Developing Talent Proceedings

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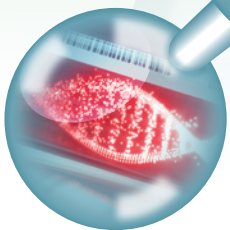
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The Developing Talent Proceedings of the British Society of Animal Science constitutes summaries of papers to be presented as part of the Developing Talent Sessions at the Society's Annual Conference.

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Welcome

The British Society of Animal Science (BSAS) aims to provide an opportunity for those with an interest in animals and animal science to exchange views, ideas and information. It is an energetic and active society with members from countries throughout the world.

Today, as ever, the Society is the natural connecting point for all of those with an interest in animal science and related sectors. Its membership is drawn from research, education, advisory work, commerce and practical animal keeping.

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Contents

Quality attributes of eggs from laying hens fed supplemental selenium and α-tocopherol

F. O. Jemiseye[1], O. A. Ogunwole[1], A. O. Mosuro[2]
[1]University of Ibadan, Ibadan, Nigeria.
[2]Lead City University, Ibadan, Nigeria.

Presenting author:
Folasade Jemiseye. E- mail: jemiseyefo@gmail.com

Application: Improvement of egg production and quality, inhibition of cholesterol and lipid oxidation during storage of eggs and cooking, improvement in the egg shelf life during storage, and most importantly the production of antioxidant-fortified eggs are some of the expected importance of inclusion of the nutrients.

Introduction: A change in egg quality can be aggravated by several features. Management and dietary modifications are available to help alleviate the problems of egg quality. Selenium and α-tocopherol are antioxidants that are associated with quality of eggs from hen. While selenium has sparing effects on vitamin E. However, there have been conflicting reports of dietary supplementation of selenium and α-tocopherol on egg quality parameters of laying.

Materials and Methods: The experiment was carried at the Poultry section of the Teaching and Research Farm, University of Ibadan, Ibadan, Oyo state Nigeria. Effects of dietary supplements of selenium and α-tocopherol on egg quality attributes were evaluated in a 20 weeks trial. ISA brown pullets (n=192) at week 31 of age were assigned to six experimental diets. Basal diet (T1) was without supplementation while other diets; T2, T3 and T4, contained 0.5, 1.0 and 1.5 mg/kg supplemental selenium, respectively. Diets T5 and T6 were supplemented with 20 and 40 mg/kg vitamin E, respectively. Each treatment comprised four replicates with eight birds per replicate allotted in a completely randomised design.

Measurements of the egg internal contents were achieved using standard methods (Monira et al., 2003). Haugh was determine as described (Haugh, 1937. Data were subjected to analyses of variance (SAS, 2003) and means were separated at α0.05 using Duncan multiple range test option of the same software.

Results: Albumin weight and haugh unit were not significantly affected (p>0.05) by the dietary supplements of selenium and α-tocopherol. Egg albumin length (69.62), yolk weight (12.74) and yolk to albumin ratio (0.35) was significantly lower in hens on 40mg/kg α-tocopherol supplementation. Yolk weight to albumin weight was increased with selenium supplementation at 0.5 (0.40), 1.0 (0.40) and 1.5 (0.41) mg/kg. Supplementation has no significant effect on egg Haugh Unit. Egg yolk weight to albumin weight was increased with selenium supplementation at 0.5, 1.0 and 1.5 mg/kg.

Conclusions: Dietary supplemental selenium at 0.5, 1.0 and 1.5 mg/kg in the hens' diet enhanced egg yolk weight to albumin weight.

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Meat quality of adult Sahelian does fed a basal diet of *Brachiaria decumbens* supplemented with probiotics and concentrates

O. Alhassan, A.A. Yunus, O. Emmanuel Lartey Kwame, A-K. Victoria, I. Frank
Kwame Nkrumah University of Science and Technology, Kumasi, Ghana.

Presenting author:
Abdul Aziz Yunus. E-mail: binyunus2010@gmail.com

Application: Probiotics could be incorporated at 100g per 100kg of concentrate supplement and fed at 1000g/d per doe for improved carcass quality.

Introduction: Ruminant production is aimed at producing good quality and healthy animal protein in the form of milk and/or meat. Such healthy animal products should have for instance lower levels of saturated fatty acids but with higher levels of the unsaturated fatty acids in the fat deposits. Adequate good quality feeding is thus a prerequisite for the realisation of this objective. The integration of agro-industrial by-products as concentrates into ruminant diets can help to alleviate the shortfall in feed supply. Goat meat is reported to be lean and rich in nutrients. Nonetheless, several factors such as genetic make-up, age, sex and type of feed all bring about variations in goat meat. Increasing concern for physical welfare and good health has heightened the need for information regarding the intake of healthy animal products. Probiotics are noted for features that promote health and so could be valuable for improving meat quality. This experiment evaluated the effects of probiotics and concentrates supplementation on meat quality of Sahelian does on *Brachiaria decumbens* grass basal diet.

Materials and Methods: Twenty-four Sahelian does averaging one year and weighing 13.3±1.16kg were randomly allocated in a 2x2 factorial arrangement to four treatments in a Completely Randomised Design with 6 replicates and fed for 14 weeks. The factors were levels of locally formulated protein/energy concentrate (500g/day and 1000g/day) and Vicbinzy powder probiotics (0g and 100g per 100kg of the concentrate). The concentrate was formulated from millet mash residue, wheat bran, vitamin premix, oyster shell and common salt while the probiotics was composed of *Clostridium butyricum* ($\geqslant 5.0 \times 10^7$), *Bacillus subtilis* ($1 \times 10^9$cfu/g) and *Lactobacillus delbrueckii* subsp (1.8×10^9cfu/g). On the final day of feeding, three goats per treatment were slaughtered. Meat samples from longissimus lumborum were taken for proximate composition and evaluation of fatty acid profile. Data taken were subjected to Analysis of Variance using the PROC general linear model (GLM) of SAS (2002) statistical package and means separated using Tukey's pairwise comparison.

Results: The results revealed that supplementing probiotics and higher levels of concentrate led to increased crude protein content while concentrate and probiotics reduced crude fat content of the meat. Additionally, the treatments imposed led to reductions in saturated fatty acid concentrations while increasing the unsaturated fatty acid concentrations of the meat samples.

Conclusions: Meat obtained from does supplemented with probiotics and higher levels of concentrates had improved nutritional value due to increased crude protein content with reduced crude fat. In addition, probiotics and higher levels of concentrate were associated with improvement in the nutritional indices of fatty acids by decreasing saturated fatty acids and then increasing unsaturated fatty acids.

In vitro study of the effects of condensed tannins in Willow on the digestive process and methane emissions in cattle

J. Thompson[1], S. Stergiadis[2], T. Yan[3], L.A. Crompton[2], K. Theodoridou[1]
[1]Queens University, Belfast, United Kingdom.
[2]University of Reading, Reading, United Kingdom. [3]Agri Food and Biosciences Institute, Hillsborough, United Kingdom.

Presenting author:
Josh Thompson. E-mail: jthompson80@qub.ac.uk

Application: Willow is a tree fodder containing condensed tannins that has potential to improve protein efficiency, reduce ammonia and methane emissions and make farming more carbon-neutral for ruminant production systems.

Introduction: Ruminants contribute to UK agricultural methane emissions and their impact on climate change is a major concern. Willow contains condensed tannins (CT) able to bind proteins, inhibit their ruminal degradation and methanogenesis [1]. This study explored the effect of willow's CT on in vitro rumen fermentation.

Materials and Methods: Samples were collected from AFBI Hillsborough, N. Ireland, freeze-dried and ground at 1-mm screen. ANKOMRF Gas production system was used and incubations were done anaerobically at 39 °C for 24h in jars containing buffered rumen juice from 3 dairy cattle from the abattoir, Coleraine, N. Ireland. Gas production, pH, methane concentration (gas chromatography) in headspace gas samples, ammonia [2] in the fermentation medium, were measured at 0h, 3.5h and 24h. To assess effects of CT, incubations were made with and without polyethylene glycol (PEG), which deactivates CT [3]. In this study, 4g of willow and silage at different inclusion rates (0:100, 25:75, 50:50, 75:25, 100:0) were incubated. Two in vitro runs were carried out. Data were analysed by two-way ANOVA with willow inclusion rate and treatment being the variables.

Results: Methane concentration was significantly ($P<0.01$) lower for the willow incubation (100%) and was reduced by 23%, in comparison to silage (100%). No significant differences ($P>0.05$) were observed between treatment (-PEG/+PEG) at each inclusion rate of willow. Ammonia production (mg/L NH3) was significantly ($P<0.05$) reduced by willow inclusion and treatment at 3.5 hours. After 24 hours, a similar trend observed increasing willow inclusion reduced ammonia production (ml/LNH3) ($P< 0.001$), however the effect of treatment and willow inclusion on ammonia production was inconclusive ($P=0.1$).

Conclusions: Willow could be a potential approach to mitigate the adverse effects of climate change and improve animal performance when used as tree fodder or in silvopastoral systems. Further in vitro trials are necessary to select the most suitable variety and harvest strategy. Willow needs also to be further evaluated in vivo to ensure it has no negative effects on animal health, productivity, or product quality.

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Impact of dietary crude protein concentration in dairy cow diets on nitrogen use efficiency and relationships with residual feed intake

Agalu Zeleke[1], Conrad Ferris[2], Jon Moorby[3], Sharon Huws[1]
[1]Queen's University, Belfast, United Kingdom. [2]Agri-Food and Biosciences Institute, Hillsborough, United Kingdom. [3]Aberystwyth University, Aberystwyth, United Kingdom.

Presenting author:
Agalu Zeleke. E-mail: zwondimagegnehu01@qub.ac.uk

Application: Understanding relationships between nitrogen use efficiency and residual feed intake will help us to select more efficient cows.

Introduction: There is evidence that cows with higher nitrogen use efficiency (NUE (%); milk N/N intake x 100) also have lower residual feed intake (RFI), although the underlying mechanism is unclear. The present study examined the relationships between NUE and RFI for cows offered diets differing in crude protein (CP) concentration.

Materials and Methods: Ninety Holstein dairy cows were offered diets containing one of three CP concentrations (15%, 16% and 17%, DM basis) for the first 180-days. Rations comprised equal proportion of grass silage and concentrates plus 0.3 kg straw/cow/day. Rumen samples were collected from all cows during weeks 4, 8, 12 and 20 post-calving. Mean performance data during four 5-week periods (weeks 2-6, 6–10, 10-14 and 18-22) was used to determine RFI. Residual feed intake was estimated for each individual cow during each 5-week period as the difference between measured DM intakes, and DM intake calculated using energy equations within FiM (Feed-into-Milk) and the metabolizable energy density of the diets offered. A univariate ANOVA with protein levels as the main fixed effect was used to analyse feed intake, lactation, and NUE data. Rumen fermentation data were analysed using the following model: $Y_{ij}=\mu+P_i+T_j+(P \times T)_{ij}+e_{ij}$, where Y_{ij}=each observation, μ=overall mean, P_i=effect of CP, T_j=sampling period effect, $(P \times T)_{ij}$=effect of treatment x sampling period interaction, e_{ij}=error term. The correlation coefficients among variables were estimated using Pearson's correlation coefficient (r) in R.

Results: Feed intake, milk yield and milk composition did not differ between treatment groups (P>0.05). Rumen ammonia-N concentrations increased (P<0.01) with increasing dietary CP concentrations, while dietary CP concentration had no effect on ruminal pH (P= 0.638) and volatile fatty acid (VFA) concentrations (P>0.567). Rumen pH, and concentrations of ammonia-N and VFA's all changed over time, while there were no treatment x time interactions for any parameters. Nitrogen use efficiency varied significantly between treatments, with a mean of 33.7%, 33.1%, and 30.6% in the low, medium, and high protein treatments, respectively. Residual feed intake was negatively correlated with NUE (r= -0.573; P < 0.001), suggesting that cows with higher NUE, particularly those receiving 16% CP, also showed lower-RFI. The correlation coefficients for 15%, 16%, and 17% CP levels were -0.55, -0.83, and -0.75 with the regression equations y= 0.7x+34.4, y= -1.2x+33, and y= -1.6x+31.3, respectively, where y=NUE (%) and x=RFI (kg/d).

Conclusions: Reducing dietary CP from 17% to 15% improved NUE with no significant impact on cow performance. Furthermore, cows with low-RFI have an improved NUE.

Guest Speaker:
An investigation into the differential effects of conventional crate and PigSAFE postnatal environments on telomere length in piglets *(Sus scrofa domesticus)*

C. McPartland
SRUC, West Mains Road, Kings Buildings, Peter Wilson Building, Edinburgh, United Kingdom

Presenting author:
Catherine McPartland. E-mail: catmcpartland@gmail.com

Telomeres are non-coding DNA sequences located at the ends of chromosomes. They play a crucial role in protecting the important genetic code of animals and without them genetic material would be lost at each cell division. The natural, age related degradation of telomeres can be accelerated by various factors such as stressors in an animal's environment.
This is important in the context of animal welfare as premature shortening of telomeres has been linked to numerous physical and psychological ailments, as well as negatively impacting production traits in livestock. This project examined the effect of two different postnatal environments, farrowing crate and PigSAFE, to determine what effect, if any, they had on telomere length in piglets over the pre-weaning period. The objectives of this study involved the collection of tissue from the ear tagging of 92 piglets across the two environments at birth and again approximately 26 days later at point of weaning. DNA was then extracted from this tissue and qPCR used to determine relative telomere length. Adjusted T/S ratios indicative of relative telomere length were calculated, and ANOVA general linear models used to compare piglet telomere length between the two environments as well as to examine associations with sow parity and litter size. A Pearson's correlation was used to determine if there was an association between piglet average daily gain and telomere length. Results showed that post-natal environment had no effect on piglet telomere length at weaning ($F_1 = 2.82$, $p = 0.098$). Piglet ADG (Pearson correlation: -0.158, $p = 0.204$) or litter size also had no effect on telomere length at birth ($F_2 = 1.40$, $p = 0.253$) or at weaning ($F_2 = 1.79$, $p = 0.176$). Sow parity did have a statistically significant effect on telomere length however, with piglets from sows of lower parity displaying longer telomeres at birth ($F_1 = 6.60$, $p=0.013$) and weaning ($F_1 = 5.22$, $p = 0.026$) than piglets from sows of higher parity.

A validation approach for constrained estimates of genetic parameters from random regression models for Suffolk and Charollais sheep with insufficient mature weight records

E McGowan[1,2], R Mrode[1], M Coffey[1], G Simm[2]
[1]SRUC, Edinburgh, United Kingdom.
[2]University of Edinburgh, Edinburgh, United Kingdom

Presenting author:
Emma McGowan. E-mail: emma.mutch@sruc.ac.uk

Application: When few records are available late in the growth cycle of sheep, random regression modelling struggles to converge. Convergence can be achieved by constraining estimates to be within the parameter space, which can be validated using a multi-trait validation.

Introduction: Random regression modelling has been used across multiple animal species to model longitudinal data (Schaeffer, 2004). However, the model may result in inflated correlations between the parameters of the Legendre polynomial when there are few weight records. This study investigated the use of a multi-trait approach to validate estimates of genetic parameters for growth in Suffolk and Charollais sheep populations with few mature weight records. In these models, the correlations between the parameters of the polynomial were constrained within the parameter boundary space.

Materials and Methods: This project was conducted with two datasets with 14,870 Suffolk sheep with a total of 42,244 records in the first dataset and 148,334 Charollais sheep with 353,958 records in the second dataset. A random regression model (Model 1) with Legendre polynomial of order 1 and fixed effects of sex, season of birth, a fixed regression on age, flock, and management group was fitted. The parameters were constrained within parameter space by fixing the correlation between the slope and intercept of the polynomial at three different levels 0.2, 0.5, and 0.7. Genetic parameters were estimated from the results of the model. For the Charollais dataset, Model 2 with Legendre polynomial of order 1 and fixed effects of sex, a fixed regression on age, birth type, and flock was fitted. The correlations were fixed to the same three levels. Validation of the fixed correlation models was done by constructing multi trait models to obtain estimated breeding values and fixed effect models to obtain corrected yields. The predictive ability and accuracy of the breeding values from the multi-trait analysis were estimated by correlating them with corrected yields, regressing the corrected yields on the breeding values and estimating bias for each weight trait.

Results: A correlation of 0.5 was initially preferred for both datasets due to the biological plausibility of the resulting genetic parameters. Model 1 and Model 2, when constrained, resulted in heritability values from 0.1 to 0.4. The validation showed the fixed correlation of 0.5 had highest correlations from 0.27-0.72 in Suffolk and 0.36-0.87 in Charollais, regression coefficients closest to 1, and lowest biases for most of the weight recording points.

Conclusions: Multi trait approach could be used to validate genetic parameters from random regression models when parameters are constrained within the parameter space for growth in sheep with few mature records.

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Association between a genetic index for digital dermatitis resistance and the incidence of foot lesions in Holstein cows

A. Anagnostopoulos[1], M. Barden[1], B.E. Griffiths[1], C. Bedford[1], M. Winters[2], B. Li[3], M. Coffey[3], A. Psifidi[4], G. Banos[3], G. Oikonomou[1]
[1]Department of Livestock and One Health, Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Leahurst Campus, Liverpool, United Kingdom.
[2]Agriculture and Horticulture Development Board (AHDB), Stoneleigh Park, Kenilworth, United Kingdom.
[3]Animal & Veterinary Sciences, SRUC, Roslin Institute Building, Easter Bush, Midlothian, United Kingdom.
[4]Department of Clinical Science and Services, Royal Veterinary College, North Mymms, Hertfordshire, United Kingdom.

Presenting author:
Alkiviadis Anagnostopoulos.
E-mail: Alkiviadis.Anagnostopoulos@liverpool.ac.uk

Application: Digital dermatitis (DD) is a polybacterial disease that is endemic to most UK dairy farms. It poses a major financial and welfare threat and is characterised by high incidence and recurrence rates. We show that animals with favourable values for a DD genetic index (published by AHDB) were less likely to develop DD, compared to those with poorer genetic merit. Breeding for DD resistance may be an effective strategy to reduce the incidence of DD in dairy herds.

Introduction: We investigated the association between the estimated genomic breeding value for resistance to digital dermatitis, the Digital Dermatitis Index (DDI), and the frequency of foot lesions in a population of Holstein dairy cows that had not been included in the reference population of DDI genetic evaluation by AHDB.

Materials and Methods: We enrolled and genotyped 2,352 cows from four farms. Foot lesion records were obtained by our research team for each animal four times throughout their production cycle, starting at approximately two months before calving and ending at the late lactation stage. Lesion records were matched to the animal's own DDI (n = 2,101) and to their sire's DDI (n = 1,812). The values of DDI ranged from -1.41 to 1.2, with positive values considered favourable for DD resistance. The relationship between the DDI and the incidence of digital dermatitis (DD), sole ulcer (SU), sole haemorrhage (SH), white line lesions (WL) and heel horn erosion (HE) was investigated using logistic regression models, with farm and parity as additional covariates.

Results: The odds of an animal being affected by DD were 2.50 times greater for every one-point reduction in the animal's DDI (95% confidence interval (CI) 1.92-3.22, P< 0.001). The adjusted probability of DD with a DDI value of -1 was 60% (95% CI 53-68%) compared to a DDI value of +1 where the probability of DD was 20% (95% CI 16-25%). Similar results were obtained with the sire's DDI, the odds of DD were 1.47 times greater (95% CI 1.23-1.75, P< 0.001) for every one-point reduction in sire DDI. The odds of SU, SH, WL and HE were 2.00 times (95% CI 1.45-2.94, P< 0.001), 1.49 times (95% CI 1.12-2, P=0.006), 1.13 times (95% CI 0.84-1.53, P=0.39), and 2.56 times (95% CI 1.96-3.33, P<0.001) greater respectively for one point decrease in the DDI.

Conclusions: Genetic predisposition plays a role in the manifestation of digital dermatitis. The results of this study further support the efficacy of claw-health genetic indexes in the reduction of DD incidence. Breeding for resistance to DD, alongside environmental and management control practices, would reduce the prevalence of the disease in dairy herds.

Investigating the Impact of CuCl2 and ZnCl2 on the microbiota of the ovine interdigital space

A. Smith[1], C. Bastos[2], N. Faria[3], J. Powell[2], F. Lovatt[1], S. Tötemeyer[4]
[1]University of Nottingham, Nottingham, United Kingdom. [2]University of Cambridge, NoBACZ Healthcare, Cambridge, United Kingdom. [3]University of Cambridge, NoBACZ Healthcare, Cambridge, United Kingdom. [4]Univeristy of Nottingham, Nottingham, United Kingdom.

Presenting author:
Ashleigh Smith. E-mail: ashleigh.smith@nottingham.ac.uk

Application: This study focuses on the use of metals as an antimicrobial to prevent the spread of infectious lameness whilst helping reduce the use of antibiotics.

Introduction: Sheep lameness is a major concern in the UK with the polymicrobial disease, footrot, being a primary cause that results in the separation of the hoof horn. Best practice is to treat clinically-affected sheep with an injectable antibiotic. Due to the risk of antibiotic resistance and associated focus on stewardship, there is increasing pressure on farms and veterinary professionals to reduce antibiotic usage.

Recently, a rapid-setting, adhesive liquid bandage that forms a topical barrier when applied has been proposed to support the control of lameness. Containing low levels of copper and zinc, the material prevents entry of environmental pathogens or their growth on its surface. However, it does not treat the affected area because its components do not migrate. This study examined what sustained levels of released copper or zinc would be required in footrot if a component-migratory bandage were developed. This study aimed to:

1. Determine the Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) of copper chloride (CuCl2) and zinc chloride (ZnCl2) on *E. coli* (control) and mixed cultures collected from the surface of healthy sheep feet.

2. Determine concentrations that inhibit *E. coli* and mixed culture biofilm formation.

Materials and Methods: MIC / MBC were determined using microbroth dilution assays with concentrations between 0.002- 5 mg/ml of CuCl2 and ZnCl2 concentrations. Biofilm inhibition was assessed using inoculated polycarbonate membranes treated with CuCl2 and ZnCl2. Inoculated membranes were incubated in treated medium for 24 hours to determine if there was growth inhibition.

Results: CuCl2 and ZnCl2 MICs against *E. coli* (n=5) were both 0.625 mg/ml. Compared to the mixed cultures (n=5), MICs were 0.625 mg/ml and 0.313 mg/ml respectively. The MBCs against *E. coli* (n=5) were 0.313 mg/ml (CuCl2) and 0.156 mg/ml (ZnCl2) whereas against the mixed cultures (n=5) it was 0.625 mg/ml for both salts.

Conclusions: Preliminary results suggest that MICs are higher for biofilm inhibition than for suspension cultures. We also conclude that for the development of a component-migratory barrier, *E. coli* could be a suitable initial model.

The association of serum biomarkers for fat mobilisation and hormonal profiles with sole ulcers in dairy cows

B.E. Griffiths[1], A. Anagnostopoulos[1], M. Barden[1], C. Bedford[1], M. Rudd[1], J. Graham- Brown[1], S. Carter[1], A. Psifidi[2], G. Banos[3], G. Oikonomou[1]
[1]University of Liverpool, Liverpool, United Kingdom.
[2]Royal Veterinary College, Hatfield, United Kingdom.
[3]Scotland's Rural College, Aberdeen, United Kingdom

Presenting author:
Bethany E. Griffiths. E-mail: hlbgriff@student.liverpool.ac.uk

Application: Sole ulcers (SU) are painful, non-infectious lameness-causing lesions. Furthering our understanding of their aetiopathogenesis will aid prevention and may lead to the development of novel treatment tools.

Introduction: Relaxin, insulin and periparturient fat mobilisation have been putatively implicated in the aetiopathogenesis of sole ulcers. Here, we evaluate whether serum biomarkers for fat mobilisation and specific hormonal profiles are associated with the odds of a cow displaying a SU in early lactation.

Materials and Methods: In two commercial dairy herds, 371 Holstein cows due to calve between April and December 2019 were prospectively enrolled. Animals were assessed at four time points relative to calving; before calving (mean: -59 days, SD: 30), immediately post-calving (mean: +5 days, SD: 4; Fresh), approximately two weeks post-calving (mean: +12 days, SD: 4; Fresh2) and in early lactation (mean: +77 days, SD: 10; EL).

At each visit, all feet were assessed for the presence of infectious and non-infectious lesions; lesions were graded for severity. Animals were also body condition scored. Serum samples were collected at Fresh, Fresh2 and EL. After the exclusion of animals with missing data, serum samples were analysed from all enrolled primiparous animals (60) and 140 randomly selected multiparous animals. Relaxin (Relaxin ELISA Kit, BlueGene Biotech, Shanghai, China), insulin (Bovine Insulin ELISA, Mercodia, 10-1201-01, Uppsala, Sweden), β-hydroxybutyrate (BHB; Ranbut, Randox, RB1007, County Antrim, UK) and non-esterified fatty acids (NEFA; NEFA, Randox, FA115, County Antrim, UK) concentrations were measured using commercially available kits.

BHB and NEFA concentrations were dichotomised as normal or elevated based on clinical reference ranges. Relaxin and insulin concentrations were binned into ordinal quartiles. The presence of a SU at EL was analysed as a binary outcome with the explanatory variables of BCS, the concentration of relaxin, insulin, BHB and NEFA from each of the three time points, and the presence of foot lesions before calving or immediately after calving. Following univariable analyses, a multivariable logistic regression model was fit following stepwise selection.

Results: Twenty-four of the 371 animals enrolled (7%) exhibited a SU at EL.
The final multivariable regression model indicated there were greater odds of a SU at EL with elevated BHB concentrations at Fresh2 (odds ratio (OR) = 8.69, 95% confidence interval (CI) =1.6-47.29, P=0.012) and elevated NEFA concentrations at EL (OR=5.5, 95% CI=1.41-21.4, P=0.014), compared to animals with clinically normal concentrations. Animals with the greatest insulin concentrations at EL were 10.75 times more likely to have a SU at EL (95% CI=1.13-101.79, P=0.038), compared to those with the lowest concentrations. Animals with a SU at Fresh tended to have an increased odds of a SU at EL (OR=4.68, 95% CI= 0.61-36.08, P=0.139).

Conclusions: This study concurs with previously described risk factors for SU and identified novel associations, such as the association between insulin concentration and SU in EL, which require further investigation.

Survival of *Streptococcus dysgalactiae* on different bedding materials found on UK sheep farms and calcium oxide (lime powder) as an effective disinfectant

LP Jackson[1,2], JS Duncan[1], D Timofte[1]

[1]University of Liverpool, Liverpool, United Kingdom.
[2]AHDB Beef and Lamb, Warwickshire, United Kingdom.

Presenting author:
Louise Jackson. E-mail: louise.jackson@liverpool.ac.uk

Application: This project aims to provide farmers with up-to-date information for the prevention of *Streptococcus dysgalactiae* joint ill, reducing economic losses and improving lamb welfare.

Introduction: *Streptococcus dysgalactiae* subspecies *dysgalactiae* 'SDSD' is the leading cause of infectious arthritis 'joint ill' in young lambs. The route of transmission is currently unknown, though exposure of lambs to environmental contamination could be a potential source of infection. Enhanced hygiene practices, including bedding/pen management are recommended for prevention, however, outbreaks still occur on farms with good hygiene (Hovers, 2014). Previously, studies have looked at the survival of SDSD on bedding materials at laboratory conditions (Rutherford 2014). This study aims to: (i) build on current work by laboratory modelling the farm lambing environment, to determine the survival of SDSD on three different common bedding substrates, in damp and dry states, and (ii) to provide farmers with practical guidelines for disinfection.

Materials and Methods: A data logger was placed in a lambing shed for 3-weeks during lambing to continuously record humidity and temperature. For laboratory modelling of the farm environment, unused bedding: straw(2g), wood shavings(3g), and soil(5g), obtained from a farm, were sterilised via autoclave and added to universals. Straw, wood shavings and soil were either added dry or dampened by adding 5ml, 2ml, or 1ml of sterile water, respectively. A suspension of a 0.5 McFarland clinical SDSD isolate was added to each substrate and stored aerobically in a humidity-controlled incubator, across 7 time points: 1, 2, 4, 7, 10, 14, and 21 days, following an initial day 0 reading. Average temperature and humidity were cycled in two-hour intervals over a 24-hour period (range: 8-13°C, 82-87% RH). The study was repeated with the addition of calcium oxide, a commonly used farm disinfectant. All samples were cultured on COBA plates at 37oC for the recovery of SDSD.

Results: SDSD was detectable at day 14 in straw and damp straw, with a 2.1 and 2.0 log reduction in average colony forming units per ml (cfu/ml) respectively, before becoming unculturable by day 21. Soil and mud maintained SDSD survival across all 7 time points; there was 0.5 and 1.3 log reduction in cfu/ml, respectively, by day 21. SDSD was unculturable from wood shavings across all time points. The efficacy of calcium oxide was found to be dependent on concentration and contact time, which varied between substrates.

Conclusions: At temperature and humidity conditions modelled on the indoor lambing environment, SDSD was able to survive on mud and soil for 3-weeks. SDSD was unculturable on wood shavings. The importance of a dry, clean lambing environment is highlighted, further supporting current advice on bedding/pen management.

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A comparison of the health and behaviour of individual and pair housing in dairy calves

S Mahendran, N Blackie, R Booth, DC Wathes
Royal Veterinary Collegre, London, United Kingdom

Presenting author:
Sophie Mahendran. E-mail: smahendran@rvc.ac.uk

Application: The way in which dairy calves are housed can have a significant impact on their health, productivity and behaviour. Individual housing is still very prevalent in the UK, but multiple studies have shown the benefits of pair housing on solid feed intake, but without an increase in disease risks. Pair housing is also thought to improve socialisation skills and reduce the occurence of abnormal behaviours, but this is an area that warrants further investigation, which is addressed by this study.

Introduction: Housing management of dairy calves is one of the factors that contributes to a successful rearing outcome. Individual housing is still prevalent, with it thought to provide enhanced biosecurity and easy monitoring. However behavioural studies have found pair housing of calves is important for social learning, with positive impacts on health and welfare.
The aim of this study was to to establish the impact of individual and pair housing on calf health, growth and behaviour on a UK commercial dairy farm.

Materials and Methods: This study was conducted over 2020 on a commercial dairy farm in England, milking 1800 cows. 164 individually housed calves and 280 pair house calves were enrolled. Calves were housed in a large shed, using a commercially available partition system (Calf-Tel, USA) allowing systematic allocation into individual or pair housing of calves until 8 weeks of age. Weekly visits were conducted for Wisconsin health scoring and weigh banding. A subset of 90 calves were fitted with a tri-axis pedometer (IceQube, Ice Robotics, UK) to measure calf activity. A novel object approach test was conducted, with placement of an umbrella into each calf pen during the sixth week of age. In addition, a subset of 27 calves had CCTV placed above their pens to enable video analysis to assess cross sucking behaviour. This footage was manually analysed for occurrence of cross sucking on another calf and sucking on inanimate objects.

The data was analysed using linear mixed effects models, binary logistic generalised estimating equations, and generalised linear model, with pen used as the experimental unit.

Results: There was no significant association between housing group and the ADLG of the calves prior to weaning ($F_{1,1114}$ = 0.091, p = 0.76), with the a mean ADLG of 0.72 kg/day. There was a significant effect of housing group on the occurrence of disease (p = 0.014), with individually housed calves having an increased odds of developing disease (OR=1.88 (1.14 – 3.12).
When assessing calf activity, pair housed calves had a higher activity value of 4503.6 ± 117.5 compared to 4388.0 ± 179.2 in individually housed calves. The novel object approach was significantly affected by housing group (p < 0.01), with individually housed calves approaching the novel object in a mean of 84.0 ± 9.4 seconds (SEM), and pair housed calves approaching in 121.2 ± 9.2 seconds (SEM).
The behavioural video analysis is still ongoing.

Conclusions: There were significant impacts of the housing type on the occurrence of disease with individually housed calves experiencing more disease. In terms of behaviour, pair housed calves being were more active overall. This indicates no detrimental impacts of pair housing, with both positive health and welfare impacts demonstrated.

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Use of survival analysis to model reproductive performance in sheep

T.J. Clough
University of Nottingham, Nottingham, United Kingdom.

Presenting author:
Thomas Clough. E-mail: thomas.clough@nottingham.ac.uk

Application: Improvements in reproductive performance on UK sheep farms is important to optimise productivity. Understanding the variables which effect tup entry to lambing interval, will allow the implementation or change of management strategies to improve performance.

Introduction: Productivity on sheep farms is largely controlled by reproductive success (Petrović et al., 2012). Understanding the variables which control reproductive success is important to optimise management decision associated with breeding. Tup entry to lambing interval can provide a means to assess reproductive success, with lower performing ewes having an increased interval.

Materials and Methods: Data collected as part of the AHDB challenge sheep project (Challenge Sheep | AHDB, n.d.) was used to construct Cox Proportional-Hazards Models. Two models were built to differentiate between parity one ewes and multiple parity ewes. The parity one model included variables; grouped ewe body condition score at tupping, ewe breed and ewe age at tupping. Additionally, the multiple parity model included; grouped body condition score change pre-tupping, previous number of lambs born and parity. The models were evaluated using hazards ratios to determine the effects of each variable on tupping to lambing interval.

Results: The parity one model showed that low and high body condition score groups at tupping had a significant effect on days to lambing ($p<0.05$). Hazard ratios were 0.90 and 1.16 respectively. Seven out of 11 breeds had a significant effect on tupping to lambing interval, with hazard ratios ranging from 0.38 to 2.24. Age had no significant effect. High tupping body condition score had a significant effect in the multiple parity model with a hazard ratio of 0.853. The number of lambs born in the previous production year had no significant effect on days to lambing. Body condition score loss and gain pre-tupping affected days to lambing with hazard ratios of 0.85 ($p = 0.064$) and 1.08 ($p < 0.05$) respectively. Nine of the breed groupings had a significant effect on days to lambing with hazard ratios ranging from 0.42 to 1.86.

Conclusions: Understanding the effects of specific variables on ewe reproductive success is important. The models constructed show that ewe parameters at and before tupping can have a significant effect on tupping to lambing interval. Understanding the effects of each variable is important to optimise reproductive success.

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