al*. (2014). Implementation of LCA accounted for the environmental impacts of the whole farm systems and their production of milk from 'cradle to the gate'. Impact assessment was conducted using IPCC methods implementing system specific data where possible (RBU 2010). Emissions intensity was determined as kilograms of carbon dioxide equivalents ($kgCO_2e$) referenced to six FU. The FU were: UK livestock units (LSU), kilograms of energy corrected milk yield (ECM), kilograms of total combined milk solids (MS), hectares of on-farm land used for production ($Land_{farm}$), hectares of total combined on- and off-farm land used for production ($Land_{total}$), and the proposed new FU - tonnes of ECM per hectare of total land used ($MY/Land_{total}$). The effect of different FU upon the emissions intensity was assessed by analysis of variance (ANOVA). In a statistical model which included production system as a fixed effect, calendar year as a random effect and a random error term.

Results ECM was the most effective FU for reflecting differences between the systems (Table 1). Functional units which incorporated a land related aspect did not find difference between systems which were managed under the same forage regime, despite their being comprised of different genetic lines. Employing on-farm land as the functional unit was found to favour grazing systems. The proposed dual functional unit combining both productivity and land-use did not differentiate between emissions intensity of systems as effectively as the productivity based units. However this dual unit displayed potential to quantify in a simple way the positive or negative outcome of trade-off conversions between land and production efficiencies.

Table 1 Least square means of missions intensity expressed as carbon dioxide equivalents ($kgCO_2e$) per functional unit

		Functional Unit					
Variable	Level	LSU LSU^{-1}	ECM kg^{-1}	MS kg^{-1}	$Land_{farm}$ ha^{-1}	$Land_{total}$ ha^{-1}	$MY/Land_{total}$ $t^{-1}\ ha^{-1}$
System	LFC	4126^{a}	0.92^{b}	12.9^{b}	16006^{b}	6278^{a}	14.9^{a}
	LFS	4398^{ab}	0.83^{a}	11.4^{a}	15971^{b}	6304^{a}	13.4^{a}
	HFC	4535^{bc}	1.10^{d}	15.2^{c}	11506^{a}	8041^{b}	21.4^{b}
	HFS	4807^{c}	1.00^{c}	13.7^{b}	11704^{a}	7467^{b}	20.5^{b}
	s.e.m	126.3	0.016	0.23	252.5	236.2	0.82

Different superscripts within a column denote significant differences between levels of same variables, ($P<0.001$) n = 615 lactating cows

Conclusions This study demonstrated that the perceived environmental efficiency of different dairy production systems in terms of their emissions intensity was susceptible to change based upon the FU employed. Energy corrected milk yields should remain the primary FU for interpretation of the LCA of a dairy production system, but combined land use and a dual FU should be employed in a secondary role in order to present a balanced analysis.

Acknowledgements The authors acknowledge work by staff at SRUC Dairy Research Centre and funding from Scottish Government

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Prediction of methane emissions from lactating dairy cows fed fresh cut grass and concentrates

D Hynes, S Stergiadis, T Yan
Agri-Food and Bioscience Institution, Co. Down, UK
Email:deborah.hynes@afbini.gov.uk

Implications Mitigating methane (CH_4) emissions from grazing cows may be achieved by improving production efficiency. Emissions of CH_4 from grazing animals can be predicted using dry matter intake (DMI) and energy corrected milk yield (ECMY).

Introduction The agricultural industry is a major contributor of atmospheric CH_4 and accounts for 41% of total greenhouse gas emissions in Northern Ireland (Jiao *et al*., 2013). The majority of CH_4, which is produced by rumen bacteria during nutrient fermentation, is eructated while smaller amounts are emitted from manure. Although the relations between CH_4 emissions with DMI and yield have been investigated on silage based diets, information for fresh grass based diets is limited in spite of grazing systems being common in temperate areas of the world. Irish and UK dairy herds spend up to 8 months annually at pasture, which represents 89% of Irish agricultural land (Hart *et al*., 2009). The aim of the current study was therefore to investigate the effect of DMI and ECMY on CH_4 emissions from dairy cows fed fresh grass-based diets.

Material and methods Twelve multiparous early lactating dairy cows, were used in a change-over experiment with 3 periods (25 days/period) using 2 breeds (6 Holstein-Friesian, 6 Holstein-Friesian crosses) and 3 concentrates with varying crude protein contents (130, 150 and 170 g/kg DM). Experimental groups were balanced for milk yield (35±3.7 L/d), live weight (544±45 kg) and days in milk (119±20.5). Grass was harvested daily and offered *ad libitum* to the cows. Concentrate feeds were offered during the two milkings at a level of 33% of total DMI, calculated from the average DMI of the previous 5 days. Cows were initially fed the experimental diet during a pro-measurement period of 18 days, with individual DMI recorded daily. Afterwards, they were housed in metabolism units for a 1-day adaptation and then in indirect open-circuit respiration calorimetric chambers for 3-days measurements of total faeces and urine outputs, with CH_4 emissions measured over the last 2 days. Cows were then transferred back to metabolism units with daily collection of total urine and faeces outputs continuing for a further 3 days. The 3-day average data obtained in chambers were used to develop prediction equations for CH_4 emissions using Residual Maximum Likelihood Analysis in GenStat. The CH_4 emissions for the first day in chambers were estimated using the average CH_4/DMI data measured in chambers.

Results The CH_4/DMI data ranged from 13.1 to 25.2 g/kg with a mean of 18.2 g/kg (s.e., 3.23) and corresponding data for CH_4/ECMY (g/kg) were 7.7, 22.3, 14.3 and 3.46. When DMI was used to predict CH_4 outputs (g/d) the explained variation was moderate. Although the effect of ECMY in the prediction of CH_4 (g/d) was not significant (results not shown), when CH_4 emissions were expressed as per kg ECMY, r^2 of the prediction was relatively high. Lower CH_4 emissions were associated with lower DMI and higher ECMY.

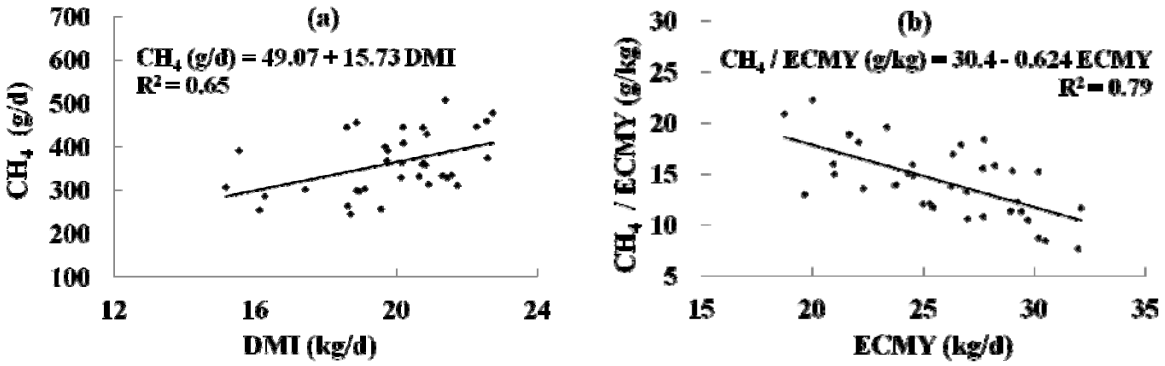

Figure 1 Relations of CH_4 emissions (g/d or per kg ECMY) with DMI (a) and ECMY (b) respectively

Conclusion The relationships in the current study may be used to predict CH_4 emissions from grazing animals in research (Eq. a) or farm (Eq. b) environment. The present study also highlights the importance of increasing milk yield per cow, at a given level of feeding, by genetic and feeding improvements, in order to reduce CH_4 emissions in pasture-based systems.

Acknowledgement This study was funded by the Department of Agriculture, Food and the Marine of Republic of Ireland.

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Methane (CH_4) outputs from grazing lactating beef cows of contrasting breed types on different pasture types

J A Rooke, C-A. Duthie, J Holland, T Waterhouse
SRUC, Scotland's Rural College, Edinburgh, UK
Email:john.rooke@sruc.ac.uk

Implications In national reporting of greenhouse gas emissions from lactating suckler cows, breed does not influence CH_4 emissions but daily CH_4 emissions were lower on rough grazing than on perennial ryegrass-based pasture.

Introduction Greenhouse gas emissions, primarily methane (CH_4), from suckler beef systems are higher than those from dairy beef because of CH_4 emissions associated with the breeding cow and the relatively low beef output per breeding female per year especially when the spring calving cow grazes on hill and upland pasture. However, these CH_4 emissions must be balanced against the conversion of grass into human-edible food of high biological value. An unknown contributor to emissions is the genotype of the cow. The hypothesis therefore to be tested was whether there were differences in CH_4 output between lactating beef cows of contrasting breed types grazed on two different pastures (hill and lowland).

Material and methods The experiment consisted of two measurement periods. Within each period, 28 lactating cows of equal numbers of two breed types (Limousin X Aberdeen Angus (LIMX) and purebred Luing (LUI)) were allocated to two sward types (reseeded predominantly perennial ryegrass (*lolium perenne*) pasture) (LOW) and rough hill grazing (semi-natural, acidic grassland, heath and rush pasture) (HILL) using a 2 x 2 factorial design. Thus a total of 56 cows (with calves) were used, balanced for parity and calving date across grazing treatment and measurement period. The two measurement periods were from 12 - 31 August (P1) and 9 - 27 September 2013 (P2), respectively. Cows and calves were weighed and cow body condition score recorded weekly. Sward height was also measured weekly (sward stick) and representative herbage samples obtained for chemical analysis. Methane production was measured using the SF6 technique. Permeation tubes containing SF6 were administered two weeks prior to any measurements. Samples were collected over two four-day periods in consecutive weeks of each period (8 samples per cow; days 8-12 and 15-19 of each period). From the 56 cows sampled, four or more of the 8 possible samples were obtained successfully for 40 cows and mean daily CH_4 emissions were calculated for these 40 cows and used in further analysis. Statistical analysis was carried out using general linear models within Genstat with the following fixed factors: the 2 x 2 arrangement of breed and grazing type and sampling period (August or September).

Results Mean cow live-weight (599 kg, SE 8.9) and body condition score (2.8, SE 0.04) did not differ between breeds, sward or period. Calf live-weights did not differ between breeds or sward but, as expected, calves in P2 were heavier than in P1 (199 vs. 156 kg, SED 7.5). Sward height was lower for LOW than HILL pasture ($P<0.05$; 8.4 vs 10.1 cm, SED, 0.78) but did not differ between periods. LOW pasture samples (Table 1) had higher crude protein (CP) and neutral cellulase digestibility (NCD) than HILL pasture. While there was little difference between P1 and P2 for LOW, sward CP and NCD decreased from P1 to P2 for HILL pasture. Methane production was 1.17-fold greater ($P<0.001$) from LOW than HILL pasture (Table 1) but there were no differences between either breeds or periods.

Table 1 Composition of herbage (g/kg dry matter) and methane production (g/day)

Sward	LOW		HILL		
Period	P1	P2	P1	P2	SED
Herbage					
CP	190	196	138	120	
NCD	722	743	661	563	
Methane					
LIMX	312	323	276	255	28.3
LUI	328	300	278	267	

Conclusion Methane emissions were influenced by sward type but not by breed of cattle. The lower CH_4 emissions from the HILL pasture probably resulted in part from lower dry matter intakes (DMI) and in part from lower forage digestibility as CH_4 adjusted for estimates of DMI (LOW, 1.11-fold HILL) and for both DMI and digestibility (LOW, 0.94-fold HILL) differed less between sward types than did total daily CH4 emissions.

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The effect of introduction of an unfamiliar individual on the social contact patterns of groups of cattle

L A Smith[1], D L Swain[2], G I Innocent[3], M R Hutchings[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]Cetral Queensland University, Rockhampton, QLD, Australia, [3]Biomathmatics & Statistics Scotland, Edinburgh, UK
Email:lesley.smith@sruc.ac.uk

Implications Agricultural mixing practices which introduce unfamiliar cattle into established groups may impact the welfare of new group members due to social isolation.

Introduction Cattle are gregarious animals that show a strong motivation for social interactions. However, the dynamics of a group are dependent on the individuals within that group, with changes in the composition representing social disruption of the group. Social stability in cattle following social disruption has previously been defined using aggressive interactions within the group, suggesting the effects of regrouping are restricted to a short period of 1-2 weeks (Boe *et al*. 2003). Here we determine the impact of social disruption on groups of cattle via the introduction on an unfamiliar individual, on the association patterns of the group. Specifically, we test the hypotheses: 1) Resident cattle will alter their patterns of association in response to social disruption; 2) The unfamiliar individual will show an increased pattern of associations with the established group members over time.

Material and methods The experimental timetable (a total of 18 days) was divided into 3 phases: Phase 1 (days 1-6), a period of 'social stability' with 6 groups of resident cattle pre-introduction of an unfamiliar individual; Phase 2a (days 7-12), a 6 day period post-introduction of an unfamiliar individual into each resident group; Phase 2b (days 13-18), a further 6 day period post-introduction of an unfamiliar individual into each resident group**.** Thirty 1yr old female Brahman cattle (*Bos indicus)* reared together since birth, were divided into 6 groups of 5 resident animals balanced for live weight. Six 1yr old female Brahman cattle were sourced from a separate herd to form the 'unfamiliar' individuals, which were allocated to a resident group, by balancing for live weight. Cattle contacts between all individuals in a group were continuously recorded using proximity data loggers (Sirtrack Ltd) which recorded the time, date and duration of all contacts. Cattle contact behaviour (frequency of contacts per cow per day; mean duration of contacts per cow per day; total duration of contacts per cow per day) was analysed by REML. To assess contact behaviour between residents during all three phases, phase (1, 2a or 2b) was included as the fixed effect and animal nested in group as the random effects. To assess contact between residents and the unfamiliar individual post-introduction, animal type (resident or unfamiliar), phase (2a and 2b only) and their interactions were included as fixed effects, animal nested in group was included as the random effects. Social network analysis (SNA) was carried out using UCINET, and social network diagrams visualised using NetDraw.

Results Post-introduction, resident cattle reduced the frequency of contacts with each other ($W = 227.79$, $df = 2$, $P < 0.001$) but increased the mean duration of those contacts ($W = 134.25$, $df = 2$, $P < 0.001$) relative to the pre-introduction phase. Post-introduction, unfamiliar individuals had a significantly lower frequency of contacts per day ($W = 65.17$, $df = 1$, $P < 0.001$), shorter mean durations of contacts per day ($W = 62.18$, $df = 1$, $P < 0.001$), and shorter total duration of contacts per day ($W = 74.25$, $df = 1$, $P < 0.001$) relative to resident cattle. Network diagrams for each group showed that the strength of contact between resident individuals and the unfamiliar individual is lower than the strength of associations between residents, and there is no increase the strength of associations with residents over phase 2a and 2b (Figure 1 shows network graphs for group 1).

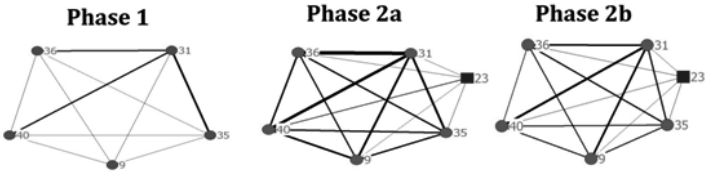

Figure 1 Social network graphs for group 1. Circles represent resident cattle; squares represent 'unfamiliar' cattle. Line thickness represents the strength of association between two individuals based on total duration spent in contact.

Conclusion Social disruption via introduction of an unfamiliar individual resulted in resident cattle spending longer bouts of time with close associates. However the contact patterns between residents and the unfamiliar individual suggests that the new individual is socially isolated from the rest of the group throughout the trial with no increase in contact pattern over time, thereby rejecting hypothesis 2. By considering animal contact patterns as a measure of social integration, this study indicated that the effects of regrouping on new group members may last for longer than previously thought.

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Vocalisations and their relationship with enrichment and welfare indicators in juvenile domestic pigs

M Friel[1], K Griffin[1], L Asher[3], N O'Connell[1], H Kunc[1], L Collins[2]
[1]Queens University Belfast, UK, [2]University of Lincoln, UK, [3]University of Nottingham, UK
Email:mfriel06@qub.ac.uk

Implications Pigs that received enrichment were more vocal during a novel object test than non-enriched pigs. Vocalisation rate in the novel object test was not related to injury score.

Introduction The vocalisations of animals can encode information about an individual's affective state, and vocalisations are increasingly being recognised as a promising indicator for animal welfare assessment. Environmental and cognitive enrichment have been shown to affect the welfare of domestic pigs. However little is known of how enrichment affects vocalisation behaviour in pigs. Here we investigated the effect of environmental and cognitive enrichment on individual vocalisation behaviour in a novel object test. The relationship between vocalisation behaviour and injury score was also investigated.

Material and methods As part of a larger experiment, five replicates of 72 commercial crossbreed (PIC 337 x (Large White x Landrace)) piglets were weaned at four weeks of age and housed in four groups of 18 where they were maintained until 10 weeks of age. Two groups per replicate were housed in barren pens which had partially slatted concrete floors with two wooden blocks hanging from the ceiling as standard enrichment. The other two groups per replicate were housed in enriched pens, which had solid floors with straw bedding replenished as required and three wooden blocks hanging from the ceiling. The enriched pens also had a greater space allowance per pig of $0.47m^2$ compared with $0.38m^2$ in the barren pens. All pigs were scored at 4, 6 and 9 weeks of age based on their level of injury to the body (from aggression) and to the tail (from harmful social behaviour). Selection for training and novel object testing was based on the individual's total injury score from ages 4 and 6 weeks. In each pen, the two pigs with the highest injury scores, the two pigs with the lowest injury scores, and two additional pigs chosen at random were selected. A total of 88 pigs, 44 barren and 44 enriched, were selected for the current experiment in this way from the five replicates (24 pigs from two replicates (total 48), 12 pigs from two replicates (total 24) and 16 pigs from the final replicate). Forty-eight of these pigs (24 barren and 24 enriched), received cognitive enrichment in the form of training to perform a cognitive bias task. Training was conducted over a maximum period of 15 days, in which each pig received 1-2 individual training sessions per day. Training sessions lasted for 5-10 minutes and were conducted in a separate room in the same building as the home pens were located. Individual vocalisation behaviour was recorded during a 5 minute novel object test which was conducted when the pigs were 8 weeks of age. To test how enrichment influences vocalisation rate we modelled vocalisation rate as function of Environmental enrichment (barren or enriched) and Cognitive enrichment (trained or non-trained) as fixed effects and Replicate as a random intercept, using linear mixed effects models. Spearman's rank correlation was used to investigate the relationship between vocalisation rate and lesion score. Results are presented with means ± SE.

Results Pigs from the enriched pens had a higher grunt rate in the novel object test than pigs from the barren environment (enriched: 19.6 grunts/min ± 1.44, barren: 16.6 grunts/min ± 1.80, $P < 0.05$). Pigs which received cognitive enrichment had a higher grunt rate in the novel object test than pigs which did not receive cognitive enrichment (trained: 20.7 grunts/min ± 1.43, non-trained: 12.6 grunts/min ± 1.53, $P < 0.001$). There was no significant correlation between grunt rate and lesion score ($r_s = 0.06$, $P > 0.05$).

Conclusion Pigs from the enriched environment and pigs that received cognitive training had higher vocalisation rates in the novel object test than non-enriched individuals. This finding suggests that enrichment does affect individual vocalisation behaviour, and pigs that have presumably higher welfare are more vocal. The reason for this may be related to lack of inhibition or fear in enriched animals and further research will be necessary to investigate this.

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Quantifying the response of aggressive behaviour in growing pigs to selection via skin lesion traits

S Desire[1], S P Turner[1], R B D'Eath[1], A B Doeschl-Wilson[2], C R G Lewis[3], R Roehe[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]Roslin Institute, Edinburgh, UK, [3]PIC, Nantwich, UK
Email:suzanne.desire@sruc.ac.uk

Implications This study quantified the potential for reducing aggressive behaviour in pigs via selection against lesions to the anterior of the body recorded 24h post-mixing, providing evidence that this trait could be used for selection purposes.

Introduction Efforts to reduce physical aggression induced by social mixing in pigs have been ongoing for several decades. Although a number of practical interventions have been explored, selective breeding may provide the most promising solution. Skin lesions resulting from physical aggression are a validated proxy measure of aggressive behaviour. While genetic correlations between skin lesion traits and certain aggressive behaviours have been shown, the response to selection in terms of reduced aggression has never been quantified. This study sought to quantify the potential behavioural response to selection via skin lesions, to determine whether significant improvements can be achieved.

Material and methods 78 new social groups were formed by mixing 15 single sex, single breed growing pigs. Skin lesion numbers were recorded for each body region (anterior, central, posterior) 24 h post-mixing (**SL24h**), and 3 wk post-mixing (**SL3wk**). Behavioural traits were defined based on the duration, intensity and outcome of aggressive interactions performed in the first 24h post-mixing. Univariate analyses were used to estimate breeding values for skin lesion and aggressive behavioural traits using the following animal model: $\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wc} + \mathbf{e}$ where the incidence matrices **X**, **Z** and **W** relate phenotypic records contained in vector **y** to fixed (**b**), additive genetic (**a**), and common environmental (pen group) (**c**) effects. Vector **e** represents residual error. Genetic line, sex, and week in which the animals were mixed were included as fixed effects for all traits, while age at time of mixing was included for SL24h and behavioural traits. EBV and phenotypic values for all traits were scaled and standardised (SD), and individuals with either: 1) EBV in the lowest 10 percent for SL24h (separately for the 3 body regions), or 2) the highest 10 percent for SL3wk were selected. These criteria target selection for low aggressive behaviour at mixing and were chosen based on previous evidence that SL24h are positively correlated with duration of reciprocal aggression at mixing (0.14 [0.06] to 0.67 [0.05]), while SL3wk are negatively correlated with reciprocal aggression at mixing (-0.30 [0.07] to -0.38 [0.05]) (Turner *et al*, 2009). Following this simulated single trait selection, the change in mean breeding and phenotypic value for each trait was compared to the mean of the population as a whole.

Results Of the 3 SL24h traits, selection against anterior lesions is expected to have the greatest effect on aggressive behaviour. Selecting individuals based on EBV for anterior SL24h is expected to genetically reduce all aggressive behavioural traits over a single generation by 0.21 SD (SE 0.10) to 1.17 SD (SE 0.09). On a phenotypic level, mean values of aggressive behaviour were reduced by 0.24 SD (SE 0.06) to 0.74 SD (0.07), with the greatest response observed for the number of pigs an individual received a reciprocal attack from. This can be quantified as a reduction of 0.71 attacks per pig, from an initial population mean of 2.86 (SD 2.32). With the exception of the duration of non-reciprocal aggression received, selection for increased SL3wk is also expected to result in a mean decrease in aggressive behaviour at mixing. Selection for anterior or central SL3wk had the greatest effect, reducing mean EBV for all behavioural traits by 0.30 SD (SE 0.09) to 0.54 SD (SE 0.10). Phenotypically, selection for increased anterior or central SL3wk is expected to reduce mixing aggression levels by 0.19 SD (SE 0.07) to 0.40 SD (SE 0.07), with the greatest response for the total number of reciprocal fights an animal was involved in. This translates to a reduction of 2.39 reciprocal fights, from an initial mean of 8.43 (SD 7.16).

Conclusion The results suggest that single trait selection against anterior SL24h or selection for anterior or central SL3wk would reduce aggression observed at mixing both on a genetic and phenotypic level. Stable lesions have higher heritabilities, and from a practical perspective, counting lesions at this time point is less time consuming, as there are fewer lesions and the animals are generally less active. However, at the present time there is very little research on the relationship between SL3wk and short and long term aggressive behaviour. In contrast, the relationship between anterior SL24h and aggressive behaviour is very well understood. Based on the current knowledge it can be concluded that anterior SL24h would be the preferable selection trait to utilise, with high potential to significantly reduce levels of aggression observed in the first 24 hours post mixing. Additional work would be required to understand the response to selection within a multi-trait situation, as well as the viability of selection, with respect to genetic associations with other production traits, such as production efficiency. Significant work is required to calculate a meaningful marginal economic value to apply to this trait.

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Evaluating environmental enrichment options for commercial broiler chickens

C L Bailie, N E O'Connell
Institute for Global Food Security, Queen's University Belfast, UK
Email:niamh.oconnell@qub.ac.uk

Implications Provision of environmental enrichment in line with that required by welfare-based quality assurance schemes does not always appear to lead to clear improvements in broiler chicken welfare. This research perhaps serves to highlight the deficit in information regarding the 'real world' implications of enrichment with perches, string and straw bales.

Introduction Earlier work showed that provision of natural light and straw bales improved leg health in commercial broiler chickens (Bailie *et al*., 2013). This research aimed to determine if additional welfare benefits were shown in windowed houses by increasing straw bale provision (Study 1), or by providing perches and string in addition to straw bales (Study 2).

Material and methods Commercial windowed houses in Northern Ireland containing ~23,000 broiler chickens (placed in houses as hatched) were used in this research which took place in 2011. In Study 1 two houses on a single farm were assigned to one of two treatments: (1) 30 straw bales per house (1 bale/44m^2), or (2) 45 straw bales per house (1 bale/29m^2). Bales of wheat straw, each measuring 80cm x 40cm x 40cm were provided from day 10 of the rearing cycle, as in Bailie *et al*. (2013). Treatments were replicated over 6 production cycles (using 276,000 Ross 308 and Cobb birds), and were swapped between houses in each replicate. In Study 2, four houses on a single farm were assigned to 1 of 4 treatments in a 2 x 2 factorial design. Treatments involved 2 levels of access to perches (present (24/house), or absent), and 2 levels of access to string (present (24/house), or absent), and both types of enrichment were provided from the start of the cycle. Each perch consisted of a horizontal, wooden beam (300 cm x 5 cm x 5cm) with a rounded upper edge resting on 2 supports (15 cm high). In the string treatment, 6 pieces of white nylon string (60 cm x 10 mm) were tied at their mid-point to the wire above each of 4 feeder lines. Thirty straw bales were also provided per house from day 10. This study was replicated over 4 production cycles using 368,000 Ross 308 birds. In both studies behaviour was observed between 0900 and 1800 hours in weeks 3-5 of the cycle. In Study 1, 8 focal birds were selected in each house each week, and general activity, exploratory and social behaviours recorded directly for 10 minutes. In Study 2, 10 minute video recordings were made of 6 different areas (that did not contain enrichment) of each house each week. The percentage of birds engaged in locomotion or standing was determined through scan sampling these recordings at 120 second intervals. Four perches and four pieces of string were filmed for 25 mins in each house that contained these enrichments on one day per week. The total number of times the perch or string was used was recorded, along with the duration of each bout. In both studies, gait scores (0 (perfect) to 5 (unable to walk)) and latency to lie (measured in seconds from when a bird had been encouraged to stand) were recorded in 25 birds in each house each week. Farm and abattoir records were also used in both studies to determine the number of birds culled for leg and other problems, mortality levels, slaughter weights, and levels of podo dermatitis and hock burn. Data were analysed using SPSS (version 20.0) and treatment and age effects on behavioural parameters were determined in normally distributed data using ANOVA ('Straw bale density*week', or 'string*perches*week' as appropriate), and in non-normally distributed data using Kuskall-Wallace tests ($P<0.05$ for significance) . Treatment (but not age) effects on performance and health data were determined using the same tests depending on normality of data.

Results Average slaughter weight, and levels of mortality, culling, hock burn and pododermatitis were not affected by treatment in either study ($P<0.05$). In Study 1 straw bale (SB) density had no significant effect on the frequency or duration of behaviours including standing, walking, ground pecking, dust bathing, pecking at bales or aggression, or on average gait score ($P>0.05$). However, the average latency to lie was greater when fewer SB were provided (30SB 23.38s, 45SB 18.62s, $P<0.01$). In Study 2 there was an interaction between perches (Pe) and age in lying behaviour, with higher percentages of birds observed lying in the Pe treatment during weeks 4 and 5 (week 3 +Pe 77.0 -Pe 80.9, week 4 +Pe 79.5 -Pe 75.2, week 5 +Pe 78.4 -Pe 76.2, $P<0.02$). There was also a significant interaction between string (S) and age in locomotory behaviour, with higher percentages of birds observed in locomotion in the string treatment during week 3 but not weeks 4 and 5 (week 3 +S 4.9 -S 3.9, week 4 +S 3.3 -S 3.7, week 5 +S 2.6 -S 2.8, $P<0.04$). There was also an interaction between S and age in average gait scores, with lower gait scores in the string treatment in weeks 3 and 5 (week 3: +S 0.7, -S 0.9, week 4: +S 1.5, -S 1.4, week 5: +S 1.9, -S 2.0, $P<0.05$). On average per 25 min observation there were 15.1 (±13.6) bouts of perching and 19.2 (±14.08) bouts of string pecking, lasting 117.4 (±92.7) and 4.2 (±2.0) s for perches and string, respectively.

Conclusion Increasing straw bale levels from 1 bale/44m^2 to 1 bale/29m^2 floor space does not appear to lead to significant improvements in the welfare of broilers in windowed houses. The frequent use of perches and string suggests that these stimuli have the potential to improve welfare. Provision of string also appeared to positively influence walking ability. However, this effect was numerically small, was only shown in certain weeks and was not reflected in the latency to lie. Further research on optimum design and level of provision of enrichment items for broiler chickens is warranted. This should include measures of overall levels of activity (both in the vicinity of, and away from, enrichment items).

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Methodology and analysis of drinking behaviour traits in turkeys

J Rusakovica[1], V Kremer[2], S Avendaño[2], I Kyriazakis[1]
[1]Newcastle University, Newcastle upon Tyne, Tyne and Wear, UK, [2]Aviagen Turkeys, Tattenhall, UK
Email:julija.rusakovica@ncl.ac.uk

Implications Drinking behaviour analysis can assist in the identification of different behavioural strategies associated with water intake and potentially breeding of birds with favourable drinking behaviour traits.

Introduction Drinking visits are episodic behavioural events occurring as separate stopovers to drinkers, which can vary between days. A bout is a number of such drinking visits clustered together. Analysis of bouts can identify common patterns of organisation in time. The latter requires identification of a bout criterion. This is the longest interval of time accepted to be within a bout, and may potentially be used to identify different strategies that birds utilise and the biological mechanisms associated with drinking behaviour. The aim of this study was to develop a methodology for the analysis of drinking behaviour in turkeys from two genetic lines and estimate drinking behaviour characteristics for each line.

Material and methods Records of visits to water stations were obtained for two turkey genetic lines (a) line A from 4627 turkeys from 6-9 weeks of age (n = 954,777 events) and (b) line B from 2351 turkeys from 10-13 weeks of age (n = 770,984 events). Birds from line A were from a male line, selected with an emphasis on feed efficiency and breast meat yield, whereas line B represented a female line, with an emphasis on reproductive performance, feed efficiency and growth. Both lines are selected for leg health and fitness traits. An electronic water station system using transponder-based data capture was used to record bird individual drinking behaviour. Video recording experiments were set up to correlate water intake records and bird drinking behaviour. Probability mixture models (PMM) used in feeding behaviour analysis by Howie *et al.* (2009) were adapted and fitted to the natural log transformed interval length between drinking visits.

Results Video observation suggested that some of the visits recorded by the automated system included very short intervals between these visits, which were the result of bird movement inside the water station. During these short intervals of less than 4 seconds, birds did not leave the drinker. Therefore, these visits were joined together into one bout. The best fit PMM was a truncated log normal distribution for within bout intervals and a log normal distribution for between bout intervals (Figure 1). The bout criterion was estimated where the two distributions crossed and resulted in significantly different estimates for the two genetic lines (Table 1). The probability of a bird visiting a drinker in the next five minutes after the last visit showed different starting probabilities for day and night visits for both genetic lines, implying different drinking behaviour organisation during the light and dark periods of the day (Figure 2).

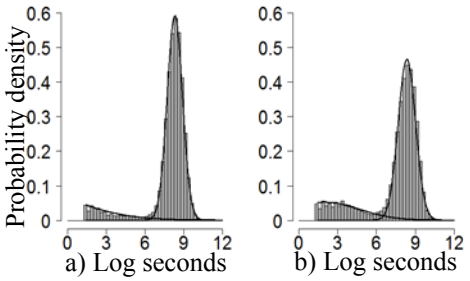

Figure 1 Fitted model for (a) genetic line A and (b) genetic line B.

Table 1 Mean (± standard error) of turkey drinking behaviour characteristics

	Genetic line A	Genetic line B
Bout criterion (s)	665	692
Bouts per day	10.45±0.113	9.92±0.116
Water per bout (ml)	73.26±0.044	76.63±0.058
N of visits per bout	1.11±0.001	1.21±0.001
Bout duration (s)	93.02±0.227	71.67±0.356

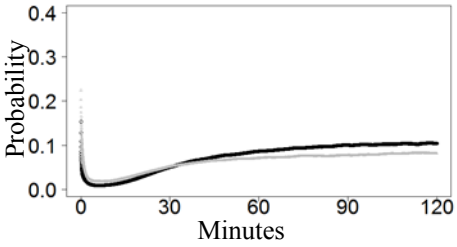

Figure 2 Starting probabilities for genetic line A (black line) and genetic line B (grey line) for the hours of light during the day.

Conclusion A method to describe drinking behaviour in turkeys was developed; the method is consistent with the biological principles of satiety. Birds from line A showed less frequent and longer visits to the water station, whereas line B showed more variation in the length of intervals between visits. The definition of these drinking behaviour characteristics, while accounting for differences in the age of the birds, can form the foundation for estimating the genetic basis of drinking behaviour in turkeys.

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The effect of routine abattoir processes on the visibility of welfare-related lesions on pig carcasses

G A Carroll[1], L A Boyle[2], D Teixeira[2], N van Staaveren[2], A Hanlon[3], N E O'Connell[1]
[1]Institute for Global Food Security, Queens University Belfast, Northern Ireland Technology Centre, 18-30 Malone Road, Belfast, BT9 5BN, UK, [2]Teagasc Pig Development Department, Animal and Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork, Ireland, [3]School of Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland
Email:gcarroll05@qub.ac.uk

Implications The increased visibility of key welfare-related lesions following scalding and dehairing of carcasses should be considered when developing abattoir-based welfare assessment schemes.

Introduction There is increasing interest in developing abattoir-based farm animal welfare measures. In addition to avoiding biosecurity issues associated with entering farms, it also avoids problems with assessing animals in crowded or poorly-lit conditions. It is important to determine the most appropriate place on the slaughter line to conduct these assessments. Routine processes such as scalding and dehairing of carcasses may either mask or unveil different types of lesions. This study aimed to determine if the visibility of different types of welfare lesions (aggression-related skin injury, tail biting injury and loin bruising) was affected by these routine processes. The study also lent itself to an assessment of the prevalence of these lesions, and the extent to which they were linked to gender and production parameters.

Material and methods Slaughter pigs processed at two abattoirs on the Island of Ireland (n = 1950 and 1939) were used. Data were collected over 6 days in each abattoir in July 2014, with an average of 400 pigs being assessed per abattoir per day. This involved assessing every second or fourth pig on the line depending on abattoir line speed. Lesion scoring took place at two points on the slaughter line: (1) at exsanguination (Slaughter Stage 1 [SS1]), and (2) following scalding and dehairing of the carcass (Slaughter Stage 2 [SS2]). Each pig was given an ink tattoo at SS1 to ensure that it was identifiable at SS2. At both observation points each whole carcass, divided into the front (everything above the loin) and the rear (the loin and everything below it excluding the tail), was assigned a skin lesion score of between 0 and 3 (0-no damage or a little superficial damage, 1-some superficial damage, clearly marked or up to three short (2-3cm) and deep injuries, 2-clear deep and or long damage (>3cm) including much superficial damage or circular areas, 3-much deep damage). The highest score of the two regions was recorded as the skin lesion score. Tails were also assigned a lesion score of between 0 and 4 (0-no evidence of tail biting, 1-healed or mild lesions, 2-evidence of chewing or puncture wounds but no evidence of swelling, 3-evidence of chewing or puncture wounds with swelling and signs of possible infection, 4-partial or total loss of the tail). Loin bruising was recorded as present when there were distinct circular bruises on the loin area, otherwise it was recorded as absent. Inter-rater reliability in lesion scoring was tested prior to data collection and good levels of agreement (>0.80) were reached. Observers also alternated between SS1 and SS2 on a daily basis. Abattoir records were used to obtain information on carcass weight (CW) and condemnation. Data were analysed using SPSS (version 20.0). Effects of observation point (SS1 or SS2) on lesion prevalence were determined using McNemar or McNemar-Bowker tests (depending on number of lesion categories) and gender effects were determined using Kruskal-Wallace tests. Individual animal was the experimental unit. Associations between welfare lesions and CW and condemnations were examined through Pearson's correlations using average values per batch of pigs submitted by a farm on a given day.

Results The percentage of pigs with a visible skin lesion (i.e. score > 0) decreased between SS1 and SS2 (54.3 vs 51.7%, SEM 0.012%, P<0.001). This decrease occurred with mild (score 1) and moderate (score 2) skin lesions, but not with severe lesions (score 3; Table 1). A greater percentage of pigs were recorded with tail lesions (i.e. score >0) at SS2 (30.8 %) than SS1 (14.7%); SEM 0.013%, P<0.001). This effect was independent of tail lesion scores (Table 1). More loin bruising was also recorded at SS2 (26.0%) than at SS1 (1.9%; SEM 0.007%, P<0.001).

Table 1 Percentage of pigs with different categories of injuries at slaughter stages 1 and 2 (SS1 and SS2)

	Mild		Moderate		Severe	
	SS1	SS2	SS1	SS2	SS1	SS2
Skin lesions	39.3	37	14.4	13.7	0.6	2.1
Tail lesions	11.9	27.3	1.4	1.9	1.5	1.6

Skin and tail lesions were more prevalent in males (M) than females (F) (SS2 values presented) (skin lesions: M 54.7%, F 51.1%, SEM 0.013%; P<0.05; tail lesions: M 33.8%, F 26.1%, SEM 0.012%; P<0.05), but there was no gender difference in loin bruising (P >0.05). Partial condemnations were correlated (P<0.001) with frequency of skin lesions (r = .358), tail lesions (r = .413), and loin bruising (r = .49). Whole carcass associations were not significant (P>0.05). Average CW was correlated (P<0.001) with frequency of skin lesions (r =. -.667), tail lesions (r =. -.615), and loin bruising (r = -.739).

Conclusion Scalding and dehairing of pig carcasses appears to improve the visibility of tail lesions and loin bruising, and also of severe skin lesions. The results also suggest that there would be both welfare and economic advantages to reducing levels of harmful social and aggressive behaviour in pigs.

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Using cognitive bias as an assessment of rabbit welfare: exploring the effectiveness of initial training

L Brooke, C Douglas
Newcastle University, Newcastle upon Tyne, UK *Email:catherine.douglas@ncl.ac.uk*

Implications These findings may help those working on cognitive bias (CB) or any rabbit training task to devise more effective tests. If successful, tests of CB could form additional assessments of rabbit wellbeing to help improve the conditions in which they are kept, improving their welfare as a laboratory specie, both in their status as pets and, importantly, as farmed animals as "more rabbits [are] farmed for meat in the EU than any other species, except meat chickens, and the vast majority of those rabbits (around 99%) are kept in barren cages all their lives",CIWF, 2014).

Introduction Cognitive bias (often described as whether a person would describe their glass as "half full or half empty") is used in human psychology to assess an individual's optimism or pessimism (or positive or negative affective state). For example a person who is anxious or depressed is more likely to make a negative judgement about an otherwise ambiguous stimulus than someone who is optimistic, who is more likely to interpret the same stimulus as positive (Harding *et al*, 2004). Whilst this is an established categorisation in human psychology, this is relatively new for assessing an animal's affective state, and thus, by extension, its welfare. Tests of cognitive bias have been used in starlings, rats, dogs, sheep and pigs as a way of assessing how an animal's environment effects its affective state; to date there are no published studies on cognitive bias in rabbits. We proposed a methodology based on Douglas *et al*'s (2012) study with pigs. The intention was to assess differences in cognitive bias between rabbits housed in a rescue shelter and pet rabbits. This paper reports on the first training stage of the methodology and possible future refinements.

Material and methods Twelve rabbits (n=7 rescue shelter, n=5 pet rabbits) of various ages, breeds and sexes underwent an initial choice test to determine their preferred food reward. Rabbits were individually placed in a hexagonal wire run "test arena" (0.94m2) and were allowed a 5 minute familiarisation (each corner numbered sequentially 1-6). The rabbit was held gently at the starting point (1), the box containing a carrot food reward was introduced at location 3 or 5 (left or right, randomly assigned to avoid any side bias); the rabbit was able to see the carrot and lettuce in the entrance to the box. The rabbit was released and the time it took to approach the box and put its head in was recorded (max 180sec allowed). The rabbit was allowed a 1 minute time out in its home pen, before being returned to repeat the test for 10 tests per training session (only 1 familiarisation session). If the rabbit was approaching in less than 180 seconds for 8 of 10 tests, it progressed to the next stage. This was a repeat of the above, however the food reward was not visible but inside the box. If the rabbit approached in less than 180 seconds for 8 out of the 10 trials, it was considered trained to associate the box with a positive outcome and would progress to the next stage introducing the non-rewarded location. Statistical analysis was ANOVA and Pearson correlation using Minitab.

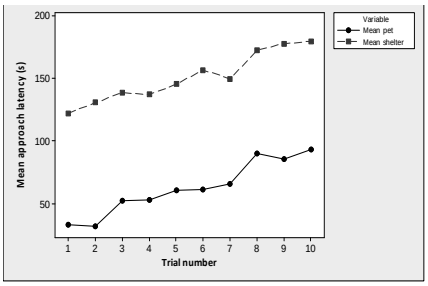

Figure 1 Mean latency to approach box for pet and shelter rabbits 1st training (food visible)

Results Shelter rabbits took longer to approach the box than pet rabbits (152sec $\pm$ 22; 63 $\pm$ 20 $p<0.001$). Figure 1 shows rabbits' increasing latency to approach the box as the tests continued (pet: $r=0.967$, $p<0.001$; shelter: $r=0.970$, $p<0.001$),. Amalgamated data found a marked increase after trial 4. This is also seen in Figure 2 in the pet rabbits who progressed to the second phase of training (n=4).

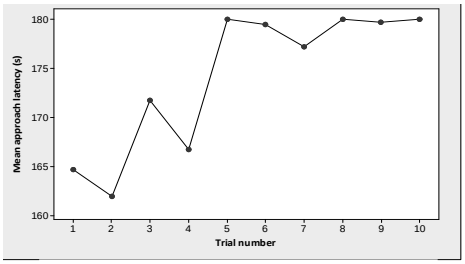

Figure 2 Mean latency to approach box for pet rabbits in the second training (food not visible)

Conclusion and Comments The data from this small pilot generated a number of refinements and hypotheses requiring further validation: A higher value treat was needed (e.g dandelion); the familiarisation period should include the box in the rewarded location; Rabbits may be susceptible to training providing training sessions involve no more than 4 trials (or we propose last no longer than 6 minutes each session); a novel arena could confound approach data so future studies should be conducted in a rabbit's home pen; a neutral or familiar experimenter should be used with both groups studied to avoid bias; we propose that a novel object test in an open arena may give a spontaneous indication of cognitive bias without the need for training and complicated protocols, demonstrated through the difference in approach latency of the rescue vs pet rabbits. However this needs to be validated through initial observations compared to data having run the full protocol.

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The relationship between water intake and oestrus behaviour in dairy cows

G Barrenho, M G G Chagunda, M D March, D J Roberts
SRUC, Scotland's Rural College, Edinburgh, UK
Email:mizeck.chagunda@sruc.ac.uk

Implications Individual cow water intake pattern has the potential to be used as an indicator of oestrus behaviour in dairy cows.

Introduction Water is necessary for life processes such as, digestion, nutrient transportation and metabolism, hydro-electrolytic balance, heat and residue elimination, and foetal development. Although there have been numerous studies on the influence of environmental and physiological factors such as: temperature, humidity, feed quality, dry matter intake, milk production, stage of lactation and diseases (Meyer, *et al*, 2004), studies quantifying the relationship between water intake and reproductive behaviour are relatively sparse. Electronic pedometers or activity tags use changes in behaviour to detect oestrus in dairy cows and heifers (Løvendahl and Chagunda, 2010). Restlessness and general physical activity increase markedly during oestrus (Van Eerdenburg *et al*., 1996). The aim of this study was to determine the relationship between water intake and oestrus behaviour in dairy cows.

Material and methods Data were obtained from SRUC Dairy Research and Innovation Centre for the period between 1st November 2013 and 23rd January 2014. During this period maximum average temperature was 8.58 °C and a minimum 3.03 °C, the highest temperature was 13.8 °C and the lowest -2.7 °C. Animals were in two sub-groups of 100 cows with different rations (home-grown and by-products). Within each of the two feeding groups cows were of either Select or Control genetic merit and hence giving rise to four systems namely, by-product x control (BPC), by-products x select (BPS), home-grown x control (HGC) and home-grown x select (HGS). Individual cow feed and water intake was measured using Hoko system (Insentec BV Marknesse, The Netherlands). Total water consumption was determined as a sum of water intake and feed water content. kg. All cows had leg mounted activity meters. Only animals with observed oestrus were included in the analysis and hence 139 oestrus periods from 60 cows were used. To determine the effect of days to oestrus on both water intake and cow activity analysis of variance was applied. The fixed factors included in the univariate mixed model were days to oestrus, production system, and parity. Random variables were cow, live weight, milk yield, age and dry matter intake. Linear regression was used to determine the relationship between water intake and cow activity.

Results Animals weighed an average of 579±69.4. Average daily total water intake for BPC, BPS, HGC and HGS was 98.64±21.9; 113.39±26.4; 82.20±18.0; and 91.96±19.2 kg/cow respectively. Dry matter intake (DMI) was BPC = 21.2±4.9, BPS = 23.3±5.0, HGC = 16.8±3.1, and HGS = 18.1±3.3kg and milk yield for the same systems was, 28.74±9.0; 33.65±9.5; 24.20±7.2; and 26.50±6.0 kg/day. Total water requirement per litre of milk produced was 3.43 kg/day for BPC, 3.37 kg/day for BPS, and the groups HGC and HGS required 3.40 and 3.47 kg/day. A productive cow weighting approximately 600 kg needs 60-70 kg of water intake for its maintenance. During oestrus, water intake decreased ($p<0.05$) while activity increased ($p<0.001$). A relationship between water intake and DMI of 5 kg water/kg DMI was found. Water intake and cow activity had a strong relationship ($p<0.001$), specially around oestrus (Fig. 1).

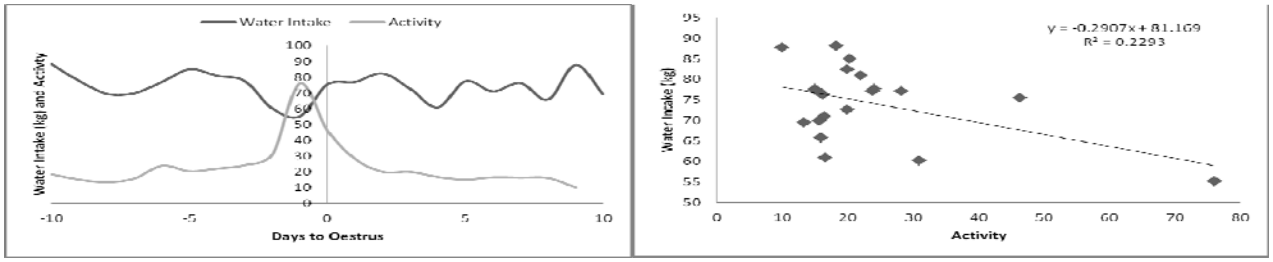

Figure 1 Profiles of water intake(kg) and animal activity (arbitrary units) relative to oestrus periods and the relationship between water intake and activity.

Conclusion Water is extremely important nutritionally and physiologically, so its consumption control can affect many food decisions and management. Water intake was strongly related to oestrus behaviour meaning that water intake would be a potential indicator of oestrus behaviour.

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The effect of social contact on weaning distress in dairy calves

S L Bolt[1], N K Boyland[2], J M Gibbons[1], D P Croft[2]
[1]AHDB, DairyCo Division, Stoneleigh Park, Kenilworth, Warwickshire, CV8 2TL., UK, [2]Centre for Research in Animal Behaviour, College of Life and Environmental Sciences, University of Exeter, Perry Road, Exeter, Devon, EX4 4QG, UK
Email:sarah.bolt@dairyco.ahdb.org.uk

Implications Pair housing calves from 5 days of age can facilitate social support to reduce stress at weaning.

Introduction In the UK dairy calves are separated from their dam almost immediately, however subsequent rearing practices vary. Around 60% of calves are individually reared (Marcé, *et al*., 2010), in an attempt to reduce the risk of disease transmission (Bach *et al*., 2011). One of the potential benefits of social contact is that it can increase social support, promoting wellbeing. Færevik *et al*., (2006) reported reduced distress in calves separated with a familiar calf compared with an unfamiliar calf or as a lone calf. De Paula Vieira *et al*., (2010) showed that social support can buffer the stress of weaning. This study compared the effects of rearing calves individually or in pairs with different contact durations on health, production and stress at weaning on a commercial dairy farm.

Material and methods Forty female Holstein-Friesian calves were randomly allocated at birth to one of three treatments: individual housing (IH) (n = 8), calves pair-housed from day 5 (P5) (n = 8 pairs), and calves pair-housed from day 28 (P28) (n = 8 pairs). All calves were stocked at a density of 2.59m^2 per calf. From day 48 these bucket-fed calves were weaned by a gradual reduction of milk over three days. Vocalisations were recorded as a behavioural response to stress, for one hour following milk feeding time, during the 3 days pre-weaning, during weaning and the first 3 days post-weaning. Daily data were collected on health (faecal and respiratory score) and feed intake from d5-55, and calves were weighed on d0 and d55. Data for pair-reared calves were averaged to give one value per pen. Treatment means were analysed using one-way ANOVA for feed intake and specific growth rates. Data from health scores were analysed using MANOVA. For analysing data over the weaning period, means were calculated for days 45-47, 48-50 and 51-53. Kruskal-Wallis tests were used to investigate the effect of treatment. Where treatment was found to have a significant effect, post-hoc Mann-Whitney tests were used to further explore the data. Where multiple tests were carried out on one dataset, false discovery rate adjusted p-values were calculated. These were quoted as a q-value using the two-stage sharpened method (Pike, 2011).

Results Treatment did not have a significant effect on health (faecal score and respiratory score) or production (feed intake and specific growth rate) as shown in Table 1. There was a significant effect of treatment on vocalisations during weaning ($p=0.008$) and post weaning ($p<0.001$). Individually reared calves vocalised four times more than P5 calves during the post-weaning period ($U = 2.0$, $q = 0.001$) and over twice as much as P28 calves ($U = 7.00$, $q = 0.007$). Moreover, during this period the P28 calves vocalised more than P5 calves ($U = 17.50$, $q = 0.048$).

Table 1 Treatment effects on production, health, and vocalisations **(**mean (±SD))

	IH	P28	P5	p value
Concentrate intake d5-55 (g/calf/d)	425.17 (±192.63)	380.61 (±123.11)	536.55 (±175.29)	n.s.
Specific Growth rate d0-55 (%)	1.12 (±0.14)	1.04 (±0.13)	1.04(±0.16)	n.s.
Respiratory score* (prop. of days above score 0)	4.57 (±6.50)	5.50 (±4.17)	4.86 (±2.10)	n.s.
Faecal score* (prop. of days above score 0)	12.72 (±8.47)	11.37 (±10.19)	8.46 (±6.06)	
Pre-weaning Vocalisations (no. /1h / calf)	0.86 ±1.72	0.10 ±0.13	0.10 ±0.9	n.s.
Weaning Vocalisations (no. /1h / calf)	2.76 ± 1.14	0.46 ±0.16	0.73 ± 0.21	0.008
Post-weaning Vocalisations (no. /1h / calf)	109.38 ±51.40	45.42 ±26.77	26.08 ±20.16	<0.001

*Wisconsin-Madison Calf Health Scoring Criteria: Faecal score; Respiratory score = sum of nasal, cough, eye and ear scores.

Conclusion Pair housing calves at 5 days after birth reduced the stress response to weaning. The duration of time calves have to socialise determines the degree of social buffering to stressors (weaning in this case). Inhibiting full social contact may leave calves less able to cope with stressful situations (such as weaning or re-grouping). This study showed that contrary to popular belief within the industry calves can be pair-reared without detriment to health or production.

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The effect of early life nutrition on future rumen function

C J Newbold[1], K Waddams[1], L Abecia[2], A Belanche[1], D R Yáñez-Ruiz[2]
[1]IBERS, Aberystwyth University, Aberystwyth, Wales, UK, [2]Estación Experimental del Zaidín (CSIC), Granada, Spain
Email:cjn@aber.ac.uk

Implications Dietary additions or manipulation in the period from birth to weaning have the potential to alter rumen function in adult sheep in later life.

Introduction Microbial fermentation in the rumen plays a central role in the ability of ruminants to utilize fibrous substrates, however rumen fermentation also has potential deleterious environmental consequences as it ultimately leads to the emission of greenhouse gases and breakdown of dietary protein leading to excessive N excretion in faces and urine. Given the importance of the rumen fermentation, it is perhaps not surprising that a great deal of effort has been devoted to investigating methods for manipulating this complex ecosystem. However, practical implementation of many dietary approaches to rumen manipulation been limited by factors related to cost and the difficulty off supplementing grazing animals. Here we report on the possibility that dietary manipulation and/or dietary additives applied during the period between birth and weaning might programme the rumen in later life

Results During rumen development, in young ruminants, ingested microbes colonise and establish in a defined and progressive sequence (Hobson and Stewart, 1997). Methanogenic archaea and cellulolytic bacteria have been found in the undeveloped rumen of lambs well before the ingestion of solid feed begins (2-4 days) and reach levels similar to those in adult animals around 10 days after birth (Fonty *et al*., 1987). Human based studies have shown that the microbial population within the gut is remarkably stable throughout adult life (Faith *et al*., 2013). Thompson *et al* (2008) suggested that the gut environment during postnatal development had a long-term impact on gut community structure, whilst Kerr *et al*., 2014 suggested **t**hat the effects of early life events on the gut microflora, are fundamental in shaping the microbial consortia in the gut throughout life.

We have reported that a simple nutritional regime (forage vs. concentrate) applied early in life of lambs modified the bacterial population colonizing the rumen and that the effect persists over 4 months (Yáñez-Ruiz *et al*., 2010). Waddams *et al*. (unpublished) have shown that treating lambs with chloroform (a potent inhibitor of methanogensis) from birth up until weaning had significant effects on methane production and rumen function 4 months after the chloroform treatment stopped and there were still indications of altered rumen function 12 months after the treatment ceased. Abecia *et al* (2014) working with goats found that treating kids and their does with bromochloromethane during the weaning period modified the archaeal community composition colonizing the rumen and although not all the effects persisted after weaning some less abundant archaeal groups remained different in treated and control 4 months after the treatment stopped.

Conclusion Clearly there is a need for more research in this area but if the concept that additives used in early life can affect rumen function in adult life can be confirmed then it will fundamentally change our approach to rumen manipulation.

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A determination of sample number requirements for nutritional analyses in sheep

N R Kendall[1], L A Stubbings[2], K D Sinclair[1]
[1]University of Nottingham, Sutton Bonington Campus, Loughborough, UK, [2]LSSC Ltd, Kettering, UK
Email:nigel.kendall@nottingham.ac.uk

Implications Sample numbers required to indicate a nutritional problem diagnostically in a group of sheep is 4.

Introduction An EBLEX workshop on Trace Elements in Sheep in 2012 highlighted the lack of definitive guidance on the number of samples required to diagnose mineral imbalances on farm. As part of an EBLEX funded project on "Validation of key efficiency measures and targeted monitoring to optimise sheep nutrition, farm performance and profitability" blood samples were taken from multiple groups at multiple times throughout the year. This dataset gave the opportunity to develop some guidance with statistical backing.

Material and methods Blood samples (n=358) were collected from sheep on 3 farms on at least 5 occasions per farm per year over a period of 12 months. Samples were taken from random sheep at each occasion from multiple management groups per farm to gain a whole farm picture of nutritional status. Samples were analysed for indicators of trace element status (erythrocyte glutathione peroxidase, serum vitamin B12, plasma selenium, cobalt, zinc, copper and selenium concentrations, serum caeruloplasmin activity, erythrocyte superoxide dismutase activity), energy status (serum Non-esterified fatty acid, Beta hydroxybutyrate and urea concentrations), liver enzymes (GGT, AST, GLDH, Tbil), basic haematology parameters (HCT, HGB, RBC) and serum total protein, albumin and globulin (by difference) concentrations. These analyses used established routine methods of the NUVetNA laboratory (School of Veterinary Medicine and Science, University of Nottingham) with the exception of serum vitamin B12 which was analysed by AHVLA using the routine commercial methodology. Data were grouped into individual management groups, according to sampling date, field, any different known dietary/supplemental treatments and sheep type (eg ewe, ram, lamb). Data were analysed using a General Linear Model (GLM, MINITAB16) using group as the model to determine the error variance of the dataset (ie the error not accountable to the grouping of the animals). Residual values were check and non-normal parameters had data log transformed to approximate normality. The square root of the error variance was used for power calculations using a one-sample t-test to determine sample size for powers of 0.8, 0.9, 0.95 and 0.99 for effect probabilities of $P<0.2$, $P<0.1$ and $P<0.05$.

Results There was huge variation between management groups, some of which reflected different types of sheep (ewes v lambs) and some the differing underlying mineral profile of fields. For example, we found that on two of the farms permanent pasture had significantly lower concentrations of selenium and cobalt than did the shorter term leys. This meant that sampling random animals on farm would be unlikely to give a full picture of the trace element profile for that farm, and implies that a targeted approach is needed, looking at individual management groups across the farm. Working with management groups and using a probability of $P<0.2$ to give a diagnostic indication, it was determined that 4 samples per management group are the minimum required. For analytical parameters which followed a normal distribution (eg plasma selenium) a target above (or below) threshold could be calculated for any diagnostic indicator. For log transformed parameters (eg serum vitamin B12) the levels above or below threshold depended on the threshold value and values above or below threshold were calculated and back transformed for each diagnostic indicator value. To achieve a higher level of significance as required experimentally (eg $P<0.05$) then this number increases to 8-10 per group. Laven and Norte (2013) had carried out a similar exercise looking at liver copper concentrations and serum selenium concentrations to diagnose copper and selenium status of dairy cattle in New Zealand. They assessed on a herd basis and did not split the herd into different management groups and used 90% confidence intervals as its criteria for recommendation of sample numbers. They recommend 12 samples of liver for assessment of copper status and 5-6 for selenium status. In this trial we did not assess liver parameters but their serum selenium is comparable to what we determined for plasma selenium remembering that we are looking at a lower level of diagnostic significance than the 90% CI, which is equivalent to $P<0.1$ using our methods.

Conclusion Nutritional status needs to be assessed on a 'management' group basis with at least 4 samples per management group.

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Effect of level and source of protein supply on the performance of ewes during late pregnancy and early lactation

R G Wilkinson, C Gauld, A M Mackenzie, S E Pattinson, J Donaldson
Harper Adams University, Newport, Shropshire, UK
Email:rgwilkinson@harper-adams.ac.uk

Implications Ewes do not respond to additional MP supply above requirements. Rape seed meal and field beans can be used to effectively replace soya bean meal in ewe diets.

Introduction The metabolisable protein (MP) requirements of ewes increase during late pregnancy and early lactation (AFRC, 1993). Failure to meet these requirements may reduce ewe and lamb performance. Over the last few years genetic selection for higher productivity has resulted in increased lamb birth weights and levels of milk production, such that current feeding standards may underestimate MP requirements (Robinson, 2001). In addition, the U.K. is heavily reliant on imported protein sources, which carry a high environmental burden, and pose a risk to food security (AHDB, 2012). The objective of the study was to investigate the effect of level and source of protein supply on ewe and lamb performance.

Material and methods 48 twin-bearing (Suffolk x Mule) ewes (84.2 kg; CS 3.3) were housed individually from 6 weeks *pre-partum* to 4 weeks *post-partum* and allocated by parity, live weight (LW) and condition score (CS) to one of 6 dietary treatments. All ewes' were offered grass silage at a restricted rate and one of 6 concentrates formulated to supply either a low (L) or high (H) level of protein, using either soya bean meal (S), rapeseed meal (R) or field beans (B) as the main protein source. All concentrates had a similar ingredient composition and were formulated to supply the same levels of ME, FME and ERDP, but different levels of CP and DUP. Concentrates L supplied 177 and 28 g/kg DM CP and DUP, whereas concentrates H supplied 212 and 56 g/kg DM CP and DUP using xylose-treated soya bean or rapeseed meal, or micronized beans. Silage was fed at 0.5 and 1.0 kg/day DM during pregnancy and lactation respectively. Concentrates were fed with silage to satisfy the ME requirements of twin-bearing ewes producing 3.0 litres of milk (AFRC, 1993) with diets L supplying 1.0 and 0.8 of MP and diets H supplying 1.25 and 1.0 of MP requirements during pregnancy and lactation respectively. Ewe LW and CS was recorded fortnightly and colostrum and milk yield were estimated at 16 hours and 21 days. Lambs were separated from the ewes, which were then injected with 1 ml oxytocin and machine milked until the udder was empty. The procedure was then repeated 4 hours later and secretion rate calculated. Litter weight and litter growth rate were recorded. From week +4 ewes were group housed within treatments and performance monitored to week +8. The experiment was analysed by ANOVA as a 2 x 3 factorial design with week -6 values being used as co-variates.

Results There was no significant effects of level or source of protein supply on ewe and lamb performance (table 1). However, numerically ewes offered soya lost less LW and CS *post-partum* than those offered soya bean meal.

Table 1 Effect of level and source of protein supply on ewe and lamb performance

	Low Protein			High Protein			SED	Probability		
	Soya	Rape	Beans	Soya	Rape	Beans		Level	Prot	Int
Pre-partum -6 to -2										
LW change (kg)	10.43	10.63	10.32	10.83	12.36	10.30	1.182	NS	NS	NS
CS change	0.33	-0.17	0.08	0.13	0.12	0.06	0.186	NS	NS	NS
Post-partum 0 to 8										
LW change (kg)	-9.42	-12.18	-9.51	-6.42	-11.74	-7.77	1.780	NS	NS	NS
CS change	-0.31	-0.71	-0.56	-0.30	-0.71	-0.89	0.278	NS	0.069	NS
Colostrum (l/day)	2.78	2.84	2.85	3.10	3.13	2.74	0.424	NS	NS	NS
Milk (l/day)	3.37	3.05	3.12	3.23	3.63	3.09	0.381	NS	NS	NS
Litter weight (kg)	9.37	11.42	10.44	10.27	9.96	10.22	0.565	NS	NS	0.022
Litter gain (g/day)	567	636	549	581	550	565	44.7	NS	NS	NS

Conclusion Ewes in good CS, fed diets formulated to supply similar levels of ME and optimise microbial protein supply showed no response to additional MP supply from DUP. However during lactation, ewes fed soya bean meal tended to maintain condition slightly better than those offered rapeseed meal or field beans.

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The effect of stocking rate and prolificacy potential on ewe production efficiency from pasture based production systems

E Earle[1,2], N McHugh[1], T M Boland[2], P Creighton[1]
[1]Animal & Grassland Research and Innovation Centre, Teagasc, Athenry, Co, Galway, Ireland, [2]UCD School of Agriculture and Food Science, University College Dublin,, Belfield, Dublin 4, Ireland
Email:elizabeth.earle@ucdconnect.ie

Implications Increasing farm output is achievable through increased stocking rates and the use of more prolific ewe breeds.

Introduction Output per ha (kg carcass) in Ireland is currently limited by low stocking rates (7 ewes/ha) and weaning rates (1.3 lambs reared per ewe), with associated poor grass production and utilisation. Performance levels of 13 ewes/ha and 1.8 lambs reared per ewe are achievable targets (Teagasc Roadmap, 2013). Grass either grazed or conserved can supply 90 to 95% of the energy requirements for sheep (Davies and Penning, 1996). Increasing stocking rates and ewe prolificacy, while maintaining optimum animal performance from pasture based production systems can increase output per hectare. The aim of the current study was to investigate the effect of stocking rate and prolificacy (based on breed type) on ewe production efficiency from a pasture based production system.

Material and methods A total of 360 primiparous hogget ewes comprising of two breed types, differing in prolificacy potential (Hanrahan, 1994), were assembled: medium prolificacy (MP) - Suffolk X ewes (n=180) with a target weaning rate of 1.5 lambs/ewe, and high prolificacy (HP) - Belclare X ewes (n=180) with a target weaning rate of 1.8 lambs/ewe. Within breed type, ewes were randomly assigned to one of three stocking rate (SR) pasture systems: a low SR (10 ewes/ha), a medium SR (12 ewes/ha), and a high SR (14 ewes/ha). The study commenced in October 2011 and was completed in October 2013 after two production cycles. Ewe body weight (BW) in kilograms and body condition score (BCS) on a 1 to 5 scale was recorded at each mating, with ewes mated to Charollais rams over a six week period. Following lambing, ewes and their progeny were rotationally grazed without concentrate supplementation. Lamb perinatal mortality was recorded as mortality within the first 24 hours of life including stillbirths. The effect of SR and prolificacy potential on lamb perinatal mortality was modelled using a fixed effect model in PROC GLM (SAS Institute 2012). The effect of SR and prolificacy on ewe production efficiency (measured as kilograms of lamb live-weight weaned per kilogram of ewe live-weight mated), BW, BCS, lamb birth weight and pre-weaning daily gains from 0 to 6 weeks and 0 to 14 weeks were analysed using the linear mixed models (PROC HPMIXED, SAS Institute 2012) with ewe included as a random effect. The predicted probability of a ewe dying within a production year was modelled using logistic regression in PROC GENMOD (SAS Institute 2012).

Results Data presented showed high SR ewes had a significantly lower BW and BCS (-2 kg, -0.10 BCS) compared to low SR ewes ($P<0.001$) over the three recorded breeding seasons as shown in Table 1. The HP ewes had lower BW and BCS (-5.1kg, 0.10BCS) compared to MP ewes, with MP ewes producing heavier lambs at birth (+0.20 kg; $P<0.05$). Similarly progeny of MP ewes had significantly higher average daily gain from 0 to 6 weeks (+12.0 g/day) and 0 to 14 weeks (+8.0g/day $P<0.01$). SR had a significant effect on average daily gain from 0 to 14 weeks ($P<0.001$) and on lamb weaning weight, with low SR lambs gaining 22 grams more per day (+2.3 kg weaning weight) compared to high SR lambs ($P<0.001$). Stocking rate and prolificacy potential had no significant effects on ewe production efficiency, culling rate or lamb perinatal mortality.

Table 1 The effect of stocking rate and prolificacy level on ewe and lamb performance and ewe production efficiency

	Stocking Rate			Prolificacy		P-value		
Parameter	Low	Medium	High	Medium	High	SR	Prolificacy	SR x Prolificacy
Ewe BW (Kg)	76.5[a]	73.9[b]	74.5[b]	77.5	72.4	<0.001	<0.01	<0.05
Ewe BCS (1-5 scale)	3.6[a]	3.5[b]	3.5[b]	3.6	3.5	<0.01	<0.01	<0.05
Lamb 0-14 weeks (ADG)	269[a]	256[b]	247[c]	261	253	<0.001	<0.01	<0.05
Weaning wt (kg) (14weeks)	32.9[a]	31.5[b]	30.6[c]	32.4	31.0	<0.001	<0.001	NS
Ewe Production Efficiency†	0.65	0.66	0.63	0.63	0.66	NS	NS	NS

a,b,c Within rows superscripts indicates significant difference ($P<0.05$) in SR, † ratio kg weaned lamb live weight to kg mated ewe live weight, ADG: Average daily gain (grams per day)

Conclusion Increased output per hectare is achievable through increased stocking rates and ewe prolificacy potential. Ewe production efficiency can be maintained despite lower ewe live weights, BCS and progeny performance.

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Effect of supplementary tannin on feed intake and digestibility in ewes offered lucerne silage during late pregnancy and early lactation

V Taha, R Wilkinson, D Davies, J Huntington
Harper Adams University, Newport, Shropshire, UK
Email:tvahel@harper-adams.ac.uk

Implications Adding tannins to lucerne silage at feeding could increase forage by-pass protein supply to the animal and thereby increase animal performance.

Introduction Tannins are a diverse group of plant secondary metabolites containing a phenol group which gives tannins the ability to bind with forage protein in the rumen to form tannin-protein complexes. These are pH dependent and resistant to rumen microbes (Muller-Harvey, 2006) but dissociate in the abomasum (pH< 3.5), facilitating protein digestion in the small intestine and generating an increased undegradable protein (UDP) supply to the animal (Makkar, 2003). Grass and legumes are the main sources (> 70%) of dietary protein for ruminants in the UK (Entec, 1998). They are high yielding (6-11 t DM /ha) and high CP (1-2 t/ha) crops but their CP contents are highly rumen degradable and could result in an oversupply of dietary rumen degradable protein (RDP) at the expense of metabolisable protein (McDonald *et al*. 1991). The objectives of this study were to investigate the effects of supplemental chestnut tannin offered with lucerne silage to ewes in late pregnancy and early lactation, on forage feed intake and digestibility.

Material and methods Approximately 20 tons of second cut lucerne was used for silage making. Chopped lucerne was wilted for 48h prior to ensiling. The clamp was filled rapidly, rolled and covered with three layers of plastic sheet and ensiled for more than 100 days. Forty singleton (Suffolk x Mule) ewes (87 kg) were used in the experiment and, from 6 to 4 weeks pre-partum, were acclimatised to lucerne silage as a group. At 4 week pre-partum, ewes were blocked according to parity, live weight (LW) and condition score (CS) and housed individually. Ewes were divided into four feeding groups (10 ewes/group). Each group was offered lucerne silage *ad libitum* and 380 g/day concentrate supplemented with tannin at 0, 25, 50 or 75 g/kg DM. Water was available ad-libitum and observations were taken between 4 weeks pre-partum and 6 weeks post-partum. Forage DM intake (DMI) was measured and ewe LW and CS were recorded weekly. At two weeks pre-partum and 4 weeks post-partum, DM and CP digestibility were measured using acid insoluble ash (AIA) methods (Van Keulen and Young, 1977). The experimental data was analysed by ANOVA as a randomised complete block design using GenStat 15 (VSN, International, Oxford, UK).

Results Supplemental tannin did not significantly affect forage DMI or ewe LW and CS change pre or post-partum. However, a high level of supplemental tannin (75 g/kg DM) significantly reduced CP digestibility, both pre-partum and post-partum, when compared with the effect of other tannin levels (25 and 50 g/kg DM) Table 1.

Table 1 Effect of supplementary tannin on dry matter intake (DMI) and diet digestibility coefficients in pregnant ewes.

	Tannin additives g/kg DM				Significance	
	0	25	50	75	SED	P
DMI	2.4	2.5	2.4	2.5	0.115	NS
Pre-partum						
LW change (kg)	9.8	7.5	6.6	10.5	2.29	NS
CS changing	-0.07	0.10	-0.03	-0.11	0.177	NS
DM $^{\text{Digestibility}}$	0.56	0.54	0.54	0.57	0.072	NS
CP $^{\text{Digestibility}}$	0.79^{a}	0.78^{a}	0.76^{a}	0.73^{b}	0.016	<0.01
Post-partum						
LW change (kg)	-11.1	-9.5	-9.1	-8.5	2.11	NS
CS changing	-0.08	-0.09	-0.12	-0.10	0.157	NS
DM $^{\text{Digestibility}}$	0.61	0.63	0.66	0.63	0.054	NS
CP $^{\text{Digestibility}}$	0.76^{a}	0.75^{a}	0.74^{a}	0.68^{b}	0.023	<0.01

Means with different letters within each row differ significantly (P<0.05).

Conclusion Supplemental chestnut tannins did not significantly affect lucerne silage DM intake by pregnant and lactating ewes but a reduction in CP digestibility at 75 g/kg DM tannin supplemention rate, could indicate a negative effect on rumen microbial metabolism and/or animal digestive enzymes (Makkar, 2003)

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The impact of concentrate supplementation on grass dry matter intake of twin suckling ewes during early lactation and subsequent effects on lamb performance

F P Campion[1], F M McGovern[1], E Levičnik[3], P Creighton[2], T M Boland[1]
[1]University College Dublin, Ireland, [2]Teagasc Athenry, Galway, Ireland, [3]University of Ljubljana, Slovenia
Email: francis.campion@ucdconnect.ie

Implications Concentrate supplementation did not improve overall dry matter intake (DMI) of ewes during early lactation. Where sufficient quantities of good quality grass are available performance is not improved by concentrate supplementation.

Introduction Up to seven weeks of age the lamb is largely dependent on milk to supply its nutritional needs (Treacher, 1973). Ewe milk production peaks approximately three weeks *post-partum*, with intake potential peaking approximately six weeks *post-partum* (Bocouier *et al*., 1987). In pasture based production systems, lambing date is planned to coincide with the onset of grass growth, with the aim of maximising the contribution of grazed grass to the nutrient requirement of the suckling ewe (Keady *et al*., 2009). The aim of this study was to investigate if concentrate supplementation during the first three or seven weeks of lactation influenced the grass intake of the ewe during early lactation and progeny performance.

Material and methods Fifty-four twin suckling ewes, blocked on body condition score (BCS) at 24 hours post-partum, were allocated to one of three dietary treatments in a randomised block design on day seven (+/- two days) of lactation. Treatment groups (n=18) were balanced for maternal age, breed, *Longissimus dorsi* muscle and fat depth at 24 hours *post-partum*, progeny sire breed, litter weight and ewe live weight (LW). Treatments were as follows: GO: *Ad-libitum* zero grazed grass, GC: *Ad-libitum* zero grazed grass and 500grams (g) fresh weight (FW) of concentrate feed for 49 days *post-partum* and GC21: *Ad-libitum* zero grazed grass and 500g FW of concentrate feed for 21 days *post-partum*. Ewes were individually penned with their progeny on expanded metal flooring from 72 hours *post-partum* until week seven of lactation. Lambs were given free access to a creep area bedded with straw and were offered fresh water and zero grazed grass. Grass was harvested each morning using a single chop zero grazer from perennial ryegrass based swards with an average pre-grazing herbage mass of 1100kg DM/ha. Individual ewe intakes were recorded daily from day seven to 49 of lactation with ewe live weights and BCS measured weekly. Milk yield was measured five times during the first seven weeks of lactation. Lambs were weighed weekly in order to calculate average daily gain (ADG). Statistical analysis was carried out using SAS 9.4 (SAS Inst., Inc, Cary, NC). The model included fixed effects of treatment, age, maternal breed and progeny sire breed as well as including lambing difficulty, combined litter weight, 24 hour *post-partum* live weight, BCS, *Longissimus dorsi* muscle and fat depths as covariates. Ewe DMI, LW, BCS and milk yield were analysed as repeated measures. Lamb ADG was calculated by regression of live weight on time and analysed as a non-repeated measure.

Results As presented in Table 1 GO ewes had higher average grass DMI compared to GC ewes ($P<0.05$) and tended to have higher average grass DMI than GC21 ewes ($P<0.10$). However, total DMI did not differ between treatments ($P>0.05$) reflecting a strong substitution effect of concentrates for grass. For each g of concentrate DM offered there was a reduction of 0.72g of grass DMI in GC ewes compared to GO ewes. Ewe live weight and BCS did not differ between treatments ($P>0.05$). Milk production, from GO (1.61kg) and GC21 (1.59kg) ewes was lower than GC (2.15kg) ewes for the final milking, six weeks *post-partum*, ($P<0.05$), and tended to be lower on average for early lactation for GC21 (1.85kg) ewes compared to GC (2.11kg) ewes ($P<0.10$). However, this was not reflected in lamb ADG during the same period ($P>0.05$).

Table 1 The effect of treatment on mean dry matter intakes from day seven to 49 of lactation (Least Square Means ± SEM)

	GO	GC	GC21	S.E.M.	P-value
Grass DMI (kg)	1.96^{ay}	1.65^{bx}	1.84^{ay}	0.078	<0.10
Total DMI (kg)	1.97	2.10	2.01	0.077	NS

[a,b,] Means within a row with common superscripts do not differ (*P > 0.05*)
[x,y,] Means within a row with common superscripts do not differ (*P > 0.10*)

Conclusion Concentrate supplementation was used by the ewe as a substitute for grass in the diet rather than improving DMI. This substitution, of a more expensive cereal based concentrate, by the ewe did not lead to benefits in flock performance with ewe LW, BCS and lamb ADG being unaffected. The differences in milk yield recorded were not immediately evident in lamb ADG.

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By-pass based protein supplementation and periparturient ewe performance

J G M Houdijk, L A Smith, J E Vipond
SRUC, Scotland's Rural College, Edinburgh, UK *Email:jos.houdijk@sruc.ac.uk*

Implications Periparturient supplementation of well-conditioned, worm-free ewes with digestible undegradable protein (DUP) may temporarily increase ewe body weight but is unlikely to increase lamb weight gain from birth to weaning.

Introduction Foetal growth and milk production increase metabolisable protein requirement (MPr) of ewes (AFRC, 1993). Additional DUP supply may increasingly be needed to meet MPr to realize ewe production potential (Houdijk and Vipond, 2014). Here, we assessed whether periparturient DUP supplementation improves ewe performance.

Material and methods Multiple-bearing Texel-mated Scottish mules, with mean body weight (BW) of 81.4±1.1 kg and condition score (CS) of 3.10±0.05 at day_{-48} (day_0 is parturition), were housed individually. They received iso-energetic rations (40% hay; 60% concentrates) at 0.85 times energy requirements (AFRC, 1993), calculated to supply 0.85 (L) or 1.20 (H) × MPr (n=24). Half of each group switched to the alternative treatment at lambing, resulting in four feeding treatment combinations during lactation (n=12). A 2:1 mixture of xylose-treated rapeseed meal (RaPass®) and soya bean meal (SoyPass®) was used to increase DUP levels from 28 to 52 g/kg. From day_7, ewes grazed one of eight 0.5 ha new grass-clover pastures (six ewes and their 12 lambs each), where H ewes were fed a pellet with 60% RaPass® and 30% SoyPass® at 400 g/head/day until day_{58}. Housed ewes were weighed weekly and CS was taken fortnightly; lambs were weighed at birth and at day_7. During grazing, ewes and lamb BW, and ewe CS, were taken on day_{24}, day_{58} and day_{100}. Ewe herbage dry matter intake was measured using the n-alkanes methodology. Data were analysed using monofactorial ANOVA during pregnancy and 2×2 ANOVA during lactation, with ewes and plots as experimental units before and after day 7, respectively.

Results Feeding more DUP during pregnancy increased ewe BW before parturition, which carried over into early lactation but did not significantly increase litter birth weight (Table 1). Ewe CS was not significantly affected, although feeding more DUP during pregnancy tended to increase CS by day 58. Feeding more DUP during lactation did not affect litter BW gain but increased ewe BW on day_{58}. Feeding treatments did not affect herbage intake, which averaged 2.89±0.12 kg/d.

Table 1 Feeding treatment effects during pregnancy and lactation on ewe performance

		Feeding treatments during pregnancy					P-values		
		Preg-L		Preg-H		s.e.d.	Preg	Lac	P×L
Ewe BW (kg)	Day_{-4}	88.4		91.6		0.98	0.002	-	-
	Day_0	75.1		76.4		0.96	0.197	-	-
Ewe CS	Day_{-7}	2.8		2.9		0.09	0.811	-	-
Litter BW (kg)	Day_0	10.1		10.6		0.51	0.342	-	-
		Feeding treatments during lactation							
		L	H	L	H				
Ewe BW (kg)	Day_7	73.1	73.3	75.8	74.4	1.22	0.035	0.512	0.345
	Day_{58}	73.6	78.1	74.9	78.7	1.86	0.500	0.035	0.774
	Day_{100}	69.3	72.0	72.6	72.1	2.19	0.338	0.516	0.364
Ewe CS	Day_4	2.6	2.3	2.6	2.7	0.14	0.119	0.456	0.075
	Day_{58}	2.3	2.2	2.4	2.3	0.09	0.100	0.542	0.347
	Day_{100}	2.5	2.8	2.7	2.8	0.12	0.209	0.118	0.279
Litter BW gain (g/d)	$Day_{0–7}$	657	618	614	669	45	0.916	0.796	0.152
	$Day_{7–58}$	696	702	653	691	49	0.483	0.558	0.679
	$Day_{58–100}$	455	380	448	408	38	0.739	0.098	0.546
	$Day_{0–100}$	572	541	543	547	34	0.655	0.610	0.508

Conclusion In this experiment, DUP supplementation temporarily increased ewe BW but did not affect litter BW gain. Since ewes had high CS, were worm-free at housing and grazed parasitologically clean pastures, the lack of DUP response may be due to high body reserves and/or low worm challenge. This hypothesis is being addressed but supported by a greater lamb BW gain than that observed in thinner, parasitized ewes grazing parasitologically dirty pastures (Kidane *et al.* 2010).

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Relationship between body condition score, back-fat and muscle depth in Suffolk x Mule ewes

R G Wilkinson, C Gauld, A M Mackenzie, S E Pattinson, J Donaldson
Harper Adams University, Newport, Shropshire, UK
Email:rgwilkinson@harper-adams.ac.uk

Implications Scanning can be used to monitor changes in body composition and nutrient supply to ewes.

Introduction Traditionally the body composition of ewes is assessed by body condition scoring (CS) (Russell, *et al*. 1969) and it is generally assumed that 1 unit of CS change is equivalent to 10.0 kg live weight (LW) (MLC, 1984), and that the energy value of LW change is 23.8 MJ/kg (AFRC, 1993). However, it is unknown whether this relationship holds true between breeds or throughout the range of LW and CS changes. Ultra-sound scanning of fat and eye muscle depth provides a more objective measurement of body composition, but is rarely carried out with ewes. The objectives of this study was to determine the relationship between measurements of CS, and back-fat and eye muscle depth in Suffolk x Mule ewes.

Material and methods 48 twin-bearing (Suffolk x Mule) ewes (84.2 kg) on an experiment to investigate the effect of level and source and protein supply on ewe and lamb performance were used in the study, which lasted from 6 weeks *pre-partum* (week -6) to 8 weeks *post-partum* (week +8). All ewes' were offered grass silage at a restricted rate and one of 6 concentrates formulated to supply either a high or low level of protein, using either soya bean meal, rapeseed meal or field beans as the main protein source. All concentrates had a similar ingredient composition and were formulated to supply the same level of metabolisable energy (ME), fermentable ME (FME) and rumen degradable protein (ERDP), but different levels of crude protein (CP) and digestible undegradable protein (DUP). Concentrates were fed with silage to satisfy the ME requirements of twin-bearing ewes producing 3 litres of milk (AFRC, 1993). Measurements of ewe condition score (CS), and ultra-sound measurements of ewe back-fat and muscle depth were recorded during weeks -6, -2, +2, +4 and +8 by the same competent person on each occasion. CS was assessed using a standard 5 point scale, with 1 being thin and 5 being fat (Russell *et al.* 1969). Scanning involved parting the wool at the third lumber vertebra at 90° to the backbone and applying liquid paraffin to give a contact. The ultra-sound transducer was then applied to the site and 3 measurements of back-fat depth obtained. The first was taken above the muscle at its deepest point, with the following two being taken at 1 cm intervals from this point, further from the backbone. A single measure of muscle depth was taken at its deepest point. Back-fat depth was calculated as the mean of the 3 measurements. The mean CS, back-fat and muscle depth of ewes on each treatment (n=8) at each time point was then calculated and subjected to regression analysis.

Results All ewes lost CS, fat and muscle depth throughout the experiment, with mean CS ranging from 3.6- 2.3, fat depths ranging from 11.1-3.0 mm and muscle depths ranging from 28.3-20.5 mm. There was a strong linear relationship between CS and fat depth (R^2=0.65), but a weaker relationship between CS and muscle depth (R^2=0.37) (Figure 1). However, the relationship between fat and muscle depth was strong (R^2=0.76). At CS 3, ewes were predicted to have a fat depth of 6.5 mm and a muscle depth of 23.7 mm, with one unit of CS change being equivalent to 5.8 mm fat and 3.7 mm muscle loss.

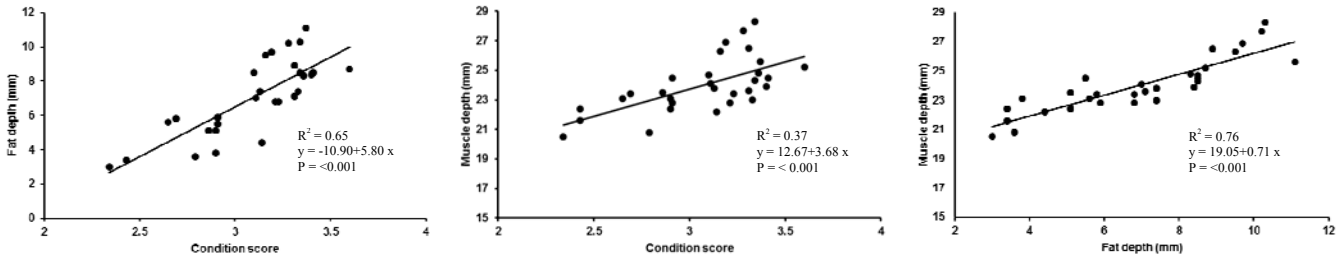

Figure 1 Relationship between CS and back-fat and muscle depth in Suffolk x Mule ewes.

Conclusion Ultra-sound scanning can be used to relate CS to body composition. The linear relationships obtained suggest that the composition of CS loss is similar throughout the range of CS changes. Further work is required to relate changes to nutrient supply, and to determine whether the relationships obtained are similar in different breeds of sheep.

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Animal science, politics and policy – a New Zealand perspective

Rt Hon Sir Lockwood Smith KNZM Ph.D.
Email:shereen.capper@mfat.govt.nz

This presentation provides an opportunity for a New Zealand perspective on the interaction between animal science and government policy. New Zealand High Commissioner, Sir Lockwood Smith, will address the topic as a former long-serving politician, Minister of Agriculture, animal scientist and livestock farmer.

The presentation covers the development of agricultural science and policy in New Zealand. It explores the role of both politics and science in shaping policy direction and considers how developments in animal science have contributed to the success of New Zealand agriculture. In examining the impact of livestock science on government policy making, it will consider whether science has adequately influenced policy, looking at examples that may provide some insight as to how to increase the impact of livestock science.

Touching on key issues concerning New Zealand agriculture – including bio-security, food safety, productivity, animal welfare and the environment – the presentation will explore some of the specific impacts of animal science research. Finally the presentation will discuss how this has helped New Zealand develop and maintain a position at the cutting edge of agriculture trade, and consider ways in which New Zealand and the United Kingdom might work together to capitalise on the contemporary opportunities presented by this truly global industry.

Methods to control the level of *Campylobacter* during poultry processing

M Howell
Howell Consulting, Buckinghamshire, UK
Email:mary.v.howell@gmail.com

Introduction Campylobacter continues to be a major cause of food poisoning with 60-80% of cases thought to be attributable to chicken. A recent attribution study reported in the 2013 Swiss Zoonosis report put the figure at just over 70%. The EU community summary report published in January 2015 by the European Food Safety Authority showed the UK had the fourth highest notification rate in humans in the EU in 2013 at just over 100 cases per 100,000 population. Surveys by the UK Food Standards agency in 2007/8 and 2014 have shown that around 70% of whole chickens on sale in major retailers are contaminated with the bacterium and in the recent study 18 % contain levels over 1000cfu/g. Chicks at the start of the production cycle are not colonised and the application of biosecurity can keep the colonisation at bay in many chicken sheds however from around 21 days of age the risk of detecting colonisation in a sample of the birds starts to increase. The process of partial depopulation (thinning) where a proportion of the birds are removed from the shed has been shown to increase the risk of colonisation by at least eight fold resulting in around 75% of UK slaughter batches being colonised at slaughter.

During processing the Campylobacter in the caeca and on the feathers results in contamination of the carcass skin.
Several studies have measured the levels of Campylobacter on the chicken at different stages during processing and shown that de feathering and evisceration are particularly important processes where contamination will increase. Chicken processors need to identify Campylobacter as a hazard in their procedures based on HACCP principles and implement a range of best practice measures and specific controls to reduce the frequency of colonisation of birds and to manage the contamination of carcasses when processing colonised birds. Scientific evidence would suggest the following measures should be considered and developed into a practical cost effective option for each processing plant. In the rearing phase birds should be sexed and reared separately with good husbandry including an active culling policy with the aim of producing even size and weight of birds with clean feathers and feet. Production should be all in all out with no thinning and birds should be sent for processing at as young an age as possible. Biosecurity should be maintained throughout the rearing process by all personnel and equipment entering and leaving the house. Feed withdrawal should be within an 8-10 hour window with birds transported to the factory in clean dry crates and modules. A gas stunning process should be managed to minimise contamination of the feathers and the scald tank maintained at 55 ^{o}C operating with a counter flow of clean water with a process to minimise and remove foaming. The carcasses should be washed with warm water pre and post pluck and plucking and evisceration machines operated with accurate settings for the size and weight of birds. The surface of the bird should be kept moist during processing and all washing processes optimized to ensure coverage of the carcass and removal of surface contamination. The chilling process should be optimised to reduce contamination levels. In addition the use of interventions to further reduce levels of contamination should be considered. Processes that can be applied within the current regulatory framework are based on raising and lowering the temperature using steam with or without ultrasonics, hot water and very cold air or nitrogen.

Bacteriophage control of *Campylobacter* in broiler chickens

I Connerton, P L Connerton
University of Nottingham, Loughborough, UK
Email:ian.connerton@nottingham.ac.uk

Implications Controlling campylobacters in poultry represents one of the greatest challenges to the agriculture and food industries if they are to achieve consumer and governmental demands to reduce human food borne disease.

Introduction The bacterial pathogen *Campylobacter jejuni* is a common cause of human diarrhoeal disease worldwide. There are over 70,000 cases reported each year in the UK but due to underreporting this belies an estimated case load of ~450,000 and 9 million across the EU (European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2011). Infection can arise from food and water-borne sources but is notably associated with the consumption of contaminated poultry products (Newell *et al*, 2011). The intestines of poultry become colonised by campylobacters often without noticeable effects on bird health but their presence represents a foodborne hazard to humans when transferred to poultry meat during processing. Bacteriophages (often abbreviated to phages) are naturally occurring predators of bacteria which are ubiquitous in the environment. Their specificity against a particular bacterial species and their lack of impact upon other flora make them attractive anti-bacterial agents and their use as such is usually referred to as phage therapy. Control of *Campylobacter* is an obvious target for phage therapy because of the large proportion of poultry reared for meat harbours these organisms as a part of their intestinal microbiota with few practical alternatives for reduction (Connerton *et al*, 2011). We will report and discuss our studies on the sustainable use of bacteriophages to control campylobacters in broiler chickens (Loc Carrillo *et al*, 2005) and on broiler meat (Atterbury *et al*, 2003).

Material and methods *Campylobacter jejuni* HPC5 was isolated from conventional barn-reared UK broiler chicken flock and cultured on horse blood agar plates (blood agar base No. 2 supplemented with 5% defibrinated horse blood), under a microaerobic atmosphere containing 5 % O_2, 5% H_2, 10% CO_2, 80% N_2 at 42 ^oC for 24 h. Bacteriophage CP30 was isolated from broiler chickens and propagated using the soft agar method and enumerated as previously described (Atterbury *et al*, 2003). Chicken portions were obtained from supermarkets and cut into 2 cm^2 sections and transferred to square Petri dishes divided into 25 sections. For *Campylobacter* enumeration skin samples were aseptically transferred into individual stomacher bags 10 ml of MRD and stomached in a Seward Stomacher 80 Biomaster for 2 min. The suspensions were diluted 1:10 in MRD. Twenty 10 µl droplets of both the neat stomachate and the 1:10 dilution were dispensed onto the surface of plates of dried mCCDA (2% agar), incubated at 42 ^oC under microaerobic conditions and the colonies counted after 48-72 h.

Results Data showing the decline in *Campylobacter jejuni* counts after storage of chicken skin at 4^oC. *C. jejuni* were applied to chicken skin at 5 $\log_{10}$ CFU/cm^2 and treated with various doses of bacteriophage (PFU/cm^2).

Days post phage treatment	10^3 PFU/cm^2	10^5 PFU/cm^2*	10^7 PFU/cm^2*	10^9 PFU/cm^2*
1	0.4	2.1	1.8	1.9
2	0.5	2.1	1.7	1.7
3	0.3	2.1	1.7	1.7

* significant differences at P= <0.05 by ANOVA
Mean decline in *Campylobacter* count ($\log_{10}$ CFU/cm^2) on broiler chicken skin (n=10)

Conclusion The application of bacteriophage can reduce the contamination of chicken meat surfaces by *Campylobacter*.

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Technical and economical performance of grass-based suckling systems of contrasting intensities

P Crosson[1], E J McGeough[2], P O'Kiely[1]
[1]Teagasc, Grange, Dunsany, Co. Meath., Ireland, [2]Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada
Email:paul.crosson@teagasc.ie

The Irish suckler cow herd is comprised of 1 million, predominantly spring-calving, crossbred cows, on grass-based systems of production. Approximately half of the 520,000 t of beef produced from the Irish beef industry derives from the suckler herd. Ninety percent of beef produced is exported with total exports valued at €2.1 billion in 2013 (DAFM, 2014). Of the predominant feedstuffs readily available for livestock production, efficiently managed grazed grass is the cheapest, followed by grass silage which, in turn, is cheaper than concentrates (Finneran *et al*., 2011). This means that maximising the proportion of grazed grass in the annual feed budget is central to sustainable suckler beef production systems. A further objective is to maximise the value of carcass beef produced per suckler cow exposed for breeding. Thus, the breeding policy should exploit breed differences and hybrid vigour or heterosis (advantage to crossbreds over the average of the parent breeds). Animals of high genetic merit should be used. Good reproductive performance is critical, and ideally cows need to first calve at 2 years old. High lifetime live weight gain of progeny i.e. attaining high weight for age during pre-weaning (combining cow milk yield and the animal's own genetic capacity for growth) and post-weaning (genetic merit, feeding management and exploiting compensatory growth), coupled with good carcass characteristics, is essential.

To maximise financial returns, the genetic potential of beef cattle must be met within grass-based systems. Compact calving before turn-out to pasture in spring in order to maximise herbage utilisation is an essential component of these systems. Mean calving date should coincide with the start of the grass growing/grazing season. Economic analysis of calf-to-beef production system comparisons at the Teagasc Grange research centre has shown that where individual animal performance remains high, stocking rate is the main driver of farm profitability (Clarke *et al*., 2013). The challenge is to achieve high levels of carcass output while also maintaining a high proportion of lifetime daily gain from a grazed grass diet. Further production benefits can be availed of by exploiting the superior growth potential of bulls over steers. However, an important issue surrounds market specifications for bull beef production systems.

In this paper we will use a bioeconomic modelling approach (Crosson *et al*., 2006) to evaluate the technical and economical performance of suckler calf to beef systems operating at different levels of intensity. For lowland, grass-based suckler calf to beef systems of the type operated in Ireland, one option involves relatively extensive systems with age at slaughter of circa 26 to 30 months and with maximum the use of home produced feeds, particularly grazed grass. An alternative option involves higher production intensities finishing cattle at younger ages, including males as bulls, and using higher inputs of purchased concentrate feeds. These systems are typically operated at higher stocking rates and achieve higher levels of lifetime daily gain for the progeny when compared to more extensive systems. Between these options there is a wide spectrum of alternatives that farmers operate subject to their farming objectives and constraints. The focus of this paper will be to evaluate a number of production systems from within this spectrum.

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An analysis of the English beef industry over the last 10 years

M Topliff
AHDB, Stoneleigh Park, UK
Email:mark.topliff@ahdb.org.uk

Introduction There is no doubt, the 10 years prior to 2005 was the most difficult period the UK and English beef sector had experienced in modern times. The consequences of BSE and human CJD cases had a significant impact on the industry, not only in economic terms but also on trade and regulation. This analysis examines at the history of the beef sector following this difficult period. The paper explores the trends in the sector from an economic, technical and production point of view, drawing mainly on the analysis of English sector data.
Currently there are around 0.7million suckler cows in England with an average herd size of 28. Approximately 0.5m tonnes of beef and veal is produced from 1.5million cattle slaughterings and the UK as a whole exports in the region of 16% of its production.

2005 - A turning point? The beef sector did well out of the support system, with around six different subsidy schemes being operated in the sector prior to 2005. However, it had been subject to some strict regulations being introduced to control the spread of BSE. A trade embargo, tight controls on the age of cattle and the type of beef material that could enter the food chain restricted the market for beef and beef products and had a negative impact on the sector.
It is important to consider the dairy sector when looking at the beef industry. Over 50% of English beef originates from the dairy herd and this increased over the last ten years with the reintroduction of cull cows and an increase in the finishing of dairy-bred males. However, whereas the English suckler herd has declined only slightly, the national dairy herd has experienced a greater decline, although at a lesser rate than earlier in the 2000s, due to improved milk prices and increased productivity.
According to the national cattle database, BCMS, there has been a mix of fortunes for the various suckler cow breeds. Although Limousin dams still largely dominate, they and most other breeds have seen a decline in numbers, more so recently. In contrast, there has been an increase in breeds such as Aberdeen Angus and Stabilisers as a result of producers looking to take advantage of supplier breed-specific premium schemes and those looking to breed cows with a lower maintenance cost.
As a result, this has led to an overall reduction in the number of prime cattle slaughtered in the last 10 years but the total beef production increasing due to cull cows being allowed back into the food chain. Further down the food chain, fresh and frozen beef sales have remained relatively steady although showing a slight decline over the past three years. So how have cattle prices trended over this time?
One the most significant features of the beef sector in the last ten years has been the significant rise in prime cattle prices, which have nearly doubled. The steady decline in prime cattle numbers while retail sales held up has certainly been a factor. However, lower beef imports and a rise in exports following the trade ban, were also significant contributors.
Following the removal of direct subsidy payments, enterprise margins were substantially impacted but the rise in cattle prices provided a much needed improvement to margins. However, profitability still remains a major issue for suckler herds due to the high cost of keeping breeding cows. The situation has been more favourable for finishing cattle enterprises although there has been more volatility due in part to the variation in feed prices.

Trends in productivity Against the background of what had been happening in the market place, there have been some interesting trends from a technical point of view, both good and not so good. One area which has not shown signs of improvement is the number of calves produced per cow put to the bull.
However, once the calf has been born, results from the EBLEX benchmarking survey show that average daily liveweight gains have increased gradually in the last ten years. Over this time, we have also seen continuous improvement in the genetic potential of cattle, particularly with regard to growth rate and muscling. However, those traits influencing ease of calving and maternal performance have not generally improved and clearly there is still a lot more that could be realised from genetic improvement by beef producers.
One of the consequences of the lifting of the Over Thirty Month Scheme in 2005, which had imposed a maximum age, was a gradual increase of prime cattle finishing at over thirty months of age. At the same time fewer cattle were finished in the age range of 21 to 30 months. Despite this, the proportion of cattle meeting the key carcase classifications increased by 10 percentage points, due to better genetics/use of different breeds and better selection of cattle for slaughtering.

Conclusions The English and UK beef industry have experienced a period of transition while adjusting to the decoupling of subsidies and the legacy of BSE, the results of which are still felt to this day. Despite better cattle prices compared with 10 years ago, profitability for the sector remains a challenge, particularly for suckler herds. To help financially, farmers have tried to reduce costs and increase weights but the average producer does not seem to have improved the productivity of their cows. Gains have been made using genetic potential and in the marketing of finished cattle. So the industry has, in many ways, come a long way since 2005 and the sector is very different in some aspects and, for that, 2005 was a turning point. Some of the changes that took place have been a necessity in a challenging environment while others are ongoing. The next ten years will no doubt see some further tough times but also some good times. A challenge for the industry is to aim to prepare itself for whatever comes its way.

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Suckler beef systems in France: recent evolution, challenges and future prospects

C Mosnier[1,2], J Agabriel[1,2], M Lherm[1,2], P Veysset[1,2]
[1]INRA, UMR1213 Herbivores, St-Genès Champanelle, France, [2]Clermont Université, VetAgro Sup, Clermont Ferrand, France
Email:cmosnier@clermont.inra.fr

Suckler beef systems are an important feature of French agriculture. Indeed the 4.1 million French suckler cows represent more than one third of all European suckler cows and supply around 65% of the beef production in France. Cull cows and old heifers represent 80 of this production. The number of cows doubled between 1984 and 2000, after the introduction of milk quotas. At the same time sales of young weaned calves was developed. Around one million weanlings are exported from France each year, mainly for a finishing in the Po Valley, in Italy (80%). French beef production remains heavily subsidised and protected since the sector plays a key role in rural development and tourism of least favoured areas such Massif Central and helps in maintaining these large areas under grassland which favours biodiversity, limits pollution and erosion and stores carbon. The he national beef herd is mainly composed of various pure breeds, and these breeds are maintained as regional particularities and are an asset for marketing. Nowadays, the number of beef cows has plateaued, while beef farm numbers (100,000 farms) are slightly decreasing together with average stocking rate. The drop in demand from Italy and increased competition from Eastern European countries are likely to reduce the weanling market over the next 10 years. Low income, increasing capital intensiveness, declining competitiveness, public support dependency are some issues of concern while in the context of globalization, decrease in meat consumption per capita, and climate change will also impact on the industry.

To improve farm income, competitiveness, and to limit input use (above all non renewable ones), the efficiency of the production process should be improved at farm level. Veysset *et al*. (2014a) analysed the evolution of the efficiency of beef production (volume of agricultural products/volume of intermediate consumptions e.g. inputs, services, machines and materials) using data from the Farm Accountancy Data Network and data from 43 farms located in the North of Massif Central collected over the period 1990-2012. The study showed that the efficiency of beef production has decreased over this period. While animal feed conversion ratio increased over the same period, Veysset *et al*. (2014a) explain that the degradation of performance can be partly due to an increase in the use of concentrate feed in animal diets and a poorer use of grazing arising from simplification of herd feeding practices and evolution of animal production toward beef products that utilise less (i.e. young bulls *vs* older steers). This efficiency ratio of production appears negatively correlated with herd size (-0.1). Over the period of study, French beef cattle farms had increased their size and labor productivity by more than 60%. Farm size per worker unit has long been a key determinant of farm income, above all by the subsidy income recoverable (Veysset *et al*., 2014b). However, this correlation has become weaker in recent years resulting from higher input prices, increasing costs from machinery and fuel (herd enlargement was accompanied by a substitution work /capital) and a slight reduction of cow reproductive performance.

Risk management could explain lower production efficiency. To reduce risk exposure, farmers could reduce the most profitable or most efficient activity to diversify their production, use less efficient but more resilient breeds and crops or they could create production overcapacity such as forage so as to enable security of fodder stock in the event of future shortages. The issue for farmers and policy makers is to find the optimal mix between self insurance (production system, savings), borrowing possibilities, and market insurance and public supports to ensure farm resilience, while limiting expenses. In the event of natural calamities on grasslands, suckler cow farmers can currently seek indemnities from a public fund. This fund will probably be replaced by subsidized insurance. However, among the 141 farmers surveyed by Mosnier *et al* (2014a), the majority preferred managing grassland production risks by themselves. Simulations (Mosnier; 2014b) show that it will remain profitable for suckler cow farmers to secure their systems against current grassland production risks (>-30% of production loss) principally as a result of forage security stocks and to a stocking rate below potential. An analysis of 1,535 farm observations over the period 2000-2009 (Mosnier *et al*., 2014a) emphasizes self insurance: the economic results are resistant to variation of grass harvested per livestock unit above -20% relative to average values but below this value, profits fall. Benefits of forage crops and grass silage on average economic results and on their variability are unclear, probably because they are associated with higher stocking rate and higher production costs.

In a context of growing uncertainties and climate change, farmers need to be able to cope with multiple risks while improving their competitiveness. To help in designing farming systems that are both efficient and resilient, a challenge is to better take into account the different dimensions of farm production: biological, ecological, technical, economical, financial and social and to provide public support and better information on regulations, , and tools to improve farmers' capabilities to manage and adapt their systems.

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U.S. suckler system sustainability - maintaining economic viability in a changing market

J L Capper
Livestock Sustainability Consultancy, Didcot, Oxfordshire, UK
Email:jude@livestocksustainability.com

Introduction The U.S. beef industry is stratified into three main components: the cow-calf (suckler) operation in which calves are born and reared on pasture until weaning; the stocker operation in which calves are fed forages and by-product based feeds and gain weight on a least-cost basis; and the feedlot, in which calves are then finished on grains, soy and by-product feeds.

Main Body Within the U.S., nearly 765,000 cow-calf operations exist, with an average herd size of 40 cows. However, this is somewhat misleading as 79.2% of herds contain less than 50 cows, yet account for only 28% of the national herd; compared to the 9.7% of herds containing 100+ cows and representing 54.6% of the national herd. Cow-calf enterprises are often secondary operations (71.9% exist as a supplemental source of income) with beef production the sole source of income for only 5.3% of operations with herds containing less than 50 cows, compared to 65.0% of operations with more than 200 cows (USDA, 2008). As in many other segments of the livestock industry, the number of cow-calf operations is declining in the U.S. and the average age of the owner-operator is 60 years (McBride and Mathews, 2011).

Economic returns are highly variable over time, with a variety of climatic factors (e.g. drought, blizzards) having noticeable impacts upon cow-calf performance. Indeed, the current U.S. beef cow herd is composed of 29.7 million head, the lowest inventory since 1951 and reflects the widespread drought over the past eight years. However, profitability is more variable between producers than can be explained by temporal changes, i.e. some producers remain profitable even when the majority are losing money. Cost differences account for more of this variability than income, including the impacts of purchased feed vs. grazed pasture; lease vs. ownership costs; and the considerable variation in pasture management, capacity and climate across the U.S. Although drought conditions have caused serious issues for some producers, retail beef prices are currently high due to the combination of reduced cattle supply and high demand.

Technology use and efficiency tend to increase with herd size, thus larger cow-calf operations have a higher adoption rate of management practices that improve productivity or add value, including castration, use of hormone implants and enrolment in the Beef Quality Assurance program (USDA, 2008). A positive correlation generally exists between improving productivity and efficiency such that when output per unit of herd bodyweight (e.g. kg of calf weaned per kg of maintenance herd bodyweight) is optimized, resource (land, animals, water, labour) use efficiency and economic returns increase accordingly. The U.S. beef industry improved resource use and greenhouse gas (GHG) emissions per kg of beef considerably between 1977 and 2007 through improvements in cattle nutrition, reproduction and management that increased slaughter weight and average daily gain (ADG; Capper, 2011). At present, 90% of cows produce a calf each year in the USA, which compared to the ideal of 100% of cows producing a calf, confers increases in land use (8.1%), water use (5.2%), GHG emissions (7.0%) and feed costs (5.5%; Capper, 2014a).

However, a conflict exists between producers' need to optimize efficiency within the confines of their operation, and the social acceptability of cattle production. As an extensive, pasture-based operation, the cow-calf producer faces less social threat than the feedlot operator, yet public concern is mounting over the use of hormones, antibiotics and parasite control products within beef production, such that currently niche markets for natural or organic beef are increasing market share. Effective parasite control is intrinsic to an economically viable cow-calf operation, as without it, calving rate is reduced from an average of 90% to 80%, and weaning weight from 248 kg to 227 kg (Capper, 2014b). If effective parasite control is removed from beef production throughout the entire chain (cow-calf, stocker and feedlot), overall mean ADG is reduced from 1.3 kg/d to 1.1 kg/d; land use increases by 15.9%, water use by 15.1%, fossil fuels by 7.1%, GHG emissions by 13.3% and feed costs by 11.8% (Capper, 2014b). A considerable proportion of these increases can be directly attributed to lost productivity in the cow-calf operation, which contributes the majority of resource use and GHG emissions per kg of beef.

Conclusion The U.S. cow-calf industry is economically viable, yet faces a number of climatic and social threats, which may intensify in future. Further research is required to help producers adapt to these challenges through improving productivity according to the characteristics of individual operations.

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Animal Electronic Recording, Transmission and Synthesis (ALERTS); decision support technologies for the farming sector

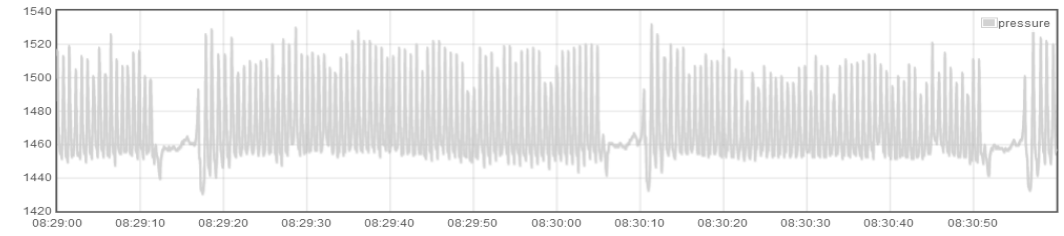
I Andonovic[2,1], C Michie[1,2], D Ross[3], M Mitchell[2], J Konka[1], C-A Duthie[3], W Thomson[4], A Loftus[5], J Hyslop[3], M Bateman[6], A Warne[7]
[1]University of Strathclyde, Glasgow, UK, [2]Silent Herdsman Ltd, Glasgow, UK, [3]SRUC, Scotland's Rural College, Edinburgh, UK, [4]Harbro, Turrif, UK, [5]Morrison's Supermarkets, Yorkshire, UK, [6]Well Cow, Edinburgh, UK, [7]NMR, Harrogate, UK *Email:i.andonovic@strath.ac.uk*

Implications A decision support platform has been developed that promotes the implementation of precision farm management through providing the farmer with information on the condition of individual animals.

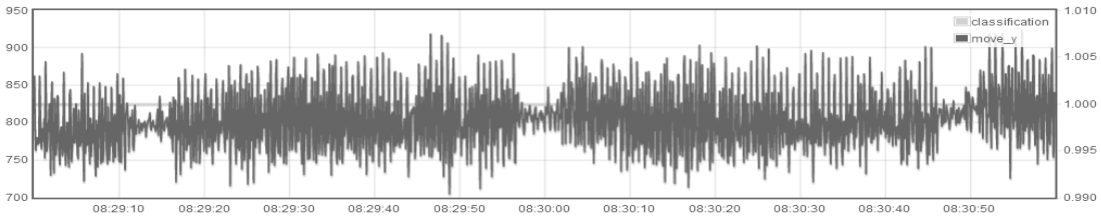
Introduction Farmers are continually challenged to balance low profits with rising feed, labour and infrastructure costs. In the recent past an average of two farms per day abandon dairy farming and those that remain operate increasingly larger herds to maximise profit through scale. As a result, there is a growing reliance on technology to carry out core functions such as identifying cows on heat. Here, a short **s**ummary is provided of the impacts from the InnovateUK-funded project entitled "Animal Electronic Recording, Transmission and Synthesis (ALERTS)".

Material and methods The foundation of the technology solutions rest on signatures derived from collars monitoring neck movement in three dimensions using an accelerometer. The methodology centres on the collection of movement data along with reliable behavioural and physiological truthing data such that software that accuratrely predicts key cow states can be robustly developed and quantified. The resultant signatures are subsequently validated under representative commercial environments. The engine of the practical solution is neck mounted collar to ease deployment and maintenance. However, for the purposes of the development, evaluation and validation of the solutions, a supporting range of technologies e.g. progesterone testing, HoKo feeders are utilised to verify collar sensor outputs.

Results A number of key signatures have been developed through the analysis of accelerometer based collar measurements; oestrus for beef/dairy, calving for beef/dairy and most strikingly an accurate indication of eating and rumination times identified through a combination of frequency and statistical analysis. A range of post processing methods have been evaluated in order to determine the most appropriate software for integration within a low power processor on the collar. In the case of eating/rumination, trials have been carried out using a rumination sensing halter to provide verification data (Figure 1). Analysis of the data over a period of several days has shown that it is possible to recover eating and rumination times at minute by minute granularity with sensitivity and positive predictive value (PPV) greater than 90%.



(a)



(b)

Figure 1 RumiWatch halter output of rumination (a); rumination signature measured using a neck mounted collar (b).

Conclusion Highly scalable and highly functional technologies that assist in the evolution of precision livestock farming are critical to the health of the farming sector. The ALERTS consortium has brought together a spectrum of disciplines ranging from world leading agricultural science and engineering researchers through to industries delivering technology solutions and operating in the dairy supply chain. The cross-disciplinary expertise across the team has prodcued a number of new integrated system solutions that facilitate the dairy industries growing demand for milk by boosting on-farm herd performance, in so doing increasing the security of the food supply.

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Insects – an alternative protein source for use in monogastric livestock feed

M E Wakefield[1], A Charlton[1], M Dickinson[1], K Robinson[1], E Fitches[1], A Booth[2], J Sissins[2], H Hall[2]
[1]The Food and Environment Research Agency, Sand Hutton, York, YO41 1LZ, UK, [2]AB Agri Ltd, 64 Innovation Way, Peterborough Business Park, Peterborough, PE2 6FL, UK
Email:maureen.wakefield@fera.gsi.gov.uk

Implications Larvae of the house fly, *Musca domestica*, have been evaluated as a sustainable source of protein in feed for monogastric livestock. Nutritional analysis has demonstrated the potential for inclusion of insect protein in animal feed.

Introduction Sustainable protein sources are required for inclusion in animal feed. More than 40 million tonnes of crop proteins, primarily soy beans and corn gluten feed, are imported annually into EU countries representing 80% of the EU's crop protein consumption (Häusling, 2011). The growing global population coupled with a change in dietary patterns, with increasing consumption of meat and fish, requires that other protein sources, less reliant on cropping systems, are available. Insects are a good source of protein and can be incorporated in animal feed for poultry, fish and pigs. Although rearing of insects with the intention of feeding to domestic animals/fish has been evaluated for several decades (e.g. Bondari and Sheppard, 1987; Newton *et al*., 2005; Hem *et al*., 2008), there has been limited adoption at a large scale. Insects can be reared on a range of organic waste products and in addition to providing valuable products (protein, oils etc) will also reduce waste volumes adding to the environmental sustainability of the system.
There are several areas of research that need to be undertaken before the use of insect protein in monogastric livestock feed can be viewed as a commercially viable proposition. Legislation in the EU does not currently permit the use of insect protein in animal feed and research needs to inform and provide evidence, particularly with regard to safety, to support the possibility of a change in legislation. Mass production methods and demonstration of acceptability and efficacy of the insect protein in the diet also need to be demonstrated. We have developed a system for rearing larvae of the house fly, *Musca domestica*, on poultry litter and have evaluated the nutritional properties of the larvae for inclusion as a protein source in feed for mongastric livestock.

Material and methods A system for rearing larvae of the house fly, *Musca domestica,* on poultry litter was established in the laboratory. Larvae egressed naturally from the poultry litter prior to pupation. The larvae were left to clear their guts prior to processing. The nutritional profile of the larvae (protein and fat content and amino acid and fatty acid composition) was determined using standard analytical techniques. Larvae were subsequently reared on a larger scale and the pepsin digestibility and mineral content were determined in addition to protein and fat analysis. An insect meal is currently being evaluated for protein digestibility in a trial with poultry.

Results Protein levels in *M. domestica* larvae reared on poultry manure generally exceed 50% on a dry matter basis. Levels of methionine, lysine, tryptophan and threonine are equivalent to or exceed those found in soymeal. Palmitic acid, palmitoleic acid, oleic acid and linoleic acid are the main fatty acids found in *M. domestica* larvae The amino and fatty acid profiles are suitable for inclusion in monogastric livestock diet in comparison with soya and fishmeal.

Conclusion The nutritional composition of *M. domestica* larvae reared on poultry manure is suitable for inclusion in monogastric livestock feed. The feeding trial will determine the digestibility of feed containing insect protein. The safety and quality of the insect protein have also been assessed. Changes in the legislation will be required before insect protein can be used in animal feed in the EU. Further research and development to establish a commercially viable insect mass rearing system is required.

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Bean starch concentrates as home grown alternative to soya bean meal in grower and finisher pig diets

L A Smith[1], M Balduino Gonçalves dos Reis[2], O Olukosi[1], J G M Houdijk[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]University of Sao Paulo, Brazil
Email:jos.houdijk@sruc.ac.uk

Implications Bean starch concentrates derived from air classified faba beans has the potential to reduce reliance on soya bean meal and wheat in growing and finishing pig diets.

Introduction Air classification of finely ground, dehulled faba bean (*Vicia faba*) produces a starch-rich co-product with moderate levels of crude protein (CP). Here, we have tested the hypothesis that such bean starch concentrate (BSC) can replace soya bean meal (SBM) in growing and finishing pig diets.

Material and methods We included BSC at 0, 60, 120, 180, 240 and 300 g/kg, gradually and completely replacing SBM from grower and finisher pig diets containing SBM at 140 and 120 g/kg, respectively. The BSC used had a CP level of 222 g/kg dry matter. Using previously established BSC digestible energy and standardised ileal digestible (SID) amino acid levels (Houdijk and Olukosi, 2014), iso-energetic diets were formulated (NE 9.3 and 9.0 MJ/kg for growers and finishers, respectively), at similar SID lysine (8.1 and 7.1 g/kg). To meet minimum requirements of methionine, threonine, tryptophan, calcium and digestible phosphorus (BSAS, 2003), levels of soya oil, pure amino acids and macro-minerals were modified. BSC replaced SBM on a SID Lysine basis, and wheat was gradually reduced from 283 to 116 g/kg and from 264 to 79 g/kg for grower and finisher diets, respectively. Barley, molasses, rapeseed meal, wheatfeed and trace element / vitamin premix levels were kept constant. Each diet was fed *ad libitum* to two groups of three male and two groups of three female terminal line grower (30 to 60 kg) and finisher (60 to 100 kg) pigs (LW × L), for three weeks, after a one-week adaptation period. Weekly live weights for individual pigs, and pen feed intakes were recorded to assess body weight gain (BWG, g/pig/day), average daily feed intake (ADFI, g/pig/day) and feed conversion ratio (FCR as ADFI/BWG). Data was analysed for feeding treatment and sex effects using a 6×2 factorial ANOVA, with initial body weight as covariate and pen as experimental unit. Contrast statements were used to locate linear and quadratic effects of dietary BSC level.

Results There were no feeding treatment effects on grower BWG, ADFI and FCR or finisher ADFI and FCR (Table 1). However, BSC quadratically affected finisher BWG; pigs grew less on 120 to 240 g/kg but not on 300 g/kg diets. There were no overall sex effects on grower or finisher performance or interactions with feeding treatment for grower BWG, ADFI and finisher performance (data not shown). However, sex and feeding treatment interacted for grower FCR (P=0.03), where FCR gradually increased from 2.21 to 2.77 in male pigs but decreased from 2.70 to 2.22 in female pigs (P=0.001).

Table 1 Effect of replacing soya bean meal with bean starch concentrates on performance of grower and finisher pigs.

	Grower Pigs			Finisher Pigs		
BSC inclusion levels (g/kg)	BWG (g/pig/day)	ADFI (g/pig/day)	FCR	BWG (g/pig/day)	ADFI (g/pig/day)	FCR
0	796	1873	2.46	1093	2867	2.61
60	805	1913	2.57	1111	2895	2.53
120	805	1951	2.51	988	2850	3.04
180	818	1923	2.36	1000	2833	2.80
240	809	2143	2.66	989	2744	2.71
300	782	1872	2.47	1079	2832	2.61
s.e.d.	42	111	0.13	52	117	0.23
P-value for BSC inclusion effect						
Linear	0.85	0.34	0.84	0.19	0.36	0.85
Quadratic	0.44	0.26	0.92	0.03	0.87	0.13

Conclusion Although we observed a biologically unclear quadratic relationship between BSC and finisher BWG, there was no effect on ADFI and FCR. This was consistent with effects of whole faba beans on finisher pig performance (Smith *et al*., 2013), and suggests that feeding pigs BSC based diets during the grower and finisher phase combined is unlikely to affect overall pig performance, indicating that BSC may be a viable home-grown alternative to SBM in pig diets.

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Relationships between dry matter intake and animal metabolic liveweight in young Stabiliser breeding bulls and finishing Stabiliser steers

J J Hyslop[1], R Fuller[2], U Taylor[2], D Thirlwell[3], D Dreux[4]
[1]SAC Consulting Ltd (SRUC), Edinburgh, UK, [2]Beef Improvement Group Ltd, Yorkshire, UK, [3]JSR Farming Ltd, Yorkshire, UK, [4]Kennan UK Ltd, Warwickshire, UK
Email:jimmy.hyslop@sac.co.uk

Implications DMI in Stabilser breeding bulls and finishing steers can be successfully determined across a wide range of animal liveweights (LW) with size of animal having little effect on the results when expressed relative to metabolic LW.

Introduction Measurements of net feed efficiency (NFE) in Stabiliser cattle requires that individual animal dry matter intake (DMI) be determined in either young breeding bulls or finishing steers. Methodologically, one question that may be asked is to what extent animals of differing LW can be used to obtain appropriate DMI estimates for such NFE determination. The objective of this data analysis was to examine how DMI varies in Stabiliser cattle of differing LWs.

Material and methods 395 Stabiliser breeding bulls between 10-13 months of age and 198 Stabiliser finishing steers between 15-18 months of age were offered a mixed forage/concentrate complete diet (CD) *ad libitum* for an adaptation period of 4 weeks and a subsequent measurement period of 56 days *via* electronic feed intake bins (Growsafe). Animals were fed these CD in 8 batches of approximately 80 animals/batch with wholecrop wheat forming the main forage for all the bulls and one batch of steers whilst the remaining steer batches were given maize silage as the basal forage. Forage:concentrate ratio in each CD was approximately 50:50 on a DM basis. Animal LW was determined weekly whilst DMI was recorded continuously using individual electronic ear tags and their associated computer software. Descriptive statistics and relationships between animal size and DMI parameters for both bulls and steers were examined in Genstat 15.

Results Descriptive statistics for LW, metabolic LW (MLW) and DMI expressed as kg/d, g/kg LW and g/kg MLW (g/kg $LW^{0.75}$) are given in Table 1. Steers were heavier than bulls due to their greater age and consequently consumed higher actual DMI levels (kg/d) and DMI increased as animal LW (kg) increased as expected (Figure 1). However, when scaled to LW, average DMI was almost identical at 21.6 and 21.8 g/kg LW for bulls and steers respectively. In addition, there was little relationship between DMI and animal metabolic LW ($LW^{0.75}$) for either bulls or steers (Figure 2).

Table 1 LW and DMI parameters in young Stabiliser breeding bulls (n=395) and finishing Stabiliser steers (n=198)

	Mean	Min	Max	s.d.	CV%		Mean	Min	Max	s.d.	CV%
Bulls						*Steers*					
LW (kg)	536	376	718	68.1	12.69	LW (kg)	597	483	680	32.6	5.46
MLW (kg)	111	85	139	10.6	8.59	MLW (kg)	121	103	133	4.93	4.08
DMI (kg/d)	11.5	7.4	15.4	1.51	13.08	DMI (kg/d)	13.0	10.4	15.8	1.13	8.70
DMI (g/kg LW)	21.6	16.5	28.1	1.93	8.94	DMI (g/kg LW)	21.8	17.5	26.7	1.53	7.03
DMI (g/kg $LW^{0.75}$)	104	80	133	8.90	9.54	DMI (g/kg $LW^{0.75}$)	108	89	130	7.52	6.99

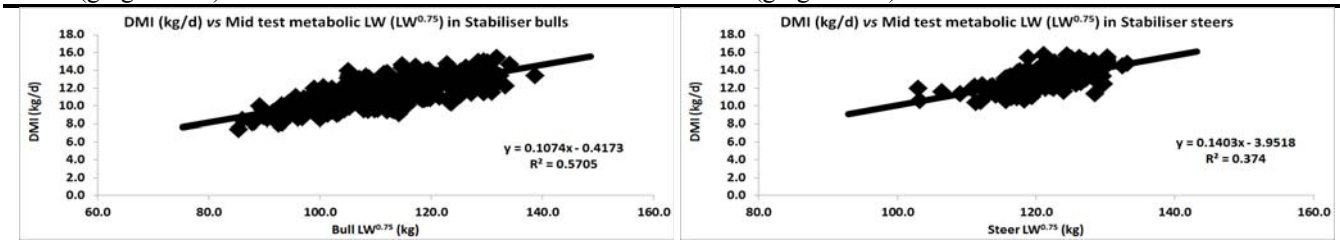

Figure 1 Individual Stabiliser bull and steer actual DMI values (kg/d) scaled to mid-test metabolic LW

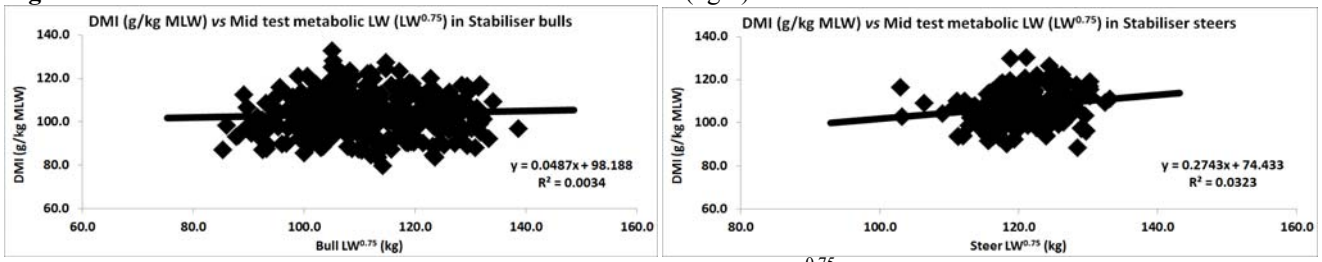

Figure 2 Individual Stabiliser bull and steer relative DMI values (g/kg $LW^{0.75}$) scaled to mid-test metabolic LW

Conclusion When scaled to animal MLW, DMI in these Stabiliser cattle has little relationship with animal size *per se*.

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Genetic determination of net feed efficiency (NFE) and other performance traits in Stabiliser beef cattle

R Roehe[1], R J Fuller[2], U Taylor[2], D Thirlwell[3], D Dreux[4], J J Hyslop[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]BIG, Southburn Offices, Driffield, UK, [3]JSR Farming Ltd, Southburn Offices, Driffield, UK, [4]Kennan UK Ltd, Stoneleigh Park, Warwickshire, UK
Email:rainer.roehe@sruc.ac.uk

Implications The magnitude of the heritability of NFE and its genetic correlations with other performance traits determines the success of breeding for feed efficiency.

Introduction Feed costs typically account for 70 to 80% of the variable costs of beef production. Consequently, genetic improvement of feed efficiency is a key breeding objective because of its large economic and positive environmental impact on beef cattle production. For an efficient selection for NFE, the heritability and its genetic correlations with other performance traits have to be known. Furthermore, the accuracy of estimation of genetic parameters may be improved by using extended pedigree information. Therefore, the objectives of this study were (i) the estimation of the heritabilities of NFE and other performance traits, (ii) the investigation of the impact of considering an extended pedigree in the analysis on the accuracy of the heritabilities and (iii) the estimation of the genetic correlations between NFE and other performance traits.

Material and methods A total of 591 Stabiliser beef cattle were performance tested on station for 56 days in 8 batches from 2012-2014. A mixed forage/concentrate complete diet was offered *ad libitum* and individual daily dry matter intake (DMI) was measured *via* an electronic feeder system Growsafe. Animals originated from 16 herds and comprised of 394 breeding bulls and 197 finishing steers with an average start (SW) and end of test weight (EW) of 507 kg (SD 64 kg) and 603 kg (SD 66 kg), respectively. Daily liveweight gain (LWG) was determined by linear regression of weekly measured LW during the 56 days test period. Feed conversion ratio (FCR) was calculated as kg DMI/kg LWG. NFE was derived for individual animals as the difference between actual DMI and estimated DMI, which was estimated using a multiple regression model including mid-test metabolic LW ($LW^{0.75}$), LWG, and fat depth at the end of test (FD) (for steers additionally killing out proportion was included in the model). The genetic analysis was alternatively carried out based on either a sire or an animal model. In the animal model, pedigree information of 5 generations, comprising of 2544 animals was considered. The fixed effects included in all models were herd of origin, batch and sex status (bull or steer), with additional linear covariables of SW or EW for the traits DMI, LWG, NFE or DMI, NFE, FD, respectively. Heterogeneous variances between different sex statuses were considered in the analysis. The univariate analyses based on a sire model were carried out using the Mixed procedure of SAS, whilst for the multivariate analysis based on an animal model the variance components estimation programme VCE was used.

Results Based on the superior animal model, the heritability of NFE was of moderate magnitude and only slightly lower than for LWG (Table 1). Substantially larger heritability was obtained for DMI. Using a sire model, the errors of estimation of heritabilities increased substantially and some traits such as FCR and DMI resulted in substantially lower estimates. Genetic correlations between NFE and LWG or FD were both 0.029 (s.e. 0.029) and thus very small and non-significantly ($P > 0.05$) different from zero.

Table 1 Means, standard deviations (SD), heritabilities (h^2) and their standard errors (SE) using a sire or an animal model

			Sire model		Animal model	
	Mean	SD	h^2	s.e.	h^2	s.e.
DMI (kg)	12.02	1.56	0.38	0.14	0.54	0.03
LWG (kg/day)	1.711	0.316	0.37	0.19	0.42	0.02
FCR (kg/kg)	7.230	1.491	0.24	0.19	0.40	0.03
NFE (kg)	-0.020	0.717	0.30	0.14	0.34	0.02
FD (mm)	5.76	1.99	0.47	0.16	0.41	0.02

Conclusion The genetic analysis showed that NFE can be efficiently used to genetically improve feed efficiency independent from growth and body composition due to its moderate heritability and its genetic correlations with LWG and FD around zero. This shows that NFE is both phenotypically and genetically independent of growth and body fatness, which is the optimal condition for an efficient use of NFE in genetic improvement. The importance of incorporating large pedigree information in the genetic analysis is shown by comparing a sire model (only sire information used) and an animal model (considering 5 generation of pedigree). This resulted not only in an increase in accuracy of the estimates but also in substantially different estimates. In particular, estimates of FCR seem to need substantial pedigree information to achieve reliable estimates. One reason may be that FCR is a ratio trait that is known to have undesirable statistical properties.

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Animal performance and efficiency of two divergent breeds of finishing steers offered either a concentrate-straw or a silage based diet *ad libitum* with either nitrate or increased dietary oil

C-A Duthie, J Rooke, S Troy, J J Hyslop, D Ross, A Waterhouse, R Roehe
SRUC, Scotland's Rural College, Edinburgh, UK
Email:carol-anne.duthie@sruc.ac.uk

Implications Inclusion of nitrate or increasing the dietary oil content in the diet of finishing beef cattle, with the primary aim to mitigate methane emissions, does not adversely affect animal performance and efficiency.

Introduction Dietary manipulation is practical and effective for mitigating methane from ruminants; however, it is important that any adopted strategy does not adversely affect production efficiency. Nutritional strategies are based on one of the following principles: (i) reducing the hydrogen production during fermentation (e.g. by increasing the level of dietary concentrate), (ii) direct inhibition of methanogenesis (e.g. by increasing the level of dietary oil), or (iii) providing alternative pathways for the use of hydrogen (e.g. supplementary nitrate). The objective of this study was to investigate the effect of key nutritional strategies, designed to reduce methane emissions, on performance and efficiency of finishing beef steers.

Material and methods The experiment was a 2x2x3 factorial design comprising 2 breed types (CHx, Charolais cross; and LUI, Luings); 2 basal diets consisting of (g/kg DM, forage:concentrate) 520:480 (Mixed) or 84:916 (Concentrate); and 3 treatments: (i) control with rapeseed meal as the protein source, (ii) rapeseed meal replaced with nitrate (18 g nitrate/kg DM) or (iii) rapeseed cake (increasing the oil to 48 g/kg DM). Steers (n=84) were group-housed in even numbers of each breed across 6 pens; each diet x treatment was allocated to 1 pen. Individual feed intake was recorded for 56 days, with feed offered *ad libitum*. Liveweights (LW) were measured weekly and ultrasonic fat depth (FD, $12^{th}/13^{th}$ rib) at the end of test. Growth was modelled by linear regression of weight against test date, to describe average LW gain (LWG), mid-test LW and mid-test metabolic LW ($MLW=LW^{0.75}$). Feed conversion ratio (FCR) was average dry matter intake (DMI, kg/day)/LWG. Residual feed intake (RFI) was calculated as deviation of actual DMI from DMI predicted based on linear regression of actual DMI on LWG, MLW and FD. Killing out proportion (KO) was (cold carcass weight (CCW)/slaughter LW)*1000. To test for breed, diet, treatment and interaction effects, the mixed procedure of SAS was used (SAS Inst. Inc.) with the random effect of pen (and slaughter batch for traits measured at slaughter).

Results Treatment did not affect animal performance. Mean values for breed*diet are given in Table 1. CHx steers had higher LWG than LUI steers (P<0.01). Mixed-fed steers had a higher level of DMI compared to Concentrate-fed steers (P<0.001). For DMI/kg LW, CHx steers consumed less (P<0.001) per kg LW than LUI steers. Consistent with FCR, CHx steers had lower RFI values (more efficient) than LUI steers (P<0.01) and Concentrate-fed steers were more efficient than Mixed-fed steers (P<0.01). A diet-by-treatment interaction effect (P<0.05) indicated that Concentrate-fed steers offered nitrate were most efficient. CHx steers had heavier CCW than LUI steers (P<0.001) and a greater KO (P<0.001).

Table 1 Effect of breed and basal diet (Mix, Mixed; Conc, Concentrate) on growth, feed intake and feed efficiency

	Mix CHx	Mix LUI	Conc CHx	Conc LUI	s.e.d.	Basal Diet	Breed	Diet*Breed
Mid-test LW (kg)	602	597	595	570	18.15	NS	NS	NS
Mid-test MLW (kg)	121.5	120.7	120.3	116.6	2.75	NS	NS	NS
LWG (kg/day)	1.62	1.45	1.49	1.32	0.07	NS	**	NS
DMI (kg/day)	11.73	12.25	10.97	11.02	0.41	***	NS	NS
DMI/LW(g/kg)	19.5	20.5	18.5	19.3	0.40	NS	**	NS
DMI/MLW(g/kg)	96.4	101.4	91.1	94.4	2.06	NS	**	NS
FD	6.4	8.5	6.5	8.0	0.53	NS	***	NS
FCR (kg, kg)	7.30	8.52	7.48	8.62	0.34	NS	***	NS
RFI (kg)	0.01	0.44	-0.40	-0.05	0.19	**	**	NS
Slaughter LW (kg)	724	717	720	683	15.91	NS	NS	NS
CCW (kg)	414.5	379.1	415.2	357.2	7.67	NS	***	*
KO	573.3	530.5	577.0	524.2	7.16	NS	***	NS

*<0.05, **<0.01, *** <0.001, NS = not significant (P>0.05).

Conclusion The key result from this study is that supplementing nitrate or increasing the level of dietary oil through the use of cold-pressed rapeseed cake does not adversely affect performance efficiency of finishing beef cattle. Nitrate may improve performance efficiency as shown by the improved feed efficiency of concentrate-fed steers offered supplementary nitrate.

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The impact of a health intervention scheme on the mobility of dairy cattle in the South West of England

F Shepherd, H Randle, P Ward
Duchy College, Cornwall, UK
Email:faye.shepherd@duchy.ac.uk

Implications Farmers who participated in 1:1 training with their vet delivered a greater reduction in lameness prevalence than farmers who only attended group training.

Introduction Lameness is a common condition in cattle, particularly in the dairy industry. It is a condition that can be extremely painful (Whay *et al*., 1997) and can greatly affect the productivity of the animal. Lameness is considered by many to be the most significant welfare issue affecting cattle. The most recent lameness prevalence (percentage of lame cows in a herd) in the UK was reported to be 36.8% (Barker *et al*., 2010). More recent data for the South West of England indicated lameness prevalence of 26.5% (Shepherd *et al*., 2012). Health intervention schemes have been used successfully to control and in some cases eradicate, diseases within the livestock industry (Presi *et al*., 2011). For this reason, there have been several health intervention schemes implemented to reduce the occurrence of lameness, with mixed success. This investigation examines the effectiveness of the Healthy Livestock Scheme, a Rural Development Programme for England (RDPE) funded scheme which ran from 2009-2014 and was aimed at improving animal health by reducing disease.

Material and methods Data were collected through the Healthy Livestock Scheme. In order for farmers to participate in the lameness strand, an initial mobility score (before any training with the farmer had taken place) and a final mobility score (after all training had been completed) was undertaken on their farm by an approved mobility scorer. The DairyCo mobility score scale was used to score every cow in the milking herd. The scores ranged from 0 (perfect mobility) through to 3 (severely lame). The number of cattle scoring scores two and three were then expressed as a percentage of the whole milking herd. In addition, a farm information questionnaire was completed for each farm which recorded information such as farm size, number of full and part time employees, farming system, housing system, number of cattle and the main breed. The veterinarian then discussed with the farmer which stages of the lameness strand would be most beneficial to the farm.
The initial sample size comprised 496 farms. Only 207 (41.7%) of the initial sample returned complete data and were subsequently used in the analysis. The dependent variables tested were the initial and final mobility scores (both of which were normally distributed). The independent variables tested were breed, herd size, farm size, farming system, housing system and number of staff working on the farm. The data was analysed using a one way analysis of variance (ANOVA) to discover whether there were any statistically significant findings between groups. Further post-hoc analysis was undertaken using the Least Significant Difference (LSD) test. Using a paired t-test the change between pre and post-intervention lameness prevalence was also analysed.

Results Pre-intervention lameness prevalence was 26.94% (n=207, ±13.3%), ranging from 3% to 77%. Post-intervention herd lameness prevalence for the sample (n=207) was 20.7% (±10.8%), ranging from 3% to 58%. A mean reduction in lameness prevalence of 6.2% was statistically significant ($p=0.001$). Farmers participating in only 1:1 stages of the Healthy Livestock lameness strand saw a mean lameness prevalence reduction of 8.4% (± 12.1%), in comparison to those who only undertook group stages of the healthy livestock strand which indicated a 2.5% reduction (±7.9%) in lameness. This difference was significant ($p=0.006$). There was no significant difference between the number of stages the farmer attended and the change in prevalence ($p=0.068$). The housing type, farming system, breed, herd size and farm size all had no significant effect on the change between pre and post intervention lameness prevalence ($p>0.005$).

Conclusion This research agrees with previous research that positive changes on farm are most likely to occur when a veterinarian is present and the farmer is undertaking 1:1 training. Although direct interaction between farmers and vets is a more expensive way of providing training than group training, it has a greater impact upon lameness levels on farm. This should be considered when shaping future health intervention schemes and funding provision.

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Prevalence of subclinical hypocalcaemia in Holstein dairy cows

V Tsiamadis[1], N Panousis[1], M Kritsepi-Konstantinou[1], A Kougioumtzis[1], G Banos[1,2], G E Valergakis[1]
[1]Faculty of Veterinary Medicine, Aristotle University, Thessaloniki, Greece, [2]SRUC, Scotland's Rural College/Roslin Institute, Edinburgh, UK
Email:etsiamad@vet.auth.gr

Implications Results from this study can contribute towards defining a pattern of subclinical hypocalcaemia prevalence prediction during the first 8 days after calving.

Introduction Calcium (Ca) balance is of great importance to the dairy cow, especially the first critical days after calving. Normally, serum Ca concentration is maintained within a narrow range, between 8.3 and 10.4 mg/dL (Divers, Peek and Rebhun, 2008). Worldwide, the overall incidence of clinical hypocalcaemia (milk fever, MF) is reported to be 5 – 7%; however, prevalence of subclinical hypocalcaemia (SHC) is much higher: it was present in 25%, 41%, 49% and above 50% for the 1 – 4+ lactation cows, respectively (Reinhardt *et al*., 2011). Our objective was to estimate the prevalence of SHC in Greek dairy herds, during the first 8 days after calving.

Materials and methods The study included 1,021 Holstein dairy cows (1–4+ lactations) in 9 herds in Northern Greece. Clinical examination and blood sampling was carried out at 1st, 2nd, 4th and 8th DIM. All cows were fed a balanced diet during the dry period, without the inclusion of anionic salts, or acidifiers. MF cases were recorded after calving. Thirty five MF animals were treated with iv Ca at 1st or 2nd DIM and were excluded from the study. Total number of repeated records summed to 3,944. Serum Ca concentrations were determined with atomic absorption spectrophotometry (AAS Perkin Elmer A 100). SHC was defined as serum Ca concentration below 8.3 mg/dL, without the presence of clinical signs of MF. Serum Ca concentrations and SHC cases were analysed with a univariate random regression model, including the fixed effect of farm, year-season of calving, parity, age at calving and DIM and the random regressions on DIM from calving associated with the additive genetic effect. Estimates of (co)variance components from this model were used to predict SHC prevalence after calving. The ASREML software was used for all statistical analysis (Gilmour *et al*., 2006).

Results Overall mean serum Ca concentration (±s.e.m.) was 8.92±0.018 mg/dL. Mean Ca concentrations for the 1st DIM were 9.14±0.05, 8.49±0.07, 8.30±0.10 and 7.94±0.11 mg/dL, for the 1st, 2nd, 3rd and 4th+ lactations, respectively. With the use of univariate random regression model, prediction lines for SHC prevalence were created for DIM 1 – 8. (Figure 1).

Table 1 Prevalence (%) of SHC cases per DIM and lactation number.

DIM	Lactation number			
	1st	2nd	3rd	4th+
1	18.6	44.6	48.4	64.9
2	26.0	40.4	56.4	45.3
4	20.4	22.5	27.7	27.7
8	14.6	16.3	19.5	23.4

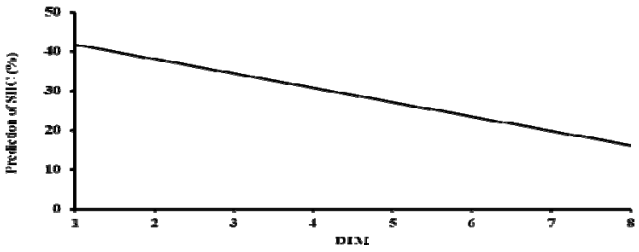

Figure 1 Subclinical hypocalcaemia prevalence (s.e.m. = 0.02).

Mean prevalence of SHC was 42% at DIM 1 and was still over 16% on DIM 8 (Figure 1). Moreover, interesting and unexpected were the following findings: a) 45 cows had serum Ca concentrations equal or below 6.0 mg/dL (which the majority of references define as the cut-off for MF) without manifesting any typical clinical sign of MF (lateral or sternal recumbency); and b) 4 cows with sternal recumbency had Ca concentrations between 6.0 and 8.3 mg/dL.

Conclusion Prevalence of SHC is high in Holstein cows during the first 8 DIM. Prevalence is higher at DIM 1, 2 and 4, especially for 3rd and 4th + lactation cows. Hence, SHC prevention with the use of nutritional/management practices is imperative. Moreover, genetic selection for enhancing (sub)clinical hypocalcaemia resistance should be attempted as it will lead to additive and permanent results. Associations between MF clinical symptoms and MF Ca concentrations may have to be re-defined.

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Development of a model to investigate the host-parasite interactions between first season grazing calves and *O. ostertagi*

Z Berk[1], S Bishop[2], A Forbes[3], I Kyriazakis[1]
[1]University of Newcastle, Newcastle-Upon-Tyne, UK, [2]University of Edinburgh, UK, [3]University of Glasgow, UK
Email:z.berk@newcastle.ac.uk

Implications As the emergence of parasite resistance to anthelmintics is a serious issue in grazing ruminants (Sutherland and Leathwick, 2011) the development of effective control strategies to reduce the rate of selection for anthelmintic resistance is an imperative. Simulation models that enable the investigation of the consequences of such strategies may constitute a cheap and faster alternative to experimentation: here we describe the development of a novel model for cattle.

Introduction Gastrointestinal (GI) parasitism poses a major challenge to the health, welfare and productivity of cattle. *Ostertagia ostertagi* is one of the most prevalent GI parasites of cattle worldwide and is responsible for health challenges to cattle in the UK. The objective of this work was to develop a deterministic, dynamic model to predict the dynamics of *O. ostertagi* and consequences to the host of different levels of infection in first season grazing cattle.

Material and methods The model stems from the principles developed by Laurenson *et al*. (2011) to represent ruminant host-GI parasite interactions. Initially, the growth of a healthy calf was simulated, taking into account genotype and nutritional conditions. Subsequently, the effects of *O.ostertagi* infection were simulated using published data sets to estimate parameters. The effect of the immune development on within-host dynamics of the parasite was assumed to be a function of larval exposure, and the subsequent phenomenon of parasite-induced anorexia was assumed to occur as a result of the rate of immune development. Abomasal damage was assumed to cause plasma loss (Fox, 1993).Worm egg production was a function of worm number and fecundity which, in turn, showed density-dependent constraints. Simulations were run over 200 days for three infection doses of 3,500, 7,000 and 14,000 infective larvae administered daily.

Results Worm burdens were greatest at higher challenge doses, but once immunity was developed the decline was steeper for higher challenges (Figure 1). Worm burdens never reached zero even when immunity was fully developed. Egg outputs (data not shown) were a reflection of the worm burdens; however the relative differences between challenge levels were smaller, due to the density dependence effects. A reduction in food intake was observed for all infection levels; with the reduction being greater for larger challenges. The point at which the maximum reduction in intake was observed was earlier for higher infection levels and all intakes returned to levels similar to a healthy host towards the latter stages of infection. As challenge level increased the losses in weight gain were disproportionately larger than the increase in challenge (Figure 2).

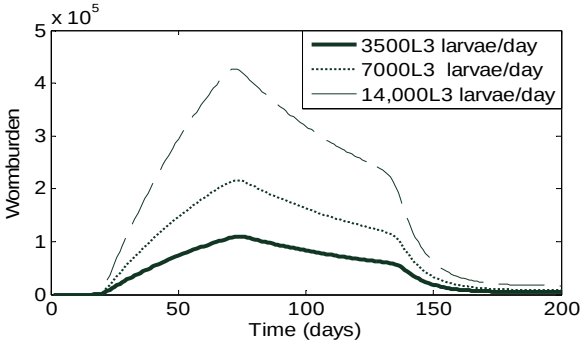

Figure 1 Simulated worm burdens over 200 days in calves administered one of 3 levels of infection of *O. ostertagi* L3 larvae

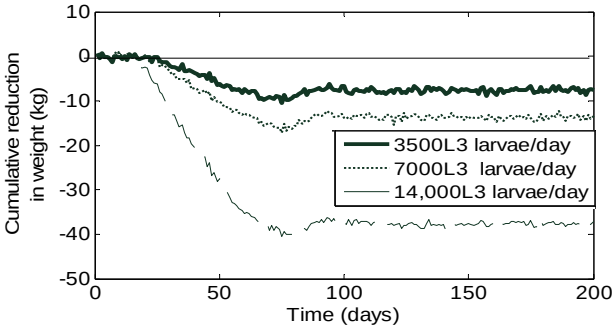

Figure 2 Bodyweight losses (compared to uninfected controls over 200 days) in calves administered one of 3 levels of infection of *O. ostertagi* L3 larvae.

Conclusion A model simulation has been developed which has behaviour consistent with our understanding of GI parasitism in sub-clinically infected calves. Predicted features of interest are: (i) the increased rate of decline in peak worm burdens for greater challenge doses, reflecting the greater immune response, (ii) smaller differences in egg outputs than worm burden with changing challenge level, due to the density-dependence effect, and (iii) disproportionately large body weight losses with increasing challenge level, due to greater parasite-induced anorexia and the inability to meet increased nutrient demands for repair. To ensure confidence in the model it must be validated against published literature studies.

Acknowledgments The authors acknowledge funding from BBSRC and Merial

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Evaluation of a model to investigate the host-parasite interactions between first season grazing calves and *O. ostertagi*

Z Berk[1], S Bishop[2], A Forbes[3], I Kyriazakis[1]
[1]University of Newcastle, Newcastle Upon Tyne, UK, [2]University of Edinburgh, UK, [3]University of Glasgow, UK
Email:z.berk@newcastle.ac.uk

Implications We show that a simulation model predicting impacts of gastrointestinal parasitism on calves produces output results that agree well with independently produced experimental data, and we identify the most influential parameters.

Introduction We have developed a model that predicts parasitological outputs (worm burdens and total egg outputs) and performance traits (food intakes and performance) for different infection modes and levels of infection in grazing calves (Berk *et al*., 2015). But before confidence can be placed in model predictions an evaluation must be conducted. The objectives of this study were to conduct a sensitivity analysis, and to compare model predictions with observations from relevant parasitological data, to validate the model concepts and parameters (Michel, 1970; Syzska and Kyriazakis, 2013).

Material and methods A sensitivity analysis was conducted on model predictions for a subset of parameters using a Latin hypercube design. Parameter combinations covered a wide scope of possibilities, whilst having relatively few simulations (250). The mean parameter values were taken as the best estimate and all parameters were assumed to be normally distributed with CVs of 20%. To analyse the impact of variation in parameter on model predictions, an ANOVA was conducted for each parameter to test for significance ($P < 0.05$). Independent sets of published experimental data were then used to independently validate model performance using both graphical comparisons and statistical tests of goodness-of-fit. Bias and root-mean-square error were calculated from differences in model predictions and reported data; these were tested for significance ($P < 0.05$). Literature studies were selected as follows (1) Infections were *O. ostertagi* alone with no other parasite species involved; (2) all calves were infected during the growing phase; (3) calves were allowed access to ad-libitum, high quality feed; (4) calves had no prior experience of parasitism at the start of the experiment. Comparisons reported here are for worm burdens (Michel, 1970) and faecal egg outputs (FECs) (Syzska and Kyriazakis, 2013).

Results The sensitivity analysis revealed that model prediction of parasitological traits were most sensitive to the rate of immune development for host-controlled larval establishment and worm mortality; this implies the immune development rate has a large impact on worm burdens and subsequent parasitological outputs. Michel (1970) investigated worm burdens following trickle infections. The simulated and observed values followed the same pattern of increasing worm burdens up to a peak followed by a decrease: the correlation between predicted and observed values was r=0.78 (Figure 1). Although there was no systematic bias in the predicted results, not all predicted values fell within the one standard deviation (SD) of true values as indicated by the RMSE. Szyszka and Kyriazakis (2013) investigated the FEC for weekly larval challenge and found that FECs started low, increased to a peak approximately 35 d post infection and decreased thereafter. There was a positive correlation (0.75) with our model predictions (Figure 2). The predicted values were mostly within the one SD as indicated by the RMSE well within the 95% confidence interval; hence there was also no significant bias.

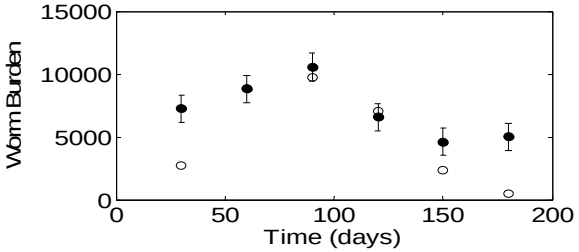

Figure 1 A comparison of the observations (●) by Michel (1970) to simulated predictions (o) for worm Burdens, from infections of 340 L3 larvae per day

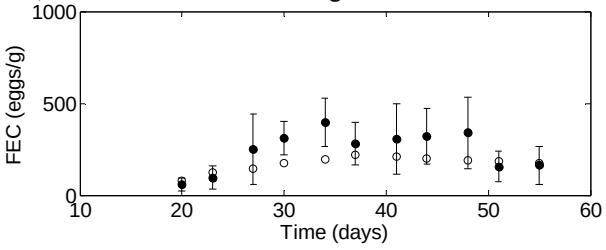

Figure 2 A comparison of experimental observations (●) from Syzska and Kyriazakis (2013) to simulated predictions (o) for FECs from an experimental infection of 50,000 L3 larvae per week.

Conclusion In general the developed model satisfactorily predicted parasitological traits, although after several comparisons with published literature (results not shown) the model was more effective at predicting the effects of sub-clinical rather than clinical challenges. Differences amongst independent published studies were large; this has been attributed to variability in calf genotypes and small samples sizes. The key question is whether development of a stochastic model incorporating variability between animals will account for the full range of experimentally observed outcomes.

Acknowledgments The authors acknowledge funding from BBSRC and Merial

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Low periconception and first trimester dietary protein affects development of immune function in beef calves

D Lomas[1], K Copping[2], R Flynn[1], T Coffey[1], V E A Perry[1]
[1]University of Nottingham, Sutton Bonington, UK, [2]University of Adelaide, Australia
Email:viv.perry@nottingham.ac.uk

Implications Low protein during the periconception period in heifers may reduce immune function in calves

Introduction Neonatal deaths in British suckler herds are surprisingly high at 8%, costing UK farmers £60 million per annum. A combination of dystocia, maternal diet during pregnancy and highly muscled genotypes have all increased susceptibility to cold stress and hence disease in the newborn. Passive immunity transferred via colostrum is affected by maternal nutrition[1]. Concomitantly, we have shown that foetal developmental is affected by the periconception (-60days) and first trimester of pregnancy (90 days) maternal diet[2,3]. The aim of the current study was to investigate the effects of maternal dietary protein during this period on colostrum quality and foetal immune development.

Material and methods Maiden yearling heifers (n=360) were selected. Prior to synchronised AI using a single sire, heifers were randomly assigned to two equal groups and individually fed a high (14%CP) or low (7%CP) protein pellet diet. 23 days post conception (dpc) (post implantation in the cow) each high or low group was again split into high (H) or low (L) protein diet treatment for the first trimester, yielding four treatment groups (HH, HL, LH, LL). Diet treatments ceased at 98 dpc. Foetuses (n= 48) and placentae were excised at 98 dpc, weighed, measured and dissected. The remaining heifers (n=64) were taken to term. Colostrum was collected at birth and calves weighed, bled and measured for morphometry prior to suckling.
Statistical analysis was completed using factorial ANOVA with diet, conception stage and fetal sex as main factors, with interactions between these being explored.

Results Immunoglobulin levels in colostrum were affected by heifer diet: IgG1 was increased by both the periconception ($p=0.03$) and first trimester low protein diet ($p<0.001$). Female calves received higher IgG1 than males. IgA and lactoferrin were both increased by the low protein first trimester diet ($p<0.05$).
Immune function: Fetal thymus size and neonatal antimicrobial use ($p<0.05$) were increased by dietary protein in the periconception period.

Conclusion Low dietary protein in the periconception and first trimester of heifer pregnancy protein may decrease immune function in the offspring. Interestingly, the dams of these immune challenged neonates may compensate by increasing production of immunoglobulins in the colostrum. Research into gene expression in the thymus and spleen and long bone in progeny is ongoing.

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The prevalence and direct financial implications of pneumonia in slaughtered cattle in Kumasi abattoir, Ghana

V Attoh-Kotoku, B Emikpe, E L K Osafo, A Donkoh, O D Tawiah
KNUST, Kumasi/Ashanti, Ghana
Email:vattoh-kotoku.agric@knust.edu.gh

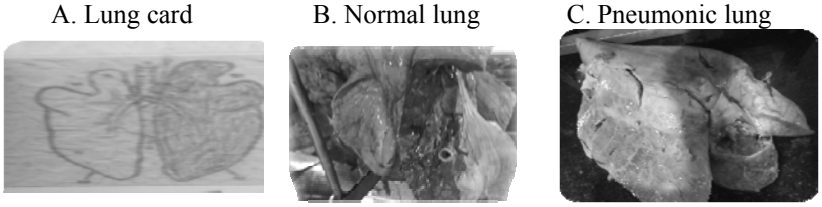
Implications Meat inspection could be handy, not only in determining the prevalence and extent of organ condemnation due to some zoonotic diseases but also to assess the direct financial loss due to organ condemnation.

Introduction A number of infections and parasitic diseases pose danger to the livestock industry in Ghana. Pneumonia an inflammation of the tissues of the lungs is one of the major disease conditions limiting the development of cattle production. Economic implications of pneumonia especially in meat breeds of cattle include treatment medications, deaths, decreased gain performance and decreased carcass value. The study seeks to determine the prevalence and pattern of pneumonia in slaughtered cattle and direct financial effect of lung condemnation.

Material and methods A cross-sectional active survey involving 1500 cattle was conducted for four months to determine the major causes of lung condemnation and estimate the direct economic loss. The lungs of 200 slaughtered animals were examined twice a week macroscopically using standard (visualisation, palpation or incision) examination procedures by trained meat inspectors under close supervision of Veterinarians to show the presence of pneumonia. Pathological lesions were differentiated and judged using guidelines on meat inspection for developing countries (FAO, 1994). The slaughtered stocks were grouped into three age groups: young (<2 years), adult (3-6 years) and mature (> 6 years) and age estimation was based on eruption of one or more incisor teeth (FSIS, 2013). Lung cards were designed to indicate the diseased portion noted by the abnormal colour of the lung. Economic losses due to condemnation of infected lungs were estimated by multiplying the cost of an average weight of healthy lungs by the total weight of infected lungs. The study cattle came to Kumasi abattoir from Kumasi and neighbouring countries in West Africa for slaughter. Collected data were analysed using Microsoft Office Excel 2007. Descriptive statistics such as mean, minimum and maximum values were used to determine the level of organ condemnation, which is the proportion of condemned organs to the total number of organs examined.

Results Table 1 shows that 36 (2.4%) cattle had pneumonia, out of which 26 (72.2%) lungs were totally condemned due to contagious Bovine pleuropneumonia while 10 (27.8%) lungs were partially affected. The total economic loss incurred due to lungs condemnation was estimated to be Gh₵1,848, about 616 USD on 1500 slaughtered cattle.

A. Lung card B. Normal lung C. Pneumonic lung



MALE; AGE: 5 ; BREED: WASH

Table 1 Number (N) of cattle slaughtered and affected with Pneumonia

Breeds	Cattle numbers (%)	Number with pneumonia (%)	Number with condemned lungs	Number partially affected
ZEBU	510 (34)	5	2	3
SANGA	270 (18)	4	2	2
N'DAMA	225 (15)	3	3	0
WASH	315 (21)	22	18	4
WHITE FULANI	180 (12)	2	1	1
TOTAL	1500 (100)	36 (2.4)	26	10

WASH; West African Short Horn

Conclusion The study revealed that pneumonia was one of the causes of lung condemnation in slaughtered cattle in Kumasi abattoir and causes significant economic loss in cattle production in Ghana.

Acknowledgements The authors would like to acknowledge the Management of the Kumasi Abattoir Company for allowing us to use their animals and facilities for the study.

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Identification of the rumen fluke *Calicophoron daubneyi* infecting cattle in Wales

K M Huson, P M Brophy, R M Morphew, N D MacKintosh
Aberystwyth University, UK
Email:kmh9@aber.ac.uk

Implications The widespread identification of rumen fluke infections in Welsh cattle highlights the need for further research into this emerging parasitic disease, in order to understand its potential impacts on animal health and production.

Introduction In recent years there has been a notable increase in reported incidences of rumen fluke parasites infecting livestock across the UK and Western Europe. In 2010 the Animal Health and Veterinary Laboratories Agency (AHVLA) began recording detection of this parasite in *post mortem* and faecal egg count examinations submitted for analysis in Britain, and in 2013 Gordan *et al* identified *Calicophoron daubneyi* as the species responsible for infection in 4 GB animals (3 cattle, 1 sheep). Clinical disease is rare, and largely associated with mass ingestion of infective metacercariae at grazing, which hatch in the duodenum and migrate to the rumen causing damage to the intestinal mucosa and clinical symptoms including diarrhoea, weight loss and mortality. Mature rumen fluke infections appear better tolerated, but their potential impact on animal production, and how they interact with both their host and the rumen environment is unknown. The aim of this study was to identify rumen fluke infections from a range of locations across Wales, and confirm the species present.

Material and methods Veterinary investigation surveillance data (VIDA) on findings of both liver and rumen fluke infections being identified in both faecal sample analyses and *post mortem* examinations performed across GB was kindly provided by the AHVLA. This data, as counts of rumen or liver fluke identifications provided by county, was grouped into 6 geographic regions based on AHVLA area coverage, and incidents of both rumen fluke infection and liver fluke infection were calculated as a percentage of total sample submissions to the AHVLA on a monthly basis from 2010-2013 inclusive. Samples of rumen fluke parasites were obtained during several visits to a local abattoir (Randall Parker Foods, Llanidloes) throughout 2014. In total, flukes were collected from 21 infected cattle from 14 farms around Wales and 1 in Shropshire. Infected animals ranged in age from 19 months to 15 years. Flukes were washed in warm (37 □C) phosphate buffered saline to remove rumen contents contamination and transported to the laboratory for storage at -80 □C. Additional 5 samples (4 cattle, 1 sheep) were provided by AHVLA Carmarthen, collected from the rumen during *post mortem* examination. For molecular species identification, genomic DNA was extracted from 3 specimens per infected animal using a Qiagen DNeasy® blood and tissue kit (Qiagen, Germany) according to the manufactures directions. Initially, 15 DNA samples (from 3 fluke per 5 infected animals) were subjected to PCR targeting the ITS-2 region of rDNA plus the flanking 5.8S and 28S sequences, as described by Gordan *et al* (2013). PCR products were then purified using a QIAquick® PCR purification kit (Qiagen, Germany), and sequenced using an ABI Prism® 3100 DNA analyser (Applied Biosystems, USA). Concensus sequences were generated using Geneious (Biomatters, NZ) and compared to reference sequences in GenBank® using BLASTn searches (http://www.ncbi.nlm.nih.gov/genbank). Remaining DNA samples were subjected to species specific PCR using the primers and protocol described for *C. daubneyi* by Martinez-Ibeas *et al* (2013) to confirm their identity.

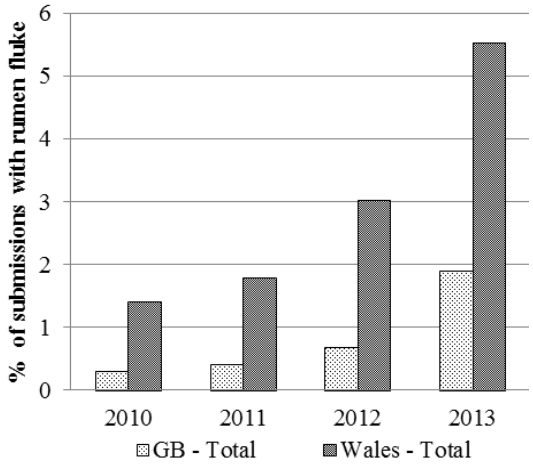

Figure 1 % of VIDA submissions diagnosable with rumen fluke annually.

Results Analysis of VIDA indicated a year on year increase in reports of rumen fluke infections across Britain (**Figure 1**). All 78 rumen fluke tested, from infections identified in 21 different bovines during slaughterhouse examination, plus samples provided by AHVLA were *C. daubneyi*. The ITS-2 sequences analysed had 100% homology with each other and the reference sequence for *C. daubneyi* deposited in Genbank® (accession number AY790883). All other samples successfully amplified with the *C. daubneyi* specific primers, confirming their identity.

Conclusion PCR based testing confirms that the rumen fluke *C. daubneyi* infects cattle finished and slaughtered in Wales. Data provided by the AHVLA suggests that this is potentially an emerging parasitic disease, thus supporting the industry's appeal for research into both the potential clinical and production impacts of rumen fluke infections, as well as a need to understand the fundamental biology of how this parasite interacts with both its host and the highly diverse rumen environment it inhabits.

Acknowledgements Many thanks to both Randall Parker Foods, Llanidloes, and Dr Sian Mitchell of AHVLA Carmarthen.

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A comparison of mastitis incidence in conventionally managed and organic dairy cows on the same farm

R Houghton, C Douglas, F da Mata
Newcastle University, Newcastle upon Tyne, UK
Email:catherine.douglas@ncl.ac.uk

Implications If organic cows are more susceptible to mastitis earlier in lactation, theoretically it could have a greater impact on their lactation milk yield. This information could be used when planning organic dry cow therapy.

Introduction Economic loss associated with a case of mastitis varies from £60 to £1148, based on drug costs, labour, reduced milk yield, non-saleable milk and culling in severe cases (DairyCo, 2013). The welfare implications of the painful condition are a major concern. Many studies have tried to compare the incidence of mastitis between conventionally managed and organic dairy herds. There are many factors confounding these comparison studies, such as genetics, milk yield, housing, differences in methods of detection and categorisation of clinical and sub-clinical mastitis and at what point it is treated. It has been suggested that organic herds have higher Somatic Cell Counts (SCC) also that farmers may be less willing to treat affected organic cows with antibiotics because of the prolonged withdrawal period and greater reduction in income, which could lead to poorer welfare in organic dairy herds (Fall *et al*., 2008).
The limited comparisons to date use data from several different farms, introducing a number of other variables. Our study compares incidence of mastitis between conventional and organic dairy production on the same site where most variables are similar. Our study explores the impact of mastitis on milk production over a 7 year period. Other research focuses on mastitis in the whole herd rather than comparisons of the cows suffering from mastitis, our study looks at whole herd and compares groups of mastitic cows within the different systems.

Material and methods The dairy herd comprises of 1 organic (O) dairy herd and 1 conventional (C) on the same farm, a rolling average of 94 organic and 95 conventional cows. Both herds are Holstein Friesians, all year round calving pattern, similar milk yields, rearing their own replacements. Cows are at grass from March until October, then housed in straw yards during winter. Cows are milked twice a day by the same stockperson at the same time but on separate sides of the parlour. Treatment for mastitis during lactation is at the same stage of the disease in both systems, using either intra muscular injection of amoxicillin/clavulanic acid (Combiclav Suspension for Injection, Norbrook) for the organic cows or intramammary suspension of cefquinome (Cobactan,) for the conventional cows. During the dry period organic cows with a SCC>200,000 cells/ml received an intramammary suspection of penethamate hydriodide, procaine penicillin and framycetin sulphate (UbroRed, Boehringer Ingelheim) while the remaining organic cows receive no treatment and conventional cows are treated with intramammary suspension of cefalonium (Cepravin, MSD Animal Health) irrespective of SCC.
Data from January 2006 to December 2012 was collected from Interherd records: parity, number of mastitis treatments, milk yield, SCC. The number of mastitis treatments was calculated by classing a treatment as a new case if it occurred >14 days after the last treatment. Milk yield per day (recorded once per month) was analysed, if a cow had mastitis on the day of milk recording, an average of the previous and subsequent months' daily yield was used. To analyse average herd milk yields (including mastitic and non-mastitic cows) the average daily milk yield for each year was calculated. Kolmogorov-Smirnov test were used, normally distributed data was analysed using t-test (milk yield) and Mann-Whitney tests were used on SCC, number of mastitis treatments, parity and lactation day.

Results There was no significant difference between O or C herd daily milk yield (C 26.2 l/day, SE = +/-0.95; O 27.3 l/day, SE = +/-0.40; P = 0.325); SCC (C 264,000 cells/ml [first quartile: 252,000; third quartile: 280,000]; O 260,000 cells/ml [first quartile: 236,000; third quartile: 287,000] P = 0.133); number of treated cases of mastitis (C 2 [first quartile: 2; third quartile: 3]; O 2 [first quartile: 2; third quartile: 2] P = 0.174). Conventional cows were older when getting mastitis (C 4 [first quartile: 3; third quartile: 6]; O 3.5 [first quartile: 2; third quartile: 5] P = 0.000). Organic cows were getting mastitis significantly earlier in lactation than conventional cows (C 120 [first quartile: 53; third quartile; 213]; O 102 [first quartile: 41; third quartile: 187] P = 0.050).

Conclusion There was no difference in incidence of mastitis or SCC due to the system, this could indicate the overall ineffectiveness of dry cow therapy as a preventative measure for conventional cows. As C cows were older when they got mastitis it may suggest dry cow therapy protects them at a younger age but is less effective as they get older. In the current study conventional cows were getting mastitis significantly later in lactation. It is proposed this could be due to better protection during the dry period but then they are susceptible later in lactation and it does not affect overall incidence.

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Effect of concentrate feed rate within a feed-to-yield system on the performance of dairy cows in early to mid-lactation

P J Purcell, R A Law, C P Ferris
Agri-Food and Biosciences Institute, Hillsborough, UK
Email:peter.purcell@afbini.gov.uk

Implications Caution is required when adopting 'high' concentrate feed rates in 'feed-to-yield' dairy systems, as these may increase concentrate intakes and decrease milk fat content without increasing milk yields.

Introduction Dairy cows on many farms are offered a 'basal' diet, which is designed to meet the cows' energy requirements for maintenance plus a given level of milk production (often termed the 'maintenance-plus' yield). In many cases, additional concentrates are then offered on a 'feed-to-yield' basis to support the milk yield of each individual cow above that supported by the basal diet. These additional concentrates are normally offered at a specific 'feed rate' for each litre of milk produced above what the basal diet can support. While a feed rate of 0.45 kg of concentrate per kg of milk is frequently adopted in practice, feed rates can be within the range 0.35 to 0.55 kg/kg. However, relatively little information exists on the effect of altering the concentrate feed rate within a feed-to-yield system. Thus, the objective of this study was to examine the effects of concentrate feed rate (CFR) on dairy cow performance in early to mid-lactation.

Material and methods Following calving, 96 Holstein-Friesian dairy cows (28 primiparous and 68 multiparous; mean calving date of 14 October (s.d. 28 days)) were offered a mixed ration (*ad libitum*) consisting of silage (grass silage and maize silage in a 70:30 ratio on a dry matter (DM) basis) and concentrates, with the latter being incorporated in the ration to achieve a target intake of 5.0 kg/cow/day. This basal diet was designed to meet the cow's energy requirements for maintenance plus 27 (multiparous) or 24 (primiparous) kg of milk/cow/day. Cows were allocated to one of four concentrate feed rate treatments at day 14 post-calving, with these feed rates set at 0.35, 0.40, 0.45, or 0.55 kg of concentrate per kg of milk produced above the milk yields assumed to be sustained by the basal diet. Cows remained on these diets until week 21 post-calving. Concentrate allocations within each of the feed-rate treatments were adjusted weekly based on the mean daily milk yield of each individual cow during the previous week. These additional concentrates were offered via an out-of-parlour feeding system. All cows were offered an additional 1.0 kg of concentrate daily via in-parlour feeders. Cows were milked twice daily. Data were analysed in GenStat using one-way analysis of variance. Where significant in the model, appropriate pre-experimental variables were included as co-variates for analysis of dependant experimental variables.

Results Cows on the 0.55 feed rate had lower (P<0.05) silage DM intakes (DMI) and higher concentrate and total DMI than cows on any of the other three feed rates (Table 1). The CFR had no effect (P>0.05) on mean daily milk yields or milk fat-plus-protein yields. Milk fat concentrations were lower for the 0.55 feed rate than for the remaining feed rates, but CFR had no effect (P>0.05) on milk protein concentrations. Liveweights and body condition scores at the end of the experiment were unaffected (P>0.05) by CFR.

Table 1 Effect of concentrate feed rate (kg/kg of milk produced above the milk yields assumed to be sustained by the basal diet) on dry matter intakes (DMI), milk yields and composition, and end-of-experiment liveweights and body condition scores

	Concentrate feed rate					
	0.35	0.40	0.45	0.55	SEM	Significance
Silage DMI (kg/cow/day)	11.6[a]	11.3[ab]	10.9[b]	10.2[c]	0.23	***
Concentrate DMI (kg/cow/day)	10.0[b]	10.0[b]	10.8[b]	12.9[a]	0.49	***
Total DMI (kg/cow/day)	21.5[b]	21.2[b]	21.7[b]	23.1[a]	0.47	*
Milk yield (kg/cow/day)	36.9	35.4	36.3	38.1	0.86	NS
Milk fat plus protein yield (kg/cow/day)	2.65	2.62	2.68	2.68	0.064	NS
Milk fat (g/kg)	40.6[a]	42.1[a]	40.9[a]	38.1[b]	0.75	**
Milk protein (g/kg)	32.5	33.0	33.3	32.5	0.35	NS
End-of-experiment liveweight (kg)	607	602	615	618	6.5	NS
End-of-experiment body condition score	2.40	2.45	2.46	2.47	0.029	NS

[a-c] Means with common superscripts within rows do not differ (P>0.05).*P<0.05.**P<0.01.***P<0.001. NS, not significant.

Conclusion Concentrate feed rates between 0.35 and 0.45 kg/kg of milk had no effect on concentrate or total DMI, or on milk yields. However, cows on the 0.55 kg feed rate had greater concentrate DMI, which resulted in lower silage DMI and milk fat content. Thus, caution is required when adopting very high feed rates.

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The effects of out-wintering replacement dairy heifers on deferred grazing, kale or fodder beet without or with a trace mineral bolus on pre-calving performance in commercial spring calving herds

N E Atkins[1], E C L Bleach[1], P R Hargreaves[2], L A Sinclair[1]
[1]Harper Adams University, Newport, Shropshire, UK, [2]SRUC Dairy Research Centre, Dumfries, Scotland, UK
Email:natkins@harper-adams.ac.uk

Implications Forage choice or trace mineral supplementation are not the main factors impacting performance of out-wintered heifers.

Introduction Most replacement dairy heifers out-wintered in the UK are from low input spring calving systems, with the common forages being grass, kale and fodder beet (Atkins *et al*, 2014). Farmers using such systems generally consider performance of heifers to be adequate, reporting mean liveweight (Lwt) gain of 0.56 kg/d – enough to reach 90% of mature Lwt by first calving (Atkins *et al*, 2014). Previous research has reported reduced performance of dairy cows out-wintered on grass (Keogh *et al,* 2009) and trace mineral nutrition may affect performance, particularly when grazing kale, a brassica low in copper and containing anti-nutritional factors (Barry, 2013). The objective of the study was to compare the performance and metabolism of heifers out-wintered on the three most common forages in commercial spring calving farms and the effect of trace mineral supplementation.

Material and methods Nine spring calving, grass based farms - three out-wintering on deferred grazing (G), three on kale (K) and three on fodder beet (F), were used. In November 2012, 40 crossbred in-calf heifers from each farm were blocked according to liveweight and randomly allocated to either without (B-), or with (B+) bolus treatment, containing the trace elements Co, Se, I and Cu (Telsol Ltd., Leeds, UK). Heifers were then managed in accordance with each individual farm's normal practice, without additional mineral supplementation. On three occasions during the winter; approximately six weeks apart and beginning in early November, heifers were weighed, body condition scored (BCS), and blood sampled via the coccygeal vein. Blood samples were subsequently analysed for 3-OHB and urea, and plasma minerals by ICP-MS. Data were analysed by repeated measures ANOVA in Genstat v.16 as a 3 x 2 factorial design nesting block within farm, with main effects of forage type and bolus.

Results Mean Lwt increased by only 20kg over the 12 week period ($P<0.001$; Table 1) but there was no effect of forage or bolus on Lwt change, which ranged across farms from 0.57 to -0.22 kg/d. Change in BCS was negative ($P<0.001$), although for treatment B+, BCS was higher ($P=0.035$) after 12 weeks compared to B-. There was no effect of forage or bolus on blood urea or 3-OHB concentrations, with both decreasing from week 0 ($P<0.001$; Table 1). There was an interaction between forage source and bolus on haematology; by week 12 haemoglobin (Hb) was lower ($P=0.031$) in animals fed K without bolus (mean values of 12.0 and 12.9 g/dL for B- and B+ respectively on K). In contrast, mean corpuscular volume (MCV) was higher ($P<0.001$) by week 12 in animals fed K (48.2 and 44.9 μm^3 B- and B+ respectively on K).

Table 1 Liveweight, body condition, blood metabolites, plasma copper and haematology measures of replacement heifers out-wintered between November 2012 and January 2013 on deferred grass (G), kale (K) or fodder beet (F), which either did not receive (B-) or received (B+) a mineral bolus.

	G	K	F	s.e.d.	*P*-value	B-	B+	s.e.d.	*P*-value
Live weight (wk 0), kg	429	400	384	20.6	0.166	404	405	1.1	0.817
Live weight (wk 12), kg	445	432	394	28.7	0.255	424	424	2.1	0.863
Body condition (wk 0)	2.73	2.72	2.55	0.152	0.467	2.67	2.67	0.019	1.000
Body condition (wk 12)	2.49	2.48	2.38	0.117	0.636	2.44	2.47	0.016	0.035
Plasma Cu, mmol/L	13.3	12.5	14.1	3.00	0.869	11.9	14.7	0.41	<0.001
Urea, mmol/L	4.26	4.64	3.41	0.504	0.117	4.15	4.06	0.070	0.204
3-OHB, mmol/L	0.38	0.39	0.37	0.079	0.963	0.39	0.37	0.013	0.177
Haemoglobin, g/dL	12.8	11.5	12.4	0.94	0.377	12.3	12.2	0.18	0.650
MCV, μm^3	44.3	46.1	42.4	1.03	0.032	44.3	44.1	0.31	0.224

Conclusion Growth and body condition of the heifers was less than expected overall and highly variable between farms. Although the trace mineral bolus increased plasma copper status, this had little effect on performance. Haematology results provide some evidence that trace mineral supplementation counteracts anti-nutritional factors of brassicas grazed by cattle.

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The effects of out-wintering replacement dairy heifers on deferred grazing, kale or fodder beet, without or with a trace mineral bolus on first lactation performance in commercial spring calving herds

N E Atkins[1], E C L Bleach[1], P R Hargreaves[2], L A Sinclair[1]
[1]Harper Adams University, Newport, Shropshire, UK, [2]SRUC Dairy Research Centre, Dumfries, Scotland, UK
Email:natkins@harper-adams.ac.uk

Implications There is little effect of out-wintering forage source on subsequent lactation performance, but the provision of a mineral bolus may improve performance and reproduction in early lactation particularly when out-wintered on kale

Introduction Out-wintering replacement dairy heifers on grass, kale or fodder beet, is most common amongst low input spring calving systems (Atkins *et al*, 2014). Farmers out-wintering heifers generally consider performance in first lactation, equal to that of housed animals (Atkins *et al*, 2014). Indeed, past research has reported comparable lactation performance in dairy cows out-wintered on forage brassicas or grass compared with housing (Keogh *et al,* 2009). Trace mineral nutrition, particularly when grazing kale, may also affect the subsequent lactation performance due to the low trace mineral concentration in forages and anti-nutritional factors. The objective of the study was to compare the effects out-wintering on deferred grazing, kale or fodder beet, without and with additional trace minerals during the out-wintering period, on first lactation performance.

Material and methods Nine spring calving, grass based dairy farms - three out-wintering on deferred grazing (G), three kale (K) and three fodder beet (F), were used. In November 2012, 40 in-calf crossbred heifers on each farm were blocked according to liveweight and randomly allocated to either without (B-), or with bolus (B+) treatment, containing Co, Se, I and Cu trace minerals (Telsol Ltd., Leeds, UK). Heifers were then managed in accordance with each individual farms normal practice, without additional supplementary minerals. From calving (February 2013), each farmer recorded health and fertility information. Milk yield was recorded in approximately 10 and 19 weeks post-partum and samples collected for fat, protein and somatic cell count (SCC) analysis (NML, Wolverhampton, UK). Continuous variables were analysed by repeated measures ANOVA in Genstat v.16 as a 3 x 2 factorial design nesting block within farm, with main effects of winter forage type and bolus using days in milk as covariate. Binomial data were analysed by logistic regression as a generalised linear mixed model with forage and bolus fitted as fixed terms, and farm and block random terms.

Results There was no effect of winter forage type on milk yield, fat, protein or SCC (Table 1). Milk fat content was higher (P=0.009) by 1.9 g/kg, and fat corrected milk yield (FCM) tended to be higher (P=0.087) in B+ during week 10 of lactation. No effect of bolus was evident in week 19. There was no main effect of forage or bolus on any of the health variables measured, nor was there any main effects on the proportion of heifers having resumed oestrous cycles at the start of the service period, receiving fertility treatment to initiate oestrous cycles or returning to first service. The proportion of heifers pregnant after the mating period was higher (P=0.032) in F, than G or K (0.95, 0.88 and 0.86 probability, respectively). Heifers fed K without bolus had the highest probability of receiving fertility treatment (0.41; P=0.030), against 0.26 when fed K with bolus, and mean probability of 0.12 and 0.21 for G and F, respectively.

Table 1 Milk performance in 1st lactation cross-bred heifers out-wintered between November 2012 and January 2013 on grass (G), kale (K) or fodder beet (F), and either did not receive (B-) or received (B+) a mineral bolus.

	G	K	F	s.e.d.	*P*-value	B-	B+	s.e.d.	*P*-value
Week 10 of lactation									
FCM, kg	18.6	19.5	17.1	1.98	0.526	18.1	18.7	0.39	0.087
Fat, g/kg	41.7	40.2	43.0	0.22	0.549	40.7	42.6	0.71	0.009
Protein, g/kg	33.8	34.3	34.2	1.48	0.925	34.2	34.0	0.25	0.625
SCC, $\log_{10}$	1.74	1.76	1.81	0.086	0.605	1.78	1.76	0.043	0.593
Week 19 of lactation									
FCM, kg	18.2	16.6	16.3	2.24	0.680	16.8	17.2	0.30	0.108
Fat, g/kg	44.6	44.3	47.2	2.83	0.556	45.4	45.3	0.61	0.866
Protein, g/kg	35.6	35.7	37.2	1.47	0.483	36.3	36.1	14.71	0.452
SCC, $\log_{10}$	1.99	1.82	1.67	0.295	0.573	1.86	1.80	0.042	0.156

Conclusion Forage used for out-wintering replacement heifers had no effect on first lactation milk production or quality in the spring calving, grass based farms studied. The results suggest that trace mineral boluses administered at the onset of the out-wintering period may have a small effect on milk and fat yield, and may benefit the fertility of heifers wintered on kale.

Acknowledgements The farmers and staff from participating farms are gratefully acknowledged, along with Stephanie Wilson, those at SRUC and the students involved in sample collection, and DairyCo. for the funding for this study.

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The effects of temperature and humidity on feeding behaviour depends on genetic merit in a temperate herd of dairy cows

D L Hill[1], E Wall[1,2]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]ClimateXChange, Edinburgh, UK
Email:davina.hill@sruc.ac.uk

Implications Continuously housed dairy cattle in Scotland decreased feed intake and made shorter feed bouts in response to increases in temperature and humidity. High genetic merit and control cows differed in their responses to prevailing weather conditions, which suggests that genetic merit affects an animal's ability to cope with thermal stress.

Introduction Climate change is expected to impact livestock through an increase in heat stress. The conditions associated with heat stress can be quantified using Temperature Humidity Indices (THI), which take into account the air's temperature and water vapour content. Cattle feeds have been formulated to provide animals with the balance of energy and nutrients that maximises milk yield. Cows produce metabolic heat during milk synthesis and so higher yielding dairy cows are expected to experience heat stress at lower THIs than lower yielders. Cows might therefore modify dry matter intake (DMI) and/or feeding behaviour to reduce heat production under conditions of heat stress. We predicted that 1) cows of high genetic merit would consume more feed and spend longer feeding than cows of average merit and that 2) cows would reduce DMI and feed bout length as THI increased. In addition, 3) the impact of heat stress on DMI and behaviour would be greater in cows of high than average genetic merit.

Material and methods We studied a Holstein Friesian dairy herd in Dumfries, UK, between April and November of the years 2004-2011. Cows belonged to 2 genetic lines: Select cows (S) were bred to bulls of the highest genetic merit for kg fat plus protein in the UK, while Control cows (C) were bred to bulls close to the UK average. The 2 lines were continuously housed and managed together. All cows were lactating (days 0-305 in milk) and milked 3x a day. They received a total mixed ration (TMR) of concentrates, brewers' grain and silage distributed into HOKO automatic feed measurement gates, available *ad libitum*. Feeders recorded the identity of the feeding cow, feed intake and meal duration. Animals remained in the study for their first 3 lactations.

Daily measurements of dry bulb temperature (T_{db}), wind speed (WS), relative humidity (RH) and the number of hours of sunshine were recorded by the British Atmospheric Data Centre (UK Meteorological Office, 2012) at a single weather station on the farm grounds. T_{db}, RH and WS were point-sampled at 0900h each day. We used these data to calculate 'adjusted THI' (THI_{adj}; Mader *et al*., 2006), a single metric that adjusts T_{db} for RH, WS and solar radiation. We estimated daily DMI based on a sample of oven-dried TMR. Meals <30 minutes apart (interval between the end of one meal and the start of the next) were summed to produce feed bouts, and we calculated the mean feed bout length/cow/test day (TD).

We analysed DMI and mean bout length as separate response variables using restricted maximum likelihood. THI_{adj}, genetic group, the interaction between THI_{adj} and genetic group, lactation number, days in milk, live weight and condition score were fitted as fixed effects. Linear, quadratic and cubic effects of THI_{adj}, live weight and days in milk were tested. We controlled for random effects of animal identity, TD and calving date.

Results S cows consumed more dry matter and made longer feed bouts than C cows (Fig 1). Both traits decreased linearly with increasing THI_{adj}, and the steepness of the declines depended on genetic merit (Fig 1). S cows showed a gentler decline in DMI but a steeper decline in bout length than C cows.

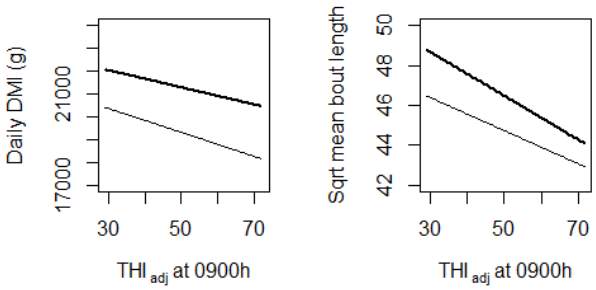

Fig 1 Effects of THI_{adj} on dry matter intake (DMI; 33900 TD records from 321 cows) and mean feed bout length (27927 TD records from 323 cows) in animals of high (thick line) and average (thin line) genetic merit. Plots are adjusted for all terms in the models (see Materials and Methods)

Conclusion Feeding cows adopted measures likely to reduce the production of metabolic heat at higher THIs. Furthermore, high genetic merit cows demonstrated different sensitivities to heat stress - or different coping tactics - from control cows.

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Replacement of grass and maize silage with lucerne in the diet of high yielding dairy cows: effects on performance and milk fatty acid profile

L A Sinclair, R Edwards, K A Errington, A M Holdcroft, M Wright
Harper Adams University, Newport, Shropshire, UK *Email:lsinclair@harper-adams.ac.uk*

Implications Lucerne can replace grass and maize silage in the diet of high yielding dairy cows without impacting on performance, and increases the content of polyunsaturated fatty acids in milk.

Introduction Increased global demand for soyabean meal in association with considerable fluctuations in availability and price has increased the importance of home grown forages in the diet of UK dairy cows. Lucerne (alfalfa) is popular in many parts of the United States and Europe as it is drought tolerant, has a low fertiliser requirement and is high in protein, complementing the low protein content found in maize silage (Broderick *et al*., 2007). Feeding lucerne silage generally results in an increase in dry matter (DM) intake, milk yield and milk fat and protein levels (Broderick *et al*., 2007). Despite this, lucerne has received relatively little commercial uptake by UK dairy farmers. The objectives of the current study were to determine the effect of rate of inclusion of lucerne silage as a replacement for grass and maize silage on the intake, performance and milk fatty acid profile in high yielding dairy cows.

Material and methods Twenty multiparous Holstein-Friesian dairy cows that were 61 (s.e. ± 6.3) days post calving received one of 4 diets in each of 4 periods of 28-duration in a Latin square design, with measurements taken during the final 7 days of each period. All dietary treatments contained 0.55:0.45 forage to concentrates (DM basis), and within the forage component the proportion of lucerne, grass and maize silage (DM basis) was varied: Control = 0.4:0.6 grass to maize silage; L20 = 0.2:0.2:0.6 lucerne to grass to maize silage; L40 = 0.4:0.6 lucerne to maize silage and L60 = 0.6:0.4 lucerne to maize silage. The lucerne silage (*vr*. Daisy) was harvested at early bud, and the grass silage was a first cut composed predominately of *Lolium perenne*. The maize silage (*vr*. Adept) was harvested at approximately 300 g DM/kg. The concentrates contained wheat, soy hulls, soyabean meal, rapeseed meal, distillers dark grains, urea and minerals/vitamins, with the soyabean and feed grade urea inclusion altered to provide a similar crude protein content of 170 g/kg DM and metabolisable protein content of 105 g/kg DM in all treatments. Cows were milked twice daily with yield recorded at each milking and samples taken on four occasions during the final week of each period for subsequent analysis. Live weight was recorded at the beginning and end of each period. Data were analysed as a Latin square design using Genstat (v. 15).

Results The lucerne, grass and maize silages contained 406, 353 and 323 g DM/kg, with a crude protein content of 183, 127 and 72 g/kg DM respectively. Intake was lowest in cows when fed L60 ($P < 0.01$), but there was no effect of treatment on milk yield, milk fat or protein content, or live weight change (Table 1). The content of both 18:2*n*-6 and 18:3*n*-3 were increased ($P<0.05$) with increasing proportion of lucerne in the ration, and there was a trend ($P<0.1$) for 18:1*t*-11 to be higher. Milk fat content of total polyunsaturated fatty acids (PUFA) was increased by 0.26 g/100g in L60 compared to the Control. The intake of soya bean meal decreased from 2.28 kg/d in cows receiving the Control diet to 1.70 kg/d when receiving L60, and the intake of feed grade urea decreased from 0.12 kg/d in the Control fed cows to 0 kg/d in L60.

Table 1 Intake, milk performance and selected milk fatty acids in cows when fed diets differing in their inclusion rate of lucerne silage.

	Control	L20	L40	L60	s.e.d.	*P*-value
DM intake, kg/d	24.5[b]	24.9[b]	24.5[b]	23.4[a]	0.40	0.004
Milk yield, kg/d	42.2	40.7	40.2	40.5	0.90	0.133
Milk fat, g/kg	41.1	40.6	40.4	41.8	0.97	0.470
Milk protein, g/kg	30.9	30.8	31.0	30.8	0.33	0.953
Live weight change, kg/d	0.21	0.23	0.13	0.05	0.207	0.814
Milk fatty acids, g/100g						
18:0	8.06	7.95	7.74	7.70	0.189	0.185
18:1*n*-9	21.83	21.67	21.72	21.39	0.319	0.561
18:2*n*-6	2.27[a]	2.37[b]	2.42[b]	2.43[b]	0.045	0.004
18:3*n*-3	0.32[a]	0.34[b]	0.36[c]	0.42[d]	0.010	<0.001
18:1*t*-11	0.47	0.55	0.57	0.59	0.049	0.092
*c*9, *t*11 conjugated linoleic acid	0.48	0.49	0.47	0.48	0.022	0.727
Total PUFA	3.26[a]	3.39[b]	3.43[b]	3.52[b]	0.063	0.002

[a]Means with a different superscript differ by $P<0.05$

Conclusion Lucerne silage can successfully replace grass and maize silage in the diet of high yielding dairy cows without affecting performance. The inclusion of lucerne also resulted in a small increase in the PUFA content of milk, and decreased the requirement for purchased protein feeds.

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The effect of supplementation with a rumen-protected fat (Megalac®) through an extended period of lactation on milk production of dairy cows in a pasture-based dairy system in Tasmania

M J Freeman[1], R M Kirkland[2]
[1]Tasmanian Institute of Agriculture, University of Tasmania, Burnie, Tasmania, Australia, [2]Volac International Ltd, Orwell, Royston, Herts., SG8 5QX, UK *Email:richard.kirkland@volac.com*

Implications Grazing cows offered a rumen-protected fat supplement based on calcium salts of palm fatty acids produced 1.3 kg additional milk per day through 200-d of lactation compared to those offered a non-fat supplemented diet.

Introduction Rumen-protected fats are common feed ingredients used in rations for lactating dairy cows, primarily to increase energy density without adding to the acid load in the rumen as is the case with fermentable starch sources of energy. Fat supplements have traditionally been targeted primarily at higher-yielding cows and there is a paucity of data available on the effects of supplementing lower-producing, pasture-based cows with this form of energy over an extended period of lactation. The objective of this study was to determine the effects of long-term supplementation with rumen-protected fat on milk production characteristics of lactating cows on a grass-based system.

Material and methods The study was conducted at the Tasmanian Institute of Agriculture's Dairy Research Facility. A total of 150 dairy cows (80 Holstein-Friesian and 70 Holstein-Friesian - crossbred) were allocated as matched pairs (based on similarity of milk yield, live weight, parity, breed and days in milk (DIM)) to either a Control (C) or fat-supplemented (M) ration at 20 DIM. From calving to the start of the study all cows were offered pasture and 4 kg concentrate/d (3.6 kg DM). From 20-220 DIM, cows in the C group continued to be offered the same concentrate at 4 kg/d, while the M cows were offered the same concentrate composition as the C group plus 250 g of Megalac rumen-protected fat (a calcium salt of palm fatty acid distillate; Volac International Ltd; to provide an additional 7.9 MJ of ME) (4.25 kg concentrate/d). Concentrates were offered as two equal individual feeds in the parlour during AM and PM milkings. Post 220 DIM all cows were treated similarly. Pasture allocations were designed to provide 12-14 kg DM/head/d, while grass silage was offered from d-103 of the study at a rate of approximately 1 kg DM/head/d until d-157, increasing to a maximum of 4.4 kg DM/head/d until the end of the study. Formulated concentration of DM, crude protein, neutral detergent fibre, fat and starch in the concentrate was 892 g/kg, 123, 165, 22 and 539 g/kg DM, respectively. Milk yield and live weight were recorded daily; milk composition was recorded monthly; and condition score was assessed on four occasions throughout the study. Data on milk yield were analysed using PROC Mixed and PROC PLM (SAS version 9.3), using an autoregressive correlation structure for repeated measures. Milk composition data were analysed by t-test, with each test adjusted for multiplicity using Holm's method.

Results Mean milk yield was 1.3 kg/d higher (P = 0.02) in the M group (Table 1) through the 200-d study period. Analysed in 10-d intervals, milk yield response in the M group was significantly (P<0.001) higher from 40 DIM to the end of the study, and a significant (P<0.05 or greater) residual response (mean +0.8 kg milk/head/d) continued to be recorded for a further 30-d following the end of fat supplementation (220 to 250 DIM). Residual numerically-higher milk yield to drying off contributed to the M cows producing a significant (P = 0.01) 349 kg additional milk in the total lactation. Treatment had no (P>0.05) significant effect on milk fat concentration, though the numerically-higher milk fat yield recorded with the M treatment fell just outside significance (P=0.056). Cows offered the C ration had higher (P<0.05) milk protein concentration, but milk protein yield was similar (P>0.05) between treatments. Neither live weight nor condition score were affected (P>0.05) by dietary treatment.

Table 1 Production performance of cows offered C and M diets from 20 to 220 DIM

Parameter	Diet		SED	Significance
	C	M		
Milk yield (kg/d)	21.7	23.0	0.55	*
Total lactation milk yield (kg)	5061	5410	141.5	*
Milk fat (g/kg)	43.4	43.0	0.68	NS
Milk fat (kg/d)	0.946	0.995	0.0250	NS
Milk protein (g/kg)	31.4	30.8	0.28	*
Milk protein (kg/d)	0.685	0.713	0.0160	NS
Mean live weight (kg)	489	494	10.2	NS
Condition score at 35 DIM #	4.18	4.18	0.08	NS
Condition score 200 DIM #	4.81	4.83	0.08	NS

* p<0.05; NS = not significant # 8-point scale

Conclusion These data indicate that low-input, pasture-based herds can respond very efficiently to supplementation with additional energy from rumen-protected fat and provide evidence that this response in milk production is maintained through to late lactation. The additional milk was produced without negative effects on either condition score or live weight.

The effect of supplementation with a rumen-protected fat (Megalac®) on fertility and blood metabolite concentration of lactating dairy cows in a pasture-based dairy system in Tasmania

M J Freeman[1], R M Kirkland[2]
[1]Tasmanian Institute of Agriculture, University of Tasmania, Burnie, Tasmania, Australia, [2]Volac International Ltd, Orwell, Royston, Herts., SG8 5QX, UK *Email:richard.kirkland@volac.com*

Implications Grazing cows offered a rumen-protected fat supplement had similar, high, levels of fertility to those offered a non-fat-supplemented ration. Blood metabolite indicators of energy status were also similar between treatments.

Introduction Grass-based dairy production systems are typically characterised by low inputs of supplementary concentrates. Rumen-protected fats are added to dairy rations to increase energy density without increasing the risk of acidosis, though scientific data are lacking on the effects of fat supplementation to cows at grass on fertility and metabolic parameters. The objective of this study was to determine effects on cow fertility and blood metabolites (as indicators of energy status) of offering a rumen-protected fat to lactating dairy cows at grass through an extended period of lactation.

Material and methods The study (matched-pair design) was conducted at the Tasmanian Institute of Agriculture's Dairy Research Facility. A total of 150 dairy cows (80 Holstein-Friesian and 70 Holstein-Friesian - crossbred) were allocated as matched pairs (based on similarity of milk yield, live weight, parity, breed and days in milk (DIM)) to either a Control (C) or fat-supplemented (M) ration at 20 DIM. From calving to the start of the study all cows were offered pasture and 4 kg of a wheat-based concentrate/d (3.6 kg DM). From 20-220 DIM, cows in the C group continued to be offered the same concentrate at 4 kg/d, while the M cows were offered the same concentrate composition as the C group plus 250 g of Megalac rumen-protected fat (a calcium salt of palm fatty acid distillate; Volac International Ltd; to provide an additional 7.9 MJ of ME) (4.25 kg concentrate/d). Concentrates were offered as two equal individual feeds in the parlour during AM and PM milkings. Post 220 DIM all cows were treated similarly. Pasture (predominantly perennial ryegrass / white clover-dominant swards) allocations were designed to provide 12-14 kg DM/head/d, while grass silage was offered from d-103 of the study at a rate of approximately 1 kg DM/head/d until d-157, increasing to a maximum of 4.4 kg DM/head/d until the end of the study. Formulated concentration of DM, crude protein, neutral detergent fibre, fat and starch in the concentrate was 892 g/kg, 123, 165, 22 and 539 g/kg DM, respectively. Servicing commenced at 76 DIM using artificial insemination (AI) and continued for a period of six weeks. At the conclusion of the AI period, bulls were introduced to the herd for a further eight-week period. Pregnancy data were determined from monitoring of Estrotect™ patches and ultrasound pregnancy testing at 161 and 270 DIM. Assessment of blood metabolites was conducted on (the same) 15 paired cows from each treatment at 3, 7, 11 and 16 weeks post-partum and analysed for non-esterified fatty acids, ß-hydroxybutyrate, glucose and urea nitrogen. Fertility data were subjected to Chi-Square analysis (SAS version 9.3), while data on blood metabolites were analysed by a mixed model analysis using PROC Mixed (SAS version 9.3).

Results Four cows from each treatment were removed from the study due to reasons not connected to the study. There were no significant (P>0.05) differences in any of the fertility parameters measured between the C and M treatments (Table 1). However, fertility was high across the herd with a mean conception to first service of 0.69, 6-week in-calf rate of 0.79 and final pregnancy rate of 0.915. Similarly, mean blood metabolite concentrations were similar (P>0.05) between the treatment groups.

Table 1 Fertility and blood metabolite concentration of cows offered C and M diets from 20 to 220 DIM

Parameter	Diet		SED	Significance
	C	M		
Fertility data				
Conception rate to first service	0.70	0.68		NS
Conception rate to second service	0.66	0.66		NS
6-week in-calf rate	0.80	0.78		NS
Days to conception	90.8	89.9		NS
Inseminations / conception	1.46	1.43		NS
Final pregnancy rate	0.92	0.91		NS
Blood metabolites				
Non-esterified fatty acids (mmol/l)	0.37	0.37	0.031	NS
ß-hydroxybutyrate (mmol/l)	0.51	0.59	0.061	NS
Urea nitrogen (mmol/l)	5.00	4.64	0.240	NS
Glucose (mmol/l)	3.56	3.58	0.063	NS

Conclusion Fertility was high in both herds in the study with average pregnancy rate of over 0.90. These data indicate that the addition of energy from fat maintained high fertility levels and energy status despite these cows producing higher milk volumes (Freeman and Kirkland, 2015).

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Effect of concentrate allocation strategy on the performance of dairy cows in early to mid-lactation

P J Purcell, R A Law, C P Ferris
Agri-Food and Biosciences Institute, Hillsborough, UK
Email:peter.purcell@afbini.gov.uk

Implications Offering concentrates using a feed-to-yield strategy may increase milk yields compared to a flat-rate strategy, but may not increase milk fat-plus-protein yields due to a reduction in milk fat and protein contents.

Introduction Dairy cows on many farms are offered a 'basal' diet, which is designed to meet the cows' energy requirements for maintenance plus a given milk yield (often termed 'maintenance-plus'). Additional concentrates are then generally offered either on a 'feed-to-yield' basis (where cows are offered specific allocations based on their individual milk yields) or at a 'flat rate' (where all cows are offered similar concentrates allocations) to support milk yields above those sustained by the basal ration. Whereas feeding-to-yield aims to meet the energy requirements of individual cows, flat-rate feeding may result in under- or over-feeding of concentrates to individual cows. These two strategies have been examined previously with lower-yielding cows. The objective of this study was to examine the effects of concentrate allocation strategy (CAS; flat-rate versus feed-to-yield) on the performance of higher-yielding cows in early to mid-lactation, when the mean concentrate intakes of cows on both strategies were similar.

Materials and methods Following calving, 48 Holstein-Friesian dairy cows (14 primiparous and 34 multiparous; mean calving date of 13 October (s.d. 27.5 days)) were offered a mixed ration (*ad libitum*) consisting of silage (grass silage and maize silage in a 70:30 ratio on a dry matter (DM) basis) and concentrates, with the latter being incorporated in the ration to achieve a target intake of 5.0 kg/cow/day. This basal diet was designed to meet the cow's energy requirements for maintenance plus 27 (multiparous) or 24 (primiparous) kg of milk/cow/day. At day 15 post-calving, cows were allocated to either a 'Flat-rate' or a 'Feed-to-yield' concentrate allocation strategy. Within the Flat-rate treatment, in addition to the basal diet, cows were offered an additional 4.0 (multiparous) or 3.0 (primiparous) kg of concentrate per day on day 15, with concentrate allocations then increased daily (by 1.0 and 0.45 kg/cow/day, for multiparous and primiparous cows, respectively) until day 20 of lactation, at which point cows were being offered 9.0 (multiparous) or 5.25 (primiparous) kg/cow/day. Within the Feed-to-yield treatment, from day 15 onwards, in addition to the basal diet cows were offered 0.55 kg of concentrate per kg of milk produced above the milk yields assumed to be sustained by the basal diet (i.e. 27 or 24 kg/cow/day). Concentrate allocations within this treatment were adjusted weekly based on the mean daily milk yield of each individual cow during the previous week. The additional concentrates in both treatments were offered via an out-of-parlour feeding system. Cows remained on these treatments until week 21 post-calving. All cows were offered an additional 1.0 kg of concentrate daily via in-parlour feeders. Cows were milked twice daily. Data were analysed in GenStat using one-way analysis of variance. Where significant in the model, appropriate pre-experimental variables were included as co-variates when analysing corresponding dependant experimental variables.

Results CAS had no effect (P>0.05) on silage (mean (SEM) across CAS of 10.5 (0.23) kg DM/cow/day), concentrate, or total DM intakes (DMI; Table 1). There was also no effect (P>0.05) of CAS on mean daily milk yields or milk fat-plus-protein yields. However, cows in the Feed-to-yield treatment tended (P<0.1) to have greater milk yields than those in the Flat-rate treatment. Milk fat and protein concentrations were greater (P<0.01) for the Flat-rate treatment. Liveweights (mean 628, SEM 6.8 kg) and body condition scores at the end of the experiment were unaffected (P>0.05) by CAS.

Table 1 Effect of CAS on DMI, milk yield and composition, and end-of-experiment liveweight and body condition score

	Flat rate	Feed to yield	SEM	Significance
Concentrate DMI (kg/cow/day)	12.8	12.9	0.38	NS
Total DMI (kg/cow/day)	23.4	23.3	0.40	NS
Milk yield (kg/cow/day)	36.9	39.0	0.86	†
Milk fat-plus-protein yield (kg/cow/day)	2.78	2.71	0.057	NS
Milk fat (g/kg)	41.5	38.1	0.85	**
Milk protein (g/kg)	34.3	32.5	0.29	***
End-of-experiment body condition score	2.46	2.47	0.031	NS

** P<0.01. *** P<0.001. † P<0.1. NS, not significant.

Conclusion CAS had no effect on intakes or body condition scores. Although feeding-to-yield tended to increase mean daily milk yields, this trend was accompanied by a decrease in milk fat and protein content, which resulted in CAS having no effect on milk fat-plus-protein yields.

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Analysis of heat stress in Greek dairy cattle and impact on milk yield and milk quality

M-A Karatzia, E Sossidou
[1]Hellenic Agricultural Organization-Demeter, Veterinary Research Institute, Thessaloniki, Macedonia, Greece
Email:mkaratz@vet.auth.gr

Implications Heat stress in dairy cattle receives the attention of researchers worldwide. Although Greek dairy farms are already facing the adverse effects of climate change, no data on its' impact on dairy cattle and milk quality are available.

Introduction Global surface temperature is expected to rise exponentially in the following years (IPCC, 2013), rendering livestock owners confronted with a hazardous situation. Heat stress is the most profound impact of climate change on dairy cattle, affecting animal health and welfare status, reducing performance and minimizing farm economic benefits.

Material and methods The study was carried out based on recent data from the period of April to September 2014, collected from a commercial dairy farm in Northern Greece. Eighty Holstein cows were milked daily and were housed in cubicles. Environmental temperature and relative humidity values were recorded in 5-minute intervals using digital relative humidity and temperature sensors. Thermal heat index (T.H.I.) was calculated using the methodology described by Burgos Zimbelman *et al*. (2009) and a threshold of T.H.I=68 was considered aggravating for high-producing cows. Thus, observations were allocated into two groups (mean T.H.I.<68 and mean T.H.I. ≥68). Average herd milk yield was calculated daily, while milk quality parameters (fat and protein percentage, freezing point, somatic cell count and total bacterial count), dry matter intake and ration cost were calculated and adjusted on a weekly basis. Bulk milk composition was determined weekly. Mean differences were statistically analysed with one-way ANOVA model at level of significance a=0.01 for all main effects using the statistical software SPSS® version 21.

Results Milk yield was significantly lower when cows were exposed to significant heat stress (T.H.I. ≥68), (P≤ 0.01). Milk composition did not appear to be significantly affected by heat stress, apart from somatic cell count that was significantly higher under circumstances inducing heat stress (T.H.I. ≥68), (P≤ 0.01). The significant reduction in dry matter intake is directly linked to heat stress and was evident when T.H.I exceeded a value of 68 (P≤ 0.01). Means and standard error values of all parameters examined are summarized in Table 1.

Table 1 Effects of heat stress on milk yield and milk composition

Parameter	T.H.I. <68		T.H.I. ≥68		P	Parameter	T.H.I. <68		T.H.I. ≥68		P
	Mean	±SE	Mean	±SE			Mean	±SE	Mean	±SE	
Temperature (°C)	17.05	0.321	25.19	0.186	0.001	Milk Fat (%)	3.73	0.030	3.82	0.025	0.06
Relative Humidity (%)	74.4	1.187	68.17	0.872	0.002	Milk Protein (%)	3.31	0.021	3.30	0.0170	0.63
Dry Matter Intake (kg/cow/day)	26.92	0.205	25.55	0.928	0.001	Milk Freezing Point (°C)	0.525	0.001	0.524	0.00004	0.70
Ration Cost (€/cow/day)	6.87	0.042	6.78	0.212	0.040	Somatic Cell Count (x10^3 cells/ml)	228.83	24.339	266.89	7.000	0.04
Milk Yield (kg/cow/day)	32.98	0.207	30.40	0.105	0.001	Total Bacterial Count (x10^3CFU/ml)	28.33	11.936	27.06	11.520	0.95

Conclusion The significant differences in milk yield dry matter intake and somatic cell count between T.H.I.<68 and T.H.I.≥68 groups throughout the examined time period are indicative of the impact of heat stress on productivity of dairy cattle in Greece, a fact that merits further investigation.

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Effect of dry cow diet on colostrum IgG concentration and volume of colostrum fed on immune status in Holstein dairy calves

A Dunn[1,4], S Morrison[1], M Welsh[5], A Ashfield[1], A Gordon[2], B Earley[3]
[1]Agri-Food and Biosciences Institute (AFBI), Hillsborough, UK, [2]Agri-Food and Bioscience Institute (AFBI), Newforge, Belfast, UK, [3]Teagasc Grange, Meath, Ireland, [4]Queens University (QUB), Belfast, UK, [5]Sisaf, Belfast, UK
Email:amanda.dunn@afbini.gov.uk

Implications Supplementing cows with concentrates during the dry period had no effect on colostrum or serum IgG level. Calves fed 10% of their birth weight (BW) in colostrum resulted in higher serum immunoglobulin G concentration than calves fed 5% BW.

Introduction Calves are born vulnerable to pathogens as they have an immature immune system due to no transfer of immunoglobulins (IgG) from their mother when in utero (Arthur, 1996). Therefore successful passive transfer of immunity from dam to calf through colostrum ingestion within 24hours is vital to reducing calf mortalities (Wells *et al*., 1996). The objectives of this study were to determine the influence of dry cow nutrition on colostrum quality and feeding different levels of colostrum to Holstein calves on performance and health.

Material and methods Thirty-eight multiparous Holstein cows were assigned to 1 of 2 treatments during the 8-week dry period, grass silage only or grass silage plus 4 kg concentrate per cow/day. Calves from these cows were assigned to 1 of 2 treatments 10% or 5% BW of colostrum from their own mother within 2.5 hours of birth. Calves within the 10% group received their 2nd feed from 1st milking. Calves received their designated BW % in colostrum from their own mother for the first 4 days. Blood samples were obtained from the jugular vein of each calf at 0, 12, 24, 48 and 72 hrs and days 7, 14, 21, 35, 49, 56 and 70 post birth and analysed for IgG (Bovine IgG ELISA kit, Bio-X Diagnostics, Jemelle). Calf live weight was recorded on a weekly basis according to their individual age. Calves were group penned from day 5 and fed through a 'Forster Technik' automatic feeding machine with milk replacer and concentrate intake recorded daily. Calves received 675 g/day of milk replacer (30% skim based) and were weaned gradually from day 40-56. Respiratory and faecal scores were recorded daily for each calf (School of Veterinary Medicine, University of Wisconsin-Madison). Statistical analyses were performed using GenStat (16th edition). An ANOVA was carried out on treatment groups for colostrum at 1st and 2nd milking and serum IgG at the time points shown above and REML repeated measures on concentrate intake and daily live weight gain with lactation, calving difficulty, and birth weight included as fixed effects with cow fitted as random effects.

Results The effects of dry cow nutrition and colostrum volume fed are shown in Table 1. Feeding calves 10% of BW in colostrum compared to 5% resulted in a greater IgG concentration in the calves' serum at 12, 24, 48 and 72 hours after birth, there was no significant difference in IgG concentration between treatments beyond this time.

Table 1 Colostrum and blood IgG level, concentrate intake and daily live weight gain across treatment groups

	Colostral Treatment		Sig.	SED	Dry cow treatment		Sig.	SED
	5% BW	10% BW			Concentrate	No concentrate		
Colostrum IgG mg/ml (1st)	68.1	50.7	0.052	8.66	62.7	52.6	NS	8.96
Colostrum IgG mg/ml (2nd)	56.5	50.3	NS	11.57	59.9	44.6	NS	11.40
Concentrate intake kg/d	0.7	0.9	<0.001	0.05	0.7	0.8	NS	0.05
DLWG kg/d (0-56 d)[1]	0.6	0.5	NS	0.04	0.5	0.6	NS	0.04
IgG mg/ml (12 hrs)	15.6	21.4	0.007	1.99	19.0	18.3	NS	2.00
IgG mg/ml (24 hrs)	12.3	20.6	<0.001	2.20	17.4	15.9	NS	2.57
IgG mg/ml (48 hrs)	20.5	16.3	0.026	1.82	18.7	18.2	NS	1.83
IgG mg/ml (72hrs)	11.3	16.0	0.001	1.34	13.4	14.1	NS	1.34

[1]DLWG - Daily live weight gain

Conclusion Feeding 10% BW resulted in greater serum IgG. Dry cow nutrition regimes used in this study did not have an impact on colostrum or calf serum IgG. However, the full impact of colostrum management on immune development is currently being investigated. Blood and colostrum samples have been collected for transcriptomics and proteomics analysis.

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Impact of routine hormone treatments for the reproductive management of dairy herds on reproductive efficiency and methane emissions: A stochastic simulation study

S C Archer, C D Hudson, M J Green
University of Nottingham, Sutton Bonington, UK
Email:simon.archer@nottingham.ac.uk

Implications Controversial management interventions for dairy cows, such as routine exogenous hormone treatments to aid in reproductive management increasingly require robust justification for their use. This paper provides a framework for decision support in terms of change in economic returns and methane emissions from herds.

Introduction The increase in demand for foods of animal origin in the first half of this century is unprecedented. However, The FAO (2006) has estimated that livestock are responsible for 18% of greenhouse gas emissions worldwide, and therefore any development in livestock production systems must be efficient with minimal adverse environmental impact.
Oestrous detection efficacy is a common limiting factor in dairy herd fertility management, and synchronisation programmes allowing fixed time artificial insemination offer a solution. Higgins *et al.* (2013) highlighted that veterinarians may be reluctant to recommend this technology for ethical reasons.
Using simulations to predict herd scenarios is useful to inform decisions around the most appropriate management strategy to adopt. Giordano *et al.* (2012) focused on the input of deterministic parameter values, and hence generated the average financial value in a particular case. In reality, decision makers may need to be more than 50% certain of a minimum return on investment to change behaviour. The impact of hormonal synchronisation programmes on the methane output of dairy herds has not previously been reported. The aim of this study was therefore to evaluate the change in cost and methane emissions associated with 3 interventions to manage the first insemination of dairy cows.

Material and methods Data for 10,000 herds of 200 cows were simulated. Probability of conception was predicted daily from the start of the study (at a calving) for each cow up to day 300 of lactation. Four scenarios of differing first insemination management were simulated for each herd using the same theoretical cows: A baseline scenario based on breeding from observed oestrous events only, synchronisation of oestrous for fixed time first insemination using 2 methods, and a regime using prostaglandin treatments followed by first insemination to observed oestrous events. Cows that did not conceive to first insemination were re-inseminated following detection of oestrous. For cows that conceived, gestation length was 280 days with cessation of milking 60 days before calving. Those cows not pregnant after 300 days of lactation were culled and replaced by a heifer. Daily milk yield was calculated for 730 days from the start of the study for each cow. Change in mean reproductive and economic outputs were summarised for each herd following each intervention. For each scenario, methane emissions were determined by daily forage dry matter intake, forage quality, and cow replacement risk.

Results Improvement in herd fertility using the programmes investigated was associated with reduced methane emissions (Table 1).

Table 1 Simulation model outputs for 10,000 dairy herds; summary statistics for the median herd (interquartile range) when 3 different reproductive management strategies were applied shown as the absolute difference from a baseline scenario of breeding to observed oestrous only

Statistic for absolute difference	Ovsynch	Ovsynch with progesterone	Double prostaglandin
Proportion of cows pregnant by 100 days in milk	0.10 (0.05 to 0.16)	0.12 (0.07 to 0.19)	0.02 (0.01 to 0.04)
Proportion of cows not pregnant by 300 days in milk	-0.06 (-0.10 to -0.02)	-0.06 (-0.11 to -0.03)	-0.01 (-0.03 to 0.10)
Mean methane production per L milk (g)	-0.4 (-1.0 to -0.0)	-0.5 (-1.0 to -0.1)	-0.1 (-0.4 to 0.17)

Conclusion For an average herd, the reduction in methane emissions was equivalent to removing 2 cars from the road.

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Effect of pre-implantation factor in an *in vitro* model of bovine *E. coli* endometritis

R E Clamp[1], M Natoli[1], E R Barnea[2,3], D Nash[1], M T Rose[1]
[1]IBERS, Aberystwyth University, Ceredigion, UK, [2]SIEP The Society for the Investigation of Early Pregnancy, New Jersey, USA, [3]BioIncept LLC, New Jersey, USA
Email:rec8@aber.ac.uk

Implications Pre-implantation factor (PIF) has the potential to be a candidate treatment for endometritis. The present study demonstrates anti-inflammatory effects of PIF on normal endometrium. Further work is needed to assess effects of PIF following low dose lipopolysaccharide (LPS) challenge.

Introduction Endometritis is a postpartum uterine infection affecting 5-26% of dairy cows, caused by bacterial contamination of the uterus. LPS is an endotoxin of *E. coli* which is a commonly isolated pathogen of endometritis. There is a call for new endometritis treatments due to increases in antibiotic resistance. An anti-inflammatory agent may reduce the disease associated inflammation that causes infertility. Pre-implantation factor (PIF) is a pregnancy specific peptide, secreted from viable embryos. PIF has immune-modulatory roles within pregnancy and as such has been shown to modulate inflammation in mouse models of autoimmune diseases (Weiss *et al*., 2012). The present study aimed to assess the use of a pre-treatment of PIF on endometrial tissue explants before LPS stimulation to investigate the immune-modulatory role of PIF within a bovine model of *E. coli* endometritis.

Material and methods Bovine uteri (n=12; n=6 dairy, n=6 beef animals) with stage I corpus luteum and absence of endometrial inflammation were used. All animals were tested for the presence of inflammation at collection by taking a cytobrush smear. Smears were fixed and stained using Diff-Quick to assess for the percentage of polymorphonuclear leukocytes (PMN) present compared to uterine epithelial cells. Tissue was sampled from the ipsilateral uterine horn to the corpus luteum. Weighed tissue explants were pre-treated with media alone or PIF at 50, 100 or 500 nM for 24 hrs, then with media alone, LPS (1µg/ml), PIF (50, 100 or 500 nM) or LPS (1µg/ml) with PIF (50, 100 or 500 nM) for a further 48 hrs Media samples were collected 24 and 48 hrs post LPS challenge and $PGF_{2\alpha}$, PGE_2 and IL-6 measured via radioimmunoassays and ELISA. Data were expressed as secretion per mg of tissue and analysed using an analysis of variance, with treatment and cow type as main effects.

Results Animals were split into two groups based on whether they were beef or dairy. There was a significantly greater production of PGE_2 from dairy explants compared to beef ($P<0.05$). LPS significantly increased $PGF_{2\alpha}$, PGE_2 and IL-6 secretion from explants at 24 and 48 hours ($P<0.001$). PIF had no effect on the secretion of $PGF_{2\alpha}$ or PGE_2 from explants with or without the presence of LPS ($P>0.05$). There was no effect of PIF on IL-6 secretion from LPS stimulated explants ($P>0.05$; Figure 1). However, PIF at 100nM and 500nM was able to significantly reduce IL-6 secretion from unstimulated explants compared to the control at 24 hours ($P<0.05$; Figure 1). This was not significant at 48 hours.

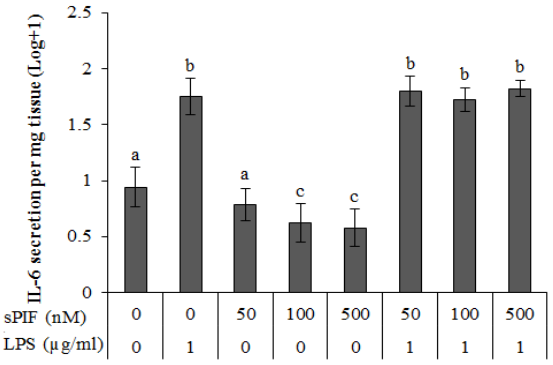

Figure 1 IL-6 secretion from bovine endometrial explants 24 hours post challenge. Differing superscripts indicate significant difference between treatments ($P<0.05$).

Conclusion PIF was shown to interact with the IL-6 pathway in un-stimulated endometrial tissue at 100nM and 500nM. There was no effect of PIF on PGE_2 or $PGF_{2\alpha}$ secretion, or LPS stimulated IL-6 secretion. However, the latter may be due to the high dose of LPS used. A lower concentration of LPS will be used in future experiments to further test the effect of PIF.
Research is needed to establish effects of PIF on components of IL-6 pathway. Furthermore, cytokines other than IL-6 should be investigated to assess the effect of PIF on other aspects of the TLR4 stimulation pathway. Earlier sample time points should be tested due to the half -life of PIF being short, at ~45min in circulation.

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The relationship between fatty acid profiles in milk identified by fourier transform infrared spectroscopy and onset of luteal activity in Norwegian dairy cows

A D Martin[1], N K Afseth[2], A Kohler[3], Å Randby[3], M Ekænes[3], A Waldmann[4], O Reksen[1]
[1]Norwegian University of Life Sciences, Oslo, Norway, [2]Nofima, Ås, Norway, [3]Norwegian University of Life Sciences, Ås, Norway, [4]Estonian Universiyt of Life Sciences, Tartu, Estonia
Email:adam.martin@nmbu.no

Implications The study shows a relationship between onset of luteal activity post-partum and the composition of milk fat in Norwegian dairy cows. These findings could be developed to allow dairy producers to manage their resources more efficiently.

Introduction Milk components represent information on the metabolic state of the milking cow. As precision farming develops it is likely that online milk component measurements will be performed at every milking in some systems. Previous work has shown milk fat:protein ratios in milk to be unreliable predictors of reproductive performance (1) and direct measures of progesterone are expensive. Fourier transform infrared spectroscopy (FTIR) has previously been used for online measurement of milk components in the wet phase (2). Drying the milk sample before analysis decreases component detection limits and improves estimate accuracy (3). This study aimed to use dry phase to measure different components of the milk fat fraction and to compare these to onset of luteal activity (OLA).

Material and methods Morning milk samples were collected thrice weekly (Monday, Wednesday, Friday) for the first 10 weeks in milk (WIM) from 87 lactations in 73 healthy Norwegian Red cows over two winter housing seasons. These samples had bronopol added to them before been frozen, thawed, and analysed by enzyme linked immunoassay to determine progesterone concentration and the proportions of the milk fatty acids which were C4:0, C14:0, C16:0, C18:0, and C18:1cis9 using dry film FTIR (3), and averaged by WIM . OLA was defined as the first day that milk progesterone concentrations were >3ng/ml for two successive measurements, the study population was categorised as early (n=47) or late (n=40) OLA, using the median value of 21 DIM as the cut off. Further milk samples were collected 6 times weekly, from morning and afternoon milkings, these were pooled by WIM and one proportional sample was analysed fresh for fat, protein and lactose content, using infrared spectrography. Feed intakes, bodyweight, milk content and yield were recorded. These data were used to calculate daily energy balance (EB) in 42 lactations before they were averaged by WIM at the cow level. Relationships were explored for each WIM using the student's t test (EB), or logistic regression (Early OLA vs. late OLA).

Results Higher proportions of medium chained fatty acids (C14:0 and C16:0) were found in the early, than in the late OLA group from WIM 1 until WIM 7 (weekly p value always <0.05). In WIM 4, a lower milk fatty acid proportion of C16:0 predicted late OLA with 74% sensitivity and 80% specificity. The proportion fatty acids that were long chained (C18:0 and C18:1cis9) was consistently lower in the milk of the early OLA group and the difference was greatest in WIM 4 and 5. A higher proportion of C18:1cis9 was seen in the milk fatty acids of the late OLA compared to the early OLA group from WIM 1 until WIM 5 (all weekly *p*-values <0,05). Animals experiencing late OLA had a more negative EB in WIM 1, 3, 4, and 5 (p-values < 0.05) than those in the early group. The greatest differences were in WIM 3 and 4. No relationship was seen between OLA and the content of either protein or fat in milk, or between OLA and the milk fat:protein ratio. The differences in milk fatty acid concentrations between the two groups were most likely the result of differences in energy balance between the two groups (4).

Conclusion This study showed that OLA is related to specific milk fatty acid concentrations. The relationships occur from WIM 1. When OLA is dichotomised as early or late, univariate analysis found prediction accuracy to be highest in WIM 4. This study also showed that dry film FTIR performed on previously frozen milk samples can determine milk fatty acid composition.

Acknowledgements The authors would like to thank Ellen Dahl for her assistance in analysing the milk samples for progesterone.

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Culling in the dairy herd: have cows paid back their cost of rearing?

A C Boulton, J Rushton, D C Wathes
Royal Veterinary College, Hertfordshire, UK
Email:aboulton@rvc.ac.uk

Implications The length of time it takes for the heifer to pay back its cost of rearing has major financial implications for the farm. Knowing what the current breakeven point is will enable farmers to make a more informed decision when culling.

Introduction High wastage levels in UK dairy herds have meant an average lifespan in 2009 of 3.5 lactations (DairyCo, 2009). The average culling rate in the UK is currently 26% with the four primary reasons for culling being health, poor reproduction, performance and management (DairyCo, 2008). The cost of rearing heifers accounts for the second largest annual expense, approximately 20% of a dairy system's production costs after feed (Bach, 2011) and heifers do not begin to repay this investment until after they enter the milking herd. The aim of this study was to determine at what point following first calving heifers repay their cost of rearing and so begin to make a profit for the farm.

Material and methods Dairy farms (n=101) across England, Scotland and Wales were visited March through August 2013. The selected farms covered a range of management systems typical of the UK with milking herd sizes ranging from 10 to 1800 cows. A questionnaire was completed during a one day interview and included 124 questions recording details and costs of heifer rearing as well as average 305-day lactation yields and farmgate price. A cost analysis workbook was developed in Microsoft Excel 2010 and costs were calculated on a per heifer basis for labour, feed, bedding, housing, veterinary and health treatments, equipment, electricity, slurry, water, grazing, reproductive management, interest and mortality. A second model to calculate the cost of rearing began at calving on day 0. Each daily time step then added on the variable cost per day of maintenance and subtracted the revenue per day from milk production. At the end of the lactation period, farms that had not paid back the cost of rearing through milk revenue were modelled through the dry period with only variable costs being added to the outstanding balance. The balance at the end of the dry period was then taken forward to the next lactation where the difference between revenue and cost was again subtracted from the outstanding balance. The cycle continued until all farms had paid back the cost of rearing. Fertility measures used to calculate the length of the dry period were taken from Cooke *et al*. (2013).

Results During the first lactation 20.8% (21/101) of farms paid back their cost of rearing, rising to 90.1% (91/101) by the end of the second lactation. The mean breakeven point was reached at 543 ± 500 days after first calving (range 179 to 2292 days, median = 299 days, n=101 herds). This translated into approximately 1.5 lactations before heifers began to make a profit for the farm. Farms that had longer repayment periods had higher mean costs of rearing (Table 1) and smaller differences between daily revenue and variable costs.

Table 1 The mean cost of rearing for farms classified according to the lactation number in which this was repaid

Lactation No.	No. farms	Mean cost of rearing (£)				
		Minimum	Maximum	Mean	s.d.	Median
1	21	10191.55	1991.12	1534.32	± 254.17	1609.14
2	70	1192.28	2644.27	1863.97	± 290.96	1874.61
3	7	1701.77	3078.67	2355.42	± 501.69	2285.76
4 -6*	1			2541.76		

*1 herd achieved payback in each of lactations 4, 5 and 6

Conclusion High culling rates particularly in the first lactation increase the risk that heifers will be disposed of before they have started making a profit. The farms that are of most concern are those in which the breakeven point is not reached until at least the third lactation. This is because the average number of lactations in the UK national herd is currently 3.5. The length of the repayment period is influenced by the cost of rearing, the farmgate price and production output.

Acknowledgements This work was supported by grants from DairyCo and the BBSRC. We would also like to thank all the UK dairy farmers who participated in the research.

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Current rearing practices for pre-weaned dairy heifer calves in Britain: is there room for improvement?

A C Boulton, J Rushton, D C Wathes
Royal Veterinary College, Hertfordshire, UK
Email:aboulton@rvc.ac.uk

Implications Awareness of current rearing practices on GB dairy farms will enable extensions services to target knowledge transfer effectively to improve the health and welfare of dairy calves.

Introduction Management of the pre-weaning period is extremely important as it will determine the heifer's future production potential and lifetime spent in the milking herd. The calf undergoes critical physiological changes during this time and is most susceptible to infections that cause enteric and respiratory disease. Much research has gone into identifying best practice for the care of dairy heifers to reduce wastage and improve productivity. The aim of this study was to record and examine current preweaning heifer rearing practices in GB.

Material and methods Dairy farms (n=103) across England, Scotland and Wales were visited March through August 2013. A questionnaire based on a study undertaken conjointly by the Université Laval, Agriculture and Agri-Food Canada, Valacta and the Université de Montréal (Vasseur *et al*., 2010) was completed during a one day interview with the farmer followed by an inspection of the rearing facilities to confirm housing type and size, feed constituents and animal movement. The survey included 60 questions on management practices related to the period from birth to weaning on the areas of neonatal care, feeding, housing, health and disease and weaning.

Results The mean duration of time spent per day on duties directly associated with heifer rearing pre-weaning was 2.14 ± 1.66 minutes per heifer. This time included feeding, mucking out and rebedding, dehorning and health treatments. All farms in the study fed colostrum to their heifer calves within 12 h of birth with an average volume at first feeding of 2.8 L and 2.4 L at second feeding. Only 32% of farms ensured both the first and second feeding were from the first milking following calving. Less than half of the farms (43%) checked the quality of the colostrum before feeding and only 42% increased the volume, used another dam's milk or artificial colostrum if the quality was not good or excellent. The routine treatment of the navel following birth was practiced by 82% of the farms surveyed with 85% of farms using an anaesthetic before dehorning and only 6/103 using an anti-inflammatory as well as an anaesthetic. Approximately 90% of farms dehorned their calves before weaning with more than half (57%) doing so between 3 and 6 weeks of age. Most farms housed their calves individually (65%) for their first accommodation if not for the entire duration of the pre-weaning period. The average size of the area allotted per calf including those group housed was 2.2 ± 2.0 m^2. Approximately half (51%) of the farms surveyed added fresh bedding daily to calf pens with pens being mucked out and rebedded normally every 4 weeks (36%): however 9% of farms only mucked out after the calves had been weaned. Disinfection occurred routinely on 76% of farms. The most common type of milk fed to calves was reconstituted milk replacer (55%) followed by whole milk (18%). The average volume of milk fed was 4.58 ± 1.33 L which equates to an average of 12.95 ± 6.15 MJ of metabolizable energy per day. The average age at weaning was 62 days with the most commonly employed method of weaning being the reduction in volume of milk fed to calves (56%) with 25% of farms ending milk feeding abruptly. Dry feed was regularly introduced to calves at <1 week of age (82/103) with free access to water during the first week of life occurring on 78% of farms (40% from day 1). Two farms did not provide access to water until after weaning. A total of 90/103 and 88/103 farms treated at least one heifer calf for scours or respiratory infection respectively during this period while 30/103 farms administered at least one type of vaccination and 10/103 farms administered multiple vaccinations most commonly for bovine respiratory diseases.

Conclusion The replacement herd is often a secondary consideration as labour constraints ensure most of the farmer's time is concentrated on managing the milking herd. While most farms followed industry and government guidelines on rearing youngstock during the preweaning period, compliance on government regulations relating to the administration of anaesthetic prior to dehorning and provision of water from birth was not practiced on 15% and 60% of farms respectively. A mean volume of milk of 4.58 L/d would not supply enough energy to achieve recommended daily liveweight gains of between 700-800 g/d particularly during the first several weeks of life when starter intake is low. Raising awareness on the importance of adhering to best practices especially regarding nutrition would improve the health and welfare of dairy calves.

Acknowledgements This work was supported by grants from DairyCo and the BBSRC. We would also like to thank all the UK dairy farmers who participated in the research.

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Effect of plane of nutrition on growth rate, feeding behaviour and systemic metabolite concentrations in pre-weaned bull calves of two contrasting dairy breeds

C Byrne[1,2], A M English[1,3], D A Johnston[1,2], S Fair[3], P Lonergan[2], D A Kenny[1]
[1]Animal & Grassland Research and Innovation Centre, Teagasc Grange, Dunsany, Ireland, [2]School Agriculture and Food Science, UCD, Ireland, [3]Department of Life Sciences, University of Limerick, Ireland *Email:colin.byrne@teagasc.ie*

Implications The performance of calves, pre-weaning, offered a high level of milk replacer does not improve when compared to calves offered a moderate level as calves on a high level of milk replacer will eat less concentrate and have lower feed efficiency. Feeding behaviour is healthier when calves are offered a moderate of level of milk replacer.

Introduction The Irish dairy herd is currently undergoing significant expansion in preparation for the abolition of milk quotas in 2015. This will result in increased availability of male dairy bred calves for beef production. The aim of this study was to characterise growth, feeding behaviour and metabolic responses in purebred male calves of two contrasting dairy breeds.

Material and methods Holstein Friesian (F) (n=42) and Jersey (J) (n=25) bull calves with a mean ± SD age and bodyweight of 21± 5.52 d, 47 ± 5.53 kg and 36 ± 8.00 d, 33 ± 4.38 kg, respectively were sourced from commercial dairy farms at two weeks of age. Calves were blocked by breed, age, weight and sire to a high (H), medium (M) or low (L) plane of nutrition. Calves were individually fed milk replacer and concentrate using a computerised calf feeding system (Förster-Technik SA 2000, Engen, Germany) which recorded all feed related events. Diets design was based on NRC 2001 guidelines. F calves on the H, M and L planes of nutrition were offered in litres (grams); 8 (1200), 6 (800) and 4 (500), of milk-replacer (MR) daily, respectively. J calves on H, M and L planes of nutrition were offered 6 (800), 4 (500) and 3.5 (350) of MR daily, respectively. Concentrates were offered *ad libitum,* to a maximum of 1.5 kg and a maximum of 1 kg daily to H, M and L calves, respectively. Calves were offered these diets for 56 days and were weaned once consuming 1 kg of concentrate, per day, for three consecutive days. Calves were weighed weekly. Blood samples were collected via jugular venipuncture on weeks 1, 4 and 7 relative to the beginning of the trial period and analysed for non-esterified-fatty acids (NEFA) betahydroxybutryate (BHB), urea and glucose. Data were analysed using ANOVA (MIXED procedure SAS v9.3). Breed and plane of nutrition with their interactions, where appropriate, were included in the model.

Results There were no interactions amongst the main effects for any animal performance or feed intake related trait ($P>0.05$). Average daily gain (ADG) was higher ($P<0.001$; Table1) in F than J calves. This higher ADG in F may be a result of the higher; total UFL intake (MR and concentrate) in F calves compared to J calves ($P<0.001$). The effect of dietary treatment approached significance ($P=0.08$), with H calves growing slightly faster than M and L calves. The difference in milk intake between treatments was in line with the design of the study; H, M and L consuming (mean litres ± s.e.m.), 5.8 ± 0.03, 4.5 ± 0.04 and 3.5 ± 0.04, respectively ($P<0.001$) and this led to higher concentrate consumption in M and L; H, M and L consuming (mean kg ± s.e.m.), 0.61 ± 0.01, 0.69 ± 0.01 and 0.64 ± 0.01, respectively ($P<0.001$). There was a tendency towards an effect of treatment on drinking speed ($P=0.07$); interestingly, the M treatment calves had the fastest rate of drinking. Feed conversion ratio (FCR) was highest for H calves ($P<0.001$). Treatment had an effect on the number of unrewarded visits for milk replacer ($P<0.001$) with L calves, making more visits than calves on either of the other two treatments. There was a breed x treatment x time interaction for plasma concentrations of BHB ($P<0.05$) manifested as J calves on L having higher concentrations during week 7, beginning of weaning, compared with their F counterparts. There was a tendency for a three way interaction of treatment x breed x time ($P=0.08$) for plasma concentrations of glucose. F calves on H had higher glucose than J calves and both breeds on M and L. Glucose levels decreased in all calves between weeks 1 and 7.

Table 1 Effect of breed (B) and plane of nutrition (T) on calf performance and feeding behaviour in the pre-weaning period

	B			T				Significance[1]		
	F	J	S.E.D.	H	M	L	S.E.D.	B	T	B*T
ADG (kg per day)	0.7	0.6	0.05	0.7	0.6	0.6	0.06	***	0.08	0.25
Total UFL intake[2]	1.9	1.7	0.05	2.2	1.8	1.4	0.59	***	***	0.18
Drinking speed(ml/min)	910.2	855.2	35.55	890.2	955.1	847.9	42.32	0.66	0.07	0.14
FCR (UFL/ kg gain)	2.8	2.7	0.10	3.0	2.8	2.4	0.12	0.31	***	0.42
Visits with feed[2]	3.5	3.6	0.16	4.3	3.0	3.4	0.20	0.41	***	***
Visits with no feed[2]	8.7	9.6	0.8	7.1	9.7	10.6	0.98	0.12	***	0.34
NEFA (mmol/l)	0.21	0.22	0.016	0.22	0.21	0.21	0.021	0.95	0.83	0.11
BHB (mmol/l)	0.11	0.19	0.012	0.14	0.15	0.16	0.014	***	0.30	***
Glucose (mmol/l)	5.69	5.44	0.139	5.88	5.41	5.51	0.171	0.07	**	0.26

[1]**=P<0.01, ***=P<0.001. [2]Average daily. ADG =average daily gain. FCR =feed conversion ratio

Conclusion Preweaning growth rate was influenced more by breed than treatment with J, as expected, growing slower than F calves. Feeding behaviour was affected by plane of nutrition, with the number of unrewarded feeding events higher in calves offered less MR. However, drinking speed, a good indicator of health, was highest for calves on the M plane of nutrition. In summary, there was no evidence of an economically justifiable improvement in performance from offering calves a higher level of MR, as although total net energy intake was increased, these calves consumed less concentrates, and had lower feed efficiency.

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Use of NIRS to describe the time course of rumen fermentation of herbage

J M Bowen[1,2], R J Dewhurst[1], S J Lister[2]
[1]Animal Bioscience Department, Teagasc, Grange, Dunsany, Co. Meath, Ireland, [2]IBERS, Aberystwyth University, Gogerddan, Aberystwyth, SY23 3EB, UK
Email:jenna.bowen@teagasc.ie

Implications NIRS was able to detect chemical differences associated with different periods of rumen fermentation, and shows promise as a rapid and low-cost technique to evaluate between-animal variation in digestion processes, without the need for calibration.

Introduction This study investigated the use of NIR spectroscopy (NIRS) to monitor the digestion of different components of fresh herbage incubated with buffered rumen fluid. A similar approach was used for a range of forages by Deaville and Givens (1998). In this work we used samples taken from the upper (mainly leaf) and lower (mainly pseudostem) parts of grass taken from two different plots. Our ultimate objective is to use NIRS to describe variation in digestion of different feed components without the need for calibration. Different incubation times were used to generate differences in digestion to simulate differences in passage rates from the rumen. Spectra from the one-hour incubation time were subtracted from spectra for each subsequent incubation time, producing difference spectra which shows the time course of degradation.

Material and methods Grass samples were collected from two different plots at Teagasc Grange during August 2013. Grass was measured and cut in half to produce upper (mainly leaf) and lower (mainly pseudostem) sections. Each section was chopped in a mixing bowl for 1 minute to simulate mastication and 30 gram samples weighed into 250 ml Duran bottles. Rumen fluid and artificial saliva was added, the space above the fluid flushed with CO_2 and bottles fitted with a rubber bung with a gas release valve. Samples were incubated in duplicate at 37^{o}C and shaken at 80 RPM for varying time periods; 1, 2, 6, 12, 24 and 48 hr. Samples were then rinsed with deionised water before being strained through forage bags (50 µm pore size; ANKOM Technology, New York) and residues dried at 100^{o}C for 48 hours before being ground through a 0.75 mm sieve. Samples were scanned between 1100-2500 nm at 2 mm intervals using a NIRSystem 6500 monochromator (FOSS, Warrington, UK). Duplicates were averaged, and spectra transformed using SNV and detrend. Spectra from 1 hr incubation residues were subtracted from spectra for each subsequent incubation time and standard deviation plots calculated (WinISI, Version 1, Infrasoft International LLC). Data was subsequently exported and visualised in Unscrambler X (Camo Software) and Excel 2010 (Microsoft Corporation).

Results Regardless of plot or grass section, dry matter of recovered sample decreased as incubation time increased on average from 34.1 to 15.5% for 1 and 48 hr respectively. Regardless of plot or section, regions associated with lipid (2310, 2350 and 2390 nm) were increasingly positive over incubation time – the peaks were also repeated in the overtone region (1728 and 1782 nm) – example Figure 1a. Increasingly negative toughs appear in regions 1450-1620 nm, previously linked with high digestibility in forages (Deaville and Givens, 1998), and 1930 and 2100 nm associated with starch/cellulose. Greater differences between grass sections is observed in the region of 1450-1660 nm of SD plot (Figure 1b), whilst greater differences between plot is observed at 2100 nm.

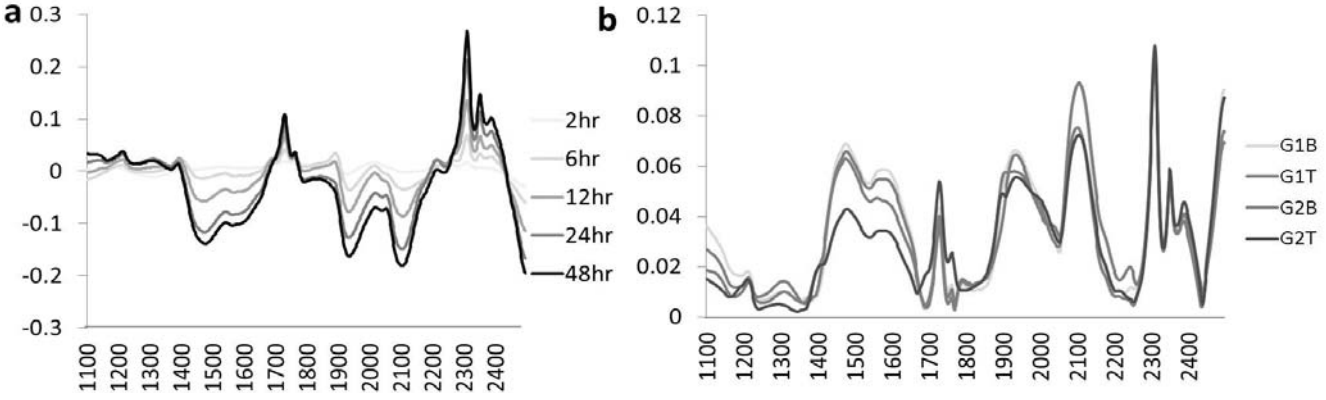

Figure 1 a) difference spectra of bottom section of plot 2 and b) SD plot of both section and plot

Conclusion Compounds associated with high digestibility (cellulose and various sugars) decreased in concentration as incubation time increased, whilst lipids increased in concentration.

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Effect of supplemental tannin (chestnut) at feeding on rumen pH and protozoa number *in vivo*

V Taha, R Wilkinson, D Davies, J Huntington
Harper Adams University, Newport, Shropshire, UK
Email:tvahel@harper-adams.ac.uk

Implications Dietary inclusion of hydrolysable tannin (chestnut) results in partial defaunation of the rumen.

Introduction Tannins are a diverse group of water-soluble, high molecular weight and polyphenolic plant secondary metabolites. The phenol groups give tannin the ability to bind with forage and microbial protein in the rumen to form tannin-protein complexes, which are pH (6-7) dependent and resistant to rumen microbes (Muller-Harvey, 2006). This complex then disassociates in the abomasum (pH< 3.5) facilitating protein digestion in the small intestine and hence increased undegradable protein supply (Makkar, 2003). Terrill *et al.* (1992) reported that tannins are inhibitory to protozoa in rumen fluid. Makkar *et al.* (1995) found that 0.1-0.4 mg ml^{-1} of tannin significantly reduced protozoa number *in vitro*. The objective of this study was to investigate the effect of supplemented chestnut tannin on the protozoa number and rumen pH of sheep fed lucerne silage.

Material and methods Four mature, ruminally cumulated whethers sheep were used. The sheep were group housed and adapted to lucerne silage over a 10 days period at 1.1 x ME requirement for maintenance (AFRC, 1993). Following the adaptation period, sheep were housed individually and offered lucerne silage once daily at 9:30 am (1.1 X ME). Water was available *ad-libitum* and the experiment was conducted for 4 weeks Each week sheep were offered lucerne silage supplemented with chestnut tannin at one of four levels (0, 25, 50 and 75 g/kg DM) subspecialty during week 1, 2, 3 and 4 respectively. On the final day of each week, 200 ml of rumen fluid/wether was collected manually via the rumen cannula at 6 time points: -0.25, 2, 4, 6, 8 and 10 h post feeding. The rumen fluid pH was measured immediately and rumen protozoa numbers were counted according to Dehority (1984). The experiment was analysed by ANOVA as a completely randomised design using GenStat 15 (VSN, International, Oxford, UK).

Results Figure 1 show that maximum protozoa number were found 2h post feeding (P <0.001, SED =5583) and highest rumen pH was observed 30 minutes pre-feeding (P <0.001, SED =0.042). Protozoa population density was significantly reduced (P= 0.01, SED =11190) as level of dietary tannin increased as shown in Figure 2. Figure 2 also shows that increasing tannin level (<50 gkg^{-1}DM) of the diet had no effect on rumen pH (P>0.05).

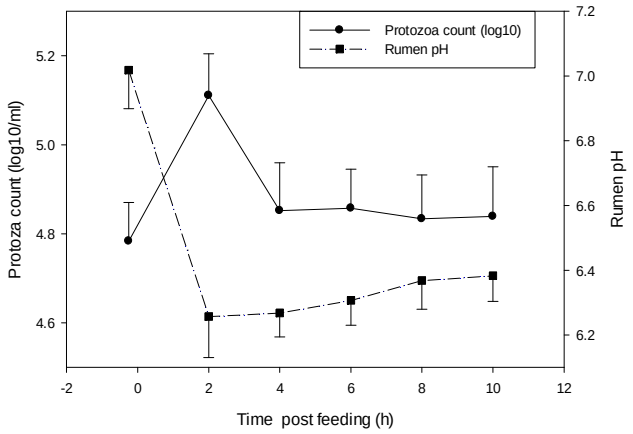

Figure 1 Changes in mean rumen protozoa counts and rumen pH with time

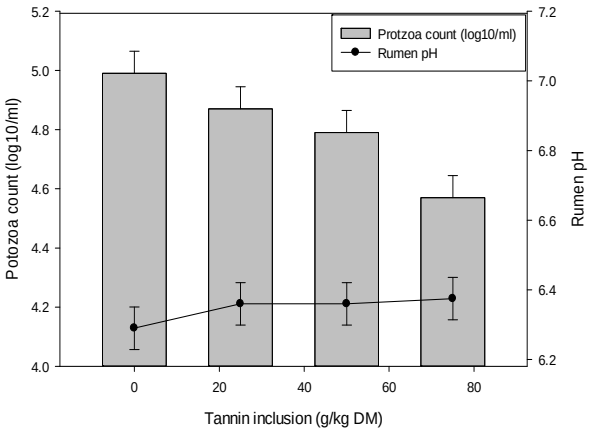

Figure 2 Mean rumen protozoa counts and rumen pH for different levels of dietary tannin.

Conclusion Maximum protozoa numbers were observed 2h post feeding. Addition of hydrolysable tannin (chestnut) (25, 50 and 75 g kg^{-1} DM) to a lucerne silage based diet significantly reduced protozoa numbers but no effect on rumen pH.

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Effects of ten whole essential oils on rumen fermentation and biohydrogenation of *n*-3 polyunsaturated fatty acids by rumen microorganisms *in vitro*

P O Eburu, S Chikunya
Writtle College, Partner of the University of Essex, UK
Email:patrickeburu@ymail.com

Implications Essential oils such as anise, cassia and cornmint oils are potentially useful inhibitors of PUFA biohydrogenation provided that inclusion doses can be optimised and the observed positive effects are replicated *in vivo.*

Introduction Using whole essential oils (EOs) and or constituent compounds (EOC) to modulate rumen function has been a prominent area of research recently (Calsamiglia *et al.* 2007; Benchaar *et al.* 2008). However, the majority of these studies have predominantly looked at their effects on protein breakdown, VFA production and methane formation; their effects on ruminal polyunsaturated fatty acid (PUFA) metabolism have been ignored. Increasing dietary intakes of PUFA such as linolenic acid (LNA, C18:3*n*-3), eicosapentaenoic acid (EPA, C20:5*n*-3), docosahexaenoic acid (DHA, C22:6*n*-3), and biohydrogenation intermediates such as conjugated linoleic acid (CLA) by humans has well documented health benefits. EOC screening trials (Sgwane *et al*. 2013; Eburu and Chikunya 2014) demonstrated that some compounds have potential to reduce disappearance of key PUFA in the rumen. This study aims to establish whether the parent oils in which some of the individual EOCs showing potential are the predominant compound are equally as effective.

Material and methods A basal feedstock of a 70:30 mixture of grass hay (*Lolium perenne)* and concentrate was formulated and milled (1 mm screen). The basal substrate was supplemented with 32.5 g oil/kg (60% fish oil + 40% ground linseed oil). Three serum bottles were incubated for 48 h in each run and repeated twice. In total 288 serum bottles were incubated, each bottle contained 80 ml buffer, 20 ml inoculum and 1 g of substrate; with 300 mg/l of EO. Rumen fluid was collected from 6 Hartline × Texel cross cull ewes on the same basal diet. In total, there were 11 treatments, with 6 replicates per EO as follows: control (CON), anise oil (ANO), cassia oil (CSO), citronella oil (CTO), clove oil (CLO), cornmint oil (CMO), eucalyptus oil (ETO), juniper berry oil (JPO), lavender oil (LVO), mandarin oil (MDO) and rosemary oil (RMO). Samples were frozen at -20^{0}C and analysed for fatty acid (FA) methyl esters by gas chromatography. Data were analysed using one-way ANOVA with experimental runs as a blocking factor using GenStat 16th Edition.

Results Effects of the ten EOs screened on biohydrogenation of PUFA are summarized in Table 1. Relative to the CON, the concentrations of 18:2*n*-6 (LA) and 18:3*n*-3 (LNA) were higher (P<0.001) across all EO. The highest (P<0.001) levels were maintained by CSO (178% and 238%) and ANO (148% and 191%) for LA and LNA respectively relative to the control. A similar pattern was also seen with 20:5*n*-3 and 22:6*n*-3 which were significantly higher (P<0.001) when ANO (124% and 30%), CSO (138% and 30) and CMO (119% and 26%) were added to the culture. With the exception of CTO and CLO, inclusion of most EO did not affect CLA concentration. Trans-vaccenic acid was increased (P<0.001) by CSO, CTO CMO and RMO. All EO, except ETO and LVO, decreased (P<0.001) total volatile fatty acid (TVFA) with CSO being the most inhibitory, inducing a 27% reduction relative to the control.

Table 1 Effects of EOs on concentration of PUFA (g/100g total FA) and total volatile fatty acids (TVFA, mmol)

	CON	ANO	CSO	CTO	CLO	CMO	ETO	JPO	LVO	MDO	RMO	*sed*	*P*
LA	2.2^{a}	5.4^{b}	6.0^{e}	4.1^{d}	3.4^{eg}	4.5^{f}	3.2^{e}	3.7^{g}	3.4^{eg}	4.6^{f}	3.9^{dg}	0.16	***
LNA	2.8^{a}	8.1^{b}	9.4^{e}	5.9^{d}	4.9^{eg}	6.9^{f}	4.5^{e}	5.3^{g}	4.8^{eg}	7.4^{f}	5.8^{dg}	0.27	***
EPA	1.4^{a}	3.0^{bc}	3.2^{b}	2.8^{cf}	2.0^{de}	3.0^{bc}	2.1^{de}	2.2^{d}	1.9^{e}	2.6^{f}	2.9^{c}	0.15	***
DHA	1.8^{a}	2.3^{be}	2.4^{b}	2.1^{c}	2.1^{c}	2.3^{be}	2.3^{be}	2.0^{cd}	1.9^{ad}	2.2^{ce}	2.3^{be}	0.09	***
TVA	1.3^{a}	1.3^{a}	1.7^{b}	1.4^{c}	1.3^{a}	1.4^{c}	1.3^{a}	1.3^{a}	1.3^{a}	1.3^{a}	1.4^{b}	0.05	***
CLA	0.10^{a}	0.11^{ab}	0.12^{bd}	0.16^{c}	0.13^{d}	0.11^{a}	0.12^{bd}	0.10^{a}	0.11^{a}	0.12^{bd}	0.12^{bd}	0.010	***
TVFA	70.0^{a}	60.6^{b}	51.0^{c}	61.1^{b}	65.6^{d}	64.1^{d}	68.3^{a}	64.9^{b}	68.2^{a}	63.5^{d}	63.2^{d}	1.37	***

Means with different superscripts are significantly different

Conclusion These results show that whole essential oils also inhibit biohydrogenation of PUFA by rumen microorganisms just like their key constituent compounds. Of those compared here; ANO, CSO and CMT show the most potential. The concomitant inhibition of VFA by the EO is undesirable and optimal doses offering the right balance need to be established.

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The effects of graded doses of 4-allylanisole, anethole, anise oil and cassia oil on fermentation and biohydrogenation of *n*-3 polyunsaturated fatty acids by rumen microorganisms *in vitro*

P O Eburu, S Chikunya
Writtle College, Partner of the University of Essex, UK
Email:patrickeburu@ymail.com

Implications Whole essential oils and individual essential oil compounds when administered at the right dose have the potential to both protect PUFA from biohydrogenation without marked reduction in VFA production *in vitro*.

Introduction In two *in vitro* studies, we established that when included at 300 mg/l both individual essential oil compounds (EOC) such as 4-allylanisole and anethole (Eburu and Chikunya, 2014) and whole essential oils (EO) particularly oils of anise and cassia (Eburu and Chikunya, unpublished) significantly inhibit the disappearance of key polyunsaturated fatty acids (PUFA) from rumen contents. However, at this level of inclusion they also caused significant reductions in VFA concentrations. The aim of this study was to investigate whether optimal doses of these substances could be established in order to achieve satisfactory inhibition of biohydrogenation but without significant reductions in VFA by evaluating these EOC and EO at graded levels of inclusion.

Material and methods A basal feedstock of a 70:30 mixture of grass hay (*Lolium perenne)* and concentrate was formulated and milled (1 mm screen). The basal substrate was supplemented with 32.5 g oil/kg (60% fish oil + 40% ground linseed oil). In total 384 serum bottles were incubated, each bottle contained 80 ml buffer, 20 ml inoculum and 1 g of substrate; with 300 mg/l of EO. Rumen fluid was collected from 6 Hartline × Texel cross lambs on the same basal diet. Increasing concentrations (0, 100, 200 and 300 mg/L) of each EO and EOC were added. There were 16 treatments (6 replicates per treatment) as follows: 4-Allyanisole (ALA 0, 100, 200 and 300 mg/L), anethole (ANE 0, 100, 200 and 300 mg/L), anise oil (ANS 0, 100, 200 and 300 mg/L) and cassia oil (CAS 0, 100, 200 and 300 mg/L). After 24 h, Samples were frozen at -20^{0}C and analysed for fatty acid (FA) methyl esters by gas chromatography. Data were analysed by Two-Way ANOVA with interaction using Genstat 16th edition.

Results All doses (of both EOC and EO) maintained higher (P<0.001) concentrations of PUFA and CLA in a linear (dose-dependent) manner (Table 1). The EO and EOC used in this study all inhibited total volatile fatty acids (TVFA), with the highest reductions being observed with ALA (11%) and CAS (14%). Irrespective of oil, the highest dose (300 mg/L) of all substances with the exception of ANE induced the most inhibition (average 12%) on TVFA. At 200 mg/L, the rest of the treatments (ANE, ALA and ANS) only marginally reduced TVFA (by about 2%) relative to the control, except for CAS which reduced TVFA by 10%.

Table 1 Effects of EOs on concentration of PUFA (g/100g total FA) and TVFA (mmol).

Treatments	Dose	18:2n-6	18:3n-3	20:5n-3	22:3n-6	CLA	TVFA
Control	0	1.7	2.1	0.63	1.7	0.15	92.5
	100	2.1	2.7	0.70	1.8	0.15	91.6
4-Allylaniaole	200	2.6	3.6	0.90	1.9	0.16	87.3
	300	3.2	4.7	1.30	2.0	0.18	75.9
	100	2.0	2.7	0.70	1.7	0.14	86.6
Anethole	200	2.5	3.4	0.90	1.8	0.15	103.5
	300	3.1	4.6	1.20	1.9	0.16	91.1
	100	2.0	2.5	0.70	1.8	0.16	98.9
Anise	200	2.4	3.4	1.00	1.9	0.18	91.8
	300	2.8	4.2	1.20	1.9	0.19	82.6
	100	2.1	2.5	0.80	1.8	0.14	85.3
Cassia	200	2.2	2.8	0.90	1.8	0.15	82.9
	300	2.6	3.7	1.20	1.8	0.18	78.5
Standard error	*Oil*	0.04	0.05	0.020	0.04	0.010	1.31
	Dose	0.04	0.05	0.020	0.04	0.010	1.31
Significance	*Oil*	0.001	0.001	NS	NS	0.001	0.001
	Dose	0.001	0.001	0.001	0.001	0.001	0.001

Conclusion Considering the effects of the tested EO and EOC and at different doses in this study, it appears that administration of these substances at 200 mg/L seems to give best balance between PUFA protection and minimal disruption to VFA production *in vitro*. Anise oil and anethole were more effective than the other two in both preventing PUFA disappearance and maintenance of optimal VFA production. It is worthwhile to investigate the mechanisms involved and whether these effects also occur *in vivo* including testing the possibility of microbial adaptation to these substances.

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In vitro screening of different biochars as antimethanogenic feed additives for ruminants

I Cabeza[1,2], R Dewhurst[1], T Waterhouse[1], S Sohi[2], J Rooke[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]School of Geosciences, University of Edinburgh, UK
Email:irene.cabeza@sruc.ac.uk

Implications The development of biochar as an animal feed additive may offer a new possibility to reduce the production of methane (CH_4) by ruminants.

Introduction Methane is a potent greenhouse gas and main source is domestic ruminant enteric fermentation. Despite extensive research undertaken to find ways of reducing CH_4 emissions from ruminants, progress has been relatively limited. Biochar is the solid product of heating biomass at high temperature without air (pyrolysis) and has been used as a soil amendment improving fertility, capturing carbon dioxide and changing soil biological community. The objective of this study was to evaluate a range of biochar samples with different compositions for their potential to reduce CH_4 emissions. The *in vitro* gas production technique was used to evaluate the effects of biochar on rumen fermentation and CH_4 production.

Material and methods Ten biochar samples with different physicochemical properties were obtained by processing five different feedstocks (wheat, miscanthus, rice husk, soft wood pellets and oil seed rape straw) at two different pyrolysis temperatures (550 and 700ºC; UK Biochar Centre, University of Edinburgh). Biochar that passed through a 2 mm sieve was used on *in vitro* incubations. Gas production was measured by anaerobic incubation of 400 mg fresh weight feed (hay: barley: rapeseed meal, 5:4:1) with either 4 or 40 mg biochar in 120 ml bottles for 24 h at 39ºC with 10 ml rumen fluid and 30 ml buffer. The experiment was repeated on four different days. On each day, each treatment was incubated in triplicate. The experimental design was a factorial arrangements of 2 biochar levels (10 and 100g/kg substrate)*2 process temperatures (550 and 700ºC) and 5 feedstocks giving 20 treatments; control (no biochar) and blank (no substrate) bottles were also included on each day giving a total of 66 bottles per day. Rumen samples were obtained by stomach tube before feeding from cattle fed *ad libitum* a diet consisting of approximately (g/kg dry matter, DM) 500 g forage, 500 g concentrate. Samples from individual animals were not pooled but three distinct rumen fluid samples were produced daily (from either one or two animals) and these made up the triplicate incubations; rumen fluid from an individual steers was not included in incubations on more than one occasion. After 24 h incubation total gas volume (pressure transducer) was measured and gas samples obtained for determination of CH_4 concentration. Rumen fluid pH was measured and samples taken to determine volatile fatty acid (VFA). Data was analysed with factorial analysis of variance using the General Linear Models procedure of GenStat. T-test done to compare mean values with controls.

Results Compare to controls, overall, the CH_4 production was reduced by 5% by addition of biochar**.** There were no interactions between the factors studied (level, temperature, feedstock), nor were there differences ($P>0.05$) in either gas or CH_4 production between adding biochar at 10 or 100g/kg. Preparing biochar at a lower pyrolysis temperature (550ºC) reduced gas (183.6 ml/g v 185.5 ml/g DM. $P=0.007$) and CH_4 production (14.8 v 15.2 mg/g DM, $P=0.007$) to a greater extent than pyrolysis at 700ºC. Gas and CH_4 production (Table 1) was reduced to the greatest extent ($P<0.05$) by biochar produced from miscanthus, with rice husk and soft wood pellets least effective, and oil seed rape straw and wheat intermediate. There were no differences between biochars in pH and VFA.

Table 1 Effects of biochars prepared from different feedstocks on *in vitro* gas and CH_4 production

	Control	Miscanthus	Oil Seed Straw	Rice Husk	Soft wood Pellets	Wheat	SEM	P-value
Gas (ml/g DM)	188.9	182.5^{a}	183.6^{ab}	186.5^{b}	185.6^{ab}	184.5^{ab}	1.59	0.09
% of control	100	96^{T}	97^{T}	99	98^{T}	98^{T}	0.8	0.11
CH_4(ml/gDM)	15.6	14.6^{a}	14.9^{ab}	15.4^{b}	15.1^{b}	14.9^{ab}	0.24	0.03
% of control	100	94^{T}	96^{T}	98	98	96^{T}	1.5	0.029

Superscript ^{T} denotes significantly different from control
^{a,b,c} Superscripts denote differences between different feedstocks.

Conclusion The observed reductions in CH_4 produced were not associated by a change in fermentation parameter, suggesting biochar primarily inhibited fermentation. Because there were differences between biochars, it will be important to investigate relationships between the physicochemical properties of biochars and antimethanogenic effects. Furthermore, it will be essential to validate the effectiveness under *in vivo* conditions.

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In vitro gas production and methane reduction in *Panicum maximum* incubated with palm kernel oil

O O Adelusi, C F I Onwuka, O J Idowu, R Y Aderinboye, V O A Ojo
Federal University of Agriculture, Abeokuta, Ogun State, Nigeria
Email:adelusioludotun@gmail.com

Implications Reduction in total rumen gas and methane (CH_4) produced in ruminants by the inclusion of palm kernel oil will result in increased post-rumen digestion which increases the nutrients obtainable from the feed consumed by animals.

Introduction Microbial breakdown of feed in the rumen generate waste gases like CO_2, CH_4 and N_2O. CH_4 represents a loss of up to 15% of consumed energy, and contributes about 30-40% of greenhouse gas from agriculture (Moss *et al.,* 2000). Dietary use of additives like oils having high ratio of medium- to long-chain fatty acids have been proposed to result in CH_4 reduction. The aim of this study was to assess the efficacy of palm kernel oil (PKO) at reducing rumen CH_4.

Material and methods The experimental design was a completely randomised design with four (4) inclusion levels of palm kernel oil (0 ml/g, 1ml/g, 2ml/g and 3ml/g) incubated with 200mg of *Panicum maximum* (substrate) as treatments. The *in vitro* gas production technique employed was that described by Menke and Steingass (1988). Rumen liquor was collected from a White Fulani cattle maintained daily on *ad libitum Panicum maximum*, into warm insulated flasks, filtered through layers of cheesecloth and used as the source of inoculums. The inoculum was then mixed with sodium and ammonium bicarbonate buffer (35g $NaHCO_3$ plus 4g NH_4HCO_3 per litre) at a ratio of 1:2 (v/v) to prevent lowering the pH of the rumen fluid which could result in decreased activities of the microbes. 200mg of substrate, replicated five (5) times for each treatment and were placed into 100ml calibrated glass syringes fitted with plungers. 2 ml syringes fitted with needles were used to draw palm kernel oil according to the treatment allocations and infused into the glass syringes through its mouth. 30ml of the buffered inoculums was then added to each syringe containing the ground. The syringes were positioned vertically in a water bath and kept at 40^{o}C. Blank syringes containing 30ml of the buffered inoculums only was included as control. Gas production was recorded at 0, 3, 6, 9, 12, 15, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51, 54, 57, 60, 63, 66, 69 and 72 hours of incubation. Methane gas was determined by introducing 4ml of NaOH solution into the glass syringes. Data obtained were subjected to one-way analysis of variance and significant means separated at $p<0.05$.

Results Palm kernel oil reduced ($p<0.05$) gas production throughout the period of incubation. Syringes incubated with 0ml/g PKO recorded the highest ($p<0.05$) volume of gas production as shown in Figure 1. The lowest ($p<0.05$) methane gas production was recorded from syringes incubated with 1ml/g level of PKO as shown in Figure 2.

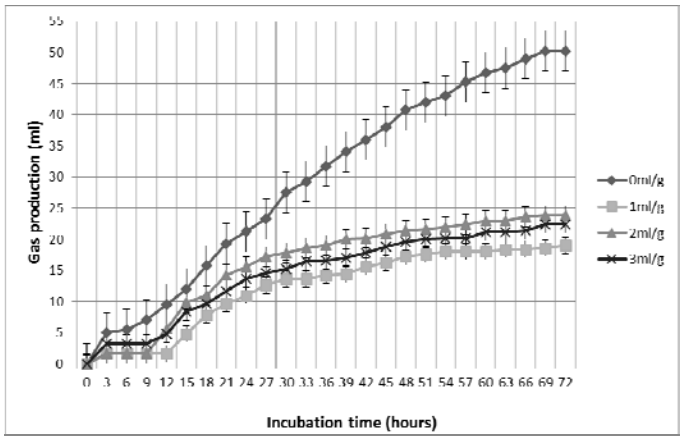

Figure 1 Effect of palm kernel oil on gas production of *Panicum maximum*

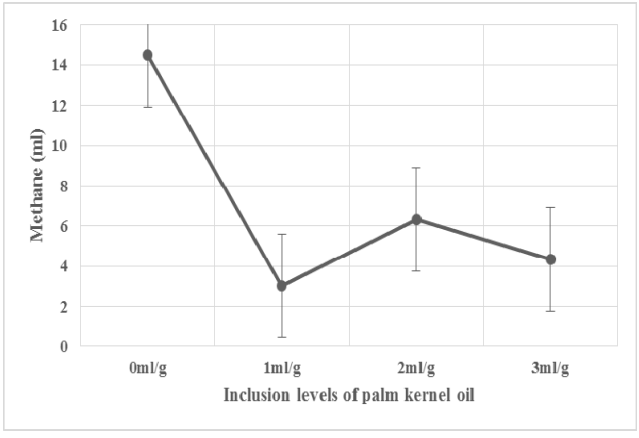

Figure 2 Methane production of *Panicum maximum* incubated with palm kernel oil

Conclusion Palm kernel oil reduced cumulative gas production meaning lowered rumen fermentation which could result in gainful digestion further down the tract while methane reduction by as much as 79% was obtained with 1ml/g PKO level.

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In vitro gas production of leaf and stem fractions of *Pennisetum purpureum* varieties fertilized with animal manures

O O Oduyemi, V O A Ojo, A O Ogunsakin, O O Adelusi, O A Okukenu, Y T Adesetan, S T Adewuyi, E D Oyebanjo
Federal University of Agriculture, Abeokuta, Ogun State, Nigeria
Email:ogunsakinao@gmail.com

Implication Animal manures can be an effective source of nutrients for forage and their applications to pastures could help substantial amounts of nutrients to be recycled through herbage production.

Introduction *Pennisetum purpureum* is high yielding perennial forage predominant in the humid tropics. It responds well to increased fertilization and good management. Grazing animals especially cattle, sheep and goats relish this forage because of its reasonable nutritive quality. It can also be used for dry season supplementary feeding as silage (Crowther and Chheda, 1982). The *in vitro* gas production technique as modified by Menke and Steingass (1988) is widely used to evaluate the nutritive value of feeds resources consumed by ruminants particularly to estimate their energy values (Makkar *et al.* (1999).
Animal manures have been reported to enhance the quality and productivity of *P. purpureum.* Olson and Paworth (2000) have reported positive effect on forage yield on the application of organic manure. This study was therefore aimed at addressing the influence of animal manure on the digestibility of the different *Pennisetum* varieties during the dry season through *in vitro* technique.

Material and methods The plot was established in organic research farms of the Federal University of Agriculture, Abeokuta in which it was planted with four varieties of *Pennisetum purpureum* (Local, Local Purple, S 13 and S 15) and fertilized with four types of animal manures (Swine, Cattle, Poultry and No manure i.e. control) in a 4x4 factorial arrangement. A quadrat of lm^2 was used on the plots and forages within it were harvested in order to determine the dry matter yield, then milled and used to carry out the *in vitro* gas production in the laboratory (Menke and Steingass, 1988).

Results The control produced higher ($P<0.05$) gas volume than other treatments both from leaf proportions at 3, 12, 24 and 48 hours of incubation. However, at 3, 24 and 48 hours, there was no significant ($P>0.05$) different in the stem fraction. The S 15 variety had higher ($P<0.05$) gas volume at 12, 24, and 48 hours for both leaf and stem fractions.

Table 1 Effects of manure types on the *in vitro* gas production of *Pennisetum purpureum* varieties (ml/200mgDM)

Factors	3hrs		12hrs		24hrs		48hrs	
	Leaf	Stem	Leaf	Stem	Leaf	Stem	Leaf	Stem
Manure								
Swine	0.00^{b}	1.50	1.38^{b}	4.25^{ab}	4.63^{b}	8.13	11.63^{c}	14.50
Cattle	0.13^{b}	1.50	1.75^{b}	4.63^{a}	5.63^{b}	9.00	14.00^{bc}	15.13
Poultry	0.00^{b}	1.13	2.12^{b}	3.63^{b}	7.00^{b}	8.88	16.38^{ab}	16.13
Control	1.00^{a}	1.38	4.25^{a}	4.63^{a}	10.25^{a}	8.88	19.63^{a}	15.50
SEM	0.11	0.14	0.39	0.27	0.93	0.50	1.25	0.64
Variety								
Local	0.00^{b}	1.00^{b}	1.38^{b}	4.38^{a}	4.37^{b}	8.75^{ab}	12.00^{b}	16.00^{a}
S13	0.25^{ab}	1.25^{b}	2.25^{ab}	3.50^{b}	7.00^{ab}	7.50^{b}	14.75^{b}	14.13^{b}
S15	0.38^{a}	2.00^{a}	3.25^{a}	5.00^{a}	8.88^{a}	10.00^{a}	19.38^{a}	17.38^{a}
Purple	0.50^{a}	1.25^{b}	2.63^{a}	4.25^{ab}	7.25^{a}	8.63^{ab}	15.50^{b}	13.75^{b}
SEM	0.108	0.144	0.392	0.268	0.934	0.496	1.247	0.639
Manure x Variety	***	*	**	***	*	*	***	*

$^{a-b}$: Means on the same column with different superscripts are significantly different ($P < 0.05$).

Conclusion The above results showed that the *in vitro* gas production of the leaf and stem fractions of *Pennisetum purpureum* that was not fertilized was higher than those fertilized with other manure types. *P. purpureum* (S15) had improved gas production and could provide better nutritive value for ruminants.

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Effects of supplementing cassava peels with cassava leaves and cowpea haulms on rumen environment parameters of West African dwarf goats

A O Oni, O M Abatan, K Adebayo, S O Iposu, O S Sowande, C F I Onwuka, O O Oni
[1]Federal University of Agriculture, Abeokuta, Ogun State, Nigeria, [2]Federal College of Education, Abeokuta, Ogun State, Nigeria
Email:profoni2003@yahoo.com

Implications The prices of conventional sources of protein in livestock ration have risen exorbitantly and this has necessitated the search for cheap alternative feed materials that are readily and cheaply available for farmers and can meet the nutritional requirements of farm animals.

Introduction Ruminant feeding systems based on poor quality tropical foliages, crop residues or agro-industrial by-products, in which protein is one of the first limiting factors, may require additional protein and roughage to maintain an efficient rumen ecosystem that will stimulate nutrient intake and improve animal performance. Cassava peel is primarily used in ruminant diets as an energy source. Cassava leaves, a by-product of cassava root harvest is rich in crude protein, minerals, vitamins and carotenes. Thus, supplementation of cassava peels (energy source) with cassava leaves (protein source) for goat feeding becomes imperative.

Material and methods A 116 d experiment was conducted to determine the effects of supplementing different proportions of cassava peels with cassava leaves and cowpea haulms on the rumen environment parameters of West African dwarf (WAD) goats. Thirty WAD bucks with average body weights of 6.25±0.12 kg were divided into 5 groups of 6 animals and each group randomly assigned in a completely randomized design. The five dietary treatments were formulated to contain cassava peels, cassava leaves and cowpea haulms at different proportions (g/kg DM) of 700:100:175 (Treatment 1); 500:200:275 (Treatment 2); 300:300:375 (Treatment 3); 400:100:475 (Treatment 4) and a control diet (Treatment 5) containing dried brewers' grains, wheat offal, palm kernel cake and rice husk. All chemical analyses were done in accordance with standard procedures. Data obtained were subjected to one way analyses of variance. Model sums of square were partitioned to test linear, quadratic and cubic trends.

Results At 0 hr post-feeding, NH_3-N values significantly ranged (L, Q, C: $P<0.05$) from 8.50 % in treatment 1 to 15.67 % in treatment 4. The acetic and propionic acids content was highest (C: $P<0.05$) in treatment 1 with values of 6.30 and 4.20 % and lowest in treatment 4 with values of 3.32 and 2.21 % respectively. Total fungi counts were similar in treatments 3 and 5 with values of 0.50 cfu/ml x 10^6 but significantly different (Q, C: $P<0.05$) from other treatments. At 8 hr post-feeding, the NH_3-N significantly (L, Q, C: $P<0.05$) increased with increasing levels of cassava leaves and cowpea haulms, and decreasing levels of cassava peels in the diets. The lowest value of 14.40% was however, obtained in treatment 5. The acetic acid values significantly (Q: $P<0.01$; C: $P<0.05$) ranged from 2.97 % in treatment 1 to 4.66 % in treatment 3; decline further to 2.50 and 2.51 % in treatments 4 and 5. Similar trend was obtained in values for propionic acids resulting into significant quadratic and cubic trend. Values obtained for total bacteria counts were 1.00, 1.00, 1.20, 1.20 and 1.10 cfu/ml x 10^6 respectively. Values for total fungi counts significantly ranged from 0.20 (cfu/ml x10^6) in treatment 2 to 0.60 (cfu/ml x10^6) in treatment 5.

Table 1 Rumen Environment parameters of West African Dwarf goats fed the experimental diets

Parameters	Treatments					SEM	Probability		
	1	2	3	4	5		L	Q	C
At 8 hr postfeeding									
Ammonia N (%)	10.63	11.80	12.33	17.40	14.40	0.57	**	**	**
Acetic acid (%)	2.92	3.32	4.66	2.50	2.51	0.20	NS	*	**
Propionic acid (%)	1.93	2.22	3.11	1.64	1.69	0.13	NS	*	**
TBC (cfu/ml x10^6)	1.00	1.00	1.20	1.20	1.10	0.03	**	**	**
TFC (cfu/ml x10^6)	0.27	0.20	0.50	0.40	0.60	0.04	*	NS	**

*P < 0.05; **P < 0.01; NS: Not significant; Probability for linear (L), quadratic (Q) and cubic (C) trends, SEM = Standard error of mean; TFC=Total fungi count; TBC: Total bacterial count

Conclusion It is concluded that feeding of cassava peels, cassava leaves and cowpea haulms at 300:300:375 promotes good rumen environment for improved animal performance in West African dwarf goats.

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Comparative study between the impact of L-ascorbic acid and α-tocopherol acetate on immune response, performance and egg composition of Egyptian native Fayoumi hens

M M Zaki, Maha M Hady
Cairo University, Giza, Egypt
Email:mmzaki@hotmail.com

Implications Improving productivity of backyard native laying hens is a critical issue concerning farmers in small villages and vitamin supplementation is one of the effective short term strategy to achieve such goal.

Introduction The native Egyptian chickens contribute to food security and serves as a source of eggs and meat which is considered as a direct income to many families in small villages. Moreover, consumers and producers are much more concerned about the nutritional quality of eggs. However, little is known about the effect of dietary L-ascorbic acid (vitamin C) in comparison with α-tocopherol acetate (vitamin E) supplementation on immune response, performance and egg quality of Fayoumi native Egyptian breed. Ascorbic acid supplementation to the diet of indigenous Venda chickens has positive effect on egg production and quality (Mbajiorgu, 2011). On the other hand, vitamin E supplementation had improved egg production and egg quality and provided health benefits to laying hens (Jiang *et al*., 2013). Regarding immune response, vitamin C has Immuno-stimulating effect in chickens vaccinated against infectious bursal disease (Wu *et al*., 2000), while vitamin E proved to have a positive effect on immune response in broiler chickens (Boa-Amponsem *et al*., 2000). The presented work deals with the comparative aspects between the effect of L-ascorbic acid and α-tocopherol acetate on Fayoumi native Egyptian hens.

Material and methods A total of 60 Egyptian native hens aging 30 weeks, were divided into 3 equal groups each of which consisted of 20 birds and assigned as group 1, 2 and 3. The birds of each group were located in 5 cages, 4 birds per each individual cage as a replicate. Birds of group 1 were fed on isocaloric and isonitrogenous basal diet mixed with L-ascorbic acid at ratio of 500 mg/kg, while birds of group 2 received the basal diet containing α-tocopherol acetate at ratio of 150 mg/kg feed. Birds of group 3 were kept as non-supplemented control. Egg production, feed consumption and eggs weight were recorded daily for a period of 10 weeks. Individual blood samples were collected every 2 weeks to be used in titration of ELISA Newcastle disease antibody titres. Dried egg samples were subjected to chemical analysis for determining protein and fat percentages in both yolk and albumen separately. All generated data were analysed statistically by "one way ANOVA" for significant differences at $P<0.05$.

Results No significant difference in ELISA antibody titers against Newcastle disease vaccination was detected in the supplemented groups, while both of them were significantly ($P<0.05$) higher than control. Weekly egg production is illustrated in figure 1.

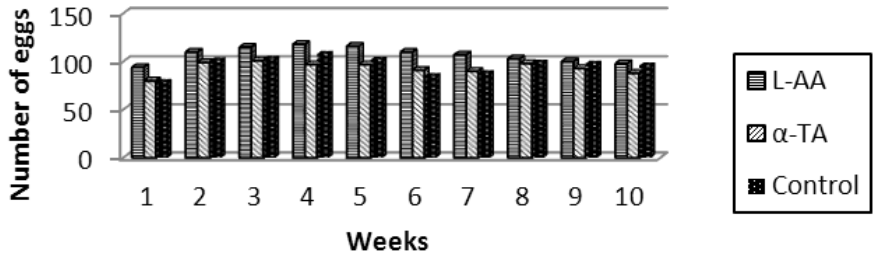

Figure 1 Egg production during 10 weeks experimental period

The best feed conversion ratio was recorded in L-ascorbic acid supplemented group followed by control and then α-tocopherol supplemented birds. No significant differences in protein and fat content were recorded between different supplemented and control groups. The role of ascorbic acid in immunity and egg production is associated with its role in the conversion of body protein and fat into energy required for production, antioxidant effect and enhancement of calcium absorption required for shell formation.

Conclusion It could be concluded that dietary supplementation of L-ascorbic acid (vitamin C) at a level of 500 mg/kg resulted in superior improvement of immune response, performance and egg composition of Egyptian native Fayoumi hens as compared with α-tocopherol acetate (vitamin E) at a level of 150 mg/kg.

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Physicochemical assessment of Quail nuggets as affected by *Ocimum gratissimum* extract

O O Olusola[1], D O Oshibanjo[1], L A Abegunde[1], J Aremu[1], O O Oyadeyi[2]
[1]University of Ibadan, Oyo, Nigeria, [2]College of Agriculture, Igboora, Oyo, Nigeria
Email:olusolaolubunmi@yahoo.co.uk

Implications Graded levels of *Ocimum gratissimum* (wild or African basil) extract have the potential for use as a phytopreservative to reduce the microbial load of quail meat nuggets.

Introduction Consumers today demand foods with high nutritional value that are free from chemical preservatives. Recently, consumers have rejected synthetic antioxidants because of their carcinogenicity (Fasseas *et al.*, 2007). *Ocimum gratissimum* extract (OGE) was used as natural preservative and antimicrobial agent at graded levels to assess the keeping quality of nugget made from Japanese quail meat. The aim of the present study was to investigate the effect of OGE inclusion in freshly prepared quail nugget.

Material and methods Fresh OG leaves were harvested from an experimental plot, washed with distilled water, drained and ground to remove the extract which were used immediately. Meat was cut into small pieces and ground twice in a meat mincer with 5 mm plate followed by 3 mm plate. All the nuggets formulations consisted of quail meat 60%, vegetable oil 6.5%, ice flakes 2.0%, refined wheat flour of varying level 14%, skimmed milk powder 2.0%, whole egg liquid 6%, table salt 1%, sugar 1%, sodium tri-polyphosphate (STPP) 0.5%, condiments 5%, spice mix 1.5% . The OGE was included at graded levels 0%, 2%, 4%, and 6% in treatments 1, 2, 3 and 4 respectively substituted with wheat flour to give 100% weight in all the products. Prepared emulsion was tightly packed in oil coated metallic mold of 3mm, arranged on the grill, then grilled for 35mins. The cooked product was cooled, weighed and removed carefully from the mold. Nuggets were packed aerobically in sterilized zip lock bags and stored at refrigerated temperature (4±1 °C) for analysis after 24hrs**.** Parameters measured were meat Swelling Capacity, Extract Release Volume, pH, Yeast and mould count, coliform and total plate count according to the methods of FSSAI (2012). Data were analysed as a completely randomised design using ANOVA, the GLM procedure of SAS (2008). Means were separated using Duncan Multiple Range Test.

Results The physical parameters of fresh quail meat as affected by increasing levels of OGE inclusion is shown on table 1. OGE did not significantly ($P<0.05$) affect the pH ranges (6.06 – 6.10) of quail nugget from the different treatments. Extract Release Volume (ERV), a determinant of incipient spoilage in meat, ranked T4 highest (38.67). ERV above 25mls indicates good meat quality for processing. Meat Swelling Capacity (MSC) increases during spoilage due to protein degradation. T4 had the least MSC. The graded levels of OGE inclusion showed there were significant difference ($P<0.05$) in microbial counts for freshly prepared quail nugget which decreased as the inclusion level of OG increased. T1 (control) had the highest values for yeast, mould, coliform and total plate count figure 1.

Table 1 Physical characteristics of quail meat

Parameters	Treatment 1	Treatment 2	Treatment 3	Treatment 4	SEM
Meat Swelling capacity	79.10	85.30	89.27	72.80	2.43
extract Release volume	32.67^{c}	32.00^{c}	35.00^{b}	38.67^{a}	3.31
pH	6.06	6.07	6.1	6.06	0.07

^{abc} Means on the same row with different superscripts are significantly different ($P<0.05$). SEM= standard error of mean.

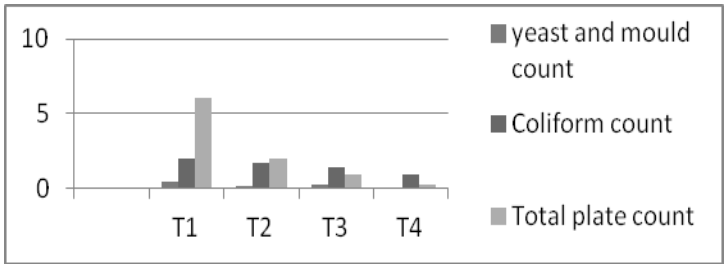

Figure 1 Microbial load counts on quail nugget (cfu/ml)

Conclusion It can be concluded that in preparation of quail nugget, *Ocimum gratissimum* extract can be used up to 6% inclusion level with beneficial effect on microbial and physical qualities.

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Utilisation of heat treated jatropha seed cake in the diets of growing Japanese quails

A F Agboola, A A Adenuga
University of Ibadan, Ibadan, Oyo, Nigeria
Email:aadebunmi@yahoo.com

Implications Lower inclusion level of Jatropha Seed Cake (JSC) resulted in improved gut integrity and overall performance of Japanese quails.

Introduction *Jatropha curcas* is a multipurpose shrub of significant economic importance because of its several potential uses. The nutrient composition of jatropha seeds compares favourably with those of conventional seeds with crude protein content of 58-64% in seed meal, 48-60% in seed cake and 60-66% in kernel meal, higher essential amino acids content (excluding lysine), and higher calcium and phosphorus than soyabean meal (Chivandi *et al*., 2005). However, the presence of toxic factors (phorbol esters) and anti-nutrients (tannins, lectins and phytate) like other conventional seeds restricts the use of jatropha in livestock feeding. The aim of the present study was to determine the effect of heat treated jatropha seed cake on gut morphology and organ weight of Japanese quails.

Material and methods The jatropha seeds used were toasted whole for about 20 minutes before oil extraction was conducted using a mechanical screw press. The press residue which was the seed cake was immersed in water and heated to about 90 ^{0}C for 45 minutes for further oil removal. Cooling was allowed to take place for separation of oil-moisture and the residue. The separated seed cake was sun dried and milled. The preparation process was done to simulate the technique carried out by the local farmers. Two hundred two-week-old Japanese quails were weighed and allotted to 5 dietary treatments consisting of 5 replicates of 8 birds each. Treatment 1 was the basal diet, a corn-soyabean meal diet without inclusion of jatropha seed cake (JSC), while treatments 2, 3, 4 and 5 contained the basal diet and 50, 100, 150 and 200g of milled JSC/kg of diet respectively in a 14-day experiment. On day 14, two birds were slaughtered by cervical dislocation and after flushing out the digesta samples, sections of the ileum were removed for ileal morphological measurements according to the methods of Iji *et al*. (2001). Also, two birds per replicate were subsequently opened up and organs such as liver and gizzard were harvested and weighed immediately using a sensitive scale. Data were analysed as a completely randomised design using ANOVA, the GLM procedure of SAS (2008). Means were separated using Duncan Multiple Range Test.

Results The effect of graded levels of heat treated jatropha seed cake (JSC) on gut histomorphological indices of Japanese quails is as shown on Table 1. Greater villus height ($P < 0.05$) was recorded for birds on 100g/kg JSC treatment relative to control though there were no differences amongst the JSC diets. Similar villus width was recorded for birds on the control and those on JSC diets. It was observed that 50 and 100g/kg JSC diets had a pronounced ($P < 0.05$) effect on the crypt depth of birds on the experimental diet. However, identical crypt depth was recorded in birds on the control diet and those on 150 and 200g/kg JSC diets respectively. There were considerable effects ($P<0.05$) of the dietary treatments on the villus height to crypt depth ratio (VH:CD) of birds on the experimental diets. Similar VH:CD was observed in birds on the control diet, 50 and 200g/kg JSC diets which differ ($P = 0.009$) from that of birds on 100 and 150g/kg JSC diets. The gizzard and liver of birds on JSC diets were ($P < 0.05$) larger than those fed the control diet. Percentage mortality increased with higher inclusion levels of JSC in the diets.

Table 1 Gut morphological parameters (μm) and relative organ weights (%) of quails on experimental diets

	Jatropha seed cake inclusion level (g/kg)						
Parameter	0	50	100	150	200	SEM	P value
Villus height	395.00^{c}	552.00^{ab}	658.50^{a}	575.63^{ab}	510.00^{ab}	58.80	0.006
Villus width	87.00^{ab}	91.50^{ab}	107.00^{a}	81.25^{ab}	73.34^{b}	6.74	0.035
Crypt depth	62.00^{b}	82.00^{a}	74.50^{ab}	63.75^{b}	61.25^{b}	5.01	0.005
VH:CD	6.48^{b}	6.82^{b}	8.98^{a}	9.14^{a}	5.75^{b}	0.81	0.009
Gizzard	4.07^{c}	4.90^{bc}	5.75^{ab}	5.27^{b}	6.46^{a}	0.29	0.007
Liver	2.81^{b}	3.36^{ab}	3.89^{a}	4.11^{a}	3.20^{ab}	0.27	0.009
*Mortality (%)	0	0	25	70	90	-	-

^{abc} Means on the same row with different superscripts are significantly different ($P<0.05$). SEM= standard error of mean. *Mortality (absolute value)

Conclusion 50g/kg heat treated JSC inclusion was the safest level for growing Japanese quails as % mortality increased with higher levels. Other detoxification methods that are less expensive and environmentally friendly should be explored.

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Evaluation of the effects of cloves (*Syzygium aromaticum*), tumeric (Curcuma longa) and African nutmeg (*Monodora myristica*) on the performance of Japanese quails (*Coturnix coturnix japonica*)

T S Olugbemi, I I Adedibu, K E Idowu
Ahmadu Bello Univerity, Samaru, Zaria, Daduna, Nigeria
Email:tsolugbemi@abu.edu.ng

Implications Tumeric as an ingredient in quail diets can be of nutritional significance

Introduction Additives are often added to poultry diets in order to optimize their performance. Feed additives are products used in animal nutrition for improving the performance of animals and also for improving the quality of feed and of food from animal origin. A relatively new class of feed additives that has recently gained increasing interest are the phytogenic feed additives otherwise called phytobiotics or botanicals. Phytobiotics are classified as herbs, spices, essential oils, or oleoresins (Windisch *et al*., 2008) and are plant – derived compounds incorporated into diets to improve the productivity of livestock through amelioration of feed properties, promotion of the animals' production performance and improving the quality of food derived from those animals. Different spices have been used as feed additives all over the globe along the history and these botanicals have received a high attention as nutraceuticals and multifunctional feed supplements, for various purposes in poultry production during recent years. Although the effects of certain spices on the performance of poultry species especially broilers have been evaluated, there is paucity on the use of spices such as cloves, turmeric and nutmeg in quail nutrition. It is on this basis that this study was carried out to evaluate the effect of clove, turmeric and nutmeg on growth and haematological indices of quails.

Material and methods One hundred and twenty (120) day-old unsexed Japanese quail chicks were used for the study which lasted for five weeks. The chicks were randomly distributed into four treatments with three replicates each, consisting of ten chicks per pen (replicate) in a completely randomized design. The same basal diet was used with varied spices representing the treatments. Treatment 1 served as the control without any spice while Treatments 2, 3 and 4 were supplemented with 1% of Clove, Turmeric and African nutmeg respectively. The quail birds were offered respective experimental diets and water given *ad-libitum* throughout the five week experimental period. During this period (5weeks), the birds were weighed on a weekly basis while daily feed intake, body weight gain and feed conversion ratio were calculated. The data generated from the study was subjected to Analysis of Variance (ANOVA) using statistical software general linear model and significant differences among means were separated using Least Square Difference (LSD).

Results Table 1 shows mean quail performance data observed. Clove and Turmeric in quail diets resulted in significant ($P<0.05$) reduction in feed intake and FCR. Turmeric had no significant ($P>0.05$) effect on weight gain while Clove showed a significant ($P< 0.05$) decrease. African nutmeg had no significant ($P>0.05$) effect on feed intake, weight gain and FCR.

Table 1 Effect of clove, turmeric and African nutmeg on the performance of growing Japanese quails

	Dietary Treatment				
	Control (1)	Clove (2)	Turmeric (3)	African nutmeg (4)	SEM
Feed intake (g/bird/5weeks)	538.07^{b}	436.40^{a}	458.96^{a}	543.37^{b}	17.48
Initial weight (g/bird)	20.83	20.77	20.80	20.76	0.41
Weight gain (g/bird/5weeks)	101.72^{a}	88.36^{b}	97.70^{a}	98.40^{a}	2.44
Final weight (g/bird)	130.70^{a}	124.91^{b}	128.06^{a}	129.23^{a}	1.35
FCR	5.29^{b}	4.94^{a}	4.76^{a}	5.53^{b}	0.15

^{ab}Means within the same row with different superscripts are significantly different ($P<0.05$)
SEM - Standard Error of Mean

Conclusion Tumeric inclusion in the diets of quails could be of advantage as it does not negatively affect the bird production indices and gives a better feed conversion.

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Metabolisable energy of oilseed rape meal is dependent on its gross energy and protein content

O A Olukosi[1], M Kasprzak[3], S Kightley[2], J Wiseman[3], P Carre[4], J G M Houdijk[1]
[1]SRUC, Scotland's Rural College, Edinburgh, UK, [2]National Institute of Agricultural Botany, Cambridge, UK, [3]University of Nottingham, Loughborough, UK, [4]CREOL, Pessac, France
Email:oluyinka.olukosi@sruc.ac.uk

Implications Oilseed rape meal is competitive with other important energy feedstuffs for poultry but its value as an energy source largely depends on the quantity of residual oil in the meal.

Introduction Oilseed rape meal (OSRM) has potential to be used as a protein feedstuff for poultry because of its relatively high protein content but its use as an energy source has not been widely investigated. The use of OSRM in poultry has been limited in the past because of potential problems associated with its high levels of glucosinolates and sinapine which may produce undesirable effects in animals or their products (Qiao and Classen, 2003; Tripathi and Mishra, 2007). Modern oilseed rape varieties and their meals are considerably lower in glucosinolates and sinapine than the older varieties and can be more safely used in poultry diets if their nutritional values are well characterised. The aim of the current experiment was to determine the metabolisable energy content of different varieties of OSRM from various parts of the UK and to relate this to some chemical components in the meal.

Material and methods A total of 273 male Ross 308 broilers at 14 days old were allocated to 13 treatments. Each treatment had 7 replicates and three birds per replicate. The treatments consisted of a maize-soybean meal reference diet and 12 test diets in which 12 varieties of OSRM (at 100g/kg diet) proportionally replaced all the energy ingredients in the reference diet. Grain samples of 12 oilseed rape varieties were defatted by crushing and subsequent hexane extraction to produce meals for the test diets. Birds received the experimental diets between days 14 and 21 and excreta were collected on days 20 and 21. Apparent metabolisable energy (AME) of the test diets was determined using the index method and the AME of OSRM samples was determined using the difference method. OSRM samples were analysed for gross energy and some chemical components and these were correlated with AME of OSRM using the CORR procedure of SAS 9.3.

Results The AME of the OSRM samples ranged from 13.01 to 13.54 MJ/kg with an average AME and coefficient of energy metabolisability of 13.1 MJ/kg and 0.684, respectively. The AME of OSRM is largely explained by its gross energy (r= 0.97); oil (r = 0.88) and protein (r = 0.57). The correlation between AME of OSRM and sinapine, glucosinolate, tannin or phytic acid contents were not significant although r for phytic acid approached a trend (P=0.11). The high correlation between AME and the GE and oil contents of OSRM suggests that the main driver of AME of the meal is its residual oil and hence processes that severely reduce the oil content of OSRM will reduce its AME concentration. The relatively high correlation between AME and protein content shows that the residual protein in the meal contributes substantially to its metabolisable energy and hence factors affecting the protein quality of the meal may also influence its energy content. Significantly, the AME of OSRM was not correlated with its glucosinolate or sinapine contents likely because these are present in the meal at relatively low levels of 14.9 µmol/g and 5.18 g/kg, respectively.

Table 1 Chemical composition (g/kg, DM basis) and correlation of AME in OSRM with its chemical composition

Chemical analysis	GE	Sinapine	CP	Glucosinolate	Tannin	Phytic acid	Oil	Aflatoxin
Average	19.2	5.18	422	14.9	1.97	21.4	33.4	1.27
Range	19.0-19.8	4.1-7.1	367-479	6.6-42.4	1.2-2.3	11-26	26-43	0.9-1.7
	Correlation coefficients							
AME (r)	0.97	-0.14	0.57	0.45	-0.40	-0.48	0.88	0.15
P-value	< 0.001	0.661	0.050	0.143	0.202	0.112	0.001	0.647

GE is gross energy (MJ/kg), CP is crude protein; AME is apparent metabolisable energy (MJ/kg); glucosinolate (µmol/g); aflatoxin (ppb)

Conclusion The metabolisable energy content of OSRM makes it a competitive energy feedstuff for poultry although its value as such will vary with its residual oil content. The AME of the OSRM samples was similar to that of wheat (13.2 MJ/kg) and lower than that of maize (14.5 MJ/kg) or sorghum (13.7 MJ/kg).

Acknowledgements
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Sexual dimorphism in haematological traits of Japanese quails (*Coturnix cotournix japonica*) fed *Moringa oleifera* seed meal

I I Adedibu, Z Aliyu, O M Akinsola, O M Daudu, T S Olugbemi
Ahmadu Bello University, Zaria/ Kaduna State, Nigeria
Email:iiipinyomi@yahoo.com

Implications There may be sex effect in haematological responses to use of additive in quail diets

Introduction Studies on the use of *Moringa oleifera* meal in poultry diets have laid more emphasis on substitution as a protein source and its effect on performance traits (Kakengi *et al.* 2007; Gadzirayi *et al.*2012). These do not usually take into consideration that haematological values may be influences and that differences may occur due to sex. This study was carried out to evaluate the response of both sexes of the Japanese quails to *Moringa oleifera* seed meal using selected haematological parameters.

Material and methods One hundred and sixty, three weeks old quail chicks comprising of eighty males and eighty females were allotted to four dietary treatments containing 0g, 5g, 10g and 15g of *Moringa oleifera* seed meal per kg respectively. The males and females were housed differently. The animals were fed *ad libitum* and all necessary medications and routine vaccinations were administered as recommended by the Ahmadu Bello University Veterinary Hospital. Blood samples were collected using a 140iμ needle gauge after six weeks from the time of commencement of the experiment. The blood was analysed for haemoglobin content, packed cell volume, white blood cell count and red blood cells. Data collected was analysed using general linear model of SAS (2001) statistical package and significant differences among means were separated using Least Square Difference (LSD).

Results There were no significant (P>0.05) differences in the haemoglobin, white blood cell and red blood cell values of both sexes of the Japanese quails (*Cotounix cotournix japonica*). The packed cell volume of both sexes differed significantly (P<0.05) at 0g/kg, 5g/kg and 1.0g/kg inclusion of *Moringa* seed meal, however there were no significant (P>0.05) differences at 1,5g/kg *Moringa* the values were low.

Table 1 Haematology values of male and female Japanese quails fed *Moringa oleifera* seed meal

		Treatments			
Parameters	Sex	0g/kg *Moringa*	5g/kg *Moringa*	1.0g/kg *Moringa*	1.5g/kg *Moringa*
PCV (%)	Male	36.75[a]	36.83[a]	35.40[a]	15.00
	Female	30.50[b]	32.17[b]	29.86[b]	18.00
	SEM	0.02	0.03	0.01	5.41
	P	0.04	0.02	0.04	0.09
Hb (g/L)	Male	12.20	12.25	11.70	4.99
	Female	10.14	10.68	9.91	5.96
	SEM	3.79	7.62	8.19	20.6
	P	0.64	0.21	0.06	0.22
WBC ($x10^9$/L)	Male	3.40	4.17	4.68	2.26
	Female	4.12	4.02	4.33	1.64
	SEM	6.12	3.70	8.14	7.06
	P	0.31	0.26	0.19	0.27
RBC ($x10^{12}$/L)	Male	6.10	6.13	5.74	2.94
	Female	5.06	5.33	5.19	3.00
	SEM	4.60	12.29	3.47	8.14
	P	0.17	0.07	0.12	0.08

[ab]Means within each column with different superscripts differ significantly (P<0.05). PCV (packed cell volume), Hb (haemoglobin), WBC (white cell volume), RBC (red blood cell)**.** SEM - Standard Error of Mean

Conclusion The inclusion of *Moringa oleifera* seed meal may not exert a difference in the haemoglobin, white cell volume, red blood cell values of male and female Japanese quails. Although there were significant differences in PCV values, it may not have been influenced by diet but sex effect because the values of the control diet (0%) where significantly different.

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Production of omega-3 fatty acids-enriched table eggs

H Al-Khalaifah, A Al-Nasser, M Al-Bahou, F Khalil, G Ragheb, M Boarki
Kuwait Institute for Scientific Research, Kuwait
Email:hkhalifa@kisr.edu.kw

Implications The current report may have the effect of increasing the consumption of n-3 fatty acids by humans. These fatty acids are known to be beneficial to treat diseases related to inflammation responses such as thrombosis, atherosclerosis, mental problems, asthma and rheumatoid arthritis. Enriching the diet of layers with flaxseed increases n-3 PUFA in eggs.

Introduction Table eggs are popular food item worldwide. There has been some interest in the enrichment of poultry eggs with long chain n-3 polyunsaturated fatty acids (PUFA) to improve intakes of these fatty acids, which are currently well below the recommendation (Froning, 1996; Lewis *et al*., 2000; Bean and Leeson, 2003). These fatty acids down-regulate inflammation responses related to many diseases and disorders such as cardiovascular disease, increased triglycerides, blood pressure, thrombosis, atherosclerosis, stress, mental problems, asthma and rheumatoid arthritis (Sellmayer et al., 2004, Schwalfenberg, 2006, Nkondjock *et al*., 2003). The objective of the current study was the production of eggs that have high levels of omega-3 (n-3) fatty acids and that are closer to the desired ratio of n-6 and n-3 fatty acids through dietary supplementation of flaxseed in the diet of laying hens.

Material and methods Twenty four wk old Lohmann Selected Line (LSL) were used. The diets were corn-soybean based with 0% (control group), 5%, 7.5% and 10% of flaxseed. The treatments lasted for thirty-two weeks, 50 hen per treatment. Eggs from the control and experimental groups were collected and fatty acid profile was analyzed using gas chromatography. Differences in the effects of the different dietary treatments were analysed using one-way analysis of variance (ANOVA) and the general linear model procedure of Minitab was applied in all the tests. Differences between the treatment groups were considered statistically different at $P \leq 0.05$. When significant differences occurred, mean treatment differences were identified by pairwise comparison using Bonferroni tests.

Results The results showed that feeding laying hens on diets with flaxseed significantly increased n-3 fatty acids in the egg samples. The total amount of n-3 was 107.49, 232.00, 226.01, and 251.96 mg/egg for the 0%, 5%, 7.5% and 10% flaxseed diets, respectively. The ratio of n-6 to n-3 was reduced from 11.73 for the control group to 6.00, 4.69, and 4.36 for 5%, 7.5% and 10% flaxseed, respectively ($P \leq 0.05$).

Conclusion In conclusion, the enrichment was successful as the recommended ratio of n-6: n-3 was achieved.

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Effect of length and storage methods on chemical composition of exotic chicken and quail eggs

I Dudusola
Obafemi Awolowo University, Ile-Ife, Nigeria
Email:iadeogun@oauife.edu.ng

Implications Poor storage conditions may result in deterioration of egg quality leading to loss and wastage of eggs which has been a major concern for poultry farmers (Jin *et al*. 2011).

Introduction Foods are known to have a shelf life, which varies depending on food type. Eggs have a relatively short shelf life, and could lose their quality rapidly during the period between production and consumption. Eggs are generally similar among species of birds, but they can differ in some aspect in their physical and chemical composition (Samli *et al*., 2005). The aim of this study was to assess effect of storage on chemical composition of exotic and quail eggs.

Material and methods 200 eggs were collected from 28 weeks old Harco layers and from 21 weeks old Japanese quail (*Coturnix coturnix japonica*). Eggs were randomly selected and divided into 5 groups of 10 eggs per group for both chicken and quail eggs and stored for 21 days. The eggs were subjected to different storage methods (room temperature, refrigeration, oiling, black polythene bags) with room temperature taking as control and analysed after 0, 3, 7, 14 or 21days. Weight loss was measured and proximate analysis was carried out according to the procedure of AOAC (1990). Data was analysed with SAS (2003) through a 4 × 5 factorial ANOVA with the four storage treatments and five sampling days.

Results With increase in storage length for both chicken and quail eggs, weight loss increased (Table 1). A high weight loss was observed for both types of egg stored for 14 and 21 days. Effects of storage methods on the egg quality parameters of chicken and quail eggs shows that the weight loss of chicken and quail eggs for all the storage methods were significantly different from each other but not different for moisture content, ash, ether extract and crude protein. Strong interactions between storage, egg type and method of storage were found for the moisture content, ether extract content and crude protein content with P values of <0.0001 (Table 2).

Table 1 Effect of storage duration on quality parameters of chicken and quail eggs

Duration of Storage								
Parameters	Egg type	0	3	7	14	21	SEM	P
WL	Chicken	-	0.17^{b}	0.54^{b}	1.23^{ab}	1.97^{a}	0.30	0.02
	Quail	-	0.74^{b}	1.30^{b}	1.83^{ab}	3.01^{a}	0.33	0.01
MC	Chicken	73.71^{c}	77.74^{a}	76.32^{b}	76.21^{b}	76.21^{b}	0.17	<0.0001
	Quail	70.90	73.82	73.65	74.30	69.72	1.05	0.20
Ash	Chicken	0.82	0.72	0.86	0.85	0.81	0.04	0.17
	Quail	1.07^{a}	0.97^{b}	0.82^{b}	1.12^{a}	1.15^{a}	0.06	0.04
EE	Chicken	1.71^{ab}	0.73^{c}	1.53^{bc}	2.59^{a}	1.94^{ab}	0.23	0.01
	Quail	0.97	1.09	1.92	1.46	1.35	0.20	0.07
CP	Chicken	8.53^{b}	9.19^{ab}	11.14^{a}	11.61^{a}	10.69^{ab}	0.66	0.05
	Quail	10.71	10.49	10.72	11.12	12.66	0.52	0.14

$^{a, b, c}$: Means within each row with different superscripts are significantly different (P<0.05); SEM = Standard Error of Mean, WL = Weight loss, MC = Moisture content, Ash = Ash content, EE = Ether extract content, CP = Crude protein content

Table 2 Effect of the studied factors and their interactions in the factor model analysis of variance

Source of variation	WL	MC	Ash	EE	CP
	P > F	P > F	P > F	P > F	P > F
Egg type (ET)	0.0001	<0.0001	<0.0001	<0.0001	<0.0001
Storage method (SM)	0.0003	<0.0001	ns	<0.0001	0.01
Storage duration (SD)	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
ET*SM	0.001	<0.0001	ns	<0.0001	<0.0001
ET*SD	ns	<0.0001	0.0004	<0.0001	<0.0001
SM*SD	0.01	<0.0001	0.01	<0.0001	<0.0001
ET*SM*SD	ns	<0.0001	0.002	<0.0001	<0.0001

Key: ns = not significant (P>0.05); other abbreviations, see Table 1.

Conclusion This study concluded that chicken and quail eggs can be effectively stored without effect on its chemical composition using any of the storage methods for at least 3 days but not more than 7 days.

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Replacement value of African pear (*Dacryodes edulis*) seed meal as a protein source in broiler diets

O O K Oko, A A Ayuk, O M Emeruwa, F E Elijah, E E Ekpe, B O Asuquo, B I Okon, L N Agwunobi
University of Calabar, Cross River State, Nigeria
Email:oluwatosin.kennedyoko@gmail.com

Implications Dietary replacement of fish meal and soya bean meal with up to 20% African pear seed meal had no adverse effects on the growth performance and carcass yield of broilers.

Introduction Shortfalls in domestic production of conventional protein sources such as soya bean meal and fish meals coupled with their high importation tariff, competitive usage as raw materials in the brewing, pharmaceutical and food industries has led to an escalation in their domestic prices. Furthermore, in the animal feed industry, they account for over 80% of production cost and the resultant high cost of animal products (Oko *et al.*, 2012). Therefore, available, local feed resources which are neglected and under-utilized are being explored as possible replacements for the expensive resources (Oko *et al.,* 2014). The African pear (*Dacryodes edulis*) is a traditional food plant in Africa with potentials in improving food security and rural development (Bratte, 2011). Its seeds, discarded products after the pulp have been consumed by man are rich in lipids, vitamins and some essential amino acids. This study was conducted to evaluate the value of African pear seed as replacement for soya bean and fish meal in broilers diets.

Material and methods African pear seed were collected, washed and air dried for 72 hours. The dried seeds were ground using a hammer mill of 2mm to obtain African pear seed meal (APSM). A corn-soybean (antibiotic–free) basal diet (treatment 1) containing 27.99% SBM and 3.00% FM was formulated according to the Hubbard Recommendation for broilers and 5, 10 15 and 20% APSM were included, with every 5% APSM replacing 1.40% soya bean meal and 0.15% fish meal to constitute treatments 2, 3, 4 and 5, respectively. A total of 300-commercial broiler chicks (Hubbard strain) were used in the 56 d study with 60 chicks assigned to each treatments (3 replicates (pen) of 20 birds) in a completely randomized design. The birds were managed under the deep litter system in a 2-phase feeding program. Diets were identical in nutrient specifications during the same age period. Feed and water were offered ad libitum. Birds and feed were weighed on a pen basis at 1, 7, 14, 28, 35, 42, 49 and 56 d of age for the determination of growth rate, feed intake, and feed conversion. On d 57, six birds per pen were randomly selected, weighed and processed for carcass evaluation. Data were statistically evaluated using the ANOVA procedure of SAS 2004. Means were separated by Tukey's honestly significant differences procedure when the overall F-test was $P<.0.05$.

Results Table 1 shows that there were no significant differences ($P>0.05$) in body weight (2799.67- 2883.33g), weight gain (49.07- 50.57g/d) and feed consumption (171.43 - 200.44g/d) between birds fed APSM diets compared to those on the control diets. Carcass yield (73.26 – 76.49%) and relative breast meat yield (21.06- 24.50%) were greater ($P>0.05$) in broiler fed 5 – 10% APSM than those on other dietary treatments.

Table 1 Broiler performance on African pear seed meal

Performance	0%APSM	5%APSM	10%APSM	15%APSM	20%APSM	SEM
Initial Body weight, g	51.56	51.59	51.66	51.72	51.58	0.36
Final body weight, g	2883.33	2863.35	2846.67	2843.68	2799.67	0.78
Daily feed intake, g/day	171.43	173.23	196.15	200.44	195.79	0.66
Daily weight gain, g/day	50.57	50.21	49.91	49.86	49.07	0.56
Feed Conversion ratio	3.39	3.45	3.93	4.02	3.99	0.12
Carcass yield, %	74.07^{b}	76.49^{a}	75.45^{a}	73.56^{bc}	73.26^{c}	0.04
Thigh weight, %LW	10.89	10.92	10.64	10.47	11.10	0.33
Breast weight, %LW	21.96^{b}	24.50^{a}	24.16^{a}	21.59^{b}	21.06^{b}	0.02
Back weight, % LW	8.89	8.99	9.43	8.89	9.12	0.45

Conclusion APSM which is regarded as a waste material can successfully replace soya bean and fish meal up to 20% without any adverse effects on the growth and carcass yield of broilers.

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Evaluation of dietary *Moringa oleifera* leaves incorporation on performance parameters and anticoccidial activity in broiler chickens

Maha M Hady, Mohamed M Zaki
Cairo University, Giza, Egypt
Email:mhhady@yahoo.com

Implications Dietary supplementation of the *M. oleifera* dry leaf powder as unconventional feed at rates of 2.5 and 5% has significant anticoccidial activity and tends to increase growth performance of broiler chickens.

Introduction Avian coccidiosis is a disease induced by *Eimeria* species and is incriminated for causing tremendous economic loss in the poultry industry due to adverse effects on mortality rates, growth and feed utilization efficiency. At present, conventional disease-control programmes essentially depend on chemotherapy and /or vaccination. However, the increase awareness of drug resistance and drug residues in poultry meat has demanded the emergence of alternative methods for controlling coccidiosis. Recently, photobiotic derived from various elements of plants has been explored as sustainable alternatives for controlling coccidiosis. *Moringa oleifera* belongs to family *Moringaceae* has nutritional and medicinal properties. *Moringa oleifera* leaves (ML) exhibit growth promoting, antioxidant and anticoccidial effects in poultry. In Egypt, Moringa plant has been cultivated in semiarid districts and strongly suggested to be utilized by poultry. The aim of this work is to evaluate nutritional and anticoccidial properties of ML in broiler diets.

Material and methods *Moringa oleifera* leaves (ML) were obtained from a local farm, dried and finely grinded then 10g sample was subjected to proximate chemical analysis (AOAC).One hundred and eighty unsexed commercial Cobb® chicks were randomly allotted into 3 treatments (each of 3 replicates). The control treatment (n=72) was equally subdivided into 3 designated groups (n=24, 8/replicate) as; non-infected non-medicated control (CN), *E. tenella*-infected non-medicated control (CP) and *E. tenella*-infected-medicated control (CPM). Meanwhile, the rest of the birds (n=108) were divided into two ML treatments (2.5 and 5 %), each of 54 birds. Each treated group were further subdivided into *E. tenella*-infected and non-infected (n=27, 9/replicate) groups. Salinomycin sodium was used as reference anticoccidial feed additive in CPM group. The birds were reared in clean pens embedded with deep litter under standard hygienic conditions. Feed and water were provided *ad- libitum*. All the birds were fed on basal formulated starter and finisher diets (maize-soya bean) to which ML was incorporated at levels of 2.5 and 5 % on partially expense of SBM to maintain the diet isonitrogenous andisocaloric. At 22 days of age, all the groups used as positive controls were orally infected with 30×10^3 sporulated oocysts of *E. tenella* (Solsby, 1986). The performance parameters such as body weight gain, feed intake and feed conversion ratio were determined for pre- and post- infection periods. The anticoccidial efficacy of treatments post infection was evaluated on the basis of survival rate, bloody diarrhea, caecal lesion score as well as the oocyst shedding. All the data were subjected to one way ANOVA at 5% level using the SPSS® and means were separated using Duncan's Multiple Range test.

Results The results of the proximate chemical analysis of ML powder demonstrate that it contains 22.7, 51.4, 9.4, 1.9 and 8.7% for crude protein, carbohydrate, crude fiber, ether extract and ash, respectively. These results emphasis the valuable nutritional value of ML. The performance parameters of the first phase (pre-infection) showed that the incorporation of both levels of ML in isonitrogenous–isocaloric diet had achieved significant ($P<0.05$) increase in body weight gain and numerical improvement of FCR which was insignificant as compared to the control group. The positive effects on broilers performance due to ML feeding might be attributed to the fact that the ML is rich not only in dietary antioxidants but also in other nutrients. In the second phase (post-infection), performance parameters were similar to the first phase in all groups except the non-medicated infected control group (CP) that demonstrated the significant ($P<0.05$) lowest body weight gain and FCR. *E. tenella* species are known to destroy the absorptive mucosal surface leading to impairment of nutrient utilization, hence, hindering bird's performance. The results of the anticoccidial response of ML fed-groups five days post-infection indicated that all the infected groups manifested bloody diarrhoea and the CP group (infected non-medicated control) recorded the most sever bloody diarrhoea, the highest mortality rate (25.8 %), caecal lesion score (4.1) and oocysts shedding (11.8×10^3/g excreta) as compared to infected medicated (GC) and both ML groups.

Conclusion From this study, it appears that ML feed additive has growth promoting and anticoccidial effects in chickens. This effect may be ascribed to the presence of a variety of antioxidants, such as β-carotene, ascorbate and α-tocopherol (Ayssiwede *et al*., 2011) which are capable of scavenging free radicals helping in limiting the cellular damage (Sies, 1997)

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Comparison of performance data and feed efficiency measurements from broiler chickens raised in a similar manner but in two different countries

F Mansoor[1], B Zebeli[2], C Donaldson[3], P Lawlor[4], R Hawken[5], E Magowan[1]
[1]Agri Food Biosciences Institute, Hillsborough, UK, [2]University of Veterinary Medicine, Vienna, Austria, [3]Devenish Nutrition, Belfast, UK, [4]Teagasc, Moorepark, Ireland, [5]Cobb-Vantress, Arkansas, USA
Email:fawad.mansoor@afbini.gov.uk

Implications Feed conversion efficiency (FCR) and residual feed intake (RFI) are both measures of feed use efficiency. Whilst animals with low FCR will also have a good RFI, it was found that when comparing data between sites FCR differed significantly whereas RFI didn't. This could suggest that RFI standardised the data and allowed between site comparisons to be made with more confidence.

Introduction Poultry meat will play a key role in supply of protein to meet the global food security challenge in coming years. Whilst poultry meat production is significantly more efficient than beef or lamb major pressures still exists to further improve its efficiency and also reduce the variation in efficiency between birds. Feed use efficiency can be measured in different ways for different reasons, for example residual feed intake (RFI) (which is the difference between the observed feed intake and the intake predicted on observed growth) is considered the most accurate measure of how efficient the animal converts feed to growth and is commonly used in breeding goals but yet feed conversion ratio (FCR) is commonly used on farm and represents a practical tool to which economics can be easily related to. The aim of current study was to understand the performance variation in relation to RFI and other feed efficiency traits [FCR, residual gain (RG) difference between actual and predicted body weight gain, and residual intake and body gain (RIG) that is a linear combination of RFI and RG] between broiler chickens reared at different sites under a common regime.

Material and methods A total of 342 Cobb 500 FF chickens were used across 6 batches/time periods across two locations. Three batches of birds were group housed at AFBI, Northern Ireland and the other 3 batches in Vetmeduni, Vienna, Austria. The 342 chickens were selected from a larger pool of chickens (540) which were sexed on day 1 after which equal numbers of females and males were housed individually from day 7 with *ad libitum* access to feed and water. The chickens were offered a starter, grower and finisher diet from day 1 to 10, 11 to 21 and 22 to 42 respectively across both locations. Diets were manufactured in each country to a common formulation which reflected commercial levels of energy and protein although there were no enzymes or coccidostats in the diets. Body weight and feed intake was measured at 7, 14, 21, 28, 35, 38 and 42 days of age. Good, poor and average feed efficient birds (FE) were shortlisted at day 21 (n=24) on the basis of RFI and further on day 38 (n=18) to identify chickens for slaughter and sampling. Blood samples were taken at slaughter to assess the relatedness of birds using Cobb's proprietary 52K Chicken SNP chip. A three-way-ANOVA using PROC MIXED of SAS was used to investigate the effect of FE classification and location on RFI, RG, RIG and FCR. Batch was used as a covariate in the analysis. RFI was calculated using regression analysis in SAS (version 9.2, SAS Stat Inc.).

Results Body weight at day 7 averaged 151g for AFBI birds and 140g for Vetmeduni birds. There was no significant effect of FE classification on body weight at day 38 but site did ($P<0.001$) with birds at AFBI being lighter (2.36kg) than those at Vetmeduni (2.60kg). Male birds were also heavier (2.66kg) than female birds (2.31kg) ($P<0.001$). FE classification had a significant effect ($P<0.001$) on FCR (as expected), RFI and RIG (Table 1). There was no effect ($P>0.05$) of location or gender on RFI or RIG but there was a significant effect of these on FCR (both $P<0.001$). The FCR of male birds was better (1.59) than that of females (1.65) and the FCR of birds at Vetmeduni was better (1.52) than that of birds at AFBI (1.71). FE classification had a significant effect ($P<0.001$, SEM 51.0) on the Total feed intake of birds (3581, 3694 and 4011 g for good, average and poor birds respectively. Location had no effect but males birds ate more (3974g) than female birds (3551g) ($P<0.001$). Sib genetic analysis for genetic relatedness suggested there was no relationship between the birds on the two locations or within the locations.

Table 1 Effect of FE classification and location on RFI, RIG and FCR over a 38 day growing period.

	AFBI			Vetmeduni				Significance	
	Feed efficiency class (FE)			Feed efficiency class (FE)					
	Good	Average	Poor	Good	Average	Poor	s.e.m	FE	Location
RFI (g)	-232	-4.69	229	-189	12	250	20	***	NS
FCR	1.61	1.69	1.84	1.44	1.52	1.61	0.016	***	***
RIG (g)	239.3	3.2	-228.2	191.5	-10.8	-244.22	20.06	***	NS

*** = $P<0.001$, NS = non significant, RFI = residual feed intake, FCR = feed conversion ratio.

Conclusion As FCR increased, RFI increased and RIG decreased. This would largely be expected. Male birds ate more and converted feed to body weight gain better than female birds. Although birds were of the same 'breed' and offered a dietary regime manufactured to a common formulation, FCR differed between locations but RFI did not. This suggested that RFI standardised the data and allowed between site comparisons to be made with more confidence.

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Lime (*Citrus aurantifolia*) juice as a source of natural organic acids can improve the growth of broiler chickens

E Ndelekwute, G Enyenihi, E Assam, U Ufot, O Otu
University of Uyo, Akwa Ibom, Nigeria
Email:gloryenyenihi@yahoo.com

Implications Feeding of 25ml of lime juice per kg diet improved growth, daily gain and feed intake at starter and finisher phases, while 20ml/kg improved growth only at the finisher phase. The juice in feed lowered bacterial load.

Introduction The ban on the use of antibiotics as feed additives has necessitated alternatives among which are organic acids. They were reported to have the capacity to improve growth (Leeson *et al*., 2005). In most developing countries, synthetic organic acids are expensive. Natural sources such as lime (Novella, 2014) abound in the ecosystem, especially in the tropics, and could be a better alternative. The aim of this study was to determine the effect of lime juice as a source of organic acids on growth performance of broilers.

Material and methods Fresh lime fruits were washed cut into halves and the juice extracted. Ascorbic and citric acid content were determined by titration (Novella, 2014). The juice's antibacterial action in the feed was determined by serial dilution method. Three hundred day-old broiler chicks were allotted to 5 dietary treatments (T) of 60 birds each, replicated thrice (20 birds per replicate) in a completely randomised design. Basal maize - soybean meal based starter and finisher diets were formulated with 0, 10, 15, 20 and 25ml of fresh lime juice/kg diet being each added to a portion of the basal diet to form treatments T1, T2, T3, T4 and T5 respectively. The experiment, in an open-sided rearing house, lasted 56d (28d each for starter and finisher). Feed and water were provided *ad libitum.* The starter feed (on DM basis) had 224g/kg CP and 12.03MJ/kg ME and the finisher diet 205g/kg CP and 12.14 MJ/kg ME. The birds were supplied heat for the first 3 weeks. Vaccination against Newcastle and Gumboro diseases was carried out. Data on feed intake and live weight were collected weekly and statistically analysed using analysis of variance. Means were separated using the Duncan multiple range test.
Results The lime juice contained ascorbic and citric acids (12g/kg and 16g/kg respectively). Above 10ml/kg bacterial load in the feed was reduced from 10^4cfu to 10^2 cfu. Table 1 shows that final live weight, daily gain and feed intake were increased by 25ml/kg lime juice supplementation at the starter phase ($P<0.05$), while both 20ml/kg and 25ml/kg gave higher final live weights ($P<0.05$) at the finisher phase (Table 2).

Table 1 Effects of dietary fresh lime juice addition (ml/kg diet) on intake and live weight gains in starter broilers

Parameters	T1 0.00	T2 (10)	T3 (15)	T4 (20)	T5 (25)	SEM values
Initial live weight (g)	40.1	40.8	40.0	40.8	40.5	10.71
Final live weight (g)	950^{b}	963^{b}	977^{b}	982^{b}	1133^{a}	80.5
Daily weight gain (g)	32.5^{b}	32.9^{b}	33.5^{b}	33.6^{b}	39.0^{a}	4.16
Daily feed intake (g)	50.9^{c}	55.0^{b}	55.5^{b}	55.6^{b}	62.0^{a}	3.00
Feed: gain ratio	1.57	1.67	1.64	1.65	1.59	0.111

abc Means along the same row with the different superscripts are significantly different ($P<0.05$).

Table 2 Effects of dietary fresh lime juice addition (ml/kg diet) on intake and live weight gains in finisher broilers

Parameters	T1(00)	T2(10)	T3(15)	T4(20)	T5(25)	SEM values
Initial live weight (g)	950^{b}	963^{b}	977^{b}	982^{b}	1133^{a}	80.5
Final live weight (g)	2755^{c}	2806^{bc}	2838^{abc}	2888^{ab}	2927^{a}	118.8
Daily weight gain (g)	64.5	65.8	66.3	68.1	64.1	6.05
Daily feed intake (g)	154.3	154.8	155.4	155.1	154.3	25.76
Feed : gain ratio	2.39	2.35	2.35	2.29	2.41	0.253

abc Means along the same row with the different superscripts are significantly different ($P<0.05$).

Conclusion The increase in live weight, feed intake, and feed: gain ratio indicated that lime juice is a potential and novel feed additive that could be used to promote growth of broiler chickens.

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Pelage colour as a non-invasive measure of blood plasma melatonin in the red deer (*Cervus Elaphus*)

D J G Charman, A H Stewart, A M Mackenzie
Harper Adams University, Shropshire, UK
Email:charmanagri@hotmail.co.uk

Implications The use of pelage colour as an on farm measurement of melatonin in breeding animals would allow animals with lower levels of melatonin to be selected for breeding, thereby improving production performance in deer farming.

Introduction The effect of altering photoperiod on *Cervus Elaphus* has been the subject of a range of research over several years including its effects on growth, reproduction and a range of hormones (Wesbter, *et. al.* 1998,2001). Despite this research and the fact that most if not all of the summaries point towards melatonin being the driving factor behind these seasonal variation, no published values for melatonin in *Cervus Elaphus* could be found. Alongside this, Rollag and Adelman (1992) suggested that "colour change" could be used as a non-invasive measure of melatonin in mammalian species. In sheep a wide range of baseline melatonin levels exist among groups of ostensibly similar animals (Zarazaga, *et. al.,* 1998). In order to both establish the range of melatonin levels in *Cervus Elaphus* and to determine if pelage colour could be used as a non-invasive measure of melatonin the following trial was conducted.

Material and methods Blood samples were collected from 42 male red deer on 8/12/2012 (10 to 18 months of age, from the same farm with carcass weights ranging from 47.0 to 68.0 kilos) at ex-sanguination. A wide range of parameters were measured in the samples, including melatonin (32 results) which was quantified by ELISA. Pelage colour was measured at the "Hip" and "Shoulder" using a Konica Minolta colorimeter measuring in the L*a*b* colour space. The results we analysed via linear regression.

Results

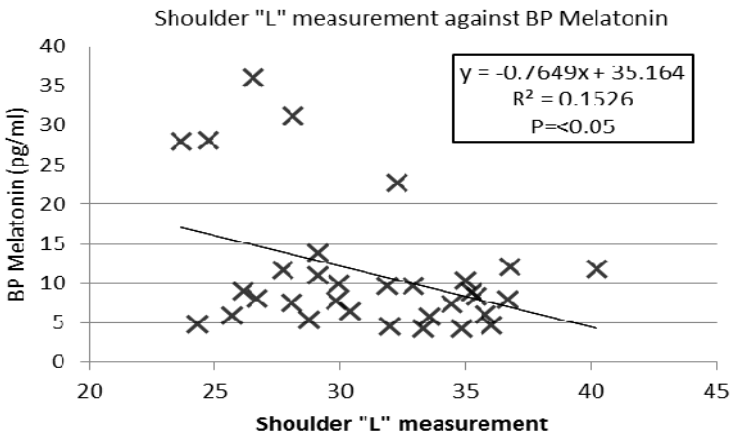

Table 1 Summary of blood plasma melatonin values in *cervus elaphus* (pg/ml).

N	Min	Max	Mean	Coefficient Variation
32	4.29	36.06	11.37	73%

The data in Table 1 shows a high level of variation among blood plasma melatonin values in October in the UK. A similar variation was observed by Todini, *et. al* .(2011) in sheep and goats.

There was a small but significant negative relationship between pelage and melatonin in the Light /Dark spectrum (L*) at the shoulder. (Figure 1).

Figure 1 Linear regression of shoulder "L*" measurement against BP melatonin (pg/ml)

Conclusion Figure 1 shows that there is a significant (p=<0.05) negative relationship between shoulder L* measurement and BP melatonin values. L* in the L*a*b* colour space represents the "lightness" of a colour or more simply sits black/white balance. That is, in an animal with a lower L* shoulder "score" will have darker pelage, and from these finding will have higher levels of BP melatonin.

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Assessing the impact of environmental tobacco smoke on the biological age of pet dogs

N C Hutchinson, C M Knottenbelt, L Nasir, D J Mellor
University of Glasgow, UK
Email:n.hutchinson.1@research.gla.ac.uk

Implications Pet dogs that live with smokers may undergo a faster rate of leukocyte telomere length loss than those in non-smoking homes.

Introduction While several studies have explored the effects of passive smoking on humans, there is little information on the impact of smoking on pet dogs in the home. This study aimed to quantify the impact of environmental tobacco smoke (ETS) by comparing measures of biological age in dogs both in smoking and non-smoking homes. Telomeres are tandem repeats of TTAGGG found at the end of chromosomes which become gradually shorter each time a cell divides. Telomere length has been used as a biomarker of aging in many human studies and telomere dynamics have been found to behave in a similar fashion in humans and dogs (Nasir *et al* 2001). An increased rate of telomeric loss has been seen in humans who smoke and it is not known whether dogs that are exposed to ETS have shorter telomeres to those who are not. One issue of using telomeres as a biomarker of aging is that they can vary somewhat between individuals depending on genetics and other factors. In the dog, a variation in telomere length has been shown to exist depending on breed (Fick *et al* 2012). Therefore the study also aimed to see if there may be another marker which would be more appropriate to use in future studies assessing biological age. One alternative biomarker of aging which has shown to be less variable than telomere length between human individuals is the cell senescence marker CDKN2A. There are no current publications looking at CDKN2A in terms of canine aging and therefore pilot data was produced to show whether this could be a viable biomarker of aging in the dog.

Material and methods 37 entire male dogs were recruited to the study and were divided into three exposure groups depending on the responses to an owner questionnaire: the dogs with non-smoking owners formed the first group, then the dogs with smoking owners were subdivided into higher and lower exposure based on the smoking behaviours of the household to form groups two and three. A physical examination was performed and a blood samples for routine biochemistry and haematology were taken to ensure the dogs were all healthy upon entering the study. The dogs were castrated and the removed tissues retained, along with spare blood from the diagnostics laboratory. DNA was extracted from leukocytes and cremaster muscle, and telomere length measured by qPCR using the method previously described by Cawthon (2002). The difference between the cremaster muscle and leukocyte telomere length adjusted for age was calculated as per Benetos *et al* (2011) in order to make the telomere lengths comparable between individuals and give an estimate of rate of loss of telomere bases. Skeletal muscle is a post mitotic tissue and unlike leukocytes, it does not undergo a massive cellular proliferation at a young age so gives a better idea of the telomere lengths the individual had at birth.
RNA and protein were extracted from one of the testes from each dog and used to determine both mRNA levels and protein levels of CDKN2A.

Results
An ANOVA test was performed in R to compare the age-adjusted leukocyte-cremaster muscle telomere lengths between the ETS exposure groups. A significant difference was found between the groups ($p=0.0487$), with the smallest age-adjusted difference between cremaster muscle and leukocyte telomere length being found in the non-smoking homes and the largest difference found in the heavy smoking homes. Results are still pending regarding the CDKN2A experiments.

Conclusion
Dogs in non-smoking homes appear to have a slower rate of telomere loss than those in smoking homes. The owners have been asked to bring their dogs back at 12 months after initial sampling so it is hoped that further data on the dogs' telomere dynamics will be elicited in the coming months.

Acknowledgements
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Bodyweight, feed intake and activity rhythms of entire and neutered female cats during the transition from autumn to winter

D G Thomas[1], J Cormier[2]
[1]Massey University, Palmerston North, New Zealand, [2]AgroSup Dijon, France
Email:d.g.thomas@massey.ac.nz

Implications Entire female cats show no bodyweight gain during the autumn to winter transition, despite eating more and being less active than neutered female cats on the same diet. This emphasises the energetic cost of reproductive cycling in the cat even at the end of the breeding season.

Introduction The cat (*Felis catus*), is a small domesticated carnivorous mammal which shows strong seasonal cycles of reproduction (Goodrowe *et al*. 1989) and coat growth (Hendriks *et al*. 1997). We have previously investigated seasonal rhythms of bodyweight, feed intake and activity of both neutered male and female cats in our colony over a complete year (Thomas *et al*., 2012). In animals exposed to a temperate climate (Temperature range: Max. 30.4°C, Min. -2.3°C), the period of the year where the most rapid changes in bodyweight, intake and activity rhythms occur is autumn. The aim of this study was to investigate the change in bodyweight, feed intake and activity of neutered and entire female cats during the transition from autumn to winter.

Material and methods Two groups of adult domestic short-haired cats; neutered females (NF: n=5) and entire females (EF: n=5), from the Centre of Feline Nutrition, Massey University, Palmerston North, New Zealand (longitude 175° 38' E, latitude 40° 22' S) were used in the study which ran from 24th March until 7th July 2014. Each group was balanced for age (mean±SEM: NF 5.67 ± 1.16, EF 5.55 ± 1.30 at the start of the study), and kept in outdoor colony cages (4.5×1.4×2.5 m) according to the Companion Cats Code of Welfare (NAWAC, 2007). Environmental conditions (temperature, rainfall and humidity), were recorded using a weather station (La Crosse Technology, La Crosse WI USA). Both groups were fed *ad libitum* with a commercial AAFCO tested wet diet (17.8% DM as is, 8.1%DM ash, 45.9%DM crude protein, 32.5%DM crude fat, 2.0%DM crude fibre and 26.0kJ/g DM gross energy). Accelerometers (Actical® Respironics Mini Mitter division, Bend, OR USA) were fitted to all cats and used to determine activity rhythms. Epoch length was set at 0.25 min on each monitor which recorded continuously. Monitors were removed briefly (<1h) once per week and data was downloaded and analysed by Actical® Software (Version 2.0). Results are presented as mean and standard errors of the mean (SEM), with differences between groups determined using general linear model (SAS, version 9.4). A probability less than 0.05 was considered significant and a probability less than 0.1 a trend.

Results Day length declined from 11 h 57 min at the start of the study to 9 h 25 min at the end. Similarly, average daytime temperature fell from 16.3°C to 9.0°C, while weekly rainfall and sunshine hours were highly variable but not different when compared at the start and end of the study. In the study NF consistently weighed more than EF ($P<0.001$), during the transition from autumn to winter. In addition NF showed a significant weight gain (3.504 ± 0.285 kg to 3.728 ± 0.268 kg: $P<0.001$) during the study, while the bodyweight of the EF remained constant (2.997 ± 0.160 kg to 2.997 ± 0.143 kg: $P>0.05$). In contrast, NF consistently ate less on a per kg bodyweight basis than EF (103.4g/kg/d vs 93.2g/kg/d respectively: $P<0.001$), although both groups showed a highly variable but slight decline in intake on a per kg bodyweight basis during the study (NF 96.2g/kg/d to 90.1g/kg/d; EF 111.2g/kg/d to 101.5g/kg/d). EF were less active than NF (48,245 vs 61,508 counts/d: $P<0.001$), with both groups more active during the day compared to the night ($P<0.001$), and less active when the moon was full then when it was a new moon ($P<0.05$). There was also a trend for both groups to be more active when the sun was shining ($P=0.087$), and for activity to decline when temperatures were lower ($P=0.055$).

Conclusion The experiment clearly showed that neuter status clearly has an effect on bodyweight, feed intake and activity in female cats. Entire female cats weighed less than NF but they ate more (on a per kg BWt basis) and were less active. This indicates that EF utilise energy differently from NF and suggests that the energetic cost of reproduction, even at the end of the breeding season, is marked in these individuals, and this process takes precedence over weight gain in these animals. The significant bodyweight increase recorded in NF during the autumn to winter transition occurred despite eating less and being more active, further emphasising the effect that neuter status had in the experiment.

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Performance of growing rabbits fed graded inclusion levels of sun-dried shrimp waste meal based diets

A Okorodudu, O O Oduguwa, A O Fafiolu, A O Ogunsakin
Federal University of Agriculture, Abeokuta, Ogun State, Nigeria
Email:okorodudurosuo@gmail.com

Implications Inclusion of sun-dried shrimp waste meal up to 66% in the diet of growing rabbits had no adverse effect on their growth performance and reduces the cost of feeding.

Introduction High cost of feed ingredients which supply protein in livestock feed formulation which can be attributed to seasonal availability and competition with man has greatly affected the production of livestock especially monogastric animals such as poultry and rabbits. Thus, there is the need for animal nutritionist to find alternative protein sources that are relatively cheap and not in competition with man. One of such alternative feed ingredients is sun-dried shrimp waste meal (SWM) which is basically the dried milled waste of the shrimp industry consisting of the head, appendages and the exoskeleton of shrimps processed and packaged for both local and export markets. This study sought to determine the feeding value of shrimp waste meal in the diets of growing rabbits.

Material and methods The experiment was carried out at the Rabbit unit, Directorate of University Farms, Federal University of Agriculture Abeokuta, Ogun State, Nigeria. A total of 48 growing rabbits were used for this experiment, divided into 4treatments and 3replicates. The rabbits were housed, 2per cell in two tier wire mesh hutches with 4cells each large enough to give room for concrete feeders and drinkers; movement and exercise. Shrimp waste was sourced from CHI limited, Lagos, sun-dried and milled. Four iso-calorific (2235kcal/kg) and iso-nitrogenous (15%crude protein) experimental diets were formulated at 0%, 33%, 66% and 100% inclusion levels of SWM replacing soybean meal. Rabbits were fed ad-libitum with access to clean water daily. Data generated during the 12 weeks of the experiment was analysed using statistical analysis system (SAS) and significant means separated using Duncan's Multiple Range Test.

Results The effect of SWM on parameters measured was significant ($P<0.05$) except at the initial weight. 0%, and 66% had similar final weight and total weight gain, however, they were higher than those fed 33% and 100% SWM. Those fed 66% SWM had highest (3.58) feed conversion ratio.

Table 1 Performance characteristics of growing rabbits fed graded levels of shrimp waste meal based diets

Parameter	0%	33%	66%	100%	SEM	P-value
Initial weight (g)	516.67	483.33	466.67	483.33	12.50	0.6140
Final weight (g)	1322.33^{a}	1319.33^{a}	1398.67^{a}	997.33^{b}	48.01	0.0001
Total weight gain (g)	805.67^{a}	769.00^{b}	923.67^{a}	514.00^{c}	48.01	0.0005
Feed intake (g)	60.10^{a}	55.09^{b}	59.01^{a}	51.83^{c}	1.01	<0.0001
Feed conversion ratio	4.19^{b}	4.07^{b}	3.58^{b}	5.66^{a}	0.25	0.0007

Conclusion The results show that SWM can be used as an alternative feed ingredient in the diet of growing rabbits to improve their performance.

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Reproductive potential of rabbit bucks orally administered exogenous organic selenium

E O Ewuola, D E Akinyemi
University of Ibadan, Oyo state, Nigeria
Email:eoewuola@gmail.com

Implications Bioavailability of organic selenium and its antioxidant properties has been adjudged to enhance reproductive efficiency in male rabbits.

Introduction Selenium (Se) is important for a myriad of biochemical processes. It is an essential component of selenoproteins that play an important role in many biological functions, such as antioxidant defence, formation of thyroid hormones, DNA synthesis, fertility and reproduction (Youcef *et al*., 2013). Reproductive characteristics of livestock also depend heavily on whether such livestock are selenium replete or selenium deficient. Many cases of infertility have been recorded in selenium deficient areas (Arechiga *et al*., 1998). Meschy, (2010) reported a remarkable increase in fertility (92% vs 45%) when supplementation with Se was provided for animals feeding on pastures very poor in Se. Organic forms of Se are more bioavailable and better retained in animals than the inorganic forms. The aim of the study was to evaluate the effect of organic Se on reproductive potential of male rabbits.

Material and methods Twenty four, 10-month old male rabbits (New Zealand White and Fauve de Bougourne) were weighed and allotted to 4 dietary treatments consisting of 6 replicates with each rabbit as a replicate in a completely randomised design. Se in the form of L-selenomethionine was orally administered by drenching at 48-hour intervals in the morning before feeding. All animals were fed the same basal diet that contained 0.1mg Se for 42 days. Treatment 1 was a control without L-selenomethionine, while treatments 2, 3 and 4 received 0.2, 0.3, and 0.4 mg L-selenomethionine / kg body weight respectively. On days 38 and 42, semen was harvested from the bucks using artificial vagina and evaluated for quality characteristics (Ewuola and Egbunike, 2010). Seminal plasma was separated from the semen and used for glutathione peroxidase (GPx) and total antioxidant activity determinations (Rotruck *et al.* 1973). Data were analysed using ANOVA, the GLM procedure of SAS (2008). Means were separated using Duncan Multiple Range Test.

Results There were no significant differences between treatments in semen volume (Table 1). Mass activity and progressive sperm motility were higher ($P<0.05$) in rabbits administered 0.3 and 0.4 mg/kg bodyweight than T2 and the control (T1). Percentage live sperm cells and sperm concentration were higher in rabbits on T4 than those in T3 and T2 respectively. Glutathione peroxidase and total antioxidant activity in rabbits was significantly increased as the level of selenium supplementation increased.

Table 1 Semen characteristics and antioxidant capability of rabbit bucks administered L-Selenomethionine

Parameters	T1 (0mg/kg)	T2 (0.2mg/kg)	T3 (0.3mg/kg)	T4 (0.4mg/kg)
Volume (ml)	0.58±0.28	0.67±0.17	0.51±0.16	0.49±0.18
*Mass activity	++	++	++++	++++
Sperm motility (%)	$63.33±11.69^{b}$	$70.83±7.36^{b}$	$82.50±7.58^{a}$	$85.83±5.85^{a}$
Live sperm cells (%)	$90.17±4.94^{ab}$	$94.25±1.23^{ab}$	$88.94±8.43^{b}$	$95.19±1.78^{a}$
Sperm concentration (x 10^{9}/ml)	$0.86±3.05^{b}$	$1.15±8.48^{b}$	$1.47±4.66^{ab}$	$2.05±9.70^{a}$
Total antioxidant Capacity (mmol/l)	$0.83±0.34^{b}$	$0.97±0.07^{ab}$	$0.98±0.04^{ab}$	$1.11±0.27^{a}$
GPx (µg GSH/min/mg protein)	$33.24±2.77^{b}$	$34.49±2.97^{b}$	$41.84±2.03^{a}$	$44.15±4.07^{a}$

a b - Means with different superscripts are significantly ($P<0.05$) different. GPx-Glutathione peroxidise
*determined subjectively by grading the wave generated due to collective activity of the sperm cells in the semen

Conclusion. L-selenomethionine supplementation in male rabbits increased antioxidant activities and improved semen quality. Therefore, 0.4mg/kg body weight is recommended to enhance the reproductive potential of the animal.

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The choice of diet affects the oral health of the domestic cat

F Mata
Newcastle University, Newcastle Upon Tyne, UK
Email:fernando.da-mata@newcastle.ac.uk

Implications The awareness of animal owners and health professionals of factors with a negative impact in on health and welfare is paramount in preventive practice. This study evidences the impact of diet choices in the oral health of the cat.

Introduction Periodontal disease (PD) is a highly prevalent disease, affecting around 70% of domestic cats over 2 years of age (Ingham *et al*., 2002) and 85% of those aged over 5 years (Verhaert and Van Wetter, 2004). Calculus formation and development of gingivitis are key aspects in the development of PD, and as these increase oral health deteriorates. A relationship between the degree of calculus and gingivitis development, signals a deterioration of the teeth health status. The calculus index (CI) proposed by Ramfjord (1967), and the gingival index (GI) proposed by Loe and Silness (1963) are used to assess the oral health of cats. The GI scoring criteria are: 0 (normal), 1 (mild inflammation, slight colour change, slight oedema, no bleeding on palpation), 2 (moderate inflammation, redness, oedema, bleeding on probing), and 3 (severe inflammation, marked redness and oedema, tendency to spontaneous bleeding). CI scoring criteria: 0 (no calculus present), 1 (supra-gingival calculus covering 1/3 of exposed tooth surface), 2 (supra-gingival calculus covering more than 1/3 but 2/3 of exposed tooth surface or presence of flecks of sub-gingival calculus or both), 3 (sub-gingival calculus covering more than 2/3 of exposed tooth surface or continuous heavy band of sub-gingival calculus around the crevice of teeth or both). The prevalence and severity of PD varies with factors such as: gender, age, breed, diet, chewing behaviour and systemic health (Clarke and Cameron, 1998). It was the aim of this study to evaluate the effect of age and type of diet on the oral health and different teeth of cats.

Material and methods Data were collected within Pet Doctors™ in the Isle of Wight in England, taken from n = 41 cats, during January 2013. The GI and the CI were assessed for each of the cats' teeth and the cat owners answer the questions about: 'age' (young <3 years, adult 3 to 8 years, old >8 years) and 'diet' (dry and wet). Data were organized by 'teeth' (incisors, canines, premolars and molars), averages for CI and GI were calculated between teeth in the same cat, and finally GI and CI were added together to create the variable teeth health status (THS). Values were rounded to the nearest unit and ranged from 0 to 6, as both CI and GI ranged from 0 to 3. A generalised estimating equations model was fit to data to account for within-subject effects of the variable teeth. A multinomial cumulative logit link function was used. The analysis was done using IBM® SPSS® Statistics 21.

Results From the factors analysed teeth (p<0.001) and diet (p<0.001) show to be significant. Age was not significant (p>0.05) as a standing alone factor, however it was found significant within first and second level interactions, together with the interactions between all the other factors: age x teeth (p<0.01), age x diet (p<0.01), teeth x diet (p<0.001) and teeth x age x diet (p<0.001). Using the parameters of the model, the probabilities of scoring each of the THS for the different combinations of teeth, diet and age, were calculated. Table 1 shows the calculations for THS 1 and 6.

Table 1 Probabilities for scoring THS 1 and 6. The other THS intermediary scores have ordered intermediary probabilities.

Variables			THS scores 1 and 6 Probabilities	
Teeth	Age	Diet	1	6
incisors	adult	dry	0.190	0.001
incisors	young	dry	0.221	0.001
canines	young	dry	0.245	0.001
incisors	old	dry	0.335	0.001
incisors	old	wet	0.353	0.002
canines	adult	dry	0.388	0.002
incisors	young	wet	0.453	0.002
premolars	young	dry	0.538	0.003
premolars	adult	dry	0.662	0.006
molars	young	dry	0.695	0.007
molars	adult	dry	0.819	0.013
canines	young	wet	0.866	0.019
canines	old	dry	0.869	0.019
incisors	adult	wet	0.886	0.022
molars	old	dry	0.923	0.034
premolars	young	wet	0.934	0.040
premolars	old	dry	0.949	0.052
canines	old	wet	0.955	0.059
canines	adult	wet	0.961	0.068
molars	young	wet	0.969	0.084
premolars	adult	wet	0.978	0.114
molars	adult	wet	0.985	0.163
molars	old	wet	0.986	0.173
premolars	old	wet	0.994	0.332

Conclusion Cheek teeth (molars and premolars) are more susceptible to poor oral health than other teeth independently of the age of the cat. Cats feeding on wet food are also more susceptible. It is important to prevent oral health deterioration from an early age with special attention paid to the cheek teeth. Dry food has abrasive properties showing to play an important role in teeth cleaning; wet canned food promotes the development of calculus and gingivitis and therefore poor oral health.

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Hip scoring for canine hip dysplasia: A comparison of British and German breeding strategies

C Douglas, F Mata, G Menem
Newcastle University, UK
Email:fernando.da-mata@newcastle.ac.uk

Implications Canine hip scoring (HS) can effectively be used in selection programs to reduce the incidence of canine hip dysplasia (CHD). By adopting the German system of mandatory HS of breeding parents and only allowing those with low scores to breed, it would appear to offer a more effective method of reducing hips scores in populations of pedigree dogs than the UK Kennel Club's voluntary system. This in turn is likely to lead to lower incidence of the painful and debilitating condition of CHD for future generations of dog breeds prone to CHD, with positive impact on welfare.

Introduction CHD is a common disorder of the locomotive system in dogs, first described in 1935. As the issue grew with the number of dogs affected increasing, HP programmes were established to allow negative selection in mating programs. HS is based on the assessment of radiographs and measurements taken are well categorised and standardised in most national and international canine institutions (Ginja *et al.*, 2010). HS has been mandatory in Germany for German Shepherd (GS) dogs since 1973, followed by the Boxer (B) and Rottweiler (R), and only unaffected animals are allowed to have their descendants registered in German Breeding Clubs that are members of the German Kennel Club. HS was introduced in the UK in 1983 (Lewis *et al.*, 2013) but on a voluntary basis and any descendent can be registered. Different countries use different HS systems with Germany using the FCI system (scoring A to E) (Fikse *et al.*, 2013). The UK HS system grades with points several criteria. CHD is a polygenetic disorder, with heritability ranging between 0.2 and 0.6 (Duan *et al.*, 2013). Therefore responsible breeding, choosing parents with low hip scores, should be able to reduce the incidence of this debilitating disease and reduce the hip score within the populations of dog breed. Our aim was to explore whether the German compulsory HS prior to breeding compared to the UK voluntary HS appeared to have had an impact on hip scores between the breeds in the 2 countries. We hypothesised that there would have been a greater reduction in hip score in German breeds as a result of compulsory HS compared to the voluntary system in the UK.

Material and methods The data were provided by The Kennel Club (UK) and its German equivalent, Breed Clubs of the Verband für das Deutsche Hundewesen. The set of data included a total of N = 100436 hip scored dogs (n = 65505 from Germany and n = 34951 from Britain) of 3 breeds and scored between the following years: B (n = 5807 from Germany – 2003 to 2012, and n = 283 from the UK – 1990 to 2013), R (n = 4391 from Germany – 2003 to 2013, and n = 7812 from the UK – 1983 to 2014) and GS (n = 55307 from Germany – 2003 to 2010, and n = 26856 from the UK – 1980 to 2014). Hip score was modelled as a function of the factors (country, breed and gender) and the covariates year and age, using Poisson models with a log link. Due to the different HS systems in use, both UK and German scores were converted to a 0-4 value for analysis. The statistical analyses was done with the package R Cran for Windows 3.0.3.

Results Figure 1 models breed, country and year as independent variables. HS decreases with year (p<0.001); Germany (p<0.05) scores below UK; R (p<0.001) scores below the others; B and GS score equally (p>0.05). However due to interaction, the Germans R (p<0.001) score higher and the Germans GS (p<0.001) scores lower.

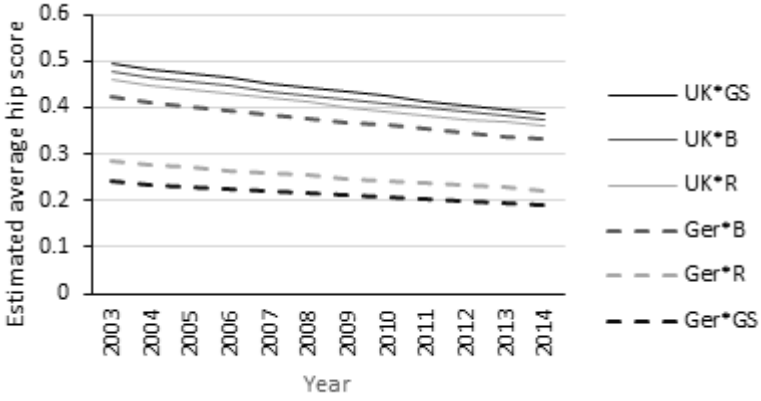

Figure 1 Estimated average scores through the years

Conclusion Heritability in CHS is high enough to allow programs of selection to be effective in few generations. Germany's established compulsory HS program for CHD promotes significantly lower hip scores for the German breeds compared to the UK. We recommend further studies to explore the incidence of CHD over time. Selection is not fully efficient if, independently of scores, dogs enter in the stud books.

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Effect of two dietary schemes in the pre- and early post-weaning phase on within-batch heterogeneity at 10 weeks of age

S P Paredes[1], T de Waele[2], J W Resink[1]
[1]Nutreco Nederland, B.V., Boxmeer, The Netherlands, [2]Trouw Nutrition Benelux, Gent, Belgium
Email:sandra.paredes@nutreco.com

Implications: The current work provides insight into the advantages of a more complex feeding scheme in early life. Opening new opportunities to the industry in terms of nutritional intervention to tackle the welfare and economic implications of genetic sow prolificacy.

Introduction With the increase in litter size there has been an increase in within-litter variation due to a larger number of light weight piglets in the herd. These light weight piglets pose an economic disadvantage to the farmer and have severe welfare implications due to their high mortality rate. A reduction in the heterogeneity of the piglet batch at 10 weeks of age might be achieved by a more complex nutritional program in early life compared to a simple diet (Beaulieu *et al*., 2012; Douglas *et al*., 2014). To test this hypothesis a 2 x 2 experiment was set up to determine whether a combination of Milk replacer + prestarter + larger quantity of a high specification weaner diet would have a beneficial effect on group homogeneity at 10 weeks of age.

Material and methods A 2 x 2experiment was designed following 48 litters from birth until 10 weeks of age. Half of the litters were provided a milk replacer (Milkiwean Yoghurt, **MR**) next to the sow milk until 14 days of age; and half were only provided sow milk (**CO**). From 14 days of age until weaning (21 days), all piglets (MR and CO) were fed a dry prestarter (Milkiwean Precoce). At weaning, half of each group was fed 5 kg (**F**) or 2.5 (**T**) kg of a complex weaner diet respectively (n = 128 piglets/group). After this a commercial starter diet was provided *ad libitum* to all piglets until they reach 10 weeks of age. All groups were followed until 10 weeks of age. The periodic weight differences between groups were evaluated including pre- and post-weaning treatment and their interaction as independent variables using the MIXED procedure in SAS. Group homogeneity was tested at weaning and at 10 weeks of age using homogeneity of variance test (Levene's and Hovtest). Blocks based on weight category were analysed to determine the benefit of the dietary treatments in weight gain, feed intake and feed conversion ratio between groups including the pre- and post-weaning treatment and their interactions as independent variables using the MIXED procedure in SAS 9.3 (2012).

Results

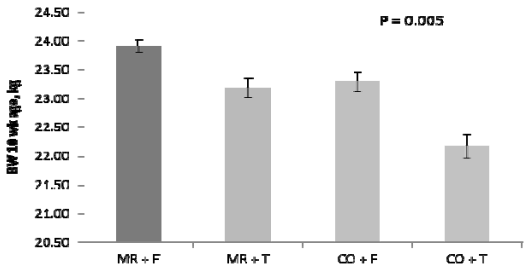

Figure 1 Effect of dietary scheme on BW at 10 weeks of **age**

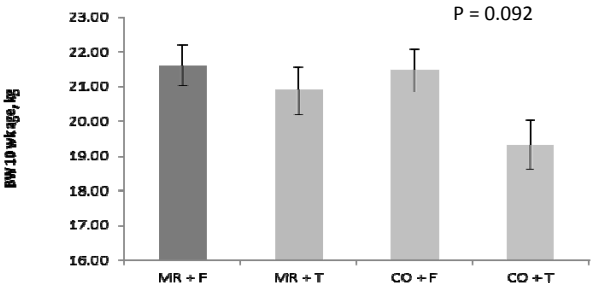

Figure 2 Effect of dietary scheme on BW at 10 weeks of age for light BW piglets.

There was a 25% reduction in the BW variation at weaning for the MR fed piglets (P = 0.001). In the post-weaning period, there was a higher 10-weeks weight for the MR+F piglets (P = 0.005; Figure 1). Compared to the other treatments, the MR + F fed piglets had a higher homogeneity (P = 0.113). When blocking by weight category, it was observed that the light weight piglets fed the MR + F treatment had a higher weight gain (P = 0.092; Figure 2). The CO + F fed piglets had the second highest weight at 10 weeks of age. The CO + T fed piglets had the lowest performance from weaning until ten weeks of age.

Conclusion

- The MR + F dietary scheme provides a more homogeneous piglet batch at 10 weeks of age
- Providing only a creep feed and 2.5 kg of weaner diet has the worst performance for piglets
- Light weight piglets benefit the most by a combination of Milk replacer and 5 kg weaner diet

Acknowledgements The authors gratefully acknowledge the team of Trouw Nutrition Benelux for their valuable contribution during the execution of the study.

Feeding values of *Pennisetum purpureum* varieties fertilized with animal manures

O G Ojambati, V O A Ojo, S A Adeoye, T K Adeleye, T B Oyekunle, O M Arigbede, E O Ojo, S O Badaru
Federal University of Agriculture, Abeokuta, Ogun, Nigeria
Email:ogunsakinao@gmail.com

Implication Forage is important to livestock production since it is the major source of ruminant feed and nutrition for sustainable animal protein and energy.

Introduction *Pennisetum purpureum* (Schumach) commonly known as elephant grass or Napier grass has been reported to be a high yielding forage grass by several authors. It has been identified as high yielding forage on smallholder farms (Orodho, 1990) and enhance the quality and productivity. Olson and Paworth (2000) have reported positive effect on forage yield on the application of organic manure. This study therefore aimed at addressing the influence of animal manures on the feeding values of the different *Pennisetum* varieties during the dry season.

Material and methods A 4×4 factorial experiment replicated 3 times which consisted of four manure types (swine, 10.16; cattle 22; poultry, 7.92 (kg/plot) and control) was established on the organic research farms of the Federal university of Agriculture, Abeokuta. The soil contained total N (0.15%), organic C (1.31%) and available P (32.87mg/ kg). The forages were harvested at 12 weeks of growth with a 1 m^2 quadrat in order to obtain subsamples and oven dried at 65^0C until constant weight was obtained. Proximate composition was analysed (AOAC, 2002). Relative feed value was calculated (Xie *et al.,* 2012). The data obtained were analysed as a two-way analysis of variance using the SPSS 20 statistical package.

Results The dry matter digestibility (DDM) contents ranged from 491.7g/kg for *P. purpureum* (purple) to 501.4g/kg for *P. purpureum* (S13). The dry matter intake (DMI) ranged from 15.6g/kg for *P. purpureum* (S15) to 16.7g/kg for *P. purpureum* (local). Relative feed value (RFV) is an index used to rank forages by potential digestible dry matter intake and it ranged from 606.5g/kg for *P. purpureum* (S15) to 652.7g/kg for *P. purpureum* (local). The feed intake (FI) ranged from 15.6g/kg for *P. purpureum* (S13) to 16.7g/kg for *P. purpureum* (local).

Table 1 Main and interaction effects of manure type on the feeding values of *Pennisetum purpureum* varieties (g/kg)

Factors	DDM	DMI	RFV	FI
Manure type				
Swine	503.4^{b}	15.9^{d}	624.0^{c}	15.9^{d}
Cattle	507.2^{a}	16.7^{a}	659.9^{a}	16.7^{a}
Poultry	472.2^{d}	16.2^{b}	593.4^{d}	16.2^{b}
Control	513.1^{c}	16.1^{c}	643.5^{b}	16.1^{c}
SEM	0.00	0.00	0.00	0.00
Variety				
LOCAL	501.4^{b}	16.7^{a}	652.7^{a}	16.7^{a}
S13	503.4^{a}	16.0^{c}	626.6^{c}	16.0^{c}
S15	499.5^{c}	15.6^{d}	606.5^{d}	15.6^{d}
PURPLE	491.7^{d}	16.6^{b}	634.9^{b}	16.6^{b}
SEM	0.00	0.00	0.00	0.00
Manure x Variety	***	***	***	***

$^{a-d}$: Means on the same column with different superscripts are significantly different ($P < 0.05$).

Conclusion Results showed that the feeding values of the local variety of *Pennisetum purpureum* were higher than the others and that fertilization of this local variety with cattle manure resulted in improved feeding values that could be used in feeding of ruminants during the dry season.

Acknowledgments The authors really appreciate the help rendered through the laboratory technologist Mr Idehen John.

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Effect of supplementation with forages of cassava, *Gliricidia* and *Leucaena*, on the growth and faecal egg count of semi intensively managed sheep

O A Fasae, J E O Omosun
Federal University of Agriculture, Abeokuta, Ogun State, Nigeria
Email:animalexp@yahoo.co.uk

Implications Sheep managed semi- intensively supplemented with either forages of cassava, *Gliricidia* or *Leucaena*, had improved growth performance with a reduction in faecal egg count.

Introduction In most sheep production areas in Nigeria, inadequate nutrition and infections with gastrointestinal parasites represent a major constraint in sheep husbandry. For many years, the control of these parasites has solely relied on the repeated use of synthetic anthelmintics. However, the emergence of resistant gastrointestinal parasites populations and the increasing concern of consumers for drug residues in animal products have provided a strong impetus towards the development of alternative strategies such as feeding forages containing tannins to control gastro-intestinal parasites. The aim of the present study was to evaluate the effect of supplementation with forages of cassava, *Gliricidia* or *Leucaena*, on the growth and faecal egg count of semi intensively managed sheep.

Material and methods West African Dwarf breed (n = 16) sheep, managed semi intensively, with an average body weight of 16.76±1.30kg, were randomly assigned to tanniferous forages of cassava, *Gliricidia*, *Leucaena*, or an unsupplemented control treatment. The animals were tagged for identification and allowed to graze natural pastures for six (6) hours daily (0800hrs – 1400hrs). Forages were harvested fresh from established plots, wilted for 24 hours to allow a reduction in the level of anti-nutritional factors as well as other materials that may have negative effect, before feeding the animals. The forages were given to the animals after grazing at a rate of 4% body weight (as fed) along with 100g of a 16% crude protein concentrate diet, comprising 10% maize, 50% maize offals, 25% brewer's dried grain, 18% soya bean meal, 3% bone meal, 0.5% salt and 0.5% vitamin premix with water provided *ad libitum*. Initial body weights of the animals were taken using a spring balance at the start and on a weekly basis thereafter during the 8 week experimental period. Faecal samples of about 2 to 4 grams were obtained directly from the rectum of each animal at the beginning of the experiment and on weekly basis for faecal egg count determination. The faecal egg count was analyzed using the Modified McMaster counting technique. Data collected were subjected to one way analysis of variance in a completely randomized design according to SAS (1999). Significant means were separated using Duncan Multiple Range Test (Duncan, 1955).

Results Growth of sheep supplemented with the cassava and *Leucaena* forages were high and were not significantly different to each other ($P < 0.05$) , but growth rates were lower ($P > 0.05$) for sheep fed *Gliricidia* (Table 1), albeit that the latter were still higher than the control treatment. A range of 65.48 to78.37 % reduction in faecal egg count was observed in sheep supplemented with forage compared to the unsupplemented control treatment.

Table 1 Weight gain and faecal egg count of sheep supplemented with forages of cassava, Gliricidia and Leucaena

Parameters	Cassava	*Gliricidia*	*Leucaena*	Control	SEM
Initial weight(kg)	16.75	17.00	16.50	16.77	1.30
Final weight(kg)	28.25^{a}	26.25^{b}	28.75^{a}	24.52^{c}	1.35
Weight gain(g/day)	20.53^{a}	16.51^{b}	21.87^{a}	13.83^{c}	3.09
Initial faecal egg count (egg/g)	712	620	689	701	9.83
Final faecal egg count (egg/g)	154^{c}	214^{b}	171^{c}	1050^{a}	7.04
% Reduction in faecal egg count	78.37	65.48	75.18	-49.79	5.80

$^{a, b, c}$ means with same superscript within the rows are not significantly different($P<0.05$)

Conclusion The improved performance of sheep in this study indicates the potential of these forages, possibly because of their tannin content, to help to increase growth and decrease faecal egg counts in sheep managed semi-intensively. It is therefore recommended that since these forages are naturalized to the tropical conditions and represent a rich, renewable, and unexplored source of protein and tannins for grazing sheep, the possibility of using feeds containing these plant materials need to be explored and the mechanism evaluated for effective sheep production.

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Effects of a blends of essential oils on rumen microbial fermentation of a 50:50 lucerne: concentrate diet in a dual-flow continuous culture system

N Khosrozad, O Azizi, H Jahani-Azizabadi
Department of Animal Science, Faculty of Agriculture, University of Kurdistan, Sanandaj, Kurdistan, Iran
Email:ho.jahani@uok.ac.ir

Implications Most *in vitro* studies for investigating the effect of essential oils (EO) have been conducted under 24-48h batch culture. The present study investigated the effect on rumen microorganisms when exposed to EO over a longer term.

Introduction Positive effects of thyme, cinnamon and clove essential oils on rumen microbial fermentation have been reported in recent studies (Benchaar *et al.*, 2007a; Jahani-Azizabadi *et al.,* 2011). No study has investigated the effects of simultaneous use of thyme, cinnamon and clove essential oils on rumen microbial fermentation characteristics. Therefore, the aim of the present study was to investigate the effects of a blend of thyme, cinnamon and clove essential oils on rumen microbial fermentation of a 50:50 forage:concentrate diet in dual flow continuous culture system.

Material and methods Six 1380-ml dual-effluent fermenters were used in two replicated periods (in each period 7d for adaptation and 3d for sampling). On the first day of each period fermenters were filled with 0.4L of pre-warmed McDougall's buffer (McDougall, 1948) that was modified to contain 1.0 g/L of $(NH_4)_2SO_4$, and 1 L of strained rumen fluid. Rumen fluid was obtained from three steers after surgery. Animals were fed twice per day with a 50:50 forage (Lucerne hay and maize silage) to concentrate diet. Fermenters were fed at 100 g of DM/d in 3 equal portions (every 8 h) with a 50:50 lucerne hay:concentrate (17% CP, 52% NFC) diet. Temperature (38.6°C), liquid (10%/h) and solid (5%/h) dilution rates were maintained constant and anaerobic conditions were maintained by infusion of N_2 at a rate of 40 mL/min. Artificial saliva (McDougall's buffer) was continuously infused into the flasks. Beginning at d 7, experimental treatments [control (non additive) and 250 and 500 mg/L of essential oil blend (50% thyme, 30% cinnamon and 20% clove essential oils)] were deposited directly into the fermenters (n=2) once daily (before morning feeding of fermenters). The measurement period was divided into 2 stages [initial (d 10 to 12) and final (d 16 to 18)]. At each sampling period, daily effluent was homogenized and strained through four layers of cheesecloth to eliminate large feed particles and the solid fraction was dried at 55°C for 48 h for the determination of DM. Undigested residues were subsequently analyzed for OM and CP. During the last day of each sampling period 50 ml of fermenter fluid was taken at 4 h after morning feeding to determine tungstic acid soluble N (**TA-N**), TCA-soluble N (**TCA-N**), and ammonia N concentration. Data were analyzed using MIXED procedure of SAS (9.1) for repeated measures. Period was considered as random effect. Means were compared at $P<0.05$.

Results Results of the present study showed that the addition of essential oil blend resulted in a decrease ($P<0.05$) in OM disappearance relative to those of the control. DM and CP disappearance of experimental diet and N-NH3, LPep-N and SPep+AAN concentration were not affected by essential oil supplementation.

Table 1 Effect of essential oil blend on ruminal fermentation characteristics of a 50:50 forage: concentrate diet measured using dual-flow continuous culture system

	Essential oil blend (mg/ L)			
Fermentation parameter	0	250	500	SEM
DM disappearance	0.585	0.556	0.480	0.018
OM disappearance	0.581[a]	0.552[a]	0.476[b]	0.017
CP disappearance	0.427	0.348	0.255	0.033
NH_3-N (mg/dl)	12.6	10.5	13.5	0.720
LPep[1] N (mg/dl)	11.1	14.5	14.1	1.41
SPep+AA[2] N (mg/dl)	3.95	2.26	4.53	0.460

Within each row, values not sharing the same superscript vary ($P<0.05$); [1]LPep N= large peptides N; [2] SPep N= small peptides plus amino acid N

Conclusion results of the present study showned that EO blend used in this study over the long term did not have a significant effect on ruminal nitrogen metabolism and DM disappearance. Further investigation is required into the effects of this EO blend on VFA concentrations and ruminal methane emissions.

Acknowledgements The authors gratefully acknowledge funding from university of Kurdistan**.**

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Prophylactic liniment mint oil cream treatment reduces cows' somatic cell counts in on-farm trials

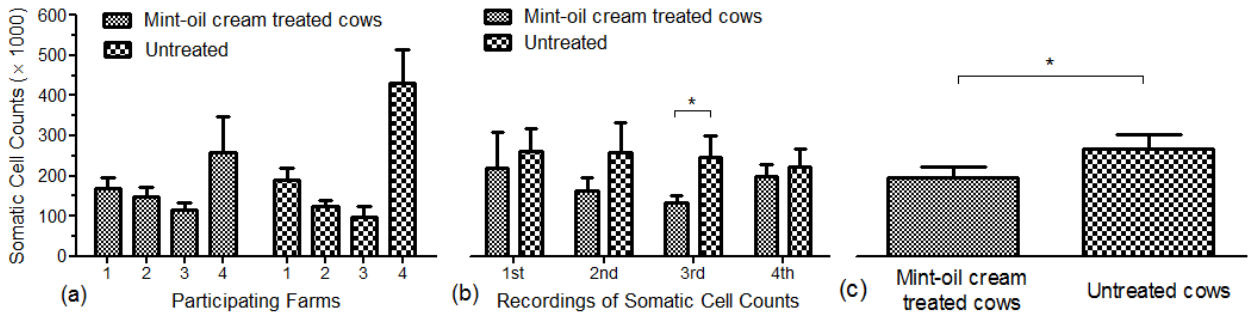
K Zaralis[1], W Waterfield[2], S Padel[1]
[1]The Organic Research Centre, Newbury, Berkshire, UK, [2]The Farm Consultancy Group, Andover, Hampshire, UK
Email:kostas.z@organicresearchcentre.com

Implications To reduce the use of antibiotics in organic livestock production, the EU-Regulation (EC/834/2007) postulates that "homeopathic and phytotherapeutic remedies shall be used in preference, provided that their therapeutic effect is effective for the species of animal and the condition for which the treatment is intended". This study presents data from on-farm trials on the effectiveness of a liniment mint oil cream in reducing somatic cells counts in organic dairy cows.

Introduction In the UK, treatment of mastitis incidences in organic dairy farms relies largely on antibiotic use (Haskell *et al*., 2009). To mitigate the use of antibiotic treatments for controlling mastitis in dairy cows, several farmers use a specially formulated liniment commercial cream containing 35% mint oil. The cream is designed for massage and absorption into the udder and it is used for softening swollen and inflamed udders as well as being used as an oedema preventative at calving time in organic farms. Somatic cells counts (SCC) in milk increase as a result of an immune response to a mastitis-causing pathogen. Mint oil is known to improve blood flow by dilation of the capillaries and it is likely that application of the mint oil cream can enhance the transportation of white blood cells to the udder and thus, can act as a prophylactic measure to prevent mastitis. Here we present results from a participatory research trial which tested the effect of a commercial liniment cream containing 35% mint oil on SCC, following treatment of the udder.

Material and methods Farmer group meetings were held quarterly during 2013 and 2014 allowing for knowledge transfer about the application of the liniment mint oil cream and communication of potential benefits. To test whether the use of liniment milt oil cream can maintain cows' SCC at optimum levels in practice, six farmers committed to -but only four succeeded in- participating in an on-farm trial during 2014. According to the experimental protocol, every second newly-calved cow was treated for 4 consecutive days with the commercial liniment mint oil cream (treatment UT). The cream was applied in a quantity of 5 ml and the udder was massaged for a minimum of 2 minutes each day before the morning milking. The control group (treatment C) consisted of untreated cows. The SCC of both UT and C cows in each farm were recorded for 4 months through National Milk Records. Data were analysed by means of a two sample t-test assuming unequal variances.

Results The average SSCs over the 4-month recording period in both UT and C cows varied between farms (panel a). The SCCs of the UT cows were systematically lower compared to those of the C cows when farm data were combined for each monthly recording, but the difference was significant (P=0.025) in the third month only (panel b). Statistical analysis performed in combined farm data across the recordings showed that the overall SCCs of the UT cows were significantly lower (P=0.04) compared to those of the untreated control cows (panel c).



Conclusion Liniment mint oil cream treatment could act as a complementary on-farm practice to prevent mastitis incidences as indicated by the cows' SCC, but the mode of action remains to be investigated.

Acknowledgements The study was financially supported by the SOLID Project and the Duchy Originals Future Farming Programme. We are grateful to the six farmers that participated in the trials.

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No effect of gonadotropin releasing hormone agonist on the cardiac function of young sheep

I Sanz[1], A Corda[1], E Barzack[1], O Marron[1], C Watson[1], C Wyse[2], D Hough[2], M Bellingham[2], M McLaughlin[1], A French[1], N Evans[2]
[1]School of Veterinary Science, Glasgow, UK, [2]Institute of Biodiversity, Animal Health and Comparative Medicine, Glasgow, UK
Email:cathy.wyse@glasgow.ac.uk

Implications Chronic peripubertal administration of gonadotropin releasing hormone agonists (GnRHa) had no detectable effect on the cardiometabolic function of sheep in this study, but further studies are required to establish if these agents might exacerbate existing cardiovascular pathology in diseased or aged animals.

Introduction Gonadotropin releasing hormone (GnRH) is a neurohormone released in the hypothalamus primarily considered to be a regulator of reproductive function, but whose non-reproductive functions are increasingly evident (Zhang *et al.,* 2013). Chronic exposure of pituitary gonadotrophs to a GnRH agonist (GnRHa) suppresses androgen secretion and is used in veterinary medicine to manipulate reproductive status and behaviour, and to inhibit benign prostate hyperplasia (Lucas, 2014). Chronic GnRHa treatment is associated with metabolic dysfunction and increased risk of cardiovascular disease in humans (Keating *et al.,* 2010), but it is not known if GnRHa affects cardiac function in animals. The aim of this study was to investigate if chronic peripubertal administration of GnRHa affects the cardiometabolic function of sheep.

Materials and methods Male sheep (mixed breeds) received either GnRHa (goserelin 3.6mg every 28 days) (n = 22) or no treatment (control) (n = 18), from 8 weeks of age. An echocardiographic and electrocardiographic examination of the heart was performed on unsedated, standing animals after 10 months of GnRHa treatment. The six lead ECG traces were digitised, and ImageJ software was used to measure heart rate (R-R interval), Q-T interval, Q-T dispersion and S-T segment depression. Values for the Q-T interval were normalised to the resting heart rate of each animal, and reported in seconds for each lead. Q-T dispersion was measured by subtracting the minimum Q-T interval of all the trace measurements from the maximum QT interval, and normalising to resting heart rate for each individual. Transthoracic echocardiographic examinations were performed using an Esaote ultrasound machine and a 2.5 MHz transducer to generate 2D and M-mode tracings and calculate geometric indices of the cardiac structures. Serum fructosamine was measured to assess glucose homeostasis, and testes size and body weight were measured every two weeks for the duration of the study. Data are presented as mean ± se, and statistical significance was tested using ANOVA and accepted at $p < 0.05$.

Results Chronic peripubertal administration of GnRHa was associated with reduced testes size in the treated compared to control sheep but there was no treatment effect ($p > 0.05$) on any of the cardiometabolic parameters (Table 1).

Table 1 Cardiac Geometry, ECG Derived Measures and Metabolic Parameters after 10 months GnRHa

	Control	GnRHa		Control	GnRHa
EDV/BSA (cm³)	36.95 ± .56	37.36 ± 0.43	LVds (mm)	15.80 ± 0.24	16.73 ± 0.19
ESV/BSA (cm³)	11.10 ± 0.25	11.51 ± 0.15	FS (%)	21.01 ± 0.33	21.12 ± 0.25
EF (%)	38.51 ± 0.55	39.63 ± 0.42	Heart Rate (bpm)	85 ± 4	88 ± 2
A:Ao	0.69 ± 0.01	0.78 ± 0.00	Q-T Interval (s)	0.44 ± 0.01	0.46 ± 0.01
IVSd (mm)	5.57 ± 0.08	5.45 ± 0.05	QT Dispersion (s)	0.07 ± 0.01	0.06 ± 0.00
IVSs (mm)	7.30 ± 0.12	7.08 ± 0.07	Fructosamine (mmol/l)	0.80 ± 0.05	0.86 ± 0.07
LVPWd (mm)	4.86 ± 0.07	4.92 ± 0.05	BW (kg)	55.8 ± 2.1	52.7 ± 1.5
LVPWs (mm)	8.01 ± 0.11	7.86 ± 0.08	Testes length (cm)/BW	0.236 ± 0.006	0.259 ± 0.006
LVdd (mm)	25.78 ± 6.95	26.57 ± 6.72			

Conclusion Chronic administration of GnRHa was associated with reduced testes size but had no effect on the cardiac or metabolic parameters of the healthy young sheep in this study. These findings suggest that GnRH blockade did not directly affect cardiometabolic function, but do not exclude exacerbation of existing cardiac pathology in diseased animals.

Acknowledgements The authors gratefully acknowledge funding from the BBSRC

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The effects of dietary digestible phosphorous, phytase and zinc oxide on the growth performance of weaner pigs

S C Mansbridge[1], A M Mackenzie[1], V Pirgozliev[1], C L Walk[2], M R Bedford[2], I Wellock[3], A H Stewart[1]
[1]Harper Adams University, Shropshire, UK, [2]AB Vista, Marlborough, UK, [3]Primary Diets, Ripon, UK
Email:smansbridge@harper-adams.ac.uk

Implications The inclusion of zinc oxide in weaner pig diets must be used with care as dietary inclusion of 2500 mg/kg in this study reduced daily live weight gain and increased feed conversion ratio in high health status pigs. Super-doses of dietary phytase fed to pigs post-weaning showed benefits on growth performance, but can only be used to full effect in low digestible P diets (2.8 g/kg of diet).

Introduction Phytase is an enzyme specific to phytate (the main storage of phosphorous in plants), and is commonly included in pig diets to improve the digestibility of phytate phosphorous. Recently, super-dosing of dietary phytase enzymes (up to 2500 FTU/kg) has shown improved pig growth rates post-weaning. However, in the presence of zinc oxide (ZnO), interactive effects have been observed with serum calcium and phosphorus, suggesting complex interactions between phosphorous, calcium, phytase and pharmaceutical ZnO (Walk *et al*., 2013; 2014). More information is now needed on how ZnO can best be used in conjunction with dietary phosphorous and phytase. The objectives of this study were to assess the effects of super doses of phytase and pharmaceutical levels of ZnO at low and high dietary digestible phosphorous levels, on the growth performance of newly weaned pigs.

Material and methods Experimental procedures were approved by Harper Adams University Research Ethics Committee and regulated procedures were conducted in compliance with the Animals (Scientific Procedures) Act 1986. A 2x2x2 factorial experiment was conducted on 320 UK commercial type pigs from weaning (~ 26 days of age) to three weeks post weaning. Pigs were housed in pens of five pigs/treatment to give 8 replicate pens/treatment, blocked in two batches. The dietary treatments consisted of two levels of digestible phosphorous (dgP) supplied using dicalcium phosphate (Low = 2.8 g/kg and High = 5.8 g/kg), zero exogenous phytase or 2500 FTU/kg phytase (supplied as a 6-phytase derived from modified *Escherichia coli* and expressed in *Trichoderma reesei* with a declared activity of 5000 FTU/g), and zero or 2500 mg/kg zinc (supplied as ZnO). One phytase unit (FTU) is defined as the amount of enzyme required to release 1 µmol of inorganic P/min from rice bran phytate at pH 5.5 and 37°C. All diets were wheat based (20.6% CP, 8.6% fat, 2.5% fibre and 6.1% ash) and formulated to be isoenergetic (10.5 MJ NE) and isonitrogenous. Performance parameters calculated were daily live weight gain (DLWG), daily feed disappearance (DF) and feed conversion ratio (FCR). Data was analysed by ANOVA in a full factorial design using GenStat 16th edition software.

Results In the first week post weaning, addition of dietary ZnO reduced DF by 19% ($P<0.001$) and DLWG by 17% ($P=0.016$) however, there was an interactive effect of phytase and ZnO on FCR (Table 1). In the second week, phytase improved DLWG by 8% ($P=0.032$) and reduced FCR from 1.17 to 1.10 ($P=0.019$). FCR was also lower in the high dgP group ($P=0.009$) in the third week post weaning and addition of ZnO increased FCR ($P=0.034$) at this time. Over the whole three week period, there was a significant phytase x dgP interaction, whereas exogenous phytase improved DLWG ($P=0.04$) and FCR ($P=0.02$) in the 2.8 dgP diets, there were no effects in the high dgP diets. The addition of dietary ZnO reduced overall DLWG ($P=0.002$) by 7.9% and increased FCR ($P=0.045$) from 1.25 to 1.30, regardless of phytase or dgP level.

Table 1 The effect of dietary phytase (2500 FTU/kg) and ZnO (2500 mg/kg) on weaner pig FCR one week post weaning

	No phytase, no ZnO	No phytase + ZnO	Phytase, no ZnO	Phytase + ZnO	Pooled S.E.D.	P value Phytase X ZnO
FCR	1.49	1.26	1.26	1.39	0.078	0.026

Conclusion The study concludes that the addition of dietary phytase at 2500 FTU/kg is beneficial for newly weaned pigs up to three weeks post weaning, especially in low dgP diets. ZnO fed at 2500 mg/kg for three weeks post-weaning has a detrimental effect on healthy pig performance and thus it should be used with consideration when fed to weaning pigs that are clearly healthy. Weaned pigs responded well to a higher level of dgP however, further research is required into the interactions of phosphorous, phytase and ZnO.

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Growth performance from day 42 post-weaning to slaughter at ~100 kg body weight in pigs divergent for residual feed intake reared at different sites across Europe

S Buzoianu[1], U McCormack[1,2], D Berry[1], G Gardiner[2], E Magowan[3], F Mansoor[3], B Metzler-Zebeli[4], P Varley[5], P Lawlor[1]
[1]Teagasc, Animal and Grassland Research and Innovation Centre, Moorepark, Fermoy, Ireland, [2]School of Science, Waterford, Ireland, [3]Agri-Food and Biosciences Institute, Hillsborough, UK, [4]Department for Farm Animals and Veterinary Public Health, University of Veterinary Medicine, Vienna, Austria, [5]Hermitage Genetics, Kilkenny, Ireland
Email:stefan.buzoianu@teagasc.ie

Implications Residual feed intake (RFI) as a selection parameter for feed efficiency (FE) in pigs requires extensive repeated recording of animal growth, intake and body composition. Similarly, it demands extensive data manipulation, which may not be feasible in commercial pig production. Despite this, RFI could be particularly useful for objectively selecting animals based on FE in multi-site experiments where different genetics, different management practices and different health status may exist. The effect of RFI ranking on other growth parameters was assessed here.

Introduction FCR is traditionally used to measure FE in pigs. However, it is correlated with growth and therefore has limited value in selection. 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), 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. 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 using PROC GLM in SAS (SAS, Cary, NC, USA), as the residuals of 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 × 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 with pooled SEM. Significance was at $P \leq 0.05$.

Results ADG was higher in Vetmeduni than in Moorepark and higher in Moorepark than in AFBI (1254, 1082 and 992 g/d, respectively; SEM = 40.3; $P<0.05$). ADFI was higher in Vetmeduni than in Moorepark and AFBI, with the latter not being different from each other (2770, 2226 and 2222 g/day, respectively; SEM = 92.6; $P<0.05$). FCR was poorer in AFBI than in Moorepark, and FCR in Vetmeduni was not different from the two other sites (2.25, 2.05 and 2.18, respectively; SEM = 0.05; $P<0.05$). Paternal ancestry also had a significant effect on ADG, ADFI, FCR and BW at birth, day 42 post-weaning and at slaughter ($P < 0.05$, data not shown). While the paternal ancestry also affected RFI and RIG, location did not ($P > 0.05$; data not shown), indicating that ranking 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. However, ranking on RFI did not result in three distinct FCR categories ($P>0.05$). Males had higher ADG, better FCR and higher slaughter BW than females ($P < 0.05$).

Table 1 Growth performance of male and female pigs divergent for RFI between day 42 post-weaning and slaughter

	Females			Males			Pooled	Significance	
Parameter	Low	Average	High	Low	Average	High	SEM	RFI rank	Gender
ADG (g/day)	1088	1090	1088	1119	1152	1117	31.4	0.69	0.03
ADFI (g/day)	2271^{b}	2440^{ab}	2542^{a}	2265^{b}	2376^{ab}	2542^{a}	72	<0.01	0.57
FCR (feed:gain)	2.08^{b}	2.23^{a}	2.34^{a}	2.01^{b}	2.05^{b}	2.28^{a}	0.039	<0.01	<0.01
RFI (g)	-149.6^{c}	-16.8^{b}	109.9^{a}	-114.6^{c}	-25.1^{b}	113.2^{a}	26.44	<0.01	0.51
RIG (g)	2321^{a}	199^{b}	-1451^{c}	1744^{a}	441^{a}	-1997^{b}	362	<0.01	0.32
Birth BW (kg)	1.60	1.68	1.55	1.71	1.74	1.66	0.082	0.27	0.09
d 42 post-weaning BW (kg)	32.3	32.8	33.2	34.3	33.5	33.4	1.21	0.98	0.18
Final BW (kg)	97.2	97.8	98.2	100.9	102.1	100.1	1.76	0.88	0.02

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

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Effect of creep feeding and use of a sweet gel post weaning on weaner pig performance

F Mansoor, E Magowan
Agri Food Biosciences Institute, Hillsborough, UK
Email:fawad.mansoor@afbini.gov.uk

Implications The use of a sweet gel increased feed 'disappearance' post weaning but there was no impact on growth rate. Dry matter intake pre weaning from milk is estimated at 220g/day, in this study it took pigs 3 days to regain this level of intake after weaning when being offered feed mixed with gel.

Introduction Weaning is a stressful event for piglets which significantly decreases feed intake and increases susceptibility to enteric diseases because of breakdown of intestinal barrier function (Campbell *et al*., 2013). Creep feeding is one common practise which helps pigs adjust to a solid, less digestible diet post weaning. Other supplements to help pigs overcome weaning include 'hydrates' rich in vitamins and minerals offered in a sweet gel form. 'Fresta gel' is such a product that has been found to improve the growth rate of piglets (EFSA, 2011). The aim of this study was to assess the effectiveness of creep feeding in combination with offering a 'sweet gel' post weaning on the feed intake and performance of weaned pigs.

Material and methods A total of 112 litters pre weaning and 960 pigs ((Lr x LW) x PIC337) post weaning were used across eight replicates over eight time periods. Treatments were based on a 2 x 6 factorial design. Pre weaning treatments included creep or no creep feed offered for 10 days pre weaning. Six treatments were then imposed post weaning (day 0). In all treatments feed was offered *ad libitum* from a dry multi space hopper but treatments differed through the offering of the sweet gel (Fresta gel) or not and with the sweet gel containing increasing amounts of feed mixed through it. The gel was offered for 5 days post weaning in a separate hopper. Therefore treatments were: T1- No gel (control), T2 - 100g of gel per day per pig, T3, T4, T5 and T6 – 100g of gel per day per pig mixed with 50, 100, 150 or 200g of feed respectively. 300g of gel was offered as a once only to all the gel treatments, immediately after weaning and thereafter the 100g/day/pig of gel was offered over three periods daily (i.e. 33g/pig in the morning, before lunch and in the afternoon). Creep feed pre weaning, daily water and feed intake from day 1 to 14 post weaning, daily gel intake for 5 days post weaning and feed intake between weaning and 7 weeks of age was recorded. Additionally, weights on days -10, 0 and 21 were recorded. Pig performance data was analysed using ANOVA in Genstat version 10.

Results There was no significant interaction between creep feeding and the use of gel on the feed intake of pigs. There was no significant ($P>0.05$) effect of creep feeding on weaning weight (9 ± 0.11kg), weight of pigs at 7 weeks of age (17 ± 0.19kg), the average daily feed intake (ADFI) (446 ± 6.6g/day), average daily gain (ADG) (407 ± 8.2g/day) or feed conversion ratio (FCR) (1.10 ± 0.01) between weaning and 7 weeks of age. ADFI was significantly higher on day 1, 3 and 4 post weaning when gel was offered (Table 1) but intake did not increase with increasing inclusion of feed mixed with gel. There was no effect ($P>0.05$) of gel inclusion on the overall feed intake between weaning and 7 weeks of age (Table 1). There was an interaction seen ($P<0.05$) between creep feeding pre weaning and gel usage post weaning on ADG between 4 and 6 weeks of age where gel mixed with 150g of feed increased ADG of pigs offered no creep pre weaning (355g/day) but had no effect on ADG of pigs offered creep pre weaning (316g/day).

Table 1 Effect of feed mixed with gel on daily feed intake immediately after weaning.

	Time Point	No Gel	Gel only	Gel + 50g/pig	Gel + 100g/pig	Gel + 150g/pig	Gel + 200g/pig	SEM	F.Pr
ADFI (g/pig)	**Day 1**	18	78	68	66	76.0	79.0	12.1	0.005
	Day 2	84	147	145	131	149	153	19.7	0.144
	Day 3	126	209	234	196	240	236	24.6	0.015
	Day 4	175	259	260	232	272	241	21.8	0.037
	Day 1-21	436	440	443	439	459	461	11.4	0.481

Conclusion Overall, although the use of a sweet gel increased feed intake in the days after weaning, there was no effect of either creep feeding pre weaning or the use of the gel on the 7 week weight or post weaning growth performance of pigs. The intake of pigs 48hrs after weaning was low and when feed was mixed with gel it took 3 days for intake to increase to a level comparable with that which would have been consumed from milk in the days before weaning i.e. approximately 220 g DM/day observed in AFBI pig herd in the past.

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The potential of co-products to reduce the environmental impact of pig systems

S G Mackenzie[1], N Ferguson[2], I Leinonen[1], I Kyriazakis[1]
[1]Newcastle Unviersity, Newcastle Upon Tyne, UK, [2]Nutreco Canada, Guelph, Ontario, Canada
Email:s.g.mackenzie@ncl.ac.uk

Implications Increased inclusions of co products, such as bakery meal and wheat shorts in pig diets can reduce the Global Warming Potential and Non-Renewable Resource Use of pig systems.

Introduction Previous Life Cycle Assessment (LCA) studies have shown that feed production causes the majority of Global Warming Potential (GWP) and Non-Renewable Resource Use (NRRU) (Mackenzie *et al*, 2014) resulting from pig systems. The level of Acidification Potential (AP) caused by pig systems is sensitive to the efficiency of nutrient supply in the diets to meet pig requirements. The aim of this study was to investigate the effect that including alternative feed ingredients (co products) in Grower/Finisher (G/F) diets can have on the GWP, AP and NRRU of Canadian pig systems.

Material and methods The diets were tested using an LCA model for pig systems in Canada (Mackenzie *et al*, 2014) which calculated the GWP, AP and NRRU of the system per kg of carcass weight. The land use change methodology followed PAS 2050 guidelines (BSI, 2011). All diets were formulated on a least cost basis using Canadian price data for 2013 and the Stein Monogastric Nutrition Laboratory nutritional matrix (2014). All diets (except the Least Cost across the G/F phase (LCGF) diet) had nutritional specifications designed for optimum feed efficiency following expert advice from industry and had four feeding phases. The control (C) diet was based on corn, soymeal, canola meal, a fat blend, limestone, amino acids, minerals and additives. 4 diets were formulated for a maximum inclusion of meat meal (MM) (5 - 7.5%), bakery meal (BM) (7.5-10%), corn DDGS (DDGS) (20-30%) and wheat shorts (WS) (20-40%) in G/F diets. Results were generated using 1000 Monte-Carlo (MC) simulations; each diet was compared to the control using parallel simulations accounting for shared uncertainty. Two further diets were formulated; one at least cost for optimum feed efficiency (FE) with BM (8.22%) and WS (2.49%) and one for least cost across the G/F phase (LCGF) accounting for compensatory feed intake with BM (8.69%) and WS (18.9%). Parallel MC simulations were used to compare the environmental impacts of the system using these two diets.

Results The BM diet produced small reductions ($P < 0.001$) in the environmental impact of the system for all categories tested (table 1). The MM diet reduced NRRU ($P < 0.001$), did not significantly affect GWP and increased AP ($P < 0.001$). DDGS caused a small reduction in AP ($P = 0.01$), but increased GWP and NRRU ($P < 0.001$). The WS diet caused the largest reductions in GWP and NRRU ($P < 0.001$) and did not significantly affect AP. The LCGF diet had lower NRRU than the FE diet but increased AP caused by the system ($P < 0.001$), GWP was not significantly different between the scenarios.

Table 1 The environmental impacts of 1 kg expected carcass weight in Canadian pig systems using different G/F diets.

	GWP (kg CO_2 e)			AP (g SO_2 e)			NRRU (g Sb e)		
	Mean	s.d.	%<C[1]	Mean	s.d.	%<C[1]	Mean	s.d.	%<C[1]
C	2.20	0.19	N/A	57.4	4.2	N/A	6.52	0.90	N/A
MM	2.16	0.20	81	61.6	5.0	0	5.95	0.82	100
BM	2.13	0.18	100	56.7	4.1	100	6.30	1.04	100
DDGS	2.58	0.21	0	57.1	4.0	99	10.3	1.8	0
WS	1.97	0.18	100	57.6	4.2	29	5.34	1.16	100
	Mean	SD	%< FE[1]	Mean	SD	%< FE[1]	Mean	SD	%< FE[1]
FE	2.16	0.19	N/A	56.1	4.3	N/A	6.42	0.91	N/A
LCGF	2.12	0.19	88	58.4	4.3	0	5.84	0.97	100

[1] %<C= Percentage of results which were smaller than the control diet, %<FE = Percentage of results which were smaller than the least cost diet for optimum feed efficiency

Conclusion It is possible to reduce the environmental impact of Canadian pig systems through the increased inclusion of co products. Increased WS and BM inclusions reduced the environmental impact of the system with no increase in any of the impact categories tested. The increased inclusion of co-products in the LCGF diet had a mixed effect on the environmental impacts in comparison to the FE diet reducing NRRU but increasing AP resulting from the system.

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The variation in finishing pig feed conversion efficiency between and within herds

E Magowan[1], V Beattie[2], S Smyth[3], K McCracken[2], G Donaldson[3], F Gordon[3], M Hawe[4]
[1]AFBI, Hillsborough, UK, [2]Devenish Nutrition Ltd, Belfast, UK, [3]John Thompson and Sons Ltd, Belfast, UK, [4]CAFRE, N. Ireland, UK
Email:elizabeth.magowan@afbini.gov.uk

Implications Variation in feed use efficiency between contract finishing units in Northern Ireland can equate to differences of £34,000 per annum in profitability (based on 5200 finishing places).

Introduction The efficient use of feed on pig farms is a key driver of profitability since feed represents at least 75% of production costs. With the increased use of contract finishing units in recent times the ability to accurately calculate finishing pig feed use efficiency (FCR) has now become possible. As such this study aimed to quantify the magnitude of FCR variation that exists between and within finishing pig units in Northern Ireland.

Material and methods Five producers were recruited who finished pigs across a range of different contract finish units. As such pigs originated from five sources where genetics and rearing system to approximately 30 kg were similar. These 5 sources finished pigs across a total of 17 finishing units and data was collected from a total of 79 batches of pigs reared through these units over an 18 month period during 2012 and 2013. The majority (85%) of units used single space wet and dry feeders, 10% used 'dry' feeders and the remaining 5% used liquid feed. With regard to terminal sire genetics, 25% of units represented Duroc (Danbred), 25% PIC 337, 15% Maxgro (Hermitage) and the remainder Landrace. Health status was considered good (mean mortality across all batches of 1.8%). It was not possible to obtain the digestible energy content of the diet but the crude protein of diets ranged from 19 to 16% and total lysine ranged from 1.2 to 0.9 (some units used phase feeding). Feed intake per house was measured by the amount of tonnage delivered per batch and an estimation of feed left in bins was made when pigs were removed. For the vast majority of batches pigs entered on the same day but at the end of the finishing period only a few units were cleared on the one day and the majority of pigs were sent for slaughter over a period of 4-6 weeks. The total weight of pigs removed at any given time point was recorded. The date and approximate weight of pigs that died was recorded. Simple statistics was performed on the data to calculate the mean, standard deviation (SD) and coefficient of variation (CoV) of the data. Using the batch data, a multi variate regression analysis was conducted to establish the relationship between average daily gain (ADG) and average daily feed intake (ADFI) with FCR.

Results The profile of data for start and slaughter weight, FCR, ADG and ADFI on a per batch basis is provided in Table 1. The CoV for FCR between batches within each unit ranged from 1.45 to 11.4% (with a mean of 4.98%) indicating that some units could achieve a consistent FCR whereas on others FCR was sporadic between batches. On a per unit basis FCR ranged from 2.48 to 2.85 with an SD of 0.095 and CoV of 3.57%. On a per source (producer) basis FCR ranged from 2.59 to 2.71 with an SD of 0.051 and CoV of 1.93%. Economically, assuming a diet cost of £250 per tonne, a weight gain of 70 kg and a kill out percentage of 78%, it cost 1.25 p/kg gain, 1.64 p/kg carcass weight or £4.55 per tonne of feed for every 0.05 unit shift in FCR. On a unit basis, if the SD of FCR is applied to the mean FCR, then 95% (Average + / - 2 SD's) of the FCR values fell between 2.47 and 2.85 which represents a 0.38 unit range in FCR. This would equate to approximately £35 per tonne of feed, 12p/kg dead weight or at least £34,000 in profitability (Assuming 5200 pigs finished per year). The 'average' average daily gain across all batches was 869 g/day and the 'average' average daily feed intake across all batches was 2304 g/day. 67.5% of batches of pigs with a below average FCR (2.66 or under) also had an above average ADG (869 g/day or over) and 62.5% of these batches had a below average ADFI (2304 g/day or under). Only 26% of batches with above average FCR had both above average ADG and below average ADFI. For batches with an FCR above the average (2.66 or higher), 53.3% of these had a below average ADG and 62.2% had an above average ADFI.

Table 1 Simple statistics on the FCR data across the 79 batches of finishing pigs

	Av pig live wt in (kgs)	Av Livewt sold (kgs)	FCR	ADG (g/pig)	ADFI (g/pig)
Min	24.8	96.9	2.24	704	2252
Max	52.8	120.0	3.08	1142	3079
Mean	38.9	111.8	2.66	870	2314
SD	5.68	5.22	0.16	95.9	268
% CV	14.6	4.67	5.99	9.6	10.1

Conclusion As expected the variation in FCR between sources (producers) is lower than between units which is lower than between batches. A 0.64 unit range in FCR can exist between batches of pigs across contract finishing units in NI. A 0.38 unit range in average FCR exists between contract finishing units which equates to a significant difference in profitability (£34,000 per annum based on 5200 finishing pigs). Within this dataset some herds had superior FCR due to superior growth rates whilst others had superior FCR due to reductions in ADFI and only 26% had above average FCR due to both ADG and ADFI being optimised.

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Pig and carcass performance when feed is offered in dry or liquid form

E Magowan, V Beattie
[1]AFBI, Hillsborough, UK, [2]Devenish Nutrition Ltd, Belfast, UK
Email:elizabeth.magowan@afbini.gov.uk

Implications The finish weight and feed intake of finishing pigs was found to increase when feed was offered in liquid form compared with when it was offered in dry form. However the carcass performance (carcass FCR) of pigs offered dry feed was significantly better (by 8%) than that of pigs offered liquid feed.

Introduction Liquid feeding systems are commonly used across Europe and Ireland, especially for finishing pigs. A key advantage of liquid feeding systems is the ability to incorporate liquid by products, especially from the cheese making industry. However, liquid feeding systems require significant investment and there is debate about the efficient use of feed in these systems. Furthermore, liquid feeding systems commonly use meal which has been found to have a lower digestibility of dry matter and energy than when the diet is in pellet form, hence reducing feed use efficiency. Overall, information on the performance and economics of rearing modern pigs using a liquid feeding system compared with offering pigs dry pelleted feed is unknown.

Material and methods Over two time periods a total of 360 pigs were penned in groups of 15 which were balanced for weight. Treatments were balanced for gender across the pens within each time period but each pen had at least 7 of each gender. The commercial facilities used contained liquid feeding equipment (Datamix multifeeder 5000, ad lib probe feeding**).** As such liquid feeding troughs were shared between two pens, therefore one trough offered feed to 30 pigs. One, single space wet and dry feeder was placed in alternate pens. Dry feed was dispensed when pigs pushed a paddle in these feeders and the trough also contained a water nipple where pigs could drink from. The pens using 'dry feed' were interspersed randomly among the pens using liquid feeding to eliminate any effects of position in the room. Overall a total of 16 pens of pigs (16 replicates) were offered dry pelleted feed through the single space wet and dry feeder and a total of 16 pens (8 replicates) were offered feed using the liquid feeding system. The feed was a commercial mix which contained, in decreasing order of inclusion: maize, barley, soyabean meal, wheat, wheat feed, rapeseed meal, calcium carbonate, vegetable oil blend, sodium chloride, mono DCP, minerals and vitamins. The diet had a digestible energy content of 13.8 MJ/kg, crude protein of 18.5%, crude fibre of 3.5% and total lysine content of 1.1%. The diet was prepared in meal and pellet form. The pellet form was offered as dry feed, *ad libitium* through the single space feeders and the meal form was mixed with water in a 3:1 meal to water ratio and offered *ad libitum*. Feed was collected at least twice per pen to determine the dry matter of the liquid feed. Pig weight was recorded on a pen basis at the start of the trial but individual pig weight was recorded as pigs were sent for slaughter. Individual carcass data (carcass weight and back fat depth at P_2) was also attained. The data was analysed using pen means for all performance parameters except finish weight which used individual pig data. ANOVA for unbalanced designs (REML) was used where replicate was included as a blocking factor. To calculate carcass gain and feed conversion efficiency a kill out percentage of 75% was assumed for start weight.

Results Pigs were on average 46kg at the start of the trial. The average dry matter of the liquid feed was 234g/kg. Pigs offered liquid feed had a significantly higher finish weight ($P<0.01$) and average daily feed intake ($P<0.05$) than pigs offered dry feed (Table 1). However the kill out percentage of pigs offered dry feed was significantly higher than that of pigs offered liquid feed and as a result the carcass feed conversion ratio (carcass FCR) of pigs offered dry feed was significantly improved ($P<0.001$) compared with that of liquid fed pigs (Table 1).

Table 1 Pig and carcass performance when offering pigs feed in dry or liquid form.

	Finish wt (kg)	ADG (g/day)	ADFI (g/day)	FCR	Back fat depth (mm)	Cold wt (kg)	Kill Out%	Carcass FCR
Liquid feed	110	924	2559	2.77	11.6	86.4	78	3.53
Dry feed	107	887	2346	2.65	11.7	87.3	79.9	3.23
SED	0.913	22.9	79.6	0.077	0.46	0.389	-0.8	0.084
P Value	0.004	0.116	0.014	0.115	NS	NS	0.024	<0.001

Conclusion Using only live pig performance it could be concluded that there was little difference in pig performance when feed was offered in dry or liquid form. However when examining the carcass data it is clear that pigs offered dry feed had a better kill out percentage which would suggest that pigs offered liquid feed had a heavier gut, perhaps driven by the higher feed intake. Overall when pigs were offered dry feed, carcass feed use efficiency was improved by 8% compared with when pigs were offered liquid feed.

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The effect of phytase on grower pig growth performance and bone ash

S Laird[1], I Kühn[2], P Wilcock[2], H.M Miller[1]
[1]University of Leeds, UK, [2]AB Vista, Marlborough, UK
Email:bs09sl@leeds.ac.uk

Implications The outcomes of this study show that supplementing pig diets with phytase at higher than typically recommended rates further improves the bone mineralisation of grower pigs.

Introduction Microbial phytases are routinely added to pig diets at a standard dose of 500 FTU/kg to improve the P availability in grain based diets and minimise P excretion. However, recent work in both pigs and poultry has shown that higher doses of phytase can further improve growth performance, nutrient digestibility and bone mineralisation. These effects are associated with greater degradation of phytate and generation of *myo*-inositol (Walk *et al*. 2014). Taking these performance benefits into consideration alongside the escalating costs of feed ingredients and the declining cost of phytase enzymes, it may be that higher inclusion rates of phytase in pig diets are warranted. At present, available literature on the effects of high doses of phytase in the grower-finisher pig is scarce. The objective of this study was to determine the effect of a conventional and a high phytase dose on grower pig growth performance and bone ash. It was hypothesised that a superior growth performance and a higher bone ash would be observed in pigs receiving the high phytase diet.

Material and methods Five hundred and seventy-six crossbred pigs [(Large white x Landrace) x Maxgro]; mean initial BW $\pm$ SE = 17.3 $\pm$ 0.2 kg, were used in this 28 day feeding experiment. Treatments were replicated 16 times with each replicate pen consisting of 9 mixed sex pigs, balanced for BW, sex and litter. Within replicate, pens were randomly assigned to one of four wheat-barley based dietary treatments which included: Positive control (**PC**); P at 0.5 g/kg above the BSAS recommendation; Negative control (**NC**); with Ca and dig-P 1.6 g/kg and 1.24 g/kg below the recommended levels respectively; NC + 500 FTU/kg (**500**); and NC + 2,000 FTU/kg (**2000**). All treatments were offered *ad libitum*. Pigs and feed refusals were weighed every 14 days for the determination of ADG, ADFI and FCR. At the end of the experiment 32 pigs (8 per treatment) were euthanised for the collection of the M3 metatarsal. All data were analysed using the GLM procedure of SPSS (version 20) with the pen and the individual pig serving as the experimental units for the growth and bone data respectively.

Results Pigs fed the NC diet had a 3.8% (P<0.01) lower ADG and a 3.9% (P<0.01) lower ADFI than pigs fed the PC diet. Adding phytase to the NC diet at either level resulted in the lost growth performance restored back to the level of the PC. Supplementing the NC diet with 2000 FTU/kg increased M3 bone ash percentage from 35.64% to 37.92% (P<0.01). This level of bone ash is similar to that of the PC and significantly higher than the 500 diet. Phytase supplementation increased bone P concentration (P<0.01) when provided at 2000 FTU/kg.

Table 1 Effect of phytase supplementation on grower pig growth performance and M3 bone ash

	Treatment					
Item	PC	NC	500	2000	SEM	*P*-value
End weight, kg	42.94 [a]	41.94[b]	42.58[a]	42.79[a]	0.20	<0.01
ADG, kg	0.914[a]	0.879[b]	0.902[a]	0.905[a]	0.007	<0.01
ADFI, kg	1.390[a]	1.336[b]	1.383[a]	1.382[a]	0.013	<0.05
FCR	1.521	1.519	1.533	1.527	0.013	NS
Bone ash, %	37.88[a]	35.64[b]	35.99[b]	37.92[a]	0.45	<0.01
Bone ash weight, g	3.38[a]	2.98[b]	3.28[ab]	3.31[ab]	0.100	<0.05
Bone P, %	6.79[ab]	6.43[b]	6.54[ab]	6.92[a]	0.096	<0.01

Conclusion In the present study supplementing the diet with 2000 FTU/kg delivered no additional benefit over 500 FTU/kg in terms of growth performance. The P requirement for maximal bone mineralisation is believed to be 0.1% higher than it is for maximal growth in the pig (Hastad *et al*., 2004). Pigs fed the PC or 2000 diet had a higher bone ash percentage than those fed the 500 diet. However, pigs fed the 500 diet performed similarly to those fed the PC or 2000 diets with regards to growth. These data suggest that the P requirement for optimal growth has been met in pigs fed the PC, 500 or 2000 diets, and the extra available P in the PC or 2000 diets has been used for bone mineral accrual rather than growth.

Acknowledgements The authors would like to express their appreciation to AB Vista for their financial support.

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Does grouping pigs according to sex at weaning improve early post-weaning performance?

A E Taylor, H M Miller
University of Leeds, Leeds, UK
Email:a.e.taylor@leeds.ac.uk

Implications Grouping pigs according to sex does not improve early post-weaning performance.

Introduction Mixing pigs at weaning is common practice in commercial farming due to the need to house pigs in the most efficient and cost effective way, however mixing pigs poses a challenge to both welfare and production as it leads to agonistic behaviour and fighting aimed at establishing a social hierarchy within a group. Fighting results in the accumulation of injuries, most notably skin lesions, which provide routes for subsequent infection. Fighting also results in an increase in energy expenditure which may amplify the negative effects already associated with weaning (Hoetzel *et al*., 2011), such as decreased feed intake and poor growth rates (Weary *et al*., 1999). Grouping piglets by sex at weaning may help to negate some of these problems as the presence of female pigs at weaning has been shown to increase aggressive behaviour in male pigs (Colson *et al*., 2006). The aim of this experiment was to determine the effects of grouping pigs at weaning according to sex on early post-weaning performance and the accumulation of skin lesions.

Materials and methods A total of 198 pigs ((Large White x Landrace) x MAXGRO) were weaned onto trial at 28 days of age and remained on trial for 20 days. The numbers of skin lesions on individual pigs were counted on the day of weaning (day 0), before entering the weaner accommodation. The pigs were restrained by hand and the total number of lesions on the forepart and the hind part of the body were counted. A lesion was categorised by a scratch to the skin measuring more than 1 cm in length. Each pig was then given a lesion score from 0-3 depending on number of lesions (0= no lesions, 3= ≥10 skin lesions or ≥5 deep lesions (Parratt *et al*., 2006)). Pigs were allocated to one of three treatments; 1) a pen composed of all females (F), 2) a pen composed of all entire males (M) and 3) a pen composed of 50 % females and 50 % entire males (FM). Pigs were assigned to 21 pens with 8 or 10 pigs per pen (7 replicates) based on weight and allocated so that each pen within replicate had the same number of unfamiliar pigs per pen. Pigs had *ad libitum* access to a standard weaner diet throughout the trial. Individual lesion scores were counted again 24 hours after weaning (day 1) and 7 days after weaning. All pigs were individually weighed at the start of the experiment (weaning) and then weighed at 7 and 20 days. Feed intake was determined for the first 24 hours and then at 7 and 20 days. The average skin lesion score data were analysed by analysis of variance specific for Repeated Measures (SPSS version 22). The performance data were analysed using analysis of variance (ANOVA) (SPSS version 22). The pen mean was the experimental unit for performance data.

Table 1 Effect of grouping pigs according to sex at weaning on growth performance.

	F	M	FM	SE	P-Value
Wean Wt, kg	7.6	7.5	7.5	0.460	0.993
7 d Wt, kg	8.4	8.5	8.4	0.171	0.897
20 d Wt, kg	14.0	13.9	13.9	0.339	0.988
24 h ADI, kg	0.019	0.018	0.015	0.003	0.728
7 d ADI, kg	0.198	0.194	0.184	0.010	0.604
20 d ADI, kg	0.330	0.334	0.327	0.013	0.938
7 d ADG, kg	0.119	0.129	0.123	0.024	0.957
20dADG, kg	0.311	0.319	0.321	0.016	0.905
7 d FCR	1.56	1.47	1.50	0.359	0.937
20 d FCR	1.06	1.06	1.03	0.048	0.878

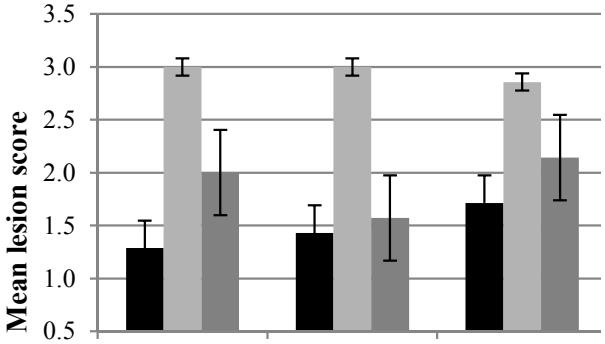

Figure 1 Mean total body lesion scores at Day 0, 1 and 7 days post weaning

Results Growth performance of the pigs during the immediate post-weaning period was not affected by grouping pigs according to sex (Table 1). There was also no difference in lesion scores at any time point between treatments (P>0.05). As expected lesion scores for the forepart and total body were greatest 24 hours post weaning (P<0.001; P<0.001). The hind part lesion score tended to be higher 24 hours post weaning (P=0.056).

Conclusions Grouping piglets according to sex at weaning did not affect piglet performance during the post-weaning period and did not reduced the aggressive behaviour observed in pigs following mixing at weaning.

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Factors affecting sow udder morphology

A Balzani[1], E Sutcliffe[2], H J Cordell[1], S A Edwards[1]
[1]Newcastle University, Newcastle Upon Tyne, UK, [2]ACMC, Beeford Driffield, UK
Email:a.balzani@ncl.ac.uk

Implications Since udder conformation in sows can influence latency to first suckling and thus neonatal mortality, understanding the causes of variation in morphology might allow the selection of sows with better nursing capacity and increase the number and weight of weaned piglets.

Introduction The sow's udder plays a very important role in piglet survival, as colostrum and milk are the main source of both energy and passive immunity for piglets and are therefore essential for their growth and health. Studies on the sow udder have previously focussed mainly on number of functional teats and mammary gland development in terms of milk production (Kim *et al*., 2000; Farmer and Sorensen, 2002). Despite its importance there are, to our knowledge, no studies about the external morphology of the udder and the characteristics which promote good piglet performance. Therefore, the aim of this experiment was to apply a standardised method to describe sow udder conformation (Balzani *et al*., 2014) to a large population of sows of two different breed types to investigate the sources of variation.

Material and methods The udder conformation of 220 sows (110 Large White X Landrace (LWL) and 110 Meidam (MDM)) of different parities was assessed by a combination of scores and metric measurements made on one row of teats shortly prior to farrowing when the sow was in a lying posture. For each teat 5 measures were taken: inter-teat distance within the same row (SAMER); distance from the base of the teats in the upper row to the abdominal mid-line (AML); length (LEN) from the tip to the base and diameter (DIA) at the tip of the teat. Scores were used to describe teat orientation (1 downward; 2 perpendicular to the gland, 3\4 towards the cranial\caudal direction; and 5 upward), and teat functionality (1 perfectly functional, 2 reduced availability of colostrum, 3 milk channel not working, including teats which were blind, inverted, or very damaged). Data were analysed using a general linear model with breed type, parity and teat position and their interactions as factors and sow as a random effect for continuous variables, and chi-square tests for ordinal data.

Results Breed differences are shown in Table 1. Teat characteristics were related to position on the udder according to three sectors (MDM in brackets had greater teat number): pairs 1-2 anterior, 3-5(6) middle and 6(7)-7(9) posterior in both breeds. Teat position had a significant (P<.001) effect on SAMER in both breeds, with less distance between middle teat pairs. AML was shorter in the rear teats than in the front and middle teats pair in LWL (48.8 v 98.2, 60.1, sem 0.75 P<.001). AML in MDM breed was significantly different between each teat pair (P<.001). LWL teat LEN was greater in the anterior and middle teats than in the posterior ones (18.3 v 15.0, sem 0.13 mm, P<.001), whereas MDM teat LEN was shorter in the front and rear teats than in middle teats pair (16.0 v 16.5, 0.15 mm, P<.001). DIA was greater in the middle teats in LWL but not in MDM (LWL: 10.6, 0.07mm; MDM: 9.7, sem 0.22 mm, P<.001). First parity (LWL) and also second parity (MDM) sows had smaller teats (P<.001) than multiparous sows. 70% of LWL and 90% of MDM teats were orientated perpendicular to the udder; there was a significant association between the teat orientation and teat position (χ^2 = 16.96, p <.05); the proportion of teats not perpendicular was higher in the anterior part (LWL 19% v 11%; MDM 16% v 2%).

Table 1 Mean and standard error of udder traits for LWL and MDM breed.

Udder Trait	LWL		MDM		P-value
	Mean(mm)	sd (mm)	Mean(mm)	sd (mm)	
LEN	17.9	3.9	16.0	4.5	0.0001
DIA	10.7	2.0	10.5	2.4	0.38
AML	78.0	23.7	71.3	21.8	0.0001
SAMER	108.1	24.8	107.5	26.6	0.86

Conclusion Udder morphology showed differences related to teat pair position, breed type and parity. LWL had anterior and posterior teats of similar type, with smaller teats and less distance between rows that in the mid section. MDM mid teats were closer to the abdominal mid-line than in LWL. Further studies are necessary to define how these udder conformation traits influence piglet suckling behaviour, survival and performance, and whether these traits are heritable and correlated with other important production traits such as prolificacy and milk production.

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Effects of short-term (7 day) treatment with growth promoters on livers of growing gilts

S Al-Doski, D Brown, M Mareko, K Ryan, J Brameld, T Parr
University of Nottingham, UK
Email:sbxsi@nottingham.ac.uk

Implications Changes in tissue weights associated with growth promoters can be caused by altered deposition of glycogen rather than protein.

Introduction Growth promoters such as beta-adrenergic agonists (BA) and Growth Hormone (GH) increase growth by partitioning nutrients into lean tissue and increasing nutrient utilisation efficiency to varying degrees. The research seeks to determine the relationships between muscle and liver, particularly the role of the liver, as it is central to the metabolism of the nutrients being utilised for lean growth and thereby has an important role in nutrient partitioning. The objective of this study was to investigate the effects of GH and BA on pig livers, particularly protein and glycogen metabolism.

Material and methods Forty five (45) Large White x Landrace gilts (PIC Ltd, UK) weighing 85(±5) kg were adapted to the feed and environment for 5 days, before being distributed to one of three treatment groups. The control group (n=15) were fed *ad-libitum* a standard commercial diet with high energy and high protein content, the β-adrenergic agonist group (BA, n=15) were also fed *ad-libitum* the same diet, but containing Ractopamine^{TM} (at 10mg/kg) and the growth hormone group (GH, n=15) were fed the same commercial diet *ad-libitum* and administered Reporcin^{TM} (10mg) by intramuscular injection on days 0, 2, 4 and 6. After slaughter on day 7, liver weights were recorded and samples of *Longissimus Dorsi* (LD) muscle and liver were collected and snap frozen in liquid nitrogen. Glycogen content was determined as described previously (Dreiling *et al.* 1987), protein was determined by Lowry assay (Lowry *et al*., 1951) and DNA content was determined using a modified fluorescence assay (Rago *et al*. 1990). Data were analysed by one way ANOVA (Genstat), followed by a *Post Hoc* Dunnett's test. Significance was accepted at $P<0.05$.

Results There was no effect of treatment on carcass weight. GH treatment for 7 days significantly increased ($P<0.001$) liver weights, compared to control groups (Table 1). GH significantly decreased ($P=0.007$) liver DNA content per unit tissue weight (mg/g liver), but had no effect on total DNA in the whole liver. Both GH and BA increased ($P<0.001$) glycogen content per unit DNA (mg/gDNA) and glycogen content per unit tissue weight (mg/g liver) compared to controls (Table 1), but only GH significantly increased ($P<0.001$) total liver glycogen. In contrast, LD muscle glycogen (mg/g muscle) was significantly decreased ($P<0.05$) with BA treatment, but there was no effect of GH. There was no significant effect of treatment on liver protein content.

Table 1 Effects of 7 days treatment with GH or BA on carcass, liver and muscle characteristics of gilts

Measurement	Control (n=15)	BA (n=15)	GH (n=15)	SED[1]	P-value
Carcass weight (Kg)	74.96	75.62	73.59	1.93	0.567
Liver weight (Kg)	1.573	1.551	1.859	0.0696	<0.001
DNA (mg/g liver)	33.2	31.57	26.82	1.913	0.007
Total DNA in whole liver (g)	53.05	48.33	50.31	4.542	0.561
Glycogen (mg/g DNA)	1.013	1.294	1.805	0.1485	<0.001
Total Glycogen in whole liver(g)	52.15	57.95	85.49	4.881	<0.001
Glycogen (mg/g liver)	32.84	38.13	46.31	2.288	<0.001
LD glycogen (mg/g muscle)	6.568	4.779	6.685	0.741	0.015
Protein (mg/g DNA)	3.995	4.122	4.268	0.1402	0.172
Total Protein in whole liver (g)	208.1	197.7	213.4	19.22	0.616
Protein (mg/g liver)	131	129.2	113.9	8.151	0.076

[1] SED = standard error of the differences of the means.

Conclusion GH increased liver weights and this appears to be due to an increase in glycogen, rather than an increase in cell number or protein content.

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Review of scientific knowledge on lactation nutrition of highly prolific modern sows

A Craig[1,2], E Magowan[1,2], A Gordon[2]
[1]Queens University, Belfast, UK, [2]Agri-Food and Bioscience Institute, Northern Ireland, UK
Email:aleslie02@qub.ac.uk

Implications In a review of recently published papers, energy content of the maternal lactation diet tended to have the greatest effect on individual piglet daily liveweight gain compared to protein and lysine content. However, the size of litters reported in the papers identified averaged only 11 piglets which is lower than litter sizes currently on commercial farms, stressing the need for more research into nutrition for sows producing larger litters.

Introduction Genetic selection for prolificacy in pig production has increased sow litter size. Litter size now commonly exceeds 12.5 pigs per litter in Ireland (O'Driscoll and Lawlor, 2014). Piglets reared per litter has increased even more significantly in Europe (BPEX, 2014). As such research emphasis has turned to redefining nutrient requirements for modern, highly prolific sows. A systematic literature review was conducted to identify recent research on the nutritional needs of the modern sow during lactation and to establish nutrient requirements for sows rearing 12 or more piglets.

Material and methods Two searches were performed and amalgamated using the Web of Science. They were 1) 'sow' AND 'lactation' AND 'diet' OR 'nutrition', and 2) sow' AND 'lactation' AND 'birth' OR 'wean* weight'. The data set was refined to references published from January 2008 to July 2014 (392 records) as it was hypothesised these papers would have had the best probability of reporting nutritional effects on piglet performance using high litter sizes. From this data set papers were further refined: removing papers not in English, not discussing pigs, not detailing the performance of piglets (weaning weight or average daily gain (ADG)) or those tested under tropical conditions, outdoor or group farrowing. This resulted in a total of 180 papers going forward for review. Out of the 180 papers, 63 were suitable to conduct a meta-analysis on as they included standard deviation (SD) or standard estimates of the mean (SEM) for performance values. These papers were sorted into groups (Energy, Protein, Fat, Minerals and Vitamins, and Misc.) by the main focus of the research. The digestible energy (MJ/Kg) (DE), crude protein (%) (CP) and total lysine (%) content of all diets used in the papers were also recorded. Three analyses were then carried out: 1) A random effects subgroup meta-analysis was used to compare estimates for piglet ADG from different types of nutrients (e.g. digestible energy, crude protein, vitamins and minerals and fat) to test if these estimates were significantly different from one another. 2) A meta-regression analysis fitted using the REML method was then used to compare the individual effects of DE, CP and lysine contents of the diets. Only papers that quoted all three parameters were used. 3) The meta-regression analysis was run again to compare the combined effects of DE, CP and lysine on piglet ADG. In the latter two tests lactation length and litter size was tested for significance.

Results Of the 63 papers, 6 focused on energy concentration, 3 considered fat vs. starch and 19 looked at fat supplementation. Also, 10 papers focused on protein concentration and 4 on lysine concentration (Table 1). Twenty three papers were classed as miscellaneous and covered topics such as yeast (7 papers), seaweed (3 papers) and plant extracts (5 papers).

Table 1 Overview of Papers Used in Meta-Analysis

	Range Used	No of Papers	Av. Litter Size
Energy	9.2 – 17.4 MJ DE/kg	28	10
Protein	10.4-19.0%	10	9.08
Lysine	1.0 – 1.3%	4	9.38

Results from the random effects subgroup analysis indicated no significant difference ($P>0.05$) between the groups (i.e. digestible energy, crude protein, vitamins and minerals and fat) and the average daily liveweight gain was 233g/day. The meta-regression indicated that DE was significantly correlated ($P = 0.038$: R^2 69.5%; Individual Piglet ADG (g/day) = 127.4 + (6.9 x DE (MJ/kg)) when comparing individual effects of DE, CP ($P = 0.508$) and lysine ($P = 0.335$) on individual piglet ADG. When DE, CP and Lysine were combined within the multi-regression analysis, none were significant ($P = 0.067, 0.234, 0.552$ respectively) and the resultant equation has no effect on the goodness of fit.

Conclusion These results would suggest that the impact of the energy content of the lactation diet on individual piglet ADG during the suckling period is greater than the impact of protein or lysine concentration. Overall this meta-analysis indicates that energy may be the driving force behind milk production. However, as litter sizes reared in these studies were low (average 11) more work needs to be undertaken to validate these results using large litter sizes.

Acknowledgements The Authors gratefully acknowledge funding from the Department of Agriculture and Rural Development in Northern Ireland.

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Measuring metabolic hormones in pig blood using a human bead-based multiplex assay

K May[1], J M Brameld[1], H V Masey O'Neill[2], J Wiseman[1], T Parr[1], S E O'Sullivan[1]
[1]University of Nottingham, UK, [2]Aunir, Towcester, Northhamptonshire, UK
Email:sbxkm2@nottingham.ac.uk

Implications Human multiplex assays can be used for detection of analytes from pig blood samples. Xylanase supplementation (XS) immediately post-weaning may affect pancreas development and satiety signals.

Introduction The aim of this study was to ascertain whether a human metabolic hormone bead-based assay could provide readings from plasma from fed and fasted pigs. As human and pig gut hormone proteins are highly conserved, and most gut hormones change in response to a fed or fasted state; we likely can predict the response of gut hormones in these states. If successful the assay would be used to analyse hormone levels when pigs feed was supplemented with xylanase. Previous studies into the supplementation of xylanase in poultry feed showed increased serum PYY levels (Singh *et al*., 2012).

Material and methods *Experiment1:* 24 male Camb12 pigs weighing 59.5±3.62 kg were assigned to two groups: fasted before slaughter (Fa) and non-fasted (Fe). Access to feed and water was *ad libitum* for one week but before slaughter Fa were fasted for ~18 hours. At slaughter, the pigs were electrically stunned and exsanguinated, with blood samples taken using EDTA coated tubes. These were centrifuged at 3000g for 10min at 4°C, the plasma was then taken off and aliquoted into new tubes and stored at -80°C for further analysis. *Experiment 2:* 32 female Camb12 newly weaned piglets weighing 8.8±1.38 kg were assigned to two diet groups in period 1 (0-2weeks post-weaning; P1), a control diet (Co) and the Co with XS. During period 2 (2-6weeks post-weaning; P2) half the pigs were kept on their original diet whilst the rest were swapped onto the other, resulting in four groups. At the end of P2 the pigs were slaughtered by electrical stunning and exsanguination. Blood samples were collected as before. *Bead-based multiplex assay analysis:* A Human Metabolic Hormone Milliplex HMHMAG-34K kit (Merck Millipore, Billerica, MA, USA) was used to simultaneously assess the concentrations of PYY, PP, Insulin, C-Peptide and GIP in plasma collected from both experiments. The assay was carried out according to the manufacturer's instructions and the internal controls were all within range. The data were analysed by a one-way or two-way ANOVA as appropriate, and significance was accepted at $P<0.05$.

Results Figures 1 and 2 show the concentrations of the metabolic hormones in blood plasma from exp. 1 and 2 respectively. In exp. 1 Fa was only seen to have a significant effect on plasma Insulin and GIP concentrations ($P=0.008$ and $P<0.001$). In exp. 2 XS in P1 tended to decrease plasma Insulin and C-Peptide concentrations ($P=0.071$ and $P=0.059$); whereas in P2 XS significantly decreased plasma PYY concentrations ($P=0.008$).

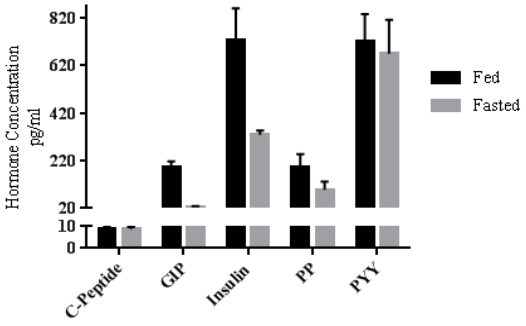

Figure 1 Concentration of metabolic hormones in fed and fasted pigs in exp 1.

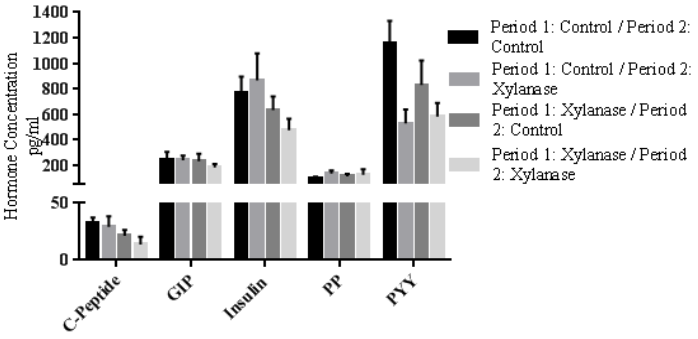

Figure 2 Concentration of metabolic hormones in pigs either fed ±xylanase supplemented diet for P1 and then ±xylanase supplemented diet for P2 in exp 2.

Conclusion The human assay was able to show the expected changes in gut hormones in exp. 1, suggesting that the human assay is a viable method for measuring porcine hormones. PP and PYY are produced in response to nutrients entering the lumen, however there was no difference in concentration between the two states in exp. 1, suggesting the average fasting time was not long enough to clear the lumen of all nutrients. The decreases in insulin and C-peptide seen in exp. 2 after XS during P1 suggests the development of the pancreas may be affected. The decrease in PYY in response to XS suggests the enzyme may influence satiety signalling, but the effect was opposite that seen previously in chicken serum.

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The use of whey permeate in the lactation diet on sow feed intake and litter performance

P McMullen[1], W Henry[2], A O'Connell[3], R Wregor[3], E Magowan[1]
[1]Agri-Food and Biosciences Institute, Hillsborough, Co. Down, UK, [2]Rektify Ltd, Gilford, Co. Armagh, UK, [3]JMW Farms Ltd, Newtownbutler, UK
Email:paul.mcmullen@afbini.gov.uk

Implications Whey has the potential to reduce the cost of pig feed and when included at 10% of the lactation diet it had no effect on sow or piglet performance.

Introduction Whey is a co product of the cheese making industry and historically it has been included in the diets of pigs offered feed through liquid feed systems. However, whey, as a co product, can be variable in composition, especially dry matter. However, it's inclusion has the potential to significantly reduce the cost of pig feed. Whey, being a product from the fermentation process, may also have beneficial effects with regard to gut microflora. However, there is a lack of research focusing on the use of whey as a pig feed ingredient since much of the nutritional research conducted uses dry feed systems. However many large producers commonly adopt liquid feeding systems (LFS) and therefore there is a need to investigate nutrition within these systems. The objective of this study was to investigate the inclusion of whey permeate in a lactation sow diet on sow and piglet performance.

Material and methods A total of 272 farrowing sows were used over sixteen time periods on a commercial farm. Within each time period sows were allocated to one of two diets. For each of the diets sows were balanced onto treatment according to weight and parity. The design of the farrowing house was such that one feed trough offered liquid feed to two sows/crates, so within each time period a 'pair' of crates was taken as one unit (as such although there were 136 sows per treatment, there were 68 replicates per treatment). The liquid to feed ratio was 3:1. Whilst sows were on a fed curve the curve essentially allowed *ad libitium* feeding with a probe in the trough controlling feed to be dispensed. The LFS used was a flush system (Big Dutchman, HydroMix system). A control (water based) diet was compared with a diet including 10% whey permeate. The diet containing the whey was balanced to meet a similar specification of energy, protein and lysine to that of the control. The main ingredients in the Control diet were (g/kg) 380 Wheat, 250 Barley, 110 Soya Meal, 100 Wheat Feed, 100 Full Fat Soya and 25 Oil, the remaining 35g/kg of the control diet was made up of a concentrate feed (JMW Lac Sow 306), Lime and Salt. The main ingredients in the Whey diet were (g/kg) 277.2 Wheat, 250 Barley, 118.3 Soya Meal, 100 Wheat Feed, 100 Full Fat Soya, 100 Whey Permeate and 25 Oil, the remaining 29g/kg of the control diets was made up of a concentrate feed (JMW Lac Sow 306), Lime and Salt. The Control diet was formulated to contain 166.1 g/kg crude protein (CP), 10.7 g/kg total lysine and 14.75 MJ/kg digestible energy (DE). The Whey diet was formulated to contain 161.7 g/kg crude protein (CP), 10.7 g/kg total lysine and 14.8 MJ/kg digestible energy (DE). Sows were offered their respective diet as soon as they had farrowed through to weaning approximately 28 days later. Daily feed intake was recorded. A 'start' litter weight was taken post cross fostering approximately 2 days after birth. Feed intake and litter performance were measured on a 'dual' crate basis. No creep feed was offered to piglets. Milk samples were taken from sows on day 7 and day 21 of lactation after administration of oxytocin. Milk samples were analysed for casein, fat, lactose, protein and urea nitrogen.

Results There was no significant effect of whey permeate inclusion at 10% on sow or piglet performance. Sow parity averaged 3.1, days in lactation averaged 26 and the average daily feed intake (ADFI) per sow averaged 7.15 kg/day (Table 1). Litter size reared and litter start weight averaged 13.2 and 25.3 kg respectively (due to start weight being approx 2 days after birth) respectively. Litter wean weight averaged 103.8kg and 103.3kg for control and whey diets respectively (Table 1). On average sows consumed 188kg and 189kg of the control and whey diets. There was no effect of diet on milk composition at day 7 or 21 with the average concentration of casein, fat, lactose, protein and urea nitrogen being 36.4, 89.1, 53.2, 46.6 and 517 g/litre respectively on day 7 and 37.0, 80.8, 53.8, 47.9 and 572 g/litre on day 21. The dry matter of the whey averaged 14.7% and over the 14 samples analysed had an standard deviation of 1.9%

Table 1 Sow and litter performance when the lactation diet contained 10% whey permeate

	Control	Whey	SEM	P Value
ADFI per Sow (kg)	7.10	7.23	0.079	0.264
Litter 'start' weight (kg)	25.6	24.9	0.422	0.220
Litter Wean Weight per sow (kg)	104	103	1.8	0.826

Conclusion In this study litter size was very high and piglet performance was good. Under these conditions and when diets were formulated to contain similar concentrations of energy, protein, and amino acids, the inclusion of 10% whey permeate had no detrimental effect on sow or piglet performance. The inclusion of whey would reduce the cost of the lactation diet and overall cost of production.

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Teat accessibility in relation to sow udder morphology

A Balzani, H J Cordell, S A Edwards
Newcastle University, Newcastle upon Tyne, UK
Email:a.balzani@ncl.ac.uk

Implications Pre-weaning mortality in pig production is a worldwide issue. Survival and growth of the piglet is determined by its ability to suckle rapidly after birth. The accessibility of teats resulting from a more suitable udder might reduce suckling latency and reduce neonatal mortality.

Introduction Piglet survival is a key issue in swine production and it has been demonstrated that the lack of early colostrum intake is the principal cause of mortality. Colostrum ejection decreases quickly after parturition, and is gradually replaced by milk, thus it is essential that the piglet obtain its first colostrum intake as soon as possible after birth, but this can be impeded by many factors. Piglets suckling behaviour in the first hour of life has been well investigated in relation to the physical environment, vitality, birth weight, and also has been studied in relation to management routines, but to date, teat suckling success has received little study in relation to the sow's udder morphology. There are many good reasons to believe that the factors that increase the latency to find a teat and suckle negatively affect piglet survival (Tuchscherer *et al.*, 2000; Vasdal and Andersen, 2012). Therefore the aim of this investigation was to determine the relationships between udder morphology and latency to find a teat and suckle.

Material and methods The udder morphology of 75 sows of differing parity was measured shortly prior to farrowing on one teat row of the sow while in a lying posture, using a standard protocol (Balzani *et al*., 2014a). From these sows, 377 piglets were weighed at birth and at 24 hours of age, and records made of vitality score and time elapsed from birth to first udder contact, and from udder contact to suckling. For each sow a colostrum sample was collected around farrowing and immunoglobulin (Ig) concentration was assessed using a Brix refractometer (Balzani *et al*., 2014b). In 38 litters, serum samples were collected from 4 piglets by puncturing the ear vein and immunoglobulin concentration was assessed using the immunocrit technique (Vallet *et al*., 2012).

Results 85 % of piglets first suckled a teat located in the upper row; 25 % of piglets chose a teat located in the rear part of the udder, 19% chose the first anterior teat, while middle teats were less often chosen. 72% of siblings suckled for the first time on the same teat. Udder morphology measures showed that posterior and anterior teats had similar conformation characteristics (Table 1). Time elapsed from udder contact to suckling was highly variable (mean 09:29 min, range 0-94:00). This time was shorter for the anterior and posterior teats (9:60 se 1.01, and 7:31 se 0.93 min) than for mid-section teats (10:30 se 1.72, $P< .01$). Investigation of teat orientation showed that piglets first suckled on 75% of occasions teats which were not perpendicular to the udder ($x^2= 14.37$; $p < .05$). Regression analysis showed that variation in litter mean serum Ig concentration and 24 h weight were not significantly explained by maternal characteristics such as colostrum quality, or piglet measures of vitality and birth weight.

Table 1 Mean and standard error of first teat suckled and of mean udder morphology

	First suckled Teat		Avergare of all teats		P.value
TEAT TRAITS	mean (mm)	se	mean (mm)	se	
Length	16.0	0.43	17.9	0.14	0.0001
Diameter	9.4	0.22	10.7	0.07	0.0001
Distance from abdominal mid line	57.0	2.41	78.0	0.85	0.0001
Inter teat distance	144.2	5.15	108.1	0.95	0.0001

Conclusion Piglets most often first accessed teats of small length and diameter, placed close to the abdominal mid line and at equal distance from one another, suggesting that udder morphology might play a role in teat accessibility. This could be especially important in large litters with high competition for teats. Udder morphology may therefore be just as important as colostrum quality and piglet vitality in acquisition of passive immunity, which was poorly explained by these factors at a litter level. Further studies are necessary to define whether udder traits are heritable and correlated with other important production traits such as prolificacy and milk production.

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Factors associated with the development of caecal dysfunction in growing turkey poults

C Rymer, D T Juniper, S Brand, K Maxam, A Tonks, R Ahmed, F Alkandari, S Indrakumar, C Poulos, M Woodward
University of Reading, UK
Email:c.rymer@reading.ac.uk

Implications Staphylococcal infection is related to the pH of caecal and gizzard digesta, and in concert with other factors may predispose the turkey poult to the development of caecal dysfunction.

Introduction Caecal dysfunction in turkeys, characterised by caecal distension and abnormal caecal droppings, is of growing concern in the turkey industry because of its negative impacts on bird welfare and economic performance. However, the aetiology of this condition is poorly understood. Including whole cereal grain in the birds' diet lowered the pH of gizzard digesta, and enhanced the populations of beneficial bacteria in the caecal microflora (Zdunczyk *et al*., 2013). The objectives of this study were to determine the effects of offering whole wheat to turkey poults on their performance and caecal health, and to identify possible causal organisms associated with the incidence of caecal dysfunction.

Material and methods Four week old turkey poults (180) were blocked by live weight and randomly allocated to one of 12 pens (15 birds per pen). Blocks of pens were randomly allocated to one of two treatments (CON and WGW, six replicate pens per treatment). CON was a proprietary, phased pelleted diet offered *ad libitum*, changed every three weeks according to the birds' changing nutrient requirements. Starter diet and whole wheat were offered in separate feeders in WGW. Feed intake, growth rate and feed conversion efficiency was calculated on a pen basis. When birds were ten weeks old, two birds from each pen were randomly selected and sacrificed. Caeca and caecal contents were scored for caecal appearance (Raman *et al*., 2011) from 0: no pathological changes to 4: complete distension with severe cell necrosis, and for caecal contents (Swayne *et al*., 2013) from 0: no pathological changes to 4: presence of thick coagulated blood. Gizzard digesta pH was recorded. Caecal digesta from the birds was pooled (on a pen basis), its pH determined, and the digesta cultured to determine the presence of *Brachyspira*, and the enumeration of *Clostridium perfringens* and *Staphylococcus* species. The effect of diet on bird performance and digesta pH was determined by ANOVA, and on caecal scores by the Kruskal-Wallis test. Relationships between caecal appearance and contents scores, digesta pH and colony counts (CFU/ml) were determined by correlation.

Results There were no clear signs of caecal dysfunction, with all birds having appearance and contents scores ≤2. Wheat intake (with WGW) averaged 72 g/d, but performance was not affected by diet (Table 1) and there was no effect of diet on the median value of appearance score (P=0.652) or contents score (P=0.284). However, gizzard digesta pH was higher in birds fed WGW. *Brachyspira* spp was present in all cultures, but no association was observed between any bacterial species and the scores for caecal digesta health. However, *Staphylococcal* spp were negatively associated with caecal digesta pH (r=-0.542, P=0.006) and positively associated with gizzard digesta pH (r=0.546, P=0.006).

Table 1 Effect of diet on bird performance and measures of gut health

	CON	WGW	SEM	P
Growth rate (g/d)	206	199	5.5	0.450
Total feed intake (g/d)	554	547	47.1	0.916
Feed conversion efficiency	2.69	2.81	0.32	0.812
Gizzard digesta pH	3.34	3.69	0.110	0.037
Caecal digesta pH	6.18	6.00	0.141	0.414
log *Clostridium pefringens* (CFU/ml)	3.98	4.57	0.185	0.109
log *Staphylococcus* sp. (CFU/ml)	3.97	4.08	0.083	0.257

Conclusion Caecal dysfunction in turkeys is a complex syndrome that may involve a *Staphylococcal* infection, but which would involve the interplay of other predisposing factors. Intake of whole wheat was low, but there was no evidence that its inclusion in the diet had a beneficial effect when birds were not stressed.

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The role of attapulgite in the colonization of potential pathogens in laying hens' caecum

S Chalvatzi, E Petridou, G Filiousis, T Poutahidis, G Papadopoulos, G Arsenos, P Fortomaris
Faculty of Veterinary Medicine, Aristotle University of Thessaloniki, Thessaloniki, 54124, Greece
Email:fortomap@vet.auth.gr

Implications The clay mineral attapulgite (or palygorskite) is a natural product that has beneficial effect as feed additive in animal nutrition

Introduction Following the ban of antibiotics as growth promoters, research was shifted towards the use of alternative resources that affect gut microbiota modulation and optimization for improved performance. Hence, dietary use of additives including probiotics, prebiotics, organic acids and enzymes has been extensively researched and widely adopted by the poultry industry. Moreover, the evidence in the literature confirms the benefits of clay mineral inclusion in animal nutrition. However the potential role of clay minerals in intestinal microflora in relation to host health and performance has not been assessed. In the present study, culture-based and molecular techniques were applied to investigate the dynamic of beneficial and potential pathogenic microbes in the caecum of laying hens that were fed diets with the clay mineral attapulgite (also known as palygorskite).

Material and methods A total of 106 *Hyline Brown* laying hens were used. These birds were obtained from an initial flock of 432 day old chicks raised in deep litter floor pens, under the same housing conditions that were equally allocated in two dietary treatments (4 replicates of 54 chicks/treatment): (i) control and (ii) 0.5% attapulgite. At the age of 18 weeks, 106 pullets were randomly selected and allocated to laying cages (7 cages of 3 birds and 8 cages of 4 birds/ treatment). Hens were fed *ad libitum* on commercial rations according to their productive stage. At the age of 22 weeks, 8 hens from each treatment (1 hen from each of the redundant cages) were euthanized and samples of caecal contents were obtained for microbiological culturing. Enumeration of Enterobacteriacae, *Escherichia coli, Enterococcus* spp., *Staphylococcus* spp., *Lactobacillus* spp. and Fungi/Moulds was performed by using Violet Red Bile Glucose (VRBG) Agar, Tryptone Bile X-Glucuronide (TBX) Agar, Slanetz -Bartley Medium and Bile Aesculin Agar, Baird-Parker Agar, de Man, Rogosa and Sharpe (MRS) Agar and Yeast Extract Dextrose Chloramphenicol Agar, respectively. Fluorescent *in situ* hybridization (FISH), using *E. coli* specific probe (5´-GCAAAGGTATTAACTTTACTCCC-3´ with a FITC-label at the 5'-end) was applied to confirm the microbiological culture results regarding this microorganism. Normality and homogeneity of variance tests were first performed in order to choose the appropriate statistical test for data evaluation.

Results Dietary inclusion of attapulgite induced a significant decrease in populations of *Escherichia coli,* Enterobacteriaceae, *Enterococcus* spp., *Staphylococcus* spp. and Fungi/Moulds in the caecum of hens, leaving counts of *Lactobacillus* spp. unaffected (Table 1). Effect on *Escherichia coli* populations was confirmed by FISH (9.1 vs 5.5 *E. coli* numbers/x100 image, for control and attapulgite groups, respectively – $P<0.05$).

Table 1 Mean values (log10CFU/g of caecal content) of microbial populations in hens' caecum according to treatment

	Treatment		
Microbial populations	Control	Attapulgite	Effect[1]
Escherichia coli	7.0	4.9	***
Enterobacteriaceae	7.8	5.8	***
Enterococcus spp.	6.7	5.0	***
Staphylococcus spp.	6.5	4.4	***
Lactobacillus spp.	6.2	6.5	NS
Fungi	3.6	1.9	***
Moulds	4.5	2.3	**

[1] NS: not significant, **P<0.01, ***P<0.001

Conclusion Overall, the results showed that 0.5% inclusion of attapulgite in the diet of laying hens reduces colonization of potential pathogens without any changes on beneficial microbes. The latter is probably associated with better utilization of nutrients in the gastrointestinal tract as a result of attapulgite presence in the diet. Hence, our notion is that attapulgite can be used in laying hens rations for the modulation of intestinal microbiota dynamics in favour of the host.

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The use of bacterial 16S rDNA restriction fragment length polymorphisms (RFLP) to monitor diet induced changes in rumen bacterial populations of cattle in an *in vitro* model of rumen fermentation

K McDermott
University of Leeds, UK
Email:katiemcdermott16@yahoo.co.uk

Implications RFLP of 16S rDNA can be used to study changes in rumen microbiome induced by differing treatments. Understanding the effect of feed on the microbiome is essential to improving animal efficiency and sustainable production.

Introduction Ruminants are exceptional in their ability to efficiently convert cellulose-rich human inedible feeds, such as forages from marginal lands, and crop and agro-industrial by-products, into high value, high protein foods for human consumption. This is made possible by the complex microbial ecosystem in the ruminant gut. Microbial ecology has previously been linked to feed efficiency (Guan 2008) and this study aimed to study shifts in rumen bacterial profiles of cattle, using an *in vitro* model of rumen fermentation and RFLP of 16S rDNA, when fed diets differing in proportion of fibre and concentrate, as well as under acidotic conditions.

Material and methods A consecutive batch culture technique was used to culture rumen fluid collected from cattle immediately after slaughter. Treatment feeds were ground to pass through a 2 mm sieve and were: Treatment 1 – all fibre (straw), Treatment 2 – build up to half fibre, half concentrate (maize/barley mix), Treatment 3 – build up to all concentrate, Treatment 4 – all concentrate (acidotic). Feed (0.5 g), 45 ml of incubation buffer (McDougall, 1948) and 5 ml of pooled rumen fluid were added to 125 ml serum bottles under CO_2. Serum bottles were prepared in quintuplet, capped and incubated at 39ºC. Gas pressure (kPa) was recorded twice daily and standardised per gram of dry matter. At 48 hour intervals for 14 days, 5 ml of fluid from each serum bottle was used to inoculate a new serum bottle containing 0.5 g of feed and 45 ml of buffer. The pH of the digesta remaining in the old bottle was recorded; the digesta was then centrifuged at 500 x g for 5 minutes to remove feed particles. The supernatant was freeze dried prior to DNA extraction. DNA was extracted using the QIAamp Fast Stool Mini Kit with the addition of a bead beating step (0.1 mm zirconium beads, 2 x 30 seconds) and an increased temperature of 95ºC to improve bacterial cell lysis. DNA quality was measured spectrophotometrically (NanoDrop ND-1000). Universal bacterial primers (8f and 1406r) were used to amplify variable regions 1-8 of 16S rDNA and the expected product was confirmed on a 2% agarose gel (1350 bp). PCR product was digested independently with three restriction enzymes (*Hae*III*, Hha*I*, Msp*I) and fragments were separated on a 12% non-denaturing polyacrylamide gel. Expected fragment lengths of some known rumen bacteria (n=10) were identified by generating primer specific regions of the 16S rRNA gene using the Sequence Manipulation Suite (Stothard, 2000) and performing *in silico* digestions (NEB cutter v2.0 http://tools.neb.com/NEBcutter2/). Cumulative gas pressure was calculated over each 48 hour period and the effect of treatment was analysed via an ANOVA with a Bonferroni *post hoc* test (SPSS Statistics 21) for both gas pressure and pH. Fragments from gels were compared for each enzyme and key differences and similarities were noted.

calculated over each 48 hour period and the effect of treatment was analysed via an ANOVA with a Bonferroni *post hoc* test (SPSS Statistics 21) for both gas pressure and pH. Fragments from gels were compared for each enzyme and key differences and similarities were noted.

Results RFLP banding patterns produced showed differences between treatments and the patterns changed accordingly with alterations in concentrate level for all treatments. The most variation was seen between Treatments 1 and 3/ 4, and the least with Treatment 2. The most rapid change was seen in the acidotic diet (Treatment 4) where novel bands were seen at the first sampling point (Day 2). Banding pattern was comparable at the start and end of the study for Treatment 1. Bands were repeatable within treatment. Some bands were universal irrespective of treatment suggesting the presence of a core microbiome. Fermentation parameters were as expected for all diets with the greatest difference observed between the high fibre and high concentrate diets (Table 1).

Table 1 Fermentation parameters of all treatments (mean ± standard error of the mean)

	Treatment 1	Treatment 2	Treatment 3	Treatment 4
Gas Pressure (kPa/gDM)	45.15 ± 2.16^{a}	115.58 ± 4.65^{b}	153.84 ± 9.56^{c}	231.06 ± 2.80^{d}
pH	6.74 ± 0.007^{a}	6.59 ± 0.012^{b}	6.45 ± 0.034^{c}	6.15 ± 0.017^{d}

[a, b, c, d] Means within the same row with different subscript differ significantly ($P < 0.001$)

Conclusion RFLP demonstrated rumen microbial profile shifts under different dietary conditions *in vitro* and supported the concept of a core microbiome. These findings merit further study at, for example, the bacterial species level with varying diets and cattle breeds with a view to identifying rumen microbial profiles associated with efficient fibre digestion.

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Effects of probiotics on the intestinal microflora of finishing broiler chickens

O O Oni[1], O M O Idowu[2], A O Oni[2], A O Oso[2], C O N Ikeobi[2]
[1]Federal College of Education, Abeokuta, Ogun State, Nigeria, [2]Federal University of Agriculture, Abeokuta, Ogun State, Nigeria
Email:onioluwakemi873@gmail.com

Implications Growing concerns about antibiotics resistance and a ban on antibiotic growth promoters in many countries necessitated increased interest in probiotics as alternatives in broilers production.

Introduction Poultry are susceptible to many enteric pathogens including parasites, bacteria and viruses. Colonization and proliferation of one or more of these enteric pathogens may result in infectious diseases that lead to increased mortality. Antibiotics growth promoters (AGP) have been used as a tool to control or reduce some of these enteric disturbances. However, the exploitation of new approaches in place of antibiotics to control enteric diseases is intensified by the continuous emergence of novel variants of established pathogens, and by the increasing public concern of antibiotic-resistant bacteria.

Material and methods Three hundred and twenty day-old Anak broiler chicks were used to assess the utilization of probiotics (*Lactobacillus sporogenes* and *Bacillus cereus*) by broiler chickens. The birds were allocated to eight treatment groups of 40 birds each with 10 birds per replicate in a 2 x 4 factorial arrangement consisting of two probiotics sources at four levels (0, 250, 500 and 750 ppm) of inclusion. At 56 days of the experiment, 5ml of gut contents were collected from two sampled birds per replicate from the ileo-caecal junction of the intestine. Microbial count was done using the method of Xia *et al.* (2004). Data obtained were subjected to 2 x 4 factorial ANOVA; significant main effects ($P<0.05$) were separated using Duncan's Multiple Range Test (Duncan, 1995).

Results Table 1 shows main effects on total salmonella count (TSC), total bacteria count (TBC) and total lactobacillus count (TLC), as probiotic strain and level did not interact ($P>0.05$). TBC was not significantly influenced by probiotic sources. TLC in *B. cereus* fed birds was significantly ($P<0.05$) greater than in *L. sporogenes* fed birds The levels of probiotic supplementation significantly ($P<0.05$) influenced the intestinal microbial count of broilers. The highest TSC was obtained at 0 ppm for probiotic levels and was significantly ($P<0.05$) different from TSC for 500 and 750 ppm inclusion levels. The TBC significantly decreased as the levels of inclusion of probiotics increased from 0 ppm to 750 ppm ($P<0.05$).

Table 1 Effects of probiotic sources and levels of inclusion on ileo-caecal microflora count (10^6cfu/g) of finishing broilers

Parameters	Probiotic Sources			Probiotic Levels				
	L. sporogenes	B. cereus	SEM	0ppm	250ppm	500ppm	750ppm	SEM
Total Salmonella Count	6.76	3.49	0.85	6.80^{a}	6.03^{a}	3.84^{b}	3.96^{b}	1.19
Total Bacteria Count	8.72	8.66	0.05	8.81^{a}	8.73^{ab}	8.67^{c}	6.43^{d}	0.06
Total Lactobacillus Count	6.85^{b}	7.17^{a}	0.13	7.54^{a}	7.17^{b}	6.91^{c}	6.43^{d}	0.1

abcdMeans on the same row having different superscripts are significantly different ($P<0.05$)

Conclusion The data support the view that inclusion of B. cereus at 750 ppm can significantly reduce the intestinal microflora of finishing broiler birds.

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Potency of dietary supplementation of some essential oils and/ or sodium butyrate on zootechnical parameters, carcass traits and intestinal integrity of broilers chickens

Maha M Hady, K N El-Den, S H El-Fattah
Cairo University, Giza, Egypt
Email:mhhady@yahoo.com

Implications The worldwide demand for safe poultry products either for the environment or for the consumers has encouraged the use of phytogenic feed additives as emergence alternative for antibiotic growth promoters. Essential oils as well as the salts of some short chain volatile fatty acids represent good, secure, practical and less costly solution.

Introduction The use of antibiotics as growth promoters (AGP) was banned as their use increases the antibiotic residues either in feed or in environment, and creates antibiotic–resistant bacteria causing human diseases. Many researchers investigated different alternatives for AGP. The class Phytogenics includes a broad range of plant materials, most of which have folklore uses in human nutrition. The essential oils (Eo) are volatile aromatic compounds derived from plants and many studies proved their anti-microbial, antifungal, antioxidant and growth promoter effects. Sodium butyrate has unique biological properties, as it is soluble in both lipids and water (Fascina *et al*., 2012). Sodium butyrate has widespread positive effects on digestive secretions, digestibility, feed efficiency, growth rate, and on defence systems in animals.

Material and methods Two hundred and forty day- old unsexed Cobb® broiler chicks were randomly allotted into four equal groups; each with three replicates of 20 birds each. All birds were raised on deep litter system and treated according to the standard management programme approved by the Animal Care Ethical Committee of Cairo University. All groups were fed on the formulated starter and finisher mash diets. Group I served as a control, while groups II ,III and IV were fed on the basal diet supplemented with essential oils (Xtract®- 100gm/ ton of feed) , sodium butyrate (Gustor®750gm / ton of feed) and a combine mixture of Xtract® and Gustor® (50gm + 375gm/ton, respectively). Feed and water were provided *ad-libitum* during the 42 days experimental period. Routine vaccination program was adopted. Zootechnical parameters (body weight development, feed consumption and Feed conversion ratio) were determined. At the end of the experiment, 9 birds as well as 3 other ones were randomly selected from each group for the sake of carcass traits and histopathological examinations. The birds were scarified by cervical dislocation and samples from different parts of the gut were collected for staining with hematoxylin and eosin for histopathological study. Data means were compared using one way ANOVA at 5% level and means were separated using Duncan's Multiple Range test (Snedecor and Cochran, 1980).

Results The results revealed that there were significant ($p<0.05$) improvement in all zootechnical parameters of chicks fed supplemented diets with either Xtract® and/or Gustor® as compared to the control group (table 1). However, no significant difference was determined in carcass trait parameters due to such treatments as compared to the control. The microscopic examination of the small intestine of all treated groups revealed a marked increase in villus surface areas in jejunum with intact epithelium which appeared as leaf like structure. Moreover, there was enhanced goblet cell density and increase in their activity in comparison with the control group. These findings confirm that the growth and nutrient absorption stimulating effects were observed in the birds as a result of Xtract® and /or Gustor® supplementation in the diets of the experimental groups.

Table 1 Overall Growth performance of broiler chickens during experimental period.

Parameter	Control	Xtract®	Gustor®	Xtract®+ Gustor
Initial body weight(g)	48.43±0.133 ^{a}	48.67±056 ^{a}	48.74±0.52 ^{a}	48.88±0.38 ^{a}
Final body weight(g)	2072.77±9.6^{c}	2202.66±1.76^{b}	2302.866±6.34 ^{a}	2494.38±6.9^{a}
Total body gain(g)	2024.33±9.5 ^{c}	2153.99±2.05 ^{b}	2254.11±6.76 ^{a}	2445.49±7.1 ^{a}
Overall FCR	2.13±0.10 ^{a}	1.84±0.57 ^{b}	1.87±0.17 ^{b}	1.73±0.016 ^{b}

Values are means ±SE, Values in the same row with different superscripts are significantly different at $P \leq 0.05$

Conclusion Dietary supplementation of commercial phytogenic feed additives products namely Xtract® at rate of 100gm/ton or Gustor® at rate 750gm/ton either solely or in combination (50 and375 gm/ ton) have positive impact on zootechnical parameters, gut health with no adverse effect on carcass traits of broiler chickens.

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Influence of L-dopa of *Mucuna pruriens* on growth response and gut mucosa integrity of broiler chickens

B R O Omidiwura, A F Agboola, M. K Adeoye, E A Iyayi
University of Ibadan, Ibadan, Oyo, Nigeria
Email:aadebunmi@yahoo.com

Implications L-dopa supplementation was found to improve gut integrity without compromising birds' performance.

Introduction *Mucuna pruriens* is a tropical legume with nutritional quality comparable to soyabeans but its utilisation as livestock feed has been limited due to presence of anti-nutritional factors like tannin, L-dopa, phytic acid etc. L-dopa (L-3, 4-dihydroxyphenylalanine) is the principal precursor for the functionality of neurotransmitter dopamine. It has been proven to be one of the few substances with the capacity to cross the blood brain barrier, converting to dopamine, and thereby stimulating the hypothalamus and pituitary to release and increase the level of growth hormone production. It was reported that when raw mucuna seeds were fed to broilers, it resulted in reduced nutrient absorption, structural disruption and collapse of intestinal microvilli (Iyayi *et al*., 2008). However, pure extract of L-dopa from *Mucuna pruriens* was adjudged to improve the performance of birds (Vadivel and Pugalenthi, 2010). The aim of the study was to evaluate the effect of L-dopa on growth performance and intestinal morphology in broilers.

Material and methods Two hundred one-day-old broiler chicks (Arbor Acre) were weighed and randomly allocated to one of 5 dietary treatments consisting of 4 replicates with 10 birds per replicate in a completely randomised design. Treatment 1 was the basal diet, a corn-soyabean meal diet without inclusion of L-dopa, while treatments 2, 3, 4 and 5 contained the basal diet and 1, 2, 3 and 4g of L-dopa/kg of diet respectively in a feeding trial that lasted for 42 days. The quantity of feed consumed was measured and birds were weighed on a weekly basis. Feed conversion ratio was computed as weight gain per unit feed intake in grams. On day 42, birds were slaughtered by cervical dislocation and after flushing out the digesta samples, sections of the ileum (5cm posterior to Meckel's diverticulum) were removed for ileal morphological measurements according to the method of Iji *et al*. (2001). Data were analysed using ANOVA, the GLM procedure of SAS (2008) was used. Means were separated using Duncan Multiple Range Test.

Results The effect of L-dopa on performance and gut morphology of birds (grower phase) is presented on Table 1. There were no statistically significant differences observed for weight gain, feed intake, feed conversion ratio (FCR), villus width or crypt depth ($P > 0.05$). However, greater villus height (1340μm) was recorded in birds receiving either both 1g or 2g/kg L-dopa supplementation compared with the control. However, there were no differences among the supplemented treatment groups. Similar trends were noticed for villus height to crypt depth ratio of birds on dietary treatments.

Table 1 Performance (g/bird) and ileal morphological indices (μm) of broilers fed L-dopa supplemented diets (d22-d42)

		L-dopa inclusion (g/kg)					
Parameter	Basal Diet	1.0	2.0	3.0	4.0	SEM	P value
Weight gain	1080.43	1179.00	1126.42	1189.02	1165.22	84.83	0.89
Feed intake	2250.00	2312.50	2245.10	2367.90	2309.10	137.86	0.64
FCR	2.08	1.96	1.99	1.99	1.98	0.31	0.74
Villus height	967.00^{b}	1340.00^{a}	1242.00^{a}	1133.50^{ab}	1132.10^{ab}	107.56	0.03
Villus width	165.70	112.76	148.29	158.91	162.81	63.39	0.31
Crypt depth	131.46	111.41	149.74	116.10	131.10	11.94	0.22
Villus:Crypt ratio	7.37^{b}	11.85^{a}	8.42^{b}	9.80^{ab}	8.97^{b}	0.99	0.04

Means on the same row with different superscripts are significantly ($P<0.05$) different, FCR: Feed Conversion Ratio, SEM: Standard Error of Mean.

Conclusion L-dopa supplementation at levels tested in broiler diets did not elicit any deleterious effect on the gut mucosa integrity and general performance of birds.

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Effect of combination of turmeric, ginger and garlic extracts on performance, microbial load and gut morphology of weaned pigs

A Adebukola Olufemi[1], Nsisongabasi P Jimmy[1], O Taiwo Olakunle[1], M Bosede Adetutu[2]
[1]University of Ibadan, Oyo State, Nigeria, [2]Moor Plantation, Oyo State, Nigeria
Email:taigadosungade@gmail.com

Implications The implication of the study is that addition of Tumeric, Ginger and Garlic Extracts can be successfully incorporated into the feeding standard of pigs as phytogenic feed additives to control intestinal microbial population without any deleterious effect or toxic residues on the animal.

Introduction Prevention and control of diseases have led during recent decades to a substantial increase in the use of veterinary medicines. Antibiotics have been extensively used as animal production to prevent pathogens and diseases so as to improve growth. However, its excessive use has resulted in resistance of bacteria to drugs as well as residue in meat which is deleterious to human who are the consumers (Sorum and Sunde, 2001). It is in view of this that attention is being focused on setting new regulations for more natural product that are friendly to animals, the consumer and the environment (Wenk, 2000). Some phytogenic feed additives have been successfully incorporated into the feeding standard of poultry birds without any deleterious effect or toxic residues (Oyekunle and Owonikoko, 2002). There are several naturally existing medicinal plants which could be used in preventing pathogens and disease which in turn improve growth. Prominent among these medicinal herb plants are turmeric (*Curcuma longa*), ginger (*Zingiber officinale*) and garlic (*Allium sativum*).

Material and methods 15 weaned pigs were used for the experiment, they were randomly allotted into 5 treatments with 3 replicates per treatment in a completely randomized design.

Experimental diet T-1 control (no extract), T-2 turmeric and ginger extracts (2 g/kg of feed, 1g each), T-3 turmeric and garlic extracts (2 g/kg of feed, 1g each), T-4 ginger and garlic extracts (2 g/kg of feed, 1g each), T-5 turmeric, ginger and garlic extracts (2 g/kg of feed, 0.67g each).

Results The result indicated a significant ($P<0.05$) variation for total microbial count, pigs ranging from 5.90 to 7.70cfu with T3 having the highest value and T2 having the least value. The result for *lactobacillus* shown on table 5 indicated no significant ($P>0.05$) variation with values ranging from 5.74 to 6.33cfu. Similarly, *Escherichia coli* had no significant ($P>0.05$) variation with values ranging from 5.77 to 6.64cfu. However, the result shows significant ($P<0.05$) difference for enterobacteria between T4 and the other treatments (T0, T1, T2, T3) with values ranging from 0.00 to 6.38.

Table 3 Microbial load of pigs fed combination Turmeric, Ginger, Garlic Diet

Treatment Parameter(CFU)	T0	T1	T2	T3	T4	SEM
Total count	6.78^{b}	6.23^{bc}	5.90^{c}	7.70^{a}	7.65^{a}	0.12
Lactobacilus	5.78	5.74	6.33	6.33	6.21	0.12
E. coli	5.77	5.53	5.58	5.64	5.43	0.25
Enterobacteria	6.38^{a}	6.20^{a}	6.23^{a}	6.29^{a}	0.00^{b}	0.03

Conclusion This study was carried out with sole aim of finding out how to make use of extracts from some phytogenic plant like Tumeric, Ginger and Garlic in pig diets because of their active ingredients which have been reported to be effective on microbes. The dietary supplementations resulted in an increase in the villus height, villus width and crypt depth of intestinal mucosa of pigs because it has been hypothesized that gut microflora decrease nutrient absorption by increasing GIT thickness, the rate of digesta passage, and also increase nutrient requirements of the host by increasing turnover of the gut mucosae and by competing with the host for a portion of the dietary energy. Therefore, these products of turmeric, ginger and garlic extracts might be promising alternatives for antibiotic growth promoters as pressure to eliminate antibiotic growth promoters in animal feed increases.

Acknowledgements Department of Animal Science, university of Ibadan

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The global livestock sector: Trends, drivers and implications for society, health and the environment

T P Robinson[1], G R W Wint[2], G Conchedda[3], G Cinardi[3], T Van Boeckel[4], B Bett[1], D Grace[1], M Gilbert[5]
[1]ILRI, Nairobi, Kenya, [2]ERGO, Oxford, UK, [3]FAO, Rome, Italy, [4]Princeton University, Princeton, USA, [5]ULB, Brussels, Belgium
Email:t.robinson@cgiar.org

Growing populations, income gains and urbanization are translating into increasing demand for livestock products, particularly in developing countries. Feeding a larger, more affluent population of over 9 billion in 2050 will require a substantial increase in agricultural production: a doubling of demand is expected for developing countries and a 70 percent increase for the world as a whole. This growth is associated with a widespread transformation of the livestock sector. While the sector provides high value food and many other economic and social functions, this rapid growth in demand is happening amidst concerns, not only about resource scarcity and climate change but also about the need for more equitable development, the urgency of poverty reduction through agricultural development and public health risks associated with agricultural intensification.

Understanding the risks and opportunities associated with a burgeoning and rapidly transforming livestock sector calls for good data on the distribution and abundance of livestock and on the production systems in which livestock are raised. Recently published global distributions of the major livestock species (http://www.livestock.geo-wiki.org), and ongoing work on mapping livestock production systems, open up the doors for analyses of the social and economic aspects of the livestock sector; the environmental impacts of livestock such as the production and management of waste, greenhouse gas emissions and livestock-related land-use change; and large-scale public health and epidemiological investigations.

This paper describes some of the trends and drivers in the livestock sector; explains the current approaches to mapping livestock and livestock production systems; and presents some examples of the use of these data in the analysis of animal and public health and zoonotic diseases.

Modelling the impact of controlling UK endemic cattle diseases on greenhouse gas emissions

J Elliott[1], G D Jones[2], A Williams[3], J Chatterton[3], B Drake[7], Z Wu[4], G Hateley[5], A Curwen[6]
[1]ADAS UK Ltd, West Yorkshire, UK, [2]Fera, North Yorkshire, UK, [3]Cranfield University, Bedfordshire, UK, [4]AFBI, Belfast,, UK, [5]AHVLA, Surrey, UK, [6]XLVet UK Ltd, Cumbria, UK, [7]University of Surrey, UK
Email:john.elliott@adas.co.uk

Implications Disease control in the dairy sector can provide cost effective GHG abatement for a range of mitigation measures (MMs) but productivity gains may lead to expansion of animal numbers and total emissions at country level.

Introduction The UK government introduced carbon budgets as part of the Climate Change Act 2008 to help the UK reduce greenhouse gas (GHG) emissions by at least 80% by 2050 from 1990 levels. Given that livestock farming is responsible for around 3% of total UK GHG emissions, Defra commissioned research to identify cost effective cattle health interventions for endemic disease control which simultaneously deliver reductions in GHG emissions. The analysis is undertaken under a fixed production constraint and separately under a supply response (to productivity gains).

Material and methods The project adopted multiple methodologies to generate three outputs; (1) a MACC illustrating the abatement potential and cost-effectiveness of animal health related MMs in the UK dairy sector, (2) quantification of the productivity dividends in terms of reduced dairy cow numbers necessary to maintain a fixed level of milk production and (3) quantification of the likely supply response from the UK dairy sector to productivity improvements arising from improved disease control. Veterinary experts within the team reviewed evidence on the prevalence and impact of 10 endemic diseases and conditions and developed around 3 MMs for each, including estimates of their efficacy and cost of implementation. Production parameter values and emissions estimates for dairy cattle, suckler beef and dairy beef, were derived using the Cranfield LCA model. The reference point for disease impact was a 'healthy animal' and parameters for the MMs reflect a point in-between the healthy and diseased animal, assuming a straight-line response. The LCA results fed into a MACC model to estimate the GHG abatement potential of MMs and associated economic benefits and costs. These were then scaled up to sector level using baseline disease prevalence and estimates of the likely uptake and the current adoption of each MM. Monte Carlo analysis was used to consider the impact of uncertainty, given the multiple parameters and value ranges. A scenario based approach was used to determine the impact of the MMs and associated land use change under a fixed output constraint. In practice it is likely that productivity gains and associated reduction in unit land requirements from improved animal health would encourage farmers to expand livestock numbers. This was simulated using a partial equilibrium macroeconomic simulation model (AGMEMOD) to estimate changes in dairy cow numbers and milk production from a relaxation of the fixed output constraint.

Results Assuming fixed output, a combination of reduced dairy animal numbers and lower GHG emissions per dairy animal produced a GHG abatement potential under two disease control scenarios (pessimistic and optimistic uptake) of 266ktCO_2e and 669ktCO_2e respectively. In addition, there is potential for GHG abatement from land use change (7-11% less grassland required for lower animal numbers); at the extreme, planting land released with conifer forest could sequester up to 1MtCO_2e. Allowing for a supply response, the AGMEMOD model estimated an increase in dairy cows numbers, driven by lower production costs resulting from improved productivity. Improvements in the technical efficiency of the dairy sector are slightly diluted by downward price pressures caused mainly by production expansion. Under the optimistic scenario, milk production is forecast to increase by 4.7% and milk price to fall by 0.4%. Increased animal numbers will contribute to an estimated increase in GHGE from the cattle sector in the UK of around 500ktCO_2e under the optimistic scenario but the intensity of emissions for milk production will be reduced by 3%.

Conclusion The research provides a 'proof of concept' that interventions aimed at improving the health and productivity of cattle can deliver positive externalities in the form of GHG abatement, both in terms of scale and cost-effectiveness. There is a business case for action by individual business owners but also for government to invest in supporting mechanisms and initiatives that encourage dairy farmers to pursue actions to improve animal health and productivity on the basis of public benefits (in terms of reduced GHG emissions intensity).

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Benefits of improving cattle health on greenhouse gas emissions (GHGE) in the UK

A G Williams[1], J C Chatterton[2], G Hateley[3], A Curwen[4], J Elliot[5]
[1]Cranfield University, Bedford, UK, [2]Unilever, Bedford, UK, [3]AHVLA, Weybridge, UK, [4]XL Vets, Carlisle, UK, [5]ADAS, Leeds, UK
Email:adrian.williams@cranfield.ac.uk

Implications Poor cattle health reduces productivity and affects welfare adversely. The use of systems-based life cycle assessment (LCA) showed how greenhouse gas emissions (GHGE) can be reduced per unit output for 10 endemic conditions in the UK.

Introduction Unhealthy cattle under-perform economically. Further, ill-health is bad for welfare. Underperformance also leads to additional environmental impacts, e.g. by premature mortalities or reduced yields. These increase the overheads of maintenance and reduce metabolic resources for production: in effect metabolisable energy requirements (MER). Direct greenhouse gas (GHG) emissions (GHGE) from digestive processes are closely related to MER (as derived in Williams *et al*., 2006). Production of feeds to meet MER also create GHGE. A life cycle assessment (LCA) perspective includes the quantification of all these factors along with manure management and other processes. All GHGE were related to functional units, which define the outputs: 1 kg carcass or 1 kg energy corrected milk (ECM) at the farm gate. The objectives were to quantify the GHGE from cattle caused by poor health and by how much these could be reduced by improving health.

Material and methods Expert practice and surveillance veterinarians quantified impacts on productivity, morbidity and mortality from the literature, AHVLA surveillance data and expert opinion derived with the Delphi method. These were converted into parameters to enhance the Cranfield agricultural systems-LCA model (Williams *et al*. 2006). The model enabled these impacts to be applied as individual parameters, including increases in mortality rates, reductions in fecundity, daily liveweight gain, milk yield and increases in feed requirements. A baseline case for healthy cattle was derived. A set of mitigation measures was compiled by the veterinarians.. These ranged from veterinary, e.g. vaccination; management e.g. better biosecurity; to engineering, e.g. improved housing ventilation. These were quantified in the LCA model to calculate the GHGE associated with implementing each intervention. The effectiveness of each intervention was estimated (by expert opinion derived with the Delphi method) to calculate the extent of potential recovery towards the healthy baseline case.

Results In affected dairy herds (assuming the maximum impact of a condition), Johne's disease, Salmonella, bovine viral diarrhoea (BVD) and infertility increased GHGE per unit milk by 15-25% above the baseline of healthy cattle. Liver fluke, infectious bovine rhinotracheitis (IBR), lameness and mastitis increased GHGE per unit milk by 7-11% above the baseline of healthy cattle. Calf pneumonia and diarrhoea had the least impacts at < 1%. BVD had the greatest potential for reducing GHGE both absolutely and relatively. Mastitis had a low absolute and relative recovery: a challenge given its prevalence. Interventions for lameness reduced GHGE twice as much as for infertility. GHGE of the interventions were relatively small: <=2% increase above healthy.

The impacts in beef were both absolutely and relatively higher than for milk. BVD roughly doubled GHGE per unit output, with Johne's, Salmonella, infertility and IBR increasing GHGE by 25-40%. Calf pneumonia and diarrhoea also had the least impacts at 4% increase in GHGE, but these are much more than for milk production, because calf mortalities (indeed all mortalities) affect beef output more directly than they affect milk production. GHGE from interventions in beef were higher for most conditions than with milk, but interventions still clearly gave net reductions in GHGE per unit output.
Sensitivity analysis showed that effectiveness of interventions was a significant factor in GHGE reductions. There were no net environmental barriers to introducing interventions, but economic costs vary considerably. Ill health is part of poor welfare and intervening thus benefits cattle welfare and GHGE.
The large impacts of BVD has policy implications, given that a voluntary approach may well not be fully effective.

Conclusion Improving cattle health reduces GHGE per unit production, with BVD, Johne's and infertility showing large potential improvements. Gains are potentially higher for beef than milk. This enhances welfare and sustainable production.

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Periparturient parasitism increases ewe methane production per kilogram lamb weaned

J G M Houdijk, B J Tolkamp, J A Rooke, M R Hutchings
SRUC, Scotland's Rural College, Edinburgh, UK
Email:jos.houdijk@sruc.ac.uk

Implications The amount of methane produced from the additional feed intake needed to overcome parasitism induced production penalties suggest that periparturient parasitism increases ewe methane production per kg lamb weaned by 13%.

Introduction We previously reported that periparturient parasitism did not affect methane yield per kg feed intake in ewes, but reduced lamb weight gain and increased maternal weight loss (Houdijk *et al*. 2012). Furthermore, parasitism may reduce feeding value. Therefore, a longer period of feeding would be needed to achieve similar metabolizable energy (ME) intake, produce similar weight of lambs and restore ewe body weight. Here, we assess periparturient parasitism impact on feed digestibility, and use the outcome to calculate the impact of parasitism on ewe methane production per kg lamb weaned.

Material and methods Twin-bearing individually housed Mule ewes were divided into 3 groups of 16 ewes of similar mean body weight (BW; 68.2±1.1 kg) and condition score (CS; 2.51±0.06) on day_{-39} (day_0 is parturition). Two groups were fed pelleted lucerne *ad libitum* and either dosed with 10,000 infective *Teladorsagia circumcincta* larvae every Mon-Wed-Fri (PAR) or sham-infected with water (CON) until day_{36}. A third group (RES) were as CON during pregnancy but fed at 80% of CON intake during lactation. Apparent total tract organic matter (OM) and nitrogen (N) digestibility was determined over 3 days around day_{28}. Lucerne gross energy (GE) and ME were analysed, and digestible energy (DE) calculated as ME/0.81 (AFRC, 1993). Earlier reported data on ewe performance and methane yield (Houdijk *et al*. 2012) were used to calculate digestible OM intake (dOMI) and methane production per kg dry matter intake (DMI), dOMI and per kg lamb weaned at 25 kg BW. The latter used total predicted DMI for lactation and restore initial BW, using 39.75 MJ/kg BW gain for CON and RES ewes (AFRC, 1993) but 49.16 MJ/kg BW gain for PAR ewes. This was deemed appropriate as PAR ewes likely lost relatively more fat than CON and RES ewes (see below), and was the average of 39.75 MJ/kg and 58.57 MJ/kg (Olthoff *et al*. 1989; ME for fat deposition only). A sensitivity analysis was undertaken for the impact of this assumption on methane production per kg lamb weaned. Feed conversion ratio (FCR) was calculated as predicted DMI divided over total lamb BW gain needed. Data were analysed through ANOVA; means were separated through Fisher's protected LSD test at $P<0.05$.

Results Observed *in vivo* OM digestibility in CON and RES ewes (Table 1) was similar to the *in vitro* 57% DE (% of GE). Parasitism reduced OM and N digestibility, resulting in reduced dOM intake. CON ewes lost less BW than PAR ewes, which in turn lost less BW than RES ewes. Treatment interacted with time for CS ($P=0.07$); CS averaged 2.46±0.06 across treatments on day_6 and reduced to 2.08, 1.84 and 2.02 on day_{29} for CON, PAR and RES ewes, respectively (s.e.d. 0.07). PAR and RES litters grew slower than CON litters. Treatments did not affect methane yield per kg DMI, but parasitism increased methane yield per kg dOMI by 15%, and per kg lamb weaned by 16% (Table 1). The latter varied from 10 to 22% when varying ME requirements for BW gain from 39.75 to 58.57 MJ/kg. Predicted FCR for CON, PAR and RES ewes was 6.65, 7.77 and 6.97, respectively (s.e.d. 0.46; $P<0.05$).

Table 1 Digestibility, performance and methane data of control (CON), parasitized (PAR) and restrictedly-fed (RES) ewes

	Treatments			s.e.d.
	CON	PAR	RES	
Digestibility (%)				
OM	54.6[a]	46.4[b]	55.8[a]	2.99
N	58.8[a]	53.4[b]	61.9[a]	2.87
Intake and performance during lactation (g/day)				
DM	4.43[a]	4.16[b]	3.45[c]	0.10
dOM	2.17[a]	1.72[b]	1.72[b]	0.13
Litter BWG	718[a]	669[b]	654[b]	24
Ewe BWG	-69[a]	-162[b]	-252[c]	37
Methane output				
Yield (g/kg DMI)	10.6	10.3	10.3	0.56
Yield (g/kg dOMI)	22.0[a]	25.2[b]	20.9[a]	1.54
Output (g/kg lamb)	57[a]	65[b]	59[a]	2.9

Conclusion Our results support the view that periparturient parasitism increases ewe methane production per kg lamb weaned, arising from increased overall FCR. Extrapolation of the latter to lambs from pen and field studies would predict that methane costs of parasitism in lambs could be considerably greater due to relatively greater impact of parasitism on FCR. We also observed that ewe parasitism reduces nutrient digestibility. The latter implies that parasitism decreases feedstuff nutritive value and further increases sheep environmental footprint arising from increased N excretion.

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New emerging infectious diseases in livestock related to climate change

W H M Van der Poel, R J Bouwstra, A R W Elbers, P T J Willemsen
Wageningen University, Lelystad, Flevoland, The Netherlands
Email:wim.vanderpoel@wur.nl

Implications Climate change plays a role in the emergence of new infectious diseases and may be associated with more frequent outbreaks of such diseases, and thereby it has an impact on both animal and human health.

Introduction There are increasing observations of climate changes supporting the emergence of infectious diseases and association of such with outbreaks of emerging diseases. Livestock diseases reduce productivity, harm animal welfare and in case of zonooses may be transmitted to humans. Livestock production contributes to economy and to farm livelihood in developing countries and provides in the growing global demand for meat, milk, eggs and other animal products, particularly because of the high quality proteins. In the list of animal infectious diseases arthropod borne and water borne diseases are most vulnerable for climate change.

Material and methods During the Schmallenberg virus outbreak in the Netherlands starting in August 2011, culicoides midges transmitting the virus were captured for speciation and characterization, and their changes in distributions were compared to literature. For pathogens of animal origin transmitted via agroproduction systems literature was also reviewed and it was evaluated how this may be influenced by climatic change. During the outbreak of highly pathogenic avian influenza H5N8 in poultry in the Netherlands starting in November 2014 (Bouwstra *et al*., 2014) the virus was identified in several species of waterfowl. Literature was reviewed for changes in spatial and temporal distributions of the involved migratory waterfowl in the region. Influences of climate change on prototypes of new emerging diseases were evaluated.

Results There is growing evidence that inter-annual and inter-decadal climate variability have a direct influence on the epidemiology of vector-borne diseases. Observations showed that the geographic range of vectors is changing. Schmallenberg virus was mainly transmitted by Culicoides Obsoletus and Culicoides Chiopterus (Elbers *et al*., 2013) which seem to have moved northwards on the northern hemisphere. A warmer climate could also cause new water-borne diseases to emerge, which was observed for enterohemorrhagic E. coli (EHEC) of livestock transmitted via manure, irrigation and green plants (Van Overbeek *et al*., 2014) . Temperature and humidity changes also affect the spatial and temporal distribution of pathogens causing non-vector borne diseases: The recently emerged H5N8 influenza virus was carried by migratory birds including wigeons (Anas penelope) and common teals (Anas Crecca). Spatial and temporal distributions of these migratory birds are altered by changes in temperature and rainfall which affect food availability. Indirectly these climate changes therefore may have triggered the emergence of new highly pathogenic avian influenza viruses in poultry.

Conclusion Changing patterns in the distributions of vectors and hosts of infectious diseases due to climate change support the emergence of new infectious agents and may result in disease outbreaks in livestock.

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Impact of early parasitic gastroenteritis and elevated environmental temperature on growth performance of lambs

S Ptochos, S Athanasiadou, M Haskell, M Hutchings, J Houdijk
SRUC, Scotland's Rural College, Edinburgh, UK
Email:sokratis.ptochos@sruc.ac.uk

Implications The impact of an early parasitic infection on feed intake was observed under elevated thermal load. Therefore, performance of parasitized lambs is expected to be penalized under the current climate projections.

Introduction As a consequence of climate change, weather conditions are expected to become warmer, with more severe and pronounced fluctuations in temperature and precipitations. This has already changed epidemiological patterns of diseases, such as parasitic gastroenteritis (PGE) in small ruminants, or lead to different host immunological responses to disease challenges (Morley and Lewis, 2014). It is expected that a higher environmental temperature and PGE will reduced feed intake. In this study, we focus on the combined impact of thermal challenge and gastrointestinal parasitism on the performance of growing lambs. The tested hypothesis is that there will be an additive effect on feed intake and growth performance of lambs when the two challenges coexist compared to when they are applied individually.

Materials and methods Forty-eight weaned, 3-month old Trichostrongyloidea naive lambs were balanced for sex and body weight (38.3±3.54 kg) and randomly allocated into pairs in 6 identical rooms with 4 pens per room. Rooms were maintained at 25±3 or 15±3 °C (n=3). Lambs in 2 pens per room were either trickle infected on 3 equally distributed days per week with a dose of 7,000 infective *Teladorsagia circumcincta* larvae, or sham-infected with tap water (n=24 lambs or 12 pens). Lambs were fed grass nuts *ab libitum* (92% dry matter (DM); 16.7% crude protein). After a two-week adaptation to the feed and housing, temperature and infection treatments were applied for 3 weeks. Infection treatment ceased by the end of week 3, when temperature of all rooms was set at 15±3 °C; data recording continued for a fourth week. Feed refusals (per pen) and lamb body weight were recorded daily and weekly, respectively, throughout. Weekly pooled samples of feed offered and pen-based refusals were analysed for DM to estimate daily DM intake per week. A repeated measures ANOVA revealed an interaction between treatments and time for DM intake ($P<0.05$). This was therefore analysed for each week separately, using a split-plot ANOVA, with room as main plot for temperature effects, and pen as split-plot for infection and temperature × infection interaction effects. Final body weight was analysed similarly, with week 1 data as covariate.

Results The effects of temperature and parasitic infection on daily dry matter intake for each of the experimental weeks are shown in Table 1. Sham-infected lambs consumed less feed than infected lambs during Week 1 at both temperatures. Infection and temperature did not affect feed intake during Week 2. However, temperature and its interaction with infection significantly affected feed intake during Week 3. Lambs kept at 25 °C ate less than lambs kept at 15 °C. Whilst infection did not affect feed intake at 15 °C, it reduced feed intake at 25 °C. This main effect of temperature and its interaction with infection were still evident during Week 4. In agreement with effects on intake, temperature and infection also interacted on final body weight ($P=0.016$); infection reduced final body weight at 25 °C (43.2 vs 44.4 kg; s.e.d. 0.61 kg) but not at 15 °C (45.1 vs 44.2 kg; s.e.d. 0.61 kg).

Table 1 Mean dry matter intake per lamb (g/day) under the double challenge of temperature and infection

Temperature (T)	Infection (I)	Week 1	Week 2	Week 3	Week 4
15±3 °C	+	1583	1506	1753	1727
	-	1468	1450	1672	1665
25±3 °C	+	1553	1469	1477	1346
	-	1398	1456	1586	1501
	s.e.d.	88.4	84.3	39.9	93.1
P values	T	0.461	0.783	<0.001	0.026
	I	0.049	0.608	0.704	0.360
	T×I	0.759	0.756	0.017	0.044

Conclusion Due to climate change extreme weather events are expected to impact the epidemiology of diseases. Thus, it is expected that PGE in small ruminants will be more frequent and severe. This trial has shown that subclinical PGE combined with elevated environmental temperature can be expected to penalize performance of growing lambs. Future work will focus on immunological biomarkers of PGE which may be affected during the early stages of infection in a warmer environment. Such insights will strengthen our understanding on the managerial and control actions needed to reduce risk of PGE under the climate change predictions.

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Effects of a two-breed and a three-breed rotational breeding strategy on ewe and lamb performance in hill flocks

A Aubry[1], R W Annett[3], D Irwin[1], A W Gordon[2]
[1]Agri-food and Biosciences Institute, Hillsborough, UK, [2]Agri-food and Biosciences Institute, Belfast, UK, [3]McLarnon Feeds, Randalstown, UK
Email:aurelie.aubry@afbini.gov.uk

Implications Horned ewes obtained from the criss-cross breeding strategy were as efficient (in terms of kg lamb/kg ewe) as ewes from the three-breed strategy, suggesting that they are the most suitable for hard hill conditions.

Introduction In order to improve the sustainability of the hill sheep sector in the UK, previous research evaluated the performance of ewes obtained from Scottish Blackface (BF) dams and a range of breeds. Crossbred ewes were found to produce up to 12% more lambs at weaning compared with pure BF ewes (Annett *et al* 2011). This study compared the performance of composite ewes obtained from a criss-cross breeding strategy (using in turn BF and Swaledale (SW) rams) or a rotational strategy where a third breed was introduced, in an attempt to increase the range of superior traits.

Material and methods This study was undertaken on six hill farms across Northern Ireland. Typically, ewes grazed improved pastures during the mating period, returned to the hill during pregnancy, were housed 2-6 weeks before lambing in Spring, and returned to the hills after lambing. Since 2006, BF ewes and their crosses (Swaledale × BF, Cheviot × BF, Lleyn × BF and Texel × BF) were mated with one of five ram breeds following two strategies: a criss-cross (CC) between BF and SW rams or a three-breed (3B) rotation combining 1) Lleyn (LL) or Belclare (Bel) to improve fertility, 2) Highlander (H) to improve lambing ease and 3) Texel (T) rams. Ewe replacements from these crosses were retained and mated first at 18 months old using another breed than its sire breed in order to continue the replacement strategies. The study includes data from 2,850 composite ewes, born between 2007 and 2012, mated between 2008 and 2013 and aged between 1.5 and 4.5 years old. Ewe live weight and body condition score (BCS) were recorded at mating. Lambing data (litter size, date of birth, lamb birth) and lamb growth to weaning (125 ± 13 days) were also determined at each farm. All data were analysed using REML in GenStat. Models for ewe traits had repeated measures with mating year, farm, age × sire breed as fixed factors and ewe as a random term. Models for lamb traits had mating year, farm, age × sire breed (of dam), ram breed as fixed factors and ewe as a random term, with additional fixed effect days to weaning for the variable kg lamb/kg ewe, and additional fixed effects litter size, sex and number of lambs reared for lamb live weight gain.

Table 1 Effects of ewe genotype on ewe and lamb performance

	Ewe breed								CC vs 3B[1]
	Three-breed strategy			Criss-cross strategy			s.e.d	P	P
	Bel ×	H ×	LL ×	T ×	BF ×	SW ×			
Ewe mating weight (kg)[2]	62.0^{a}	60.5^{ab}	59.5^{bc}	62.5^{a}	56.5^{d}	57.5^{cd}	0.62	***	***
BCS at mating	3.63^{b}	3.56^{a}	3.68^{bc}	3.70^{c}	3.77^{d}	3.75^{d}	0.019	***	***
Litter size/ewe lambed	1.61^{cd}	1.69^{d}	1.53^{bc}	1.41^{ab}	1.32^{a}	1.52^{bc}	0.078	***	0.019
Lamb live weight gain (g/d)	226	218	222	224	208	214	4.9	NS	0.024
No. reared/ewe lambed	1.30^{ac}	1.40^{c}	1.33^{ac}	1.15^{ab}	1.14^{a}	1.27^{abc}	0.082	***	NS
Efficiency[3]	0.69^{ac}	0.76^{d}	0.73^{acd}	0.64^{ab}	0.64^{a}	0.72^{abcd}	0.045	***	NS

[1]Combining ewes within the 3B or CC strategy, [2]4.5 year old ewes only, [3]weight (kg) of lamb weaned/ewe body weight (kg)

Results Breed effects on ewe and lamb traits are given in Table 1. The 3B ewes were heavier than the CC ewes, with mature Bel × and T × ewes being 5-6 kg heavier at mating. However, the 3B ewes had a 0.12 unit lower BCS than the CC ewes, with the H × ewes having the lowest BCS. Lamb output for 3B ewes was greater than CC ewes at birth (by 0.11 lambs on average) but not at weaning, despite the highest weaning rates obtained with the H × ewes (+0.25 lambs compared to T × and BF× ewes). Lambs from 3B ewes tended to gain more weight up to weaning (+ 12g/day on average, P = 0.024), however, due to their greater body weight, 3B ewes had similar efficiency to CC ewes. Low weaning rates for T × and BF × ewes led to low efficiencies, whereas high weaning rates for H × ewes led to higher efficiency of 0.76. The efficiency of SW × ewes were similar to H × and LL × ewes due to their lower body weight, compensating for a lower weaning rate.

Conclusion Overall, ewe efficiency was similar regardless of breeding strategy, despite weaning rates being particularly higher for H × ewes (+0.25 lambs compared to BF × ewes). The assessment of longevity and ease at lambing of these composite ewes will help to better target ewe breeding programmes for the hill sector.

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Effect of a colostrum alternative and milk replacer on animal performance, health, rumen fermentation and blood metabolites in lambs

A Belanche[1], C L Faulkner[1], E Jones[1], H J Worgan[1], J Cooke[2], C J Newbold[1]
[1]IBERS, Aberystwyth University, UK, [2]Volac International Ltd., Orwell, Cambridgeshire, UK
Email:aib@aber.ac.uk

Implications Good farm practices based on a correct use of colostrum alternatives and milk replacer can maximize the number of lambs weaned in flocks with a high prolificacy rate, but special care must be taken to maximize the rumen development and creep intake before weaning in order to prevent potential problems after weaning.

Introduction Genetic selection, cross-breeding and use of gonadotrophic hormones have substantially increased prolificacy in sheep. However, this increase is also associated with a greater rate of lamb deaths as a result of hypothermia, weak immune system and pathologies arising from insufficient nutrient intake. The use of colostrum alternatives (CA) and milk replacer (MR) may help to minimize these problems; but they represent a substantial cost to the producer which requires justification. This experiment aims to evaluate the effectiveness of CA and MR compared to ewe-rearing in terms of lamb health, viability and performance.

Material and methods A total of 24 pregnant ewes carrying triplets were used. Within each triplet set, lambs were classified as lightest, medium and heaviest and then randomly allocated to the experimental treatments to give similar initial live weight across treatments: 1) EE: ewe's colostrum and ewe's milk. 2) EA: ewe's colostrum and MR and 3) AA: CA and MR. All lambs were kept with their mothers for 24h after birth and AA lambs received 50g of CA (Lamb Volostrum, Volac®). Then EA and AA lambs were placed in independent pens and fed with MR *ad libitum* (Lamlac Instant , Volac®), while EE lambs were kept with the ewes. All lambs had free access to ryegrass hay, creep feed (NuGro, CCF) and fresh water. Health incidents, animal performance and intakes were recorded. Blood and rumen samples were taken just before weaning at 45d of age. Serum metabolites were analysed using RX Daytona+ Randox equipment and all data were analysed by ANOVA blocking by ewe and considering the treatment as a fixed factor.

Results All lambs remained healthy and there was just one death. Lambs fed MR had a greater incidence of mild diarrhoea than EE lambs; however they fully recovered and were weaned with similar body weights as EE lambs. No rumen protozoa were observed in lambs fed MR, while EE lambs showed a greater ruminal concentration of total VFA and a higher molar proportion of butyrate. Similar levels of nutrients were observed in blood across treatments (proteins, albumin and cholesterol), while EA and AA lambs had greater calcium levels as a result of the high milk intake (2.9 L/d). EE lambs had greater levels of amylase and β-hydroxybutyrate than lambs fed MR, possibly as a result of their greater creep feed intake (256 vs 116 g/d), and ultimately a greater rumen fermentation.

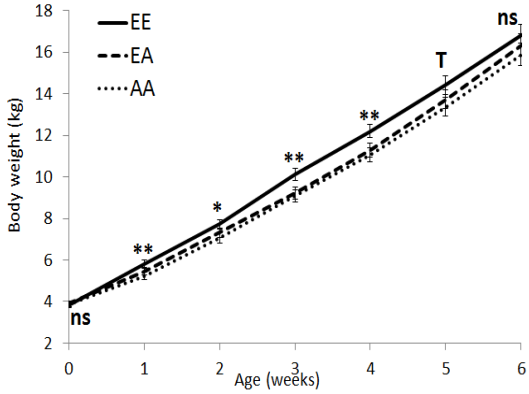

Figure 1 Lamb's weight up to weaning

Table 1 Animal performance, rumen function and blood metabolites

	EE	EA	AA	SEM	*P*
Animal performance					
Deaths, n° of lambs	0	0	1	0.03	ns
Diarrhoea score, 1 to 5	1.10[b]	1.58[a]	1.78[a]	0.144	***
ADG light-triplets, g/d	288	291	303	27.1	ns
ADG medium-triplets, g/d	340	333	318	63.5	ns
ADG heavy-triplets, g/d	347	372	335	22.8	ns
Rumen parameters					
pH	6.32[b]	6.29[b]	6.49[a]	0.07	*
mg NH_3-N/dL	4.88[b]	6.84[a]	5.96[ab]	0.70	*
Total VFA, mM	94.8[a]	76.2[b]	57.7[c]	8.24	***
Acetate, %	61.0[b]	64.9[a]	66.2[a]	1.77	*
Propionate, %	20.3	19.8	18.5	1.66	ns
Butyrate, %	13.1[a]	8.78[b]	8.40[b]	0.87	***
Lactate, mM	16.6	13.3	15.1	2.02	ns
Protozoa, log cells/mL	5.42[a]	0[b]	0[b]	0.188	***
Serum metabolites					
Calcium, mM	2.37[b]	2.52[a]	2.48[a]	0.03	***
Total Protein, g/L	45.4	46.7	46.3	0.79	ns
Albumin, g/L	32.9	33.5	33.3	0.42	ns
Cholesterol, mM	2.82	2.91	2.80	0.20	ns
HDL, mM	1.91[a]	1.65[b]	1.67[b]	0.12	T
Alk. Phosphatase, U/L	636[b]	841[a]	834[a]	55.1	***
Amylase, U/L	25.6[a]	20.2[b]	18.5[b]	1.92	**
β-Hydroxybutyrate, mM	0.26[a]	0.10[b]	0.10[b]	0.015	***

*** P<0.001; ** P<0.01, * P<0.05, T P<0.1, ns not significant (*n*=24)

Conclusion Use of CA and MR facilitated the successful artificial rearing of lambs and gave similar weaning weights to those lambs reared on ewes. But special care must be taken to maximize the rumen development before weaning.

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Prediction of nitrogen excretion in lowland lambs offered fresh grass based diets

Y G Zhao[1,2], A Aubry[1], R Annett[1], N E O'Connell[2], T Yan[1]
[1]Agri-Food and Biosciences Institute, Hillsborough, UK, [2]Queen's University Belfast, UK
Email:yiguang.zhao@afbini.gov.uk

Implications Nitrogen (N) excretion in lowland lambs can be predicted from N intake (NI) or live weight (LW) plus dietary N content ($N_{content}$). The accurate prediction of N output is essential to reduce the environmental impact of sheep production systems.

Introduction Nitrogen excretion from sheep production systems is considerable sources of nitrate and nitrous oxide responsible for groundwater pollution and global warming. The European Union introduced the Nitrates Directives (European Union, 1991) which aims to minimise the nitrate pollution of groundwater and surface water arising from agricultural sources. Therefore, there is increasing interest to estimate N output in sheep production systems. The aim of the present study was to develop prediction equations for N excretion from lowland lambs.

Material and methods Forty eight lowland lambs were used in a 2 breed (Highlander vs. Texel) × 3 sex (female vs. entire male vs. castrated male) × 2 diet (fresh grass vs. fresh grass plus 0.5 kg/d fresh pelleted concentrates) factorial design study with a single period (23 days). Animals were at approximately 5 months old and 36 ± 5.0 kg LW in the commencement of the study and allocated to 2 diet treatments balanced for sex, breed and LW. Fresh grass was harvested daily from the 1st regrowth of perennial ryegrass sward and offered *ad libitum.* Concentrates contained (g/kg fresh basis): 325 barley, 250 beet pulp, 250 soybean meal, 100 maize meal, 30 molaferm, 20 intensive lamb 20 and 25 Vit/Min supplement (V/M 208). The animals were individually housed in pens and fed experimental diets for 19 days before being transferred to individual calorimeter chambers for a further 4 days with N intake and output measured. Live weight was measured at the beginning of the study and before entering and after leaving the chamber. Grass and concentrate contained (g/kg DM): ash 107 and 60; CP 202 and 210; ADF 257 and 138; NDF 508 and 279; and GE 18.8 and 18.1 (MJ/kg DM), respectively. Data were analysed using the linear and multiple regression techniques with effects of sex, breed and diet removed. The statistical programme used in the present study was Genstat statistical package with a probability level of $P = 0.05$ for significance in relationships.

Results The prediction equations for N excretion in lowland lambs are presented in Table 1. All relationships were significant ($P < 0.001$) and each predictor had a significant effect on the relationship ($P < 0.001$). The best single predictor for N output in faeces, urine and manure was NI, and r^2 values for prediction of manure N output was higher than for faeces and urine N excretion (0.76 vs. 0.69 or 0.55). Similarly, when using both LW and dietary $N_{content}$ as predictors, the r^2 values were still relatively higher for prediction of manure N than for faeces and urine N excretion (0.63 vs. 0.58 or 0.48). However, using NI, rather than LW and dietary $N_{content}$, produced higher r^2 values and lower SE values for prediction of N output in faeces, urine and manure.

Table 1 Prediction equations for nitrogen excretion in lowland lambs (n = 48)[1]

Equations		SE	r^2
Faecal N (g/d)	$= 0.266_{(0.0544)}$ NI (g/d) $- 0.44_{(2.610)}$	1.59	0.55
	$= 0.275_{(0.0790)}$ LW (kg) $+ 0.502_{(0.5570)}$ $N_{content}$ (g/kg DM) $- 15.9_{(19.20)}$	1.74	0.48
Urine N (g/d)	$= 0.409_{(0.0542)}$ NI (g/d) $- 1.98_{(2.600)}$	1.59	0.69
	$= 0.404_{(0.0847)}$ LW (kg) $+ 1.246_{(0.5970)}$ $N_{content}$ (g/kg DM) $- 41.6_{(20.60)}$	1.87	0.58
Manure N (g/d)	$= 0.675_{(0.0730)}$ NI (g/d) $- 2.42_{(3.500)}$	2.14	0.76
	$= 0.680_{(0.1230)}$ LW (kg) $+ 1.748_{(0.8660)}$ $N_{content}$ (g/kg DM) $- 57.5_{(29.90)}$	2.71	0.63

[1]Values in subscript parentheses are SE.

Conclusion Nitrogen intake is an accurate predictor for N excretion in lowland lambs. Live weight and dietary N content together can be used to predict N output when N intake is not available.

Acknowledgements This work was funded by DEFRA, the Scottish Government, DARD, and the Welsh Government as part of the UK's Agricultural GHG Research Platform project (www.ghgplatform.org.uk).

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The effects of supplementation with cobalt, alone or in combination with vitamin B12 and selenium, on post-weaning performance of lambs on pasture

T W J Keady[1], S P Fagan[2], J P Hanrahan[1]
[1]Teagasc, Athenry, Co Galway, Ireland, [2]DAFM, Regional Veterinary laboratory, Athlone, Co Westmeath, Ireland
Email:tim.keady@teagasc.ie

Implications The response to supplementing lambs with cobalt post weaning increased as the season progressed. There was no benefit to including vitamin B12 and selenium in the supplement.

Introduction A high level of lamb growth post weaning can be achieved from grazed grass as the sole diet (Keady and Hanrahan 2010). However many commercial producers are unable to finish lambs without concentrate supplementation. While lamb growth rate from grazed pasture is predominantly affected by grass feed value and parasite control, a mineral deficiency in the herbage also reduces animal performance. It is known that the concentration of minerals in pasture varies during the grazing season. The aim of the current study was to evaluate the effects of providing supplementary Co, offered either alone or in combination with vitamin B12 and Se on the performance of lambs post weaning.

Material and methods Recently weaned lambs (n= 205;sired by Suffolk, Charollais and Belclare rams from Belclare and Belclare x Scottish Blackface dams) (mean initial live weight 34.5 kg) were allocated to one of the following 3 supplementation treatments on 12 July: no supplement (Control), Co (cobalt) or Co, vitamin B12 plus Se (VitMin). The Cobalt treatment contained cobalt sulphate (2.1 mg/ml); VitMin treatment contained B12 (200 µg/ml), cobalt acetate (10 mg/ml) and sodium selenite (0.25 mg). Lambs on the Cobalt and VitMin treatments received 10 ml and 2.1 ml of drench orally, fortnightly. All lambs were grazed on predominantly perennial ryegrass swards in a rotational grazing system. Lambs were drafted for slaughter on 26 Aug (day 49), 23 Sep (day 76), 4 Nov (day 117) and 16 Dec (day 159) at live weights of 45 and 46 kg for ewe and ram lambs, respectively. Blood, liver and kidney samples were taken from the lambs slaughtered on 4 Nov and 16 Dec for the analysis of Se, Co and Se, respectively. The data were analysed as a randomised study using Proc MIXED of SAS to fit a model with fixed effects for treatment, sex and breed.

Results The effects of supplementation on animal performance are presented in Table 1. Supplementation with either Co alone or with B12 + Co + Se increased final live weight, carcass weight, live-weight gain, carcass fat class and dressing proportion. Relative to the untreated lambs the benefit of supplementation for live-weight gain increased as the grazing season advanced. Except for live-weight gain from day 76 to117 there was no significant difference (P>0.05) between the Co only and the VitMin treatments. Supplementation increased Co concentration in liver and the difference between the Co and VitMin treatments approached significance. Treatment had no effect on the concentration of Se in kidney tissue.

Table 1 The effects of supplementation on lamb performance

	Treatment					Contrast[1]		
	Control	Cobalt	VitMin	s.e.	Sig.	VitMin *v* Co	Suppl None	*v*
Final live weight (kg)	45.6	47.2	47.5	0.50	***	NS	***	
Live-weight gain (g/d)								
- day 1 - 49	179	179	172	10.3	NS	NS	NS	
- day 49 - 76	169	193	237	19.9	**	*	**	
- day 76 - 117	81	150	159	28.2	***	NS	***	
- day 117 - 159	113	212	172	18.1	***	NS	***	
- day 0 - 159	169	178	189	9.2	NS	NS	P=0.07	
Carcass weight (kg)	19.1	20.3	20.6	0.27	***	NS	***	
Fat class[2]	2.70	2.90	2.96	0.090	NS	NS	**	
Dressing proportion (g/kg)	417	430	431	3.5	***	NS	***	
Co in liver (mmol/l)	0.17	0.73	0.99	0.081	***	P=0.06	***	
Se - blood (mmol/l)	1.02	1.07	1.70	0.144	***	***	***	
- kidney (µmol/kg)	17.8	17.5	16.8	1.35	NS	NS	NS	

[1]VitMin *v* Co = VitMin minus Cobalt, Suppl *v* None = supplementation minus no supplementation. [2]Scale 1 (thin) to 5 (fat)

Conclusion Supplementation with cobalt either alone or in combination with vitamin B12 and selenium increased lamb performance post weaning. The benefit to supplementation increased later in the grazing season.

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Effects of growth promoters on expression of serine biosynthetic pathway genes in ovine liver and skeletal muscle

S Al-Doski, K Hemmings, Z Daniel, J Brameld, T Parr
University of Nottingham, UK
Email:sbxsi@nottingham.ac.uk

Implications The capacity for enhanced muscle growth is linked to an increased potential to synthesise serine.

Introduction Animal production systems seek to increase growth by partitioning nutrients into lean tissue and increasing nutrient utilisation efficiency. The growth promoters, beta-adrenergic agonists (BA) and growth Hormone (GH), induce muscle hypertrophy which is associated with changes in nutrient mobilisation and utilization (Bell *et al*., 1998). Recent research has demonstrated that hyperplastic growth and switch to glycolytic metabolism in some cancers is associated with up regulation of the serine synthesis pathway, which then is utilised by additional biosynthetic pathways (Amelio *et al*., 2014). Therefore, the aim of this study was to investigate whether the muscle hypertrophy stimulated by growth promoters was associated with increased gene expression of the metabolic pathway responsible for serine biosynthesis.

Material and methods Male lambs (120 days old) were all fed a high protein/ energy diet *ad-libitum,* with the GH group (n=10) receiving a single subcutaneous injection of bovine GH (3.75mg/kg body weight, POSILAC, Monsanto) on day 1; the BA group (n=10) receiving BA (cimaterol) at 10mg/kg in the feed, whereas the control group (C, n=11) only had the *ad-libitum* feed. After **6 days** sheep were slaughtered and samples of Longissimus dorsi (LD), Supraspinatus (SS) muscles and liver were snap frozen in liquid nitrogen and stored at -80^{o}C. Frozen samples were crushed prior to analysis. Total RNA was extracted (Trizol) and first strand cDNA generated using random primers. Using primers specific for the mRNAs, expression was determined using quantitative RT-PCR analysis (Roche) relative to total cDNA as determined using Quant-iT OliGreen (Life Technologies). Treatment groups were compared using one-way ANOVA (Genstat) and *Post hoc* Dunnett's test, error bars are standard error of the mean. Significance was accepted at P<0.05.

Results BA but not GH significantly (P<0.05) increased phosphoglycerate dehydrogenase (PHGDH) and phosphoserine aminotransferase 1(PSAT1), but not phosphoserine phosphatase (PSPH), mRNA expression in both SS and LD muscles relative to control; whilst there was no effect on liver (Figure 1A). BA significantly (P<0.05) decreased isocitrate dehydrogenase (ICDH) mRNA in both muscles, but not liver (Figure 1B).

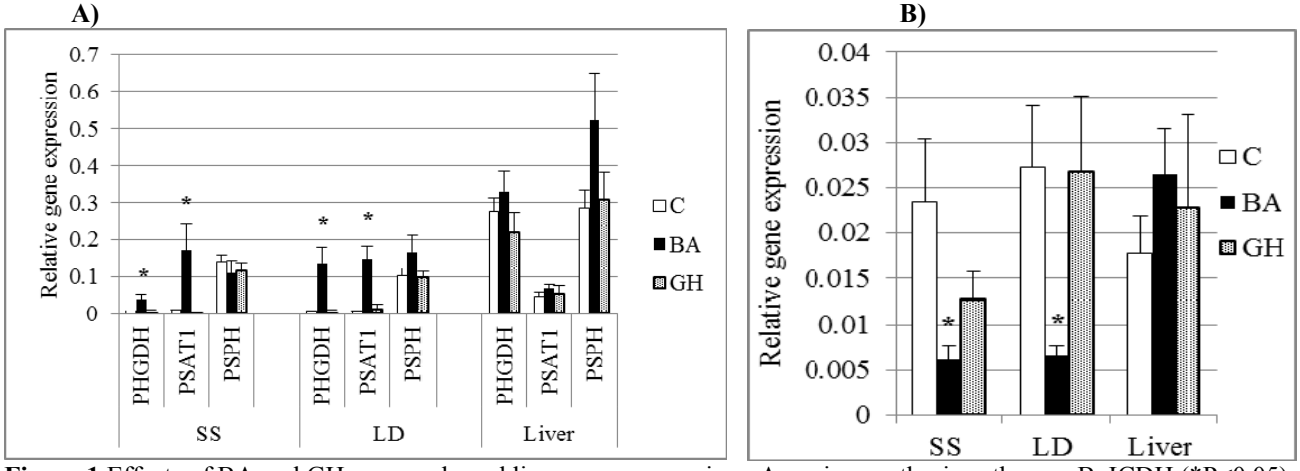

Figure 1 Effects of BA and GH on muscle and liver gene expression. A. serine synthesis pathway. B. ICDH (*P<0.05)

Conclusion Treatment of sheep with BA, but not GH, for six days increased muscle mass and caused a switch to a fast glycolytic fibre type (Hemmings *et al*., 2014). This appears to be associated with a decrease in ICDH gene expression, suggesting a decrease in TCA cycle activity. BAs increase muscle's glycolytic potential and this is associated with a capacity to increase the synthesis of serine and presumably other related metabolites required for growth.

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Relationship between body condition score and ultrasound measurements of backfat thickness in dairy Chios ewes

S-A Termatzidou, G E Valergakis, M N Patsikas, G Bramis, G Arsenos
Aristotle University, Thessaloniki, Greece
Email:sofia.termatzidou@gmail.com

Implications Results from this study can contribute towards the development of an objective scale for body condition scoring in dairy sheep.

Introduction Body condition scoring (BCS) in sheep has been a long standing practical approach for assessing energy reserves (Russel *et al.*, 1969). The thickness of subcutaneous adipose tissue is a reliable indicator of changes in body condition of sheep (Mendizambal *et al*., 2003) and it has been accurately assessed by implementing ultrasound techniques, particularly for meat producing sheep (Thériault *et al*., 2009). However, the latter is not applicable in dairy breeds of sheep, because they differ from meat breeds and there are also large conformation differences between dairy breeds. The objectives of this study were two-fold; (1) to compare ultrasound measurements between two different anatomical regions and (2) to investigate the relationship between estimations of BCS and ultrasound measurements of backfat thickness in dairy ewes of Chios breed.

Material and methods The study was carried out at the university farm of the Faculty of Veterinary Medicine, Aristotle University of Thessaloniki, Greece. Thirty six adult ewes (2^{nd} and 3^{nd} parity equally distributed among groups) were selected on the basis of their stage of production as follows: Group A: ewes at 3^{rd}-6^{th} month of lactation, Group B: ewes at 7^{th}-8^{th} month of lactation and Group C: dry ewes. At those stages the ewes had the most characteristic differences in their BCS. From each group, 12 ewes were randomly selected. BCS was performed by palpation of the dorsal lumbar region (5-point scale, with 0.25 and 0.5 increments). The thickness of subcutaneous adipose tissue was measured by ultrasound between transverse processes of 12^{th} and 13^{th} thoracic and 3^{rd} and 4^{th} lumbar vertebrae, using Agroscan A16 with 7.5 MHz linear probe; thickness is displayed in whole and half mm. Statistical analysis regarding differences among groups for BCS and ultrasound measurements was performed using descriptive statistics and analysis of variance. Pearson's correlation coefficient (r) was used to display the relationship between the measurements in the above anatomical regions and the relationship between ultrasound measurements and assessments of BCS.

Results Across groups there was a significant difference ($P<0.05$) for both BCS and ultrasound measurements. BCS estimates ranged from 1.50 to 3.75. Lumbar and thoracic vertebrae ultrasound measurements ranged from 2.5 to 9.0 mm and 2.0 to 9.0 mm, respectively (Table1). Increments of BCS at 0.25 points did not always correspond to distinct ultrasound measurements. The correlation between measurements in the two anatomical regions was high ($r = 0.974$, $P<0.05$). Correlation coefficients between BCS and ultrasound measurements in thoracic and lumbar regions were 0.931 ($P <0.05$) and 0.916 ($P <0.05$), respectively.

Table 1 Backfat thickness (mm) range between transverse processes of 3^{rd} and 4^{th} lumbar and 12^{th} and 13^{th} thoracic vertebrae, for each scale assessment of BCS.

Body condition score (scales)	Backfat thickness between transverse processes of 3^{rd} and 4^{th} lumbar vertebrae (mm)	Backfat thickness between transverse processes of 12^{th} and 13^{th} thoracic vertebrae (mm)
1.50	2.5-3.0	2.0-2.5
2.00	3.5-4.0	3.5
2.25	3.5-4.0	3.5
2.50	4.5-6.0	4.0-5.0
2.75	5.5-6.5	5.0-6.0
3.00	6.0-8.0	5.0-7.5
3.50	8.0-9.0	7.5-8.5
3.75	9.0	9.0

Conclusion Ultrasound measurements performed in the two anatomical regions revealed similar results. Hence, in practice either location can be used. The high correlation between BCS and ultrasound measurements suggests that the development of a scale for BCS in dairy sheep would be facilitated by ultrasound technique. More data are needed for the refinement of the scale. Considering that this was a pilot study, the application of such methodology to a larger sample of ewe or even at population level of certain breed will strengthen the results, providing a widely accepted methodology.

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Application of a mechanistic model to analyse the environmental factors that affect lactation curves of dairy sheep

J C Angeles Hernandez[1,2], B Albarrán Portillo[5], A H Ramirez Perez[2], A C Lizarazo Chaparro[3], O A Castelan Ortega[4], M Gonzalez Ronquillo[4]
[1]Programa de Maestría y Doctorado en Ciencias de la Producción y de la Salud Animal, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de Mexico, Mexico, [2]Departamento de Nutrición Animal, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Mexico, [3]Centro de Enseñanza Practica e Investigación en Producción y Salud Animal, Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, Mexico, [4]Departamento de Nutrición Animal, Facultad de Medicina Veterinaria y Zootecnia, Universidad Autónoma del Estado de México, Mexico, [5]Centro Universitario UAEM Temascaltepec, Universidad Autónoma del Estado de México, Mexico *Email:mvzjuancarlos@comunidad.unam.mx*

Implications The mechanistic model of lactation curve developed by Pollott, can be used to analyse the biological and environmental factors that affect milk production in Mexican dairy ewes

Introduction Milk yield is the product of cell number, secretory activity per cell and gradual reduction of number of secretory cell as results of apoptosis. External factors like environmental effects, nutrition, pregnancy and health can affected this biological process.
The Pollott functions have been specifically design to describe milk production patterns in sheep based on known biology of milk production (Pollott, 2000). This model has been compared with empirical and mechanistic models of lactation curve fitting, the Pollott model has been the most accurate method when dealing with weekly records of milk yield to model lactation curve in dairy ewes. Furthermore the model has the advantage of providing parameters which have biological interpretation, thus it could be use to analyse the biological and environmental factors that affect milk sheep production. The aim of the present study was to investigate the factors that influence milk production in crossbred sheep in commercial farms in Mexico using the Pollott model.

Material and methods A total of 10,008 weekly test-day records (TD) from 556 lactations of crossbred sheep from 4 commercial farms allocated in Mexico were analysed, to investigate some of the factors that influence in milk production in dairy sheep using a mechanistic model. Ewes were milked mechanically once daily. Only data with ewe´s identification, lambing date, lambing number, type of lambing and with the first TD record within 30 days post lambing, were considered for the analysis. Analysed lactations averaged 18.3 weekly TD records of milk yield per lactation.
The 5-parameters reduced additive model described by Pollott (2000) was fitted to each lactation using an iterative non linear procedure (NLIN, SAS Institute, 2002): The model is:
$M = ((MS_{max}/(1 + ((1 – 0.999999)/0.999999)*exp(–GR\ (n-150))) – (MSL_{max}/(1 + ((1 – NOD)/NOD)*exp(–DR\ n)))$ (1)
Where: M = milk production in kg/d on day *n* of lactation, MS_{max} = maximum milk secretion potential of the lactation, GR = relative proliferation rate of secretory cell number during early lactation, MSL_{max} = maximum milk loss potential, DR = relative decline rate in cell number, NOD = proportion of parenchyma cells death at parturition.
The total milk yield (TMY) observed was computed using the Fleishmann method (Ruiz *et al*., 2000). The biological parameters of the Pollott model were used to estimate total milk yield (TMYc). The general linear model procedure (GLM, SAS Institute, 2002) was used to determined the effect of type of lambing (single or twin), lambing number (1st, 2nd, 3rd and 4th), farm (1, 2, 3 and 4) and season of lambing (spring, summer, autumn and winter) over traits of lactation curve (TMY and TMYc) and parameters of Pollott model (MS_{max}, MSL_{max}, DR, GR and NOD). The goodness of fit of the Pollott model was evaluated using the mean square of prediction error (MSPE) and the correlation coefficient (r) between TMY and TMYc.

Results The Pollott model showed an adequate goodness of fit (MSPE = 0.013 and r = 0.86). The data analysed showed that the ewes had an average milk yield for 140 days of lactation of 72 kg. The TMY and TMYc were higher (P = 0.04) for twin lambing when compared to single lambing (TMYc = 89.01 kg *vs* 66.93 kg, respectively); For lambing number, the third lambing ewes showed the highest milk yields (TMY = 95.8 kg); Farm also affected TMY and TMYc (P = 0.001). First lambing ewes showed the lower TMY (71 kg) and TMYc (68 kg), this could be due to the significantly lower values observed for MS_{max} (2.8 kg). MLS_{max} was not affected by the environmental factors analysed. The relative GR was greatest (P = 0.05) during the first lambing (0.059) and then it was decreasing as the lambing number increased. The DR, however, was low in first lambing ewes (0.201) and increased throughout life (P = 0.04). The NOD also was affected by the farm (P = 0.001). The season on which lambing occurred did not affect milk yields and biological parameters of the Pollott model.

Conclusion Environmental factors, number of lambing and type of lambing had affects on milk yield produced by the evaluated ewes. The analysed parameters of the Pollott model were able to explain with a biologically approximation the dynamics of differentiation, secretion and death of mammary cells in dairy ewes of Mexican farms.

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A better way to feed the performance horse

M J S Moore-Colyer
Royal Agricultural University, Cirencester, UK
Email:meriel.moore-colyer@rau.ac.uk

Nutrition is not a 'short-term fix' for improving performance but long-term maintenance of 'ideal' body condition and provision of the correct balance of substrates for work, while minimising the chances of metabolic and behavioural disorders that stress the animal and reduce performance.

Current problem Traditional diets where horses are meal fed cereal-based concentrates accompanied by restricted forage in 2 hay nets per day are still common place for many performance horses. Such diets ignore equid digestive physiology and feeding behaviour and pre-dispose to diet-related metabolic disorders such as gastric ulcers, colic, acidosis, laminitis and Recurrent Airway Disorder (RAO). Furthermore meal feeding and restricting access to fibre can 'switch-on' aberrant behaviours such as crib biting, box walking and weaving which are 'coping mechanisms' employed by some horses to cope with the stressful environment.

Nutrient Requirements Energy requirements are the first consideration when deciding what to feed a horse. Recent surveys of diets fed to National Hunt, Show and Leisure horses by Mather and Shave (2011) found higher amounts of feed were given per day than the official recommendations set by NRC (2007) and Coenen (2005). This suggests that:
1. energy recommendations are being underestimated
2. digestion and metabolism is not occurring efficiently
3. the balance of feed types is not ideal for the activity required.

Good foundations Careful matching of diets with work type and requirements and consideration of digestive physiology and feeding habits will maximise nutrient utilisation. Trickle feeding is key, ensuring that the concentration and flow of non-structural carbohydrates, protein and fat matches the level of enzyme secretion in the small intestine so that starch, amino acids, glycerol and fatty acids can be completely digested and absorbed yielding maximum value to the horse. A flow of readily fermentable structural carbohydrates into the hind gut will produce a significant amount of slow-release energy in VFAs, top-up muscle glycogen reserves from propionate metabolism and maintain vitamin and water circulation. The fact that digesta rate of passage in the horse alters according to diet can be used to target nutrient delivery and gives a flexibility to diet formulation not seen in ruminants. However, this same feature pre-disposes horses to digestive disorders so diet type, meal size, meal frequency and consumption time must be carefully balanced with nutrient content and potential digestibility.

Diet formulation Horses evolved on high fibre diets and this should be the first consideration when formulating a diet. The often cited negative aspects of fibre such low DE content / kg DM and low digestibility coupled with high metabolism losses (heat increment and methane output), unnecessary gut ballast and a compromised respiratory tract from dusty forage can all be mitigated with careful thought. High-quality fibres such as grass, young leafy well conserved hay or haylage, addition of 'super fibres' alfalfa and sugar beet pulp will all minimise unnecessary hind gut ballast. Providing readily fermentable fibres maximises VFA production in the hind gut and as exercising horses readily utilise acetate (Pratt, *et al.,* 1999), and 60% of the glucose synthesised in the liver comes from propionate (Simmons and Ford, 1991) a highly fermentable fibre source is energetically valuable to the horse. Jansson and Lindberg (2008) have demonstrated that racehorses fed all fibre diets compare favourably with those on a high concentrate diet as they maintained performance, had lower blood lactate levels and decreased breathing frequency after exercise. Furthermore, fibre feeds have high hemicellulose and pectin contents and so hold water which can help prevent dehydration and electrolyte loss during exercise while the DCAB of fibre maintains gut pH and provides available minerals in a naturally chelated form. Certain fibre feeds also release their soluble protein in the small intestine (Moore-Colyer, 2006) thus contributing to the amino acid pool that can be used for anabolic purposes. Feeding high fat diets to endurance horses is now common place but high fat diets can also be used to good effect in horses working at VO_2 max. Fat is 2-3 time more energy dense than cereals, and with proper adaptation the horse will preferentially use fat for aerobic activity (most of the daily energy expenditure) sparing glucose and thus increasing the time to fatigue. Targeting small intestine fat digestion is important as long and medium chain fatty acids (PUFA) entering the hind gut can compromise cellulolytic bacteria activity (Zeyner, 2008). Cereal-based concentrates, particularly those thermally processed, are a useful source of fast-release energy. Offering several small meals per day (maximum of 1.1g starch / kg LW /meal (Vervuert, and Bergero, 2010), ensures SI digestibility and contributes to liver and muscle glycogen stores. Feeding small amounts of cereals i.e., 30% of the diet can enhance cellulolytic activity in the hind gut (Moore-Colyer, 2000; Julliand *et al.,* 2001) and thus improve fibre degradation. Micronutrients are key components of many metabolic reactions and should be provided in readily available forms. Horses can lose 20.4 litres of sweat during intense exercise and the hidden loss of electrolytes that accompanies this can be seriously detrimental to performance, thus supplementation must be considered.

Effect of supplementation with selenium and vitamin E on serum malondialdehyde and creatinine phosphokinase concentrations in horses under moderate exercise

E Velazquez-Canton[1], A H Ramirez-Perez[1], L A Zarco-Quintero[1], F Meschy[2], D A Castillo-Mata[1], J C Angeles-Hernandez[1]
[1]FMVZ-UNAM, Mexico City, Mexico, [2]INRA, France
Email:eliasvelcanton@hotmail.com

Implications Physical work of skeletal muscle increases mitochondrial O_2 uptake, intensifies oxidative stress and free radical formation, which could cause muscle damage in human athletes and horses. It can be reduced by feeding with antioxidants.

Introduction Oxidative stress is directly associated with exercise intensity. It causes free radical formation and injury in muscle which cause severe damage to cellular membrane. Hence, lipid peroxides could increase (Kenichiro *et al*., 1990) due to membrane phospholipid damage. Oxidative stress is measured by serum malondialdehyde (MDA), while muscular damage is detected by serum creatinine phosphokinase (CK) concentrations (Piccione *et al*., 2012). The aim of this study was to evaluate the effect of supplementation with selenium (selenium methionine) and vitamin E (α-tocopheryl) on the serum MDA and CK concentrations in horses under moderate exercise.

Materials and methods Institutional Animal Care and Use Committee of the Faculty of Veterinary Medicine of the National Autonomous University of Mexico approved the experimental protocol for the use of the horses in this study. The research was carried out in the Mounted Police Unit of Mexico City (2,240 m above mean sea level) from January to April 2014. We used 24 clinically healthy horses, aged 5 to 15 years and weighing 450 kg. They did not perform physical labor the month prior to this study. Animals were randomly arranged in 4 experimental groups of 6 horses each; in a factorial design (2 selenium (Se) levels × 2 vitamin E (E) levels) with repeated measures. The recommendations of Se and vitamin E were taken from the National Research Council (2007) publications for horses under moderate or intense exercise. Hence, supplementation levels were low (L) and high (H). The experimental treatments were: LSeLE, HSeLE, LSeHE and HSeHE (LSe, 0.1; HSe, 0.3 mg Se/kg of DM and LE, 1.6; HE, 2 IU vitamin E/kg of BW). Selenium was undetectable (<2 µg/kg DM), while vitamin E reached 14.4 IU/kg DM in the daily ration used. Thus, Se and E were fully supplied using experimental supplements. The study lasted 11 weeks (w); w0, corresponded to the baseline measurement of MDA and CK before starting the experimental supplementation. The experimental periods were as follows: w0 to w3, adaptation period; w4 to w7, exercise period (3 consecutive days per horse; daily exercise included 5 min of warm up, 20 min of moderate gallop and 5 min cool down); w8, rest and w9, end of supplementation. Once a week, jugular blood samples were taken. At w4 to w7, the blood sample was taken at the end of last day of exercising. Blood was centrifuged and serum was frozen until MDA and CK were quantified (Gutteridge, 1975; spectrophotometry, Randox Daytona™; respectively). Data were analysed using the PROC MIXED function of SAS (9.1) using the model: $Y_{ijkl} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + Ck_{(ij)} + \Upsilon_t + (\alpha\beta\Upsilon)_{ijt} + \varepsilon_{ijkt}$, where: μ is the overall mean, α the effect of the Se level (i =1 and 2), β the effect of the E level (j = 1 and 2), $(\alpha\beta)$ the effect of the interaction between α_i and β_j, $Ck_{(ij)}$ the random effect of the horse (1 – 24), Υ effect of experimental week (t = 0 – 11), $(\alpha\beta\Upsilon)$, the effect of the interaction of $\alpha_i \times \beta_j \times \Upsilon_t$ and ε_{ijkt} was the experimental error $N(0, \sigma_e^2)$.

Results The only significant (P<0.001) effect on serum MDA (nmol/mL) and CK (U/L) concentrations, was the experimental week (Table 1). The highest serum MDA concentrations were obtained at w1; which could be attributed to the initiation of horse handling. In contrast, serum CK concentrations increased at w3. A second increase for both MDA and CK concentrations was seen at w6, which can be explained by exercise similar to other studies. After w6, both serum MDA and CK concentrations decreased, while at week 11 (non-supplemented period) these levels increased again.

Table 1 Serum MDA (nmol/L) and CK (U/L) concentrations in horses

	Weeks of adaptation period				Weeks of moderate exercise						No supplementation	
	0	1	2	3	4	5	6	7	8	9	10	11
MDA[1]	$0.6^{d,e}$	1.8^{a}	0.7^{d}	0.4^{e}	0.7^{d}	0.8^{d}	1.2^{b}	1.0^{c}	0.7^{d}	0.5^{e}	0.8^{d}	1.0^{c}
CK[1]	$180.5^{b,c}$	164.4^{c}	$182.5^{b,c}$	224.8^{a}	$168.7^{b,c}$	$186.3^{b,c}$	227.9^{a}	$199.5^{b,c}$	194.8^{b}	159.4^{c}	$197.1^{b,c}$	$217.5^{a,b}$

[1]SEM, MDA, 0.1; CK, 10.4

Conclusion The serum MDA and CK concentrations in horses that received 0.3 mg Se/kg DM and 2.0 IU vitamin E/kg of BW, were not different from those who received 0.1 mg Se/kg DM and 1.6 IU vitamin E/kg of BW. It is important to note that MDA and CK concentrations increased during exercise weeks, however CK concentrations were not high enough to consider muscle damage, which was not the goal of this study.

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The equine atheletic heart

C M Marr
Rossdales Equine Hospital and Diagnostic Centre, Newmarket, Suffolk, UK
Email:celia.marr@rossdales.com

The horse is uniquely adapted for athletic performance, and this is particularly true in respect of the cardiovascular system. In order to sustain a cardiac output of up to 250 l/min, the horse achieves a heart rate of up to 230 bpm, a stroke volume of around 1L and pulmonary intravascular pressures are high. Oxygen delivery to muscles is augmented by the splenic resivour of red blood cells and at the level of the muscle, oxygen extraction is extremely efficient. In Thoroughbreds, the heart mass is about 1% of its body weight. Heart size is related to its maximal output and performance, particularly in Steeplechasers.

Heart murmurs commonly occur in horses with completely normal hearts, variously described as "physiological" or "flow" murmurs. The second commonest cause of heart murmurs is leaking, or regurgitation, in one or more of the heart valves. Regurgitaiton can be considered as physiological (i.e. present with normal valve structure) or pathological (due to various forms of valve pathology. Echocardiographic imaging has revealed that actually, at rest, equine heart valves can often have small leaks. This is particularly so in racehorses and large scale studies have shown that these leaks, and the murmurs they are associated with have no impact on racing performance.

There are various possible disease processes that can affect the valves, but the most common is due to degeneration linked to the ageing process. There is AN increase in the prevalence of this form of murmur with increasing age such that they are found in around 3% of horses aged less than 7 years; 8% of horses aged 8 – 14 years, around 14% of horses aged 15 – 23 years and about 15% of those older than 24 years. However, degenerative valvular disease rarely affects the horse's lifespan.

Echocardiography is the primary tool used to identify the cause of murmurs and evaluate the severity. A two-dimensional image of the heart provides an assessment of its internal structures. This is coupled with Doppler echocardiography that allows the speed and direction of blood flowing through the heart to be documented. Thus, with valvular regurgitation, echocardiography will demonstrate valvular thickening and provide a semi-quantitative assessment of the degree of regurgitation. Documentation of chamber dimensions over time is an additional indicator of progression.

The ECG is the primary tool that is used to determine heart rhythm. An ECG is essentially a road map of how the electrical impulse makes its way through the different chambers of the heart. In equine practice, it is recorded by placing at least two electrodes on the surface of the horse's body, detecting the electrical signal and displaying that as a waveform, either on paper – or more commonly with modern units, digital outputs are analysed in real time or subsequently. Dysrhythmia is the term used to describe any form of irregularity of cardiac rhythm. Physiological dysrhythmis are common: Surveys of healthy horses have shown that around 40% of horses have second degree atrioventricular block

Atrial fibrillation is the commonest form of clinically significant dysrhythmia. In some horses, the atrial fibrillation occurs in isolation with no underlying heart diseaseand is known as "loan atrial fibrillation'. However, in some horses, the atrial fibrillation is accompanied by pathology in the heart and therefore is part of a much more complex problem. Loan atrial fibrillation can self-correct, usually within 24 to 48 hours after its onset and this is called paroxsysmal atrial fibrillation. This form of atrial fibrillation is actually rather common in Standardbred and Thoroughbred racehorses and it accounts for around 1.5% of disappointing race performances. If loan atrial fibrillation does not self-correct, it may have to be treated. There are two basic approaches. Atrial fibrillation can be treated with various drugs, of which quinidine sulphate it the most common. Alternatively, some horses are treated with electrocardioversion. Both options have pros and cons. The drugs require very careful monitoring and side-effects mainly relating to gastrointestinal problems are common. Horses which have had atrial fibrillation for a fairly short period of time will typically respond well to quinidine sulphate treatment. Electrocardioversion requires specialist equipment and personal. It also involved general anaesthesia. Its main advantage is that horses which have had atrial fibrillation for several weeks are likely to respond better to electrocardioversion. It is important to recognise that the overall safety of the two approaches is fairly similar. Atrial fibrillation is a recurrent condition. There are various factors that will influence, the likelihood of recurrence but the duration that the dysrhythmia has been present is important.

Atrial fibrillation can also occur in horses with underlying heart disease and horses can also develop different forms of cardiac rhythm irregularity. Ventricular dysrhythmias are more unstable than supraventricular depolarisations and either form of dysrhythmia can occur with primary myocardial damage or secondary to other system disease processes. The key to appropriate management of these dysrhythmias is to establish the underlying cause, and to treat that if possible.

A comparison of a traditional treed saddle and a working prototype which utilises an innovative structure

T E Ward
The Royal (Dick) School of Veterinary Studies, Edinburgh, UK
Email:trace@abouttack.com

Implications The use of the innovative saddle structure tested reduces peak and average pressure, as well as peak and average force under the saddle.

Introduction Back injury in ridden horses is a common complaint. In previous studies, pressure mats used under saddles have recorded high pressures that would be expected to cause pain and damage. Several studies have recommended a re-design of saddles in order to address this concern. The aim of this study was to assess the effectiveness of an innovative saddle structure as compared with a standard treed saddle.

Material and methods Two saddles were used for the study. One was a treed saddle (Treed), and the other was a prototype using a dynamic load redistribution system (DRS). Both saddles had air panels, were fitted by a saddle fitter qualified through the Society of Master Saddlers, and were adjusted as required for each horse. Six horses and four riders participated in the study. Two riders rode two horses, no horse was ridden by more than one rider. Horses were assessed as sound and free from clinical back pain by a veterinarian prior to their involvement in this study. Trials were conducted on a woodchip surface in an indoor arena. Data was captured using a Tekscan Conformat sampling at 10hz. Circle boundaries were marked by poles (small 9m, large 18m). Straight lines were marked down the long side of the arena. Four trials were conducted. Two trials were at canter on a large circle to the right (CLCR), one trial in 2-point position (CLCR2) and one sitting (SCLCR). Two further trials were at sitting trot (ST), one on a straight line (STSL) and one on a small circle to the right (STSCR). All four trials were performed twice by each horse and rider, for each saddle type. The study looked at peak (Fpeak) and average force (Fmean) and peak (Ppeak) and average pressure (Pmean), and average area (Amean). A linear mixed-effect model was used where which horse being ridden was nested within the rider as random effects, trial added as a confounding fixed effect, and saddle the main fixed effect. $P<0.05$ was taken to indicated statistical significance,

Results Significant differences were found between the DRS and Treed saddles for Ppeak, Pmean, FtotMax, Fmean and Amean in the canter data. Significant differences were also found between DRS and Treed for Ppeak, Pmean, FtotMax, Fmean and Amean in the Trot data.

Table 1 A comparison of force, area and pressure under two different types of saddle

Trial	Saddle	Fpeak (N)	Fmean (N)	Amean (cm2)	Ppeak (kPa)	Pmean (kPa)
CLCR2	DRS	99.6**	53.9***	1434.4***	24.2*	3.7***
	Treed	111.9**	61.4***	1223.2***	27.0*	5***
CLCR	DRS	106.5**	54.5***	1489.4***	22.5*	3.6***
	Treed	130.4**	66.1***	1322.3***	28.2*	4.9***
STSCR	DRS	93.5***	48.4***	1512.5***	20.4**	3.1***
	Treed	120.6***	61.6***	1375.4***	23.1**	4.4***
STSL	DRS	86.6***	47.4***	1503.3***	16.0**	3.1***
	Treed	116.2***	60.7***	1350.8***	21.2**	4.4***

* = $P \leq 0.05$
** = $P \leq 0.01$
*** = $P \leq 0.001$

Conclusion The reduced peak and average force and pressure measured under the DRS saddle indicates that this new design may offer benefits over a Treed design. Given the significantly larger contact area (Amean) of the DRS, a commensurate reduction in pressure is logical. However, the larger contact area (Amean) under the DRS does not explain the reduction in peak and average force, and warrants further investigation.

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The effects of manual chiropractic (McTimoney) and instrument assisted chiropractic on spinal mechanical nociceptive thresholds (MNTs) in flat racehorses without clinical signs

N Rossa[1,2], S Charlton[3], C Cunliffe[4]
[1]McTimoney Animal Association/Private Practice, Berkshire, UK, [2]McTimoney Chiropractic Association, Oxfordshire, UK, [3]McTimoney Animal Association/Private Practice, Staffordshire, UK, [4]McTimoney College of Chiropractic, Oxfordshire, UK
Email:sally@charltons.info

Implications Manual chiropractic technique (McTimoney) and instrument assisted chiropractic using an Integrator both increase MNTs, an indicator of reduced pain perception, compared to no treatment, on thoroughbred racehorses.

Introduction Chiropractor's core clinical action is spinal adjustments aiming to correct spinal joint misalignments. Research into the therapeutic effect of correcting spinal joint misalignments using chiropractic techniques on horses is limited. Numerous adjusting 'techniques' exist and various adjusting instruments have been developed over the years. The aim of this study was to objectively assess the influence of manual chiropractic technique (McTimoney) compared with instrument assisted chiropractic using an Integrator on pain perception levels using pressure algometry as an established method for the measurement of mechanical nociceptive thresholds (MNTs) to indicate pain perception (Haussler and Erb, 2003).

Material and methods Thoroughbred flat racehorses (n=24) from the same yard on the same training schedule were selected (mean bodyweight 461kg ±69kg, mean wither height 15.3hh±½ hh). The horses were clinically sound with no history of pre-existing back problems. They were randomly assigned into 3 equal groups, a control group (no treatment intervention) and two treatment groups (manual chiropractic or instrument assisted chiropractic using an Integrator). Treatments were undertaken by a qualified, experienced McTimoney Animal Practitioner and McTimoney Chiropractor. Triplicate MNTs were measured 8-10cm lateral to the dorsal midline at five bilateral anatomical sites along the thoracic and lumbar musculature using a digital pressure algometer by a single examiner blinded to the groups. Measurements were taken before treatment, immediately after treatment, and at 1, 3, 7 and 10 days post treatment on all animals between 2pm and 5pm. Normal distribution of data was assessed using the Komolgorov-Smirnov test. Paired t-test compared left-right comparisons for each measurement site. Pooled left and right MNT values were used to evaluate differences between groups. Paired t-test compared MNT differences within each treatment group. Percentage differences in MNTs were compared pre and post treatment and data analysed using repeated measures ANOVA.

Results There were no significant left to right side differences in 28 out of 30 (93%) measurement sites.
Both the Integrator and McTimoney groups showed significant increases in post-treatment MNTs over time compared to pre-treatment MNTs; a significant increase in MNTs, for the control group only occurred pre-treatment to day 1 (table 1).

Table 1 Statistical change in post treatment MNTs compared to pre-treatment MNTs at each time point (mean±SEM)

Group	Pre-Tx to day1	Pre-Tx to day 3	Pre-Tx to day 7	Pre-Tx to day 10
Integrator	1.38±0.25***	0.88±0.15***	1.07±0.22***	0.56±0.22*
McTimoney	1.15±0.22***	0.61±0.20**	0.74±0.23**	1.21±0.38**
Control	1.39±0.41*	-0.27±0.36 NS	0.45±0.36 NS	0.49±0.42 NS

*P<0.05, **P<0.01, ***P<0.001, NS P>0.05

There were significant differences in MNTs between the treatment groups on Day 10 (p=0.035) after treatment compared to pre-treatment. MNTs were significantly increased (p<0.05) for McTimoney group compared to the Integrator group (figure 1).

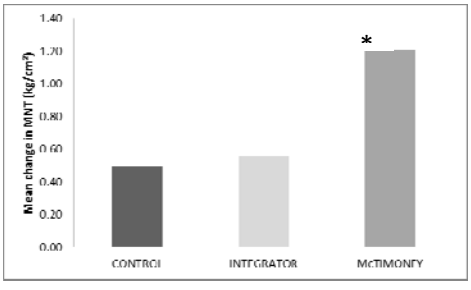

Figure 1 Mean change in MNTs from Pre-Treatment to day 10. * denotes significant difference

Conclusion Horses treated with manual chiropractic (McTimoney) and instrument assisted chiropractic using an Integrator show a significantly increased pain pressure threshold as indicated by increased MNTs across measurement sites compared with the control group on Days 1, 3, 7 and 10 post treatment. The McTimoney treatment appears to have a longer lasting effect, to day 10, on increasing MNTs compared to treatment with the Integrator. Further research to evaluate effects of the different treatments on horses with back pain would be of interest.

Acknowledgements Gratitude to Mr Sam Smith for the McTimoney treatments and Roseanne Heagerty for the Integrator treatments.

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The effect of manual chiropractic (McTimoney) treatment on pressure measurements beneath the saddle

A Crosby-Jones[1], N Routledge[2], C Cunliffe[3]
[1]McTimoney Animal Association/Private Practice, Wiltshire, UK, [2]McTimoney Animal Association/Private Practice, Devon and Somerset, UK, [3]McTimoney College of Chiropractic, Oxfordshire, UK
Email:sally@charltons.info

Implications A reduction in mean pressure beneath the saddle following manual chiropractic (McTimoney) treatment has implications for saddle fit, and the sequence of back treatment and saddle fitting.

Introduction Back problems in horses are recognised as an important factor in performance impairment. Saddle fit is considered a key factor in the aetiology of back problems (Harman 1995; de Cocq *et al* 2006) and has been shown to affect the forces acting on the horse's back (Meschan *et al* 2007). An integrative approach to solving back pain increasingly involves complementary therapies. Quantifiable scientific research of relationships between effects of manual chiropractic treatment (McTimoney) and saddle pressure would be useful.

Material and methods Twelve horses of varying breeds and ages (age 4-16 years; 8 geldings and 4 mares; height 15.1-16.3hh) were randomly assigned into two groups. Each horse was ridden in their own saddle by the same rider (61kg) along a straight 30m track. The rider was blind to the horse groups. The treatment group (n=6) received manual chiropractic (McTimoney) treatment; the control group (n=6) received an assessment but no treatment intervention.
Mean overall pressure (MOP) and mean peak pressure (MPP) were measured at walk, rising trot and sitting trot using a TekScan CONFORMat pressure sensing system. Readings were taken before and one day after treatment/no intervention.
Pressure differentials (KPa) were calculated by comparing pre and post pressure values. Data was analysed by Levene's test. Repeated Measures General Linear Model assessed relationships between pre and post activity pressure differential (PD), gait on pre-post PD, treatment on pre-post PD and interactions. Statistics were performed using SPSS 18 software package, with significance set at $P<0.05$.

Results Manual chiropractic treatment (McTimoney) significantly reduced MOP ($P<0.001$) and MPP ($P<0.001$) at all gaits. Differentials in MOP were greatest at rising trot(15%), sitting trot(12.5%) and then walk(9.5%) (table 1). Differentials in MPP were greatest at rising trot(11.4%), sitting trot(11.2%) then walk(8%). There was no significant difference in pre/post MOP ($P=0.183$) or MPP ($P=0.792$) for the control group. Pressure differentials were not affected by changing gait.

Table 1 Pre/post MOP(KPa) for treatment and control groups with differential, percentage change and standard deviation

	Treatment group			Control group		
	Walk	R.trot (av)	S.trot (av)	Walk	R.trot (av)	S.trot (av)
Pre	14.75	12.18	12.26	12.92	12.43	12.53
Post	13.35	10.31	10.73	13.88	11.76	11.82
Differential	1.40	1.87	1.53	-0.97	0.66	0.72
% change	9.5	15.0	12.5	7.5	5.3	5.7
St. Dev.	0.99	1.32	1.08	0.68	0.47	0.51
P-value	P<0.001	P<0.001	P<0.001	NS	NS	NS

R.trot= rising trot, S.trot = sitting trot NS= not significant ($P>0.05$)

Conclusion The results provide positive evidence that manual chiropractic (McTimoney) treatment has an effect on the equine back and reduces mean pressure values beneath a saddle up to one day following treatment. Further research is required to understand the longer term effect of chiropractic treatment on saddle pressure and the effect on saddle fit. Further research could ascertain the appropriate sequence of back treatment and saddle fitting.

Acknowledgements Supported by the Saddle Research Trust; McTimoney College of Chiropractic; McTimoney Animal Association.

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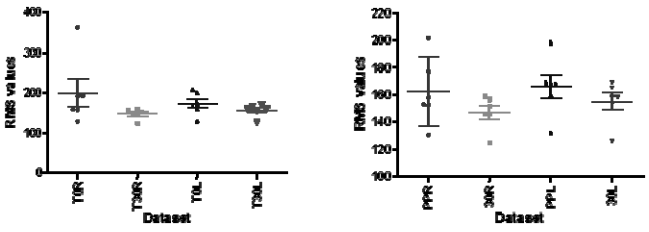
A preliminary study of the effect of manual chiropractic treatment on the splenius muscle in horses when measured by surface electromyography

J Langstone[1,4], J Ellis[2], C Cunliffe[3]
[1]McTimoney Animal Association/Private Practice, Oxfordshire, UK, [2]Warwickshire College, Moreton Morrell Centre, Warwickshire, UK, [3]McTimoney College of Chiropractic, Oxfordshire, UK, [4]International Equine Body Worker Association, Oxfordshire, UK
Email:sally@charltons.info

Implications Measuring muscle activity may be a useful and effective way of determining the effectiveness of chiropractic treatment in horses.

Introduction The McTimoney chiropractic method has been practised for over 70 years but there is limited scientific data to support the physiological improvements with animals. This method uses short lever, high velocity, low amplitude thrusts using the hands, to induce a therapeutic response in joint structures, muscle function and nerve reflexes. Much research to date has concentrated on the thoracic and lumbar and not the cervical area of the spine. A quantifiable measure of muscle activity related to the cervical spine will provide further understanding of the equine athlete. Surface Electromyography (sEMG) is a non-invasive method of measuring muscle activity. The splenius muscle is in part a stabilising muscle of the cervical spine and therefore shows activity when the horse is at rest. Measurement of the activity in a stabilising muscle and assessment of any changes may provide evidence based support for chiropractic techniques. The aim of this study was to determine if there is a relationship between objective measurable muscle parameters and misalignments and muscle tension in the cervical spine of equines.

Material and methods A controlled paired randomised study was designed using 14 privately owned horses (10 geldings, 4 mares) stabled on the same yard with mean age 9.9 years (range 5 to 25), mean height 157.8cm (range 127-173cm) . The horses were distributed between the control and treatment group by matching work, management regime, age, sex and breed. The treatment group (n=7) received McTimoney method chiropractic treatment for the neck, back and pelvis following palpation. The control group received palpation only. A Delsys 4 sensor system was used for data collection. The probes were positioned as recommended by De Luca (2002), at a half-way point between C1/C2 joint and the crest of the neck on the left and right sides, between the tendon insertion and the motor point to maximise the signals. sEMG readings were taken from the splenius muscle at time zero (0), immediately post palpation (PP) and 30 minutes post palpation (30). Each reading was taken for 20 seconds. Methodology was similar to Licka *et al* (2009).
The Delsys analysis software averaged and smoothed the data providing a root mean square value of the signal amplitude at each datum point. After testing for normality, data was analysed by one-way ANOVA for a global inter-group analysis and by two-tailed, non-parametric, paired T-test (Wilcoxon matched pairs) between control and time-points and treatment and time-points and also control and treatment groups combined and time-points, for both left and right side. Control and treatment group were combined at time zero and post palpation as this is before treatment and hence the individuals have all received identical procedure. Statistical significance was accepted at $p<0.05$.
Results Pre-treatment, there was a significant difference ($p<0.05$) between sEMG analysis at 0 and PP for control and treatment groups combined but no significant difference between left and right sides at these time points.
Post treatment, there was a significant decrease ($p<0.01$) in sEMG activity for treatment group at 0 to 30 and PP to 30 (left and right combined). There was a significant decrease ($p<0.05$) in sEMG for right side for treatment group at 0 to 30 (figure 1a) and PP to 30 (figure 1b). There were no such significant effects for the control group. The majority (83%) of horses had atlas rotation and tilt to the right.



Figures 1a and b Comparison of RMS values for treatment group, left and right, at time points 0 to 30 and PP to 30

Conclusion This preliminary study supports the use of sEMG as a means of assessing muscle activity of equines. This study suggests a statistically significant reduction in splenius muscle activity is observed following manual chiropractic (McTimoney) treatment although the benefit to the horse is unknown. The reduction in splenius muscle activity post palpation may be due to therapeutic touch and/or habituation. Further research is recommended to establish measureable effects in relation to performance parameters.

Acknowledgements McTimoney College of Chiropractic, Oxford for assistance with the hiring of the equipment.

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Causes of early equine pregnancy loss: are we making progress?

A M de Mestre
The Royal Veterinary College, London, UK
Email:ademestre@rvc.ac.uk

Reproductive efficiency is important for both the economic success and the health and welfare of mares and stallions in equine breeding programs. Pregnancy losses remain a significant contributor to reproductive wastage with approximately 15% of pregnancies confirmed at 15 days post ovulation subsequently lost. Internationally there is variation in whether these losses occur more commonly in the embryonic period (prior to day 42), as observed in Thoroughbred breeding programs in the UK, or late in gestation, as is seen in the USA. The largest published epidemiological study of early pregnancy loss in UK Thoroughbreds was performed in 2002 and showed that around 8% of pregnancies are lost prior to day 42, a figure that represents 60% of all pregnancies lost (Allen *et al*, 2007). Whilst the loss of a pregnancy late in gestation has a more obvious financial consequence, studies have shown that failure of early pregnancies can also have a significant financial impact due to a 'drift' in foaling dates that results in a season without a foal. Indeed, mares need to produce a foal in six out of seven years to be financially viable (Bosh *et al*, 2009).

Despite the clear importance of early pregnancy loss (EPL), we still know very little about what causes this condition and as a result, a definitive diagnosis is rare. Poor progress in this area is exacerbated by the fact that most cases of EPLs are diagnosed retrospectively and complete sets clinical data for mares that experience EPL are limited. Our laboratory has been focusing on identifying novel causes of EPL in the mare. We propose that a proportion of cases of unexplained EPL, particularly in older mares, arise due to gross chromosomal defects. Recently we have developed a method to isolate and culture cells from failed early equine conceptuses that will enable us to perform these genetic studies. Over the 2013 and 2014 breeding seasons, 29 failed conceptuses have been submitted to the laboratory, of which 23 were placed in culture. Cells were successfully cultured from 18/23 (78%) conceptuses. Cells are currently being karyotyped using array Comparative Genomic Hybridisation (a-CGH) and fluorescent *in situ* hybridisation (FISH). Alongside this study, we are performing a prospective cohort study to determine the current incidence of EPL, identify risk factors, and better define clinical characteristics associated with the condition. Preliminary analysis of data collected on 1007 pregnancies in the 2013 breeding season has been performed. The total incidence of EPL was 8.3% between days 15 and 65, with 6.4% of pregnancies lost between days 15 and 42 and 2% between days 43 and 65. This suggests that the incidence of EPL has changed little in the 14 years that have passed since the last epidemiological study of reproductive efficiency (Allen *et al*, 2007).

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Effect of Single Layer Centrifugation (SLC) on mitochondrial membrane potential and reactive oxygen species production by stallion spermatozoa

J Morrell, A Lagerqvist, P Humblot, A Johannisson
SLU, Uppsala, Sweden
Email:jane.morrell@slu.se

Implications The reduced hydrogen peroxide production could explain the longer retention of fertilizing capacity seen in SLC-selected sperm samples, with implications for prolonging sperm storage for artificial insemination.

Introduction Additional methods for evaluating fresh stallion sperm quality are needed to determine which ejaculates are potentially capable of fertilization. Studies on human sperm have shown that low mitochondrial membrane potential (ΔΨm) is associated with fertility problems in men but evaluation of this parameter is not routinely used when assessing stallion spermatozoa. Single Layer Centrifugation (SLC) has been shown to select robust stallion which result in a higher pregnancy rate than controls after artificial insemination (AI). The purpose of this study was to measure ΔΨm and reactive oxygen species (as a measure of metabolic activity) before and after SLC.

Material and methods Ejaculates from 14 stallions were prepared as commercial semen doses and were sent to the laboratory for SLC with Androcoll-E and evaluation 24h after semen collection. Sperm motility was analysed by computer assisted motility analysis using the SpermVision motility analyser (Minitűb GmbH, Tiefenbach, Germany). The following flow cytometric analyses were performed [1]: membrane integrity was evaluated by staining with SYBR14 and propidium iodide; chromatin integrity was analysed using the sperm chromatin structure assay (SCSA), staining with acridine orange. The measurement of ΔΨm was made by staining with the lipophilic substance 5,5,6,6-tetrachloro-1,1,3,3-tetraethylbenzimidazolyl carbocyanine iodide (JC-1). Superoxide and hydrogen peroxide were measured with dihydrodichlorofluoresceindiacetate (H_2DCFDA) and hydroethidine (HE); the method was modified from [1] in that the sperm samples were not washed before staining. Data were analysed by ANOVA using a Generalized Linear Model (SAS version 9). Results are presented as Lsmeans ±s.e.m..

Results Sperm motility, membrane integrity and chromatin integrity were higher in the SLC-selected sperm samples than in control samples (Table 1). The SLC-selected sperm samples contained a significantly lower proportion of hydrogen peroxide producing sperm (H2O2+) than controls, although other categories of ROS-production were not different between treatment groups (Table 2). There was no difference in the ΔΨm between the two groups (Table 1).

Table 1 Various parameters of sperm quality before and after Single Layer Centrifugation (n=14)

Group	Tot mot	Prog mot	Living	Dead	Dying	%DFI	Low ΔΨm	High ΔΨm
Control	71±14***	47±15***	70±13*	24±12*	1.4±1	16.5±7*	50±22	45±22
SLC	82±12***	59±15***	78±11*	19±10*	1.5±1	13.2±8*	59±26	36±26

Difference between treatments * P<0.05; *** P<0.001.

Table 2 Various parameters of ROS production before and after Single Layer Centrifugation (n=14)

Group	Live SO-	Live SO+	Dead SO+	Live H202-	Live H2O2+	Dead H2O2-	Dead H2O2+
Control	49±14	11±7*	40±13***	7±7***	54±12***	2.4±2.3***	36±13***
SLC	53±16	16±7*	31±15***	70±14***	0.38±0.5***	30±14***	0.2±0.4***

Difference between treatments * P<0.05; *** P<0.001.

Conclusion Mitochondrial membrane potential is not influenced by SLC; other parameters of sperm quality are significantly better in the SLC samples than in controls. The lower hydrogen peroxide in SLC samples warrants further investigation.

Acknowledgements We thank Lövsta Stuteri for sending the semen samples used in this study.

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The effect of a sperm washing step on flow cytometric evaluation of reactive oxygen species production by stallion spermatozoa

J.M. Morrell[1], A. Georgakas[1,2], D. Nash[2], M.C.G. Davies Morel[2], A. Johannisson[3]
[1]Department of Clinical Sciences, Swedish University of Agricultural Sciences (SLU), Uppsala, Sweden, [2]Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, Aberystwyth, Wales, UK, [3]Department of Anatomy, Physiology and Biochemistry, Swedish University of Agricultural Sciences (SLU), Uppsala, Sweden
Email:equus.athan@gmail.com

Implications A sperm washing step before flow cytometric (FC) measurement of reactive oxygen species (ROS) production by stallion spermatozoa might affect the results of the assay, and therefore it should be avoided.

Introduction The use of FC measurements for the assessment of ROS production in stallion spermatozoa allows an objective assessment of spermatozoa quality and thus possibly a prediction of fertility. The impact of a sperm washing step before FC evaluation of ROS production in stallion sperm samples was assessed in order to develop a more effective method for ROS analysis.

Material and methods Ejaculates (n=31) were collected from 9 Warmblood stallions. The gel-free portion of each ejaculate was extended with INRA96 at 37°C to prepare semen doses for AI, containing approximately 1 billion motile spermatozoa per dose. The semen doses were packed (at approximately 6°C) and sent overnight to the laboratory for treatment and evaluation at approximately 24h after semen collection. Upon arrival at the laboratory all the materials (semen samples, CellWash) were equilibrated at room temperature of approximately 22°C for 30 minutes. Each semen sample was split to form two treatment groups: washed and not washed. For the sperm washing treatment, 500 µL of semen samples were extended in 2500 µL CellWash and centrifuged for 10 min at 400 x g and 20°C. The supernatant was discarded and 500 µL CellWash added. Aliquots (500 µL) of extended semen that had not been washed were also available. From all samples, 30 µL were removed into new, labeled tubes and 270 µL of CellWash were added to each tube, for staining for ROS evaluation. As described in Morrell *et al*. (2009) a LSR flow cytometer (Becton Dickinson) equipped with standard optics was used for the analysis. The reagents used for analysis of ROS formation were H2DCFDA and HE whereas Hoechst 33258 was added to differentiate sperm viability. Menadione was used to stimulate ROS formation, as a control that the spermatozoa were capable of producing ROS (Guthrie *et al*., 2008). Briefly, Hoechst 33258 (final concentration 1.2 µM), HE (1.2 µM) and H2DCFDA (60 µM) were added to 300 µL semen samples and incubated for 30 min at 37°C. Stimulation of ROS formation was assessed after addition of menadione (200 µM) to the samples just before incubation. Data analysis was performed with the Statistical Analysis Systems software (version 9.2; SAS Institute Inc., Cary, NC, USA), using the procedure known as Differences of Least Squares Means to examine differences in treatment means.

Results Sperm washing had a significant effect on peroxide production of non-stimulated preparations and on superoxide generation in menadione-stimulated sperm samples. The proportion of living, superoxide positive spermatozoa was significantly increased ($P < 0.01$) after cell washing. Peroxide generation was significantly higher in unwashed living spermatozoa (41.18 versus 2.42%; $P < 0.01$). The percentage of dead cells that generated peroxide was significantly reduced after the sperm-washing step (from 20.62 to 0.59% $P < 0.001$). Menadione stimulation of washed stallion spermatozoa resulted in a significant decrease of living, superoxide negative spermatozoa (from 45.3 to 23.9%; $P < 0.001$) and an increase of living, superoxide positive cells (from 11.8 to 39.9%; $P < 0.001$).

Table 1 Effects of sperm washing on ROS production of extended stallion spermatozoa

	Living SO-	Living SO+	Dead SO+	Living P-	Living P+	Dead P-	Dead P+
No wash	60.78±2.47	2.59±2.46	36.43±2.11	34.5±8.58	41.18±8.36	14.66±5.22	20.62±6.18
Sperm wash	59.23±4.32	8.3±7.67[a]	31.79±5.34[b]	63.43±6.56[b]	2.42±3.22[a]	30.47±5.25[b]	0.59±0.36[b]

Values shown as Least Squares Means (± SD). Statistical significance between treatments is [a] ($P < 0.01$) and [b] ($P < 0.001$). For Living SO- non-significant differences were observed.

Conclusion Sperm washing before FC evaluation of spermatozoa might interfere with the evaluation of ROS production. A washing step before FC evaluation of ROS-production in sperm samples should be avoided.

Acknowledgements Thanks to Dr Nils Lundeheim for performing the statistical analysis. Semen samples were collected and sent to the laboratory by the personnel of the National Stud of Sweden (Flyinge A.B.).

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Restriction of daylength does not influence the time of the final ovulation during the autumn transition in mares

J Newcombe
Equine Fertility Clinic, Warren House Veterinary Centre, Walsall, UK
Email:john@warrenhousevets.com

Implications Decreasing daylength is thought to be primarily responsible for the reduction and cessation of follicular activity of mares in the autumn transition.

Introduction The resumption of ovulatory activity in mares during the spring transition is highly correlated with increasing day length and occurs within a relatively short window of time (April and May) with just a few mares ovulating earlier in late March or not until June (Northern Hemisphere). In addition, it can be accelerated by artificially increasing the daily exposure to white or blue light.
Conversely, the last ovulation of the breeding season occurs over a much longer window, anytime from September to January with a few mares ceasing to ovulate in July and August or remaining cyclic until February. Also a small number of mares even continue to cycle throughout the winter. To what extent is follicular activity during this autumn transition influenced by decreasing day length?

Material and methods Twenty three (23) cyclic Irish Draught and cross-bred mares (Group 1) were housed in darkened stables from the first week of October and restricted to 8 hours daylight. Another 60 mares from the same herd (Group 2) acted as controls. These were housed from the same date but subjected only to ambient day length.
From the first week of December, both groups were subjected to 15-16 hours day length, comprised both of ambient and artificial lighting. Mares were examined at least once daily and all developing follicles were followed until they had ovulated or regressed
Mares which had their last ovulation in or before the first week of October, were not included in the study

Results The mean date of the last ovulation before an extended period of anoestrus was December 5th and December 6th for Groups A and B respectively
The percentage of mares which had last ovulations in November were 35% and 38%, in December were 57% and 50%, and in January were 9% and 12% for Groups A and B respectively.
Two mares (8.7%) in Group A and 5 mares (8.3%) in Group B continued to cycle throughout the winter and through to spring.

There was no statistical difference ($p<0.05$) between Groups of either the mean ovulation date, the percentage of mares ovulating in each month, or the percentage of mares which continued to cycle throughout the winter (student t-test).

Conclusion The relatively small reduction in daylength before the autumn equinox suggests that those mares which cease to ovulate in July, August and September are either very sensitive to this reduction or are influenced by other factors. The results of this study further suggest that decreasing ambient day length has only a limited influence on the autumn transition. The influence of other factors, especially the possibility of entrainment by previous short-day and long-day cycles needs investigation.

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Effect of mating to ovulation interval on foal gender, live foal rate and pregnancy rate in Thoroughbred horses

N Tarapor[1], M Davies-Morel[1], J Newcombe[2]
[1]Aberystwyth University, Ceredigion, UK, [2]Warren House Veterinary Centre, Brownhills, West Midlands, UK
Email:natashatarapor@hotmail.com

Implications Mating to ovulation interval had no effect on foal gender. Spermatozoa survived for up to 5 days in the mares' reproductive tract and fertilized ova without causing a significant decline in live foal rate (LFR) and pregnancy rate (PR).

Introduction The viability of sperm and ova determine the maximum interval at which a mare can be covered prior to or post-ovulation (Woods *et al.*, 1990). Therefore, optimum timing of both insemination and mating should increase reproductive efficiency (LFR and PR). Evidence suggests that a number of factors affect the variation in mammalian offspring sex ratio (SR) (Clutton-Brock and Iason, 1986). It is hypothesised that there are equal numbers of sperm bearing the X and Y chromosome and the probability of ovum fertilization is unrelated to the sex chromosome (James, 1996). This indicates that physiological and environmental factors may be responsible for any variation in SR; however, the specific cause of variation is yet to be established. Thus, the aim of this study was to investigate whether distinct mating to ovulation intervals should receive particular attention when trying to attain a foal of a specific gender and maximise LFR and PR.

Material and methods The retrospective records for 2,675 Thoroughbred mare pregnancies (2001-2012) were recorded for mating to ovulation interval and resulting pregnancy outcome recorded as gender of foal, barren or lost (slipped, aborted or dead foals) obtained from Weatherby's Return of Mares. From the data collected, the proportion of colts and fillies born, LFR and PR were calculated. All mares were examined at 48 h intervals and from this, ovulation time was determined to within ±12 h. Matings were carried out 120 h before to 24 h after ovulation. Data from all 12 breeding seasons were pooled for analysis. Chi-square tests and stepwise regression procedures were used to analyse the data.

Results Mating to ovulation interval was found to have no significant effect on foal gender (Figure 1), LFR (Figure 2) and PR (Figure 3).

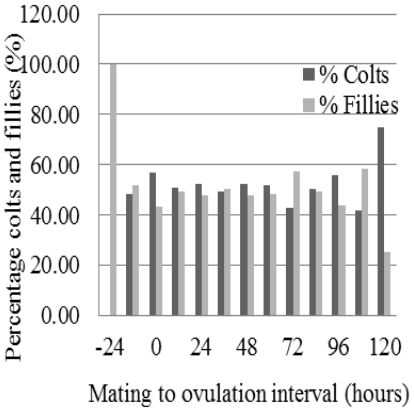

Figure 1 Effect of mating to ovulation interval on foal gender

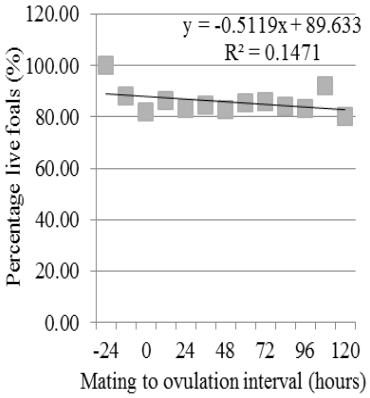

Figure 2 Effect of mating to ovulation interval on live foal rate

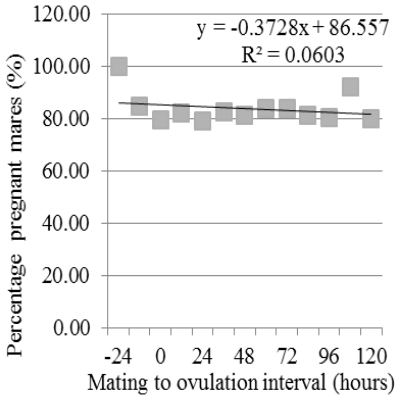

Figure 3 Effect of mating to ovulation interval on pregnancy rate

Conclusion The study found no consistent pattern in the SR of foals associated with mating to ovulation interval. The results also show that equine spermatozoa have the ability to survive for up to 120 h (5 days) within the mares' reproductive tract without having a significant effect on LFR and PR. While current management advice suggests covering mares every 48 h within oestrus for best fertility rates, this study indicates that covering mares at 120 h intervals might suffice, so as to reduce the workload placed on stallions. The use of stallions every 120 h, rather than 48 h, will reduce the incidence of endometritis and increase financial return. It would allow for more mares to be covered per season and reduce the number of coverings per mare per foal, which is of particular significance to mares that suffer from persistent post-coital endometritis.

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Education in partnership with industry: what BEF does and what we could do

J Rogers, J Dixon
British Equestrian Federation, Abbey Park, Stareton, Kenilworth, Warwickshire CV8 2RH
Email:jan.rogers@bef.co.uk

The British Equestrian Federation (BEF) is the National Governing Body for horse sports in the UK. It exists to provide leadership, vision and purpose and supports the direction of equestrianism through its Strategic Plan.

The BEF is responsible for distributing Government funding to the equestrian sports. Funding from UK Sport and Sport England supports the BEF's work from developing the best riders, with the aim of winning medals for Great Britain, to encouraging new and returning riders to improve their fitness by taking part in sport.

The BEF is an umbrella organisation representing the interests of 4.2 million riders, vaulters and carriage drivers in Great Britain via 19 independent member bodies (15 members and 4 associates). Established in 1972 it is the largest representative body within the equestrian industry and influences informed policy development, in collaboration with other key industry bodies through the Equine Sector Council and the British Horse Industry Confederation (BHIC).

The BEF's Equine Development portfolio has responsibility for Federation research matters and has its own committee dedicated to research. This committee is Advancing Equine Scientific Excellence (AESE) and is chaired by Prof Pat Harris and administered by Dr Georgina Crossman.

Our session at CFER will be jointly presented by Jan Rogers (BEF Head of Equine Development) and Dr Jo Dixon (Senior Research Fellow) who is able to share some specific practical examples of how BEF data is currently being used by students to complete Research Master Degree programmes, and how these analyses have benefitted horse owners.

Delegates can expect to find out about how important data is to inform industry decisions, AESE's collaborative studies and case studies, industry partnerships for PhDs, how BEF datasets have been used and European funding for genetics research.

Preliminary investigation into equine coat colour bias within the British Breeding Futurity young horse evaluations

A Fisker Hansen[1,2], H Randle[2], J Dixon[2,3]
[1]Plymouth University, UK, [2]Duchy College, Callington, UK, [3]Plymouth Marine Laboratory, UK
Email:anna.fiskerhansen@plymouth.ac.uk

Implications 'Blocked Coloured' (BC) and 'Spotted' (Sp) horses had significantly lower Premium Scores than 'Solid' (S) coloured horses, suggesting a negative horse coat colour bias influencing potential performance horse evaluations.

Introduction The British Equestrian Federation (BEF), under the auspices of the British Breeding Futurity, annually evaluates >700 young horses (Foals-3yo) for their potential as future performance horses. Individual horses are evaluated on a discipline basis (Dressage, Show Jumping, Eventing or Endurance). Feedback from participants has suggested that a bias in the evaluations according to the horses coat colour exists. Since the premium scores awarded at the Futurity can influence the 'worth' of a horse, any bias in scoring could have financial implications for the British equine sector. Judging bias according to athletes' uniform colour has been found in several studies e.g. that of Hageman *et al.* (2008) and changing 'fashions' in horse coat colour is apparent through history as described by Linderholm and Larson (2013). However, no prior research has investigated judging bias according to the coat colour of the horse. The aim of this preliminary research project was to (1) investigate whether equine coat colour bias exists within the Futurity evaluations and (2) evaluate in which discipline or part of the evaluation process this occurs.

Material and methods Premium scores awarded to horses exhibited in the 2012 BEF Futurity (n=750) were used as the dependent variable, comparing horse coat colour groups, using descriptive statistics, Oneway ANOVA and Tukey HSD post hoc analysis in IMB SPSS statistics 21. Horse colours were grouped according to phenotype similarities: Bay (n=422): light bay, bay, dark bay; Chestnut (n=126): chestnut, dark chestnut; Black (n=64); Block Coloured (BC) (n=49): piebald, skewbald; Grey (n=47); Dilutions (n=29): dun, buckskin, palomino and Spotted (Sp) (n=13): spotted, appaloosa, roan. Descriptive statistics and conditional formatting in Microsoft Excel 2013 were used to ascertaining apparent changes in the mean premium scores awarded between disciplines Dressage (n=274), Show Jumping (n=151), Eventing (n=306) and Endurance (n=19), and in component scores of the different aspects of the evaluation process (veterinarian, frame and built, walk, trot, canter and athletism).

Results BC and Sp horses had the lowest mean premium score across all disciplines (Table 1), and in all aspects of the evaluation process. Low premium scores of a few individual Sp horses however skewed the mean of this coat colour group. Not all horse coat colour groups were represented in the Endurance evaluations. BC coloured horses had significantly lower Premium scores compared to all other 'Solid' (S) coat colour groups (Table 1). No other coat colour group had significantly different premium scores from other coat colour groups.

Table 1 Significant levels of horse coat colour group comparisons (BC to all other colour groups)

Coat Colour Group (I)	Coat Colour Group (J)	Mean Premium Score	Mean Difference (I-J)	Standard Error
Block Coloured (Mean Premium Score=8.03)	Bay	8.41	-.39*	.06
	Chestnut	8.38	-.35*	.07
	Black	8.41	-.38*	.07
	Spotted	8.13	-0.10	.12
	Grey	8.34	-.31*	.08
	Dilutions	8.43	-.40*	.09

*. The mean difference is significant at the 0.05 level.

Conclusion 'Blocked Coloured' and 'Spotted' horses had significantly lower premium scores than 'Solid' coloured horses. This did not differ according to discipline or in the different aspect of the evaluation process. Further analysis of data from multiple years of Futurity evaluations, will allow investigation of this apparent bias and its significance with a larger sample size.

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