

The role of animals

in human and planetary health

**Developing Talent Proceedings
of the British Society of Animal Science**

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Welcome

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Understanding public perceptions of dairy cow welfare

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Application: Better understanding public perceptions of dairy farming would allow industry to improve communication and adapt farming systems to align with societal expectations.

Introduction: The viability of dairy farming is threatened by concerns over animal welfare. Access to pasture appears a key concern in this debate, questioning the future of systems that house cows year-round. Despite support for grazing, public preferences for how cows are managed appear diverse, with a range of other aspects prioritised including comfort and health and welfare (Jackson et al., 2020). However, what underpins these preferences is not clear, especially: how the public make sense of dairy cow welfare through their own experiences; or how they perceive the different systems in which farmers keep cows.

Materials and Methods: Face-to-face semi-structured interviews about dairy farming were conducted with a diverse group of 60 people from across the UK. Interviews were recorded, transcribed and uploaded to NVivo 12 software to aid coding and analysis. Inductive thematic analysis first established different interpretive frames through which participants understood the dairy cow and farmer. Thematic analysis was then used to explore how participants understood three different dairy farming systems described to them verbally and visually. Linguistic analysis using LIWC then Friedman's Test on related samples and post-hoc pairwise comparison with Bonferroni's correction was used to determine differences in style and tone when participants discussed each system. Results were triangulated to qualitative results to provide additional insight.

Results: Frame analysis identified that participants perceived the cow in three ways and the farmer through two. Cow frames revealed unexpectedly strong connections between participants and cows despite superficial contact, framing cows as companions, subordinates or 'revered' beings. Farmers were traditional or modern but in conflicting positive and negative lights, creating confusion about care of the cow. Qualitative analysis by system suggested participants saw the cow as wild but also domesticated, and best managed in

a scenario combining access to nature with protection when needed. However, they also deferred to others for guidance on how a cow should live – including the cow herself. Various dairy farming practices were seen as problematic depending on whether the cow was inside or out. Triangulation of these results using linguistic analysis found emotional reactions against housing year-round and confusion about whether grazing year-round was viable, confirming a housing-grazing combination was most logical and acceptable to participants.

Conclusions: These findings suggest the public feel a greater stake in dairy farming than industry currently acknowledges. Conflict about the farmer's motives towards dairy cow welfare create confusion. A system combining access to pasture and housing when needed is emotionally and cognitively most acceptable to the public, and optimal in addressing the cow's needs.

Acknowledgements: The authors would like to thank the Agriculture and Horticulture Development Board (AHDB) for its kind sponsorship of this study.

References: Jackson A, Green M, Millar K and Kaler J 2020. Is it just about grazing? UK citizens have diverse preferences for how dairy cows should be managed. *Journal of Dairy Science* 103, 3250–3263.

Towards preventing transmission of digital dermatitis treponemes by cattle foot trimming knives

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Application: Develop a protocol to eliminate a bovine digital dermatitis (BDD) treponeme infection reservoir, communicate to end users and identify if advice is used.

Introduction: BDD is a highly prevalent infectious foot disease of cattle. Active lesions cause pain and lameness making BDD an important economic and welfare concern. Spirochaetes of the genus *Treponema* are the most commonly implicated microbes within BDD lesions. Treponemes contaminate cattle hoof knives during foot trimming, and lack of washing of hoof trimming equipment has been identified as a risk factor for high BDD prevalence; therefore, hoof knives are considered an infection reservoir^{1,2}.

The aims were:

- 1) determine survival time of BDD treponemes on hoof knife blades,
- 2) develop a disinfection protocol to eliminate treponemes from hoof knife blades,
- 3) communicate the protocol to those working with cows' feet and determine its uptake.

Materials and methods: To determine survival time, BDD-associated treponemes (two species) were applied to hoof knife blades and swabs collected at five time points. Five disinfectants were tested in the laboratory using a 20-second contact time, then three progressed to field trials, where 133 feet with BDD lesions were trimmed and blades swabbed before and following hoof-trimming and after blade disinfection. Swab DNA extraction and PCR were used for treponeme detection, as well as swab inoculation into culture media and phase contrast microscopy and PCR after 6 weeks' anaerobic incubation. After promoting the disinfection protocol, a survey was undertaken to assess research impact on foot-trimming hygiene knowledge and practice.

Results: Treponemes were viable (culturable) for two hours on hoof trimming knives. 2% Virkon, 2% sodium hypochlorite and 1:100 FAM30 were efficacious for preventing growth of laboratory applied BDD treponemes³. In field (farm) trials, 1/22 cases exhibited treponeme culture from a hoof knife after foot-trimming when no direct BDD lesion contact was made, whilst lesion contact in 47/111 cases produced viable cultures, indicating potential for transmission⁴. Washing hoof knives in 1:100 FAM30, 2% sodium hypochlorite or 2% Virkon for 20 seconds (full AHDB protocol: <https://ahdb.org.uk/reducing-spread-of-DD>) prevented treponeme culture from knives³. After advertising and knowledge exchange of the AHDB protocol for hoof-trimming equipment disinfection: 35/80 end users surveyed were more aware of the risk of BDD transmission via this route, and 36/80 had enhanced hygiene practices⁵.

Conclusion: Foot-trimming knife blade disinfection can reduce the risk of spread of viable BDD treponemes between cows. Communication of a recommended disinfection protocol by AHDB Dairy and University of Liverpool has enhanced awareness and influenced those working with cows' feet to improve their hygiene practices.

Acknowledgements: Many thanks to foot trimmers/farmers/vets involved in the study and for BBSRC/AHDB Dairy funding.

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The performance of bivalent, flock-specific footrot vaccines compared to a multivalent footrot vaccine in commercial sheep flocks in South-West England

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Application: A more effective vaccination strategy would reduce lameness prevalence and the reliance on antibiotics as the primary control method for footrot.

Introduction: Lameness prevalence in UK sheep flocks needs to be reduced because it is a welfare concern. Footrot, caused by the bacterium *Dichelobacter nodosus*, is endemic in UK flocks and remains the most common cause of lameness (Winter, et al., 2015). Current 'best practice' for control of lameness includes prompt treatment of individual cases of footrot with antibiotics but there is pressure on the agricultural sector to reduce antibiotic use. The existing footrot vaccine, Footvax[®], only reduces flock lameness prevalence by an average of 20% (Winter, et al., 2015). This could be due to 'antigenic competition' because this vaccine contains all nine serogroups present in UK flocks (Raadsma, et al., 1994). Bivalent, flock-specific serogroup vaccines are available commercially in Australia (Custom R-Pilus[®]), and have been successfully used to reduce or eliminate footrot in some flocks (Dhungyel, et al., 2013). The objective of this study was to compare lameness and footrot incidence, and antibiotic use between treatment groups, within three commercial flocks where approximately one third of sheep received no vaccine, a flock-targeted bivalent footrot vaccine, or Footvax[®].

Materials and methods: Three commercial flocks participated in a clinical trial that commenced in August 2020, from which 175, 197 and 196 ewes were enrolled respectively. Following examination and scoring of foot lesions, ewes were stratified by breed, condition score and infectious foot lesion severity into three groups within each flock, which were then randomly allocated to received Footvax[®], saline, or the Custom R-Pilus[®] bivalent vaccine. The farm workers and the researcher carrying out observations were blinded to the treatments received by each ewe. The bivalent vaccine contained serogroups H and I, H and A, and H and C for the three flocks respectively. Two doses of the allocated treatment were given four weeks apart. The trial sheep were kept together in each flock, but separate from non-participating sheep. Sheep locomotion was scored every week for 25 weeks, and lame sheep were caught, examined and scored for footrot lesions, which were treated with antibiotics. Whole flock foot examinations were repeated 16 weeks after the trial started, and after ewes lambed, which was at 24 - 29 weeks. Throughout the trial, the interdigital skin of all ewes with footrot lesions was swabbed for *D. nodosus* quantification by qPCR and serogroup identification by PCR.

Results: Swabs from 474 examinations where footrot was observed were analysed by qPCR. The two most prevalent serogroups on week 1 of the trial were contained in the three bivalent vaccines. Treatment identities remain blinded for ongoing analysis of results.

Acknowledgments: The authors acknowledge funding from BBSRC and AHDB.

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Identification of factors associated with variation in gastrointestinal nematode faecal egg counts in periparturient ewes; towards development of targeted selective treatment guidance.

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Application: Gastrointestinal nematode (GIN) faecal egg counts (FEC) in peri-parturient ewes are associated with body condition score (BCS), age, DAGG scores and breed. These traits can form the basis of targeted selective treatment (TST) guidance for peri-parturient ewes to control GINs whilst limiting anthelmintic resistance (AR) development.

Introduction: GIN infections cost the European sheep industry €157-477 million annually (Mavrot et al., 2016). Anthelmintic treatment of peri-parturient ewes against GIN maximises flock productivity, however, anthelmintic applications must be limited to minimise AR development. TST can reduce anthelmintic use without affecting productivity, and reduces AR development (Kenyon et al., 2013), however, only 29% of GB farmers implement ewe TST (Williams et al., 2021a) despite evidence of its applicability (Williams et al., 2021b). Identifying ewes for TST can be challenging, therefore the aim was to evaluate traits associated with varying peri-parturient FECs to guide future TST protocols.

Materials and Methods: Faecal samples were collected from 226 ewes, 48h post-lambing on 7 Welsh farms. Ewes had lambed indoors and their age, breed, BCS, DAGG score, number of lambs scanned and born alive was recorded. Ewe breeds included Mule (n=153), Suffolk/Suffolk X (n=31), Texel/Texel X (n=27) and hill breeds (n=15), with each breed present on at least 4 farms. FECs were conducted within 24h of collection using the Mini-Flotac method. Multivariate negative binomial mixed models were created using glmmTMB package in R to identify factors significantly associated with FEC. A random intercept was added to the model to account for variation in FECs between farms and models were built using stepwise process where non-significant variables were removed from the model sequentially. The model with best fit was identified using the Akaike Information Criterion (AIC) and validated using residual diagnostic tests via DHARMA and Performance packages in R.

Results: A mean ewe FEC of 440 eggs per gram (range 0 – 4575), litter size of 1.87, BCS 2.56 and mean age 3.46 was observed, with 5% of ewes displaying DAGGs. The final model (Table 1) identified BCS and age as significant factors negatively associated with ewe FEC ($P < 0.01$). Suffolk/Suffolk X ewes and ewes with a DAGG score > 0 displayed significantly higher FECs ($P < 0.001$). Measures of mean litter size were not present in the final model ($P > 0.05$)

Conclusion: BCS, age, DAGG score, and breed are significant indicators of peri-parturient FEC and should be considered in TST protocols. Future research is required to identify optimal proportion of peri-parturient ewes treated to maximise production and minimise pasture contamination, whilst maintaining sufficient susceptible GINs in refugia to dilute resistant population.

Acknowledgements: Aberystwyth University, HCC, KESS2.

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Table 1. Best fit negative binomial mixed model identifying factors associated with peri-parturient ewe FEC.

Variable		B	S.E	Z	P
Intercept		7.03	0.34	20.83	<0.001
BCS		-0.22	0.08	-2.74	0.006
Age		-0.20	0.06	-3.49	<0.001
Dagg score	>0	0.71	0.21	3.36	<0.001
	0	Reference	-	-	-
Breed	Suffolk or Suffolk X	0.63	0.18	3.54	<0.001
	Texel or Texel X	0.31	0.18	1.68	0.092
	Hill breed	-0.46	0.26	-1.79	0.073
	Mule	Reference	-	-	-

Undergraduate Thesis of the Year Winner

MeDIP-AFLP; a novel approach for the discovery of DNA Methylation Biomarkers

Sara Lind Valdimarsdottir

DNA methylation is the most well-studied epigenetic mechanism of gene control in mammals and has been implicated in the response of individuals to stress, dietary change, cancer, and other diseases. These associations have raised the appetite for the use of specific methylation sites, so-called epimarkers, as a diagnostic tool for illness. To date, most work focussed on the isolation of epimarkers for use in human health, but there is also considerable scope for veterinary applications. For example, several veterinary diseases such as Ovine Pulmonary Adenocarcinoma (OPA) currently lack reliable diagnostic tests. The central problem with using methylation for diagnostic purposes is the process of identifying diagnostic sites amongst the millions of methylations across the genome. In the absence of huge resources, there is a need to reduce the genome complexity in this search. In this study, we sought to evaluate a novel strategy to screen for a subset of the genome for polymorphic epimarker sites. For this, we used a combination of Amplified Fragment Length Polymorphism (AFLP) with an embedded Methylated DNA immunoprecipitation (MeDIP) step. The method (MeDIP-AFLP) was trialled as a proof of concept to assess its ability to identify candidate methylation sites that can differentiate between tissues taken from the same animal (one sheep and one cow). MeDIP-AFLP electropherograms recovered from replicated tissue samples exhibited simplified and more distinct peak profiles than those observed from AFLP. Principal Coordinate Analysis (PCoA) showed clear differences between organs taken from the same animal. For both species, several strong peaks were identified that were consistently present across all technical replicates but differed in their presence between organs. These were deemed candidate epimarkers for tissue identification. The potential of this approach as a low-cost approach for the generation of diagnostic epimarkers in non-human species is explored, as well as the scope for its application for the production of epimarkers for diseases and cancers in veterinary medicine.

PRAISE Award Winner

Understanding and improving the behaviour and welfare of artificially reared goat kids

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My research is creating an essential knowledge base on goat kid behaviour and welfare, with the milk feeding and weaning transition being identified as high-risk periods for kid welfare, my research is addressing the following key areas.

1. Current rearing strategies and attitudes to change

A survey of goat farmers receiving 242 responses from 16 countries (currently under peer review) has characterised current kid management practices and attitudes towards change, and will help ensure future research is tailored towards prevalent systems. As farmers implement management practices daily, the survey investigated their willingness to change and perceived barriers (focusing on gradual weaning techniques and the provision of environmental enrichment – as both are evidenced to improve welfare in other species). Findings highlighted common concerns (including safety, feasibility, and health), that create barriers to change and is the first study to examine goat farmers' attitudes. Using qualitative work to inform quantitative research is a mixed-methodology approach that can help ensure research has the best chance of being implemented on commercial farms and improve the welfare of as many animals as possible.

2. Understanding behaviour and welfare under natural conditions

A detailed behavioural observation study is investigating behaviour of kids reared with their dams using CCTV footage and focal kid sampling to enable comparison with artificially reared kids.

3. Investigating the impacts of current artificial milk feeding strategies, and trial strategies aiming to improve overall welfare

Most dairy goat farms use ad libitum milk feeding systems that allow unrestricted milk access (Anzuino et al., 2019; Bélanger-Naud et al., 2019). Weaning can be abrupt, (sudden and complete milk removal), or gradual (incremental reduction before removal), and it has been noted that further investigation into weaning methods is needed (Anzuino et al. 2019). Artificial weaning is stressful as kids are weaned younger, without dam cues that cause a gradual decrease in milk consumption alongside increasing solid feed intake.

Calf research suggests that whilst animals fed on ad libitum milk may have increased weights and express more natural behavioural repertoires, lower solid feed intake and slower rumen development may be an issue. However, the lack of species-specific research must be addressed to understand how this applies to goats. Whilst calf gradual weaning research is extensive and suggests that it improves welfare, it focuses on individualised technological methods (such as computerised feeders that step-down individual milk allowance) not currently utilised on goat farms, and therefore has limited applicability. Automatic ad libitum feeders supply milk to multiple pens of kids of different ages, with individual intake unknown, so species-specific pen-level strategies are required. Teat removal is a gradual weaning method feasible for on-farm use and the results of my first study indicate that it could be recommended to improve welfare. With support from Volac providing a computerised feeder, detailed observations of the behaviour of individual kids on abrupt and gradual weaning schedules is being conducted and average daily gains measured to provide an understanding of how kids use ad libitum feeding systems, and how weaning strategies impact their welfare.

Risk Factors Associated with Joint Ill Occurrence on UK Sheep Farms in 2020

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

Introduction: Neonatal infectious arthritis (joint ill) is a debilitating condition of one or more of the synovial joints, caused by the bacteria *Streptococcus dysgalactiae*. Although the bacterial source and route of transmission are currently unknown, previous studies into joint ill risk factors have found lambing hygiene (Rutherford et al., 2014) and the intensity of indoor lambing (Smistad et al., 2020) associated with outbreaks. To aid our understanding of joint ill risk factors, we produced a survey to estimate the prevalence and identify farm level drivers of disease on UK sheep farms in 2020.

Materials and methods: The target population was UK sheep farmers who had or had not experienced joint ill problems in their flocks. 322 eligible responses were utilised in subsequent analysis. Univariate and multivariate analyses were conducted via binary logistical regression. Multivariate models were built using an automated stepwise approach.

Results: 206 farms experienced at least one case of joint ill in the 2020 lambing season – a prevalence of 64.0%, with a median of 8.5 cases per farm (IQR, 3-20). Proportionally, this equates to 1.4% of lambs born at participant farms going on to develop joint ill.

Across all farms, flock size had a positive linear occurrence with joint ill occurrence. A greater number of joint ill cases were observed on farms with longer lambing periods (in weeks;OR, 1.2;95% CI, 1.0-1.4). Farms giving all lambs antibiotics after joint ill cases had already been reported in the flock, had more reports of joint ill (87.5%) compared to other methods of prevention, such as giving antibiotics to only 'high-risk' lambs (57.7%;OR, 0.4;95% CI, 0.0-4.6).

In outdoor systems, giving antibiotics prophylactically was associated with a reduction in reported joint ill, from 76.3% to 60.0%, compared to not using antibiotics (OR, 15.1;95% CI, 2.4-94.4). Providing shelter to outdoor lambing ewes was associated with lower reports of joint ill (36.4%), compared with farms who did not provide shelter (75.9%;OR, 3.0;95% CI, 1.2-7.8). Farms that cleaned ear tags and equipment reported less joint ill (43.6%) than those who did not clean (65.8%; OR, 5.7;95% CI, 1.5-21.4) and did not ear tag (74.7%;OR, 3.8;95% CI, 1.3-11.4).

In indoor systems, upland farms were associated with an increase in reported joint ill (80.3%), compared with lowland farms (61.2%;OR, 3.2;95% CI, 1.3-7.8). The number of ewes per quantity of mothering pens was positively correlated to joint ill occurrence (OR, 1.1;95% CI, 1.0-1.2).

Conclusions: A pattern of intensity of lambing impacting joint ill occurrence was observed on participating farms in 2020. Understanding risk factors associated with joint ill occurrence can aid prevention and reduction strategies.

Acknowledgements: The author acknowledges funding from University of Liverpool and AHDB Beef and Lamb.

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The application of an in vitro egg hatch test to identify albendazole sensitivity to *Fasciola hepatica* isolates from sheep and cattle

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Application: Liver fluke, is a major welfare and economic concern, costing the UK livestock industry over £40.4 million per annum. We determined the drug sensitivity of liver fluke isolates from sheep and cattle, to allow farmers to make informed decisions based on drug efficacy, thus reducing the impact of liver fluke.

Introduction: *Fasciola hepatica* (liver fluke), causes severe morbidity and mortality in ruminant livestock. It typically presents as acute disease in sheep, resulting in sudden death. Farmers have relied on triclabendazole due to its high efficacy (>99%) against *F. hepatica* (Boray et al. 1983). However, triclabendazole resistance has led to a reliance on alternative flukicide drugs, like albendazole (>80% effective from 12 weeks post infection). Previously an isolate of *F. hepatica* (isolate E) from sheep was suspected of being albendazole-resistant, however, we confirmed albendazole susceptibility by in vivo trial (>99% efficacy against >12-week-old fluke). To determine if we could detect albendazole sensitivity in vitro, we employed an egg hatch test (Ceballos et al. 2019), for five fluke isolates, including isolate E.

Materials and Methods: For each isolate, five replicates (~200 eggs/well) were exposed to three drug concentrations (5, 0.5 and 0.05 µM albendazole) or methanol only (control, >70% egg development). % ovicidal activity was calculated as [(%eggs developed in control - %eggs developed after drug incubation)/%eggs developed in control] x100. Using the discriminating dose (0.5 µM), isolates were identified as a) resistant = ovicidal activity <40% and no statistical difference (by pairwise t-test) between egg development in albendazole-treated vs controls, b) susceptible = ovicidal activity >70% and a significant difference between egg development in albendazole-treated vs controls or c) equivocal = they did not meet either criterion.

Results: Table 1 Ovicidal Activity (%) (mean ± SD) in albendazole egg hatch test for five *Fasciola hepatica* isolates.

Conclusion: At 0.5 µM an ovicidal activity of 74% and statistical difference in egg development ($p < 0.001$) indicates isolate E is susceptible to albendazole, consistent with our in vivo observations. An ovicidal activity of 32.4% and lack of statistical difference in egg development in control vs drug exposed (0.5 µM, $p = 0.5063$) suggests isolate D21 is albendazole resistant. Isolates D20, B and S do not meet the criteria for resistance or susceptibility at 0.5 µM, so fall within the equivocal range indicating further evaluation is required.

Acknowledgements: The authors acknowledge funding from BBSRC DTP, University of Liverpool and Hybu Cig Cymru. References: Boray et al. 1983 Vet Record, 113,14: 315-7, Ceballos, et al. 2019. Vet Parasitol, 271: 7-13

Table 1: Ovicidal Activity (%) (mean ± SD) in albendazole egg hatch test for five *Fasciola hepatica* isolates.

Isolate	Ovicidal Activity (%)			Egg development in control vs. 0.5 µM p-value
	5 µM	0.5 µM	0.05 µM	
E	92.0 ± 4.1	74.0 ± 4.4	54.8 ± 7.4	$p < 0.001$
D20	76.8 ± 4.3	43.8 ± 4.6	19.7 ± 7.6	$p < 0.001$
D21	78.5 ± 7.2	32.4 ± 1.5	22.0 ± 4.1	$p = 0.5063$
B	92.4 ± 1.7	59.0 ± 3.9	6.6 ± 2.7	$p < 0.001$
S	89.7 ± 1.1	35.6 ± 4.0	4.2 ± 2.7	$p < 0.001$

Characterising immune gene expression in sheep from whole blood and sorted immune cells as a tool to empower transcriptome-informed breeding

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Application: Breeding healthier animals is a key goal for the UK sheep industry, providing both cost and welfare benefits. Providing a robust set of immune-related variants for use in genomic selection can help improve the health of the UK sheep flock.

Introduction: Genomic selection has accelerated genetic gain in livestock species such as dairy cattle but is currently underutilised within sheep breeding. Understanding how the genome is expressed can provide a foundation for understanding the link between genotype and phenotype; and can add an additional layer of information that can inform breeding strategies (Daetwyler et al., 2019).

Although gene expression has been characterised for many tissue and cell types in sheep these studies have involved only small numbers of animals. It is possible to investigate gene expression at a flock level by carrying out an eQTL (expression-Quantitative Trait Loci) study. This study type scans for genomic markers that explain a proportion of the variance in a gene expression phenotype. They have been carried out in livestock species such as cattle and pigs, however only a few have been conducted in sheep (e.g., Yuan et al., 2021).

This study aims to identify functional immune variants by i) characterising gene expression in whole blood for an eQTL cohort, and ii) deconvoluting expression patterns of immune cell types in a smaller subset of animals.

Methods: Peripheral blood samples were collected from 102 Scottish Blackface or cross-bred lambs from two UK farms (52 and 60 lambs each), aged 6 to 8 months old. Total RNA was extracted using a Tempus spin kit and checked for quality using Nanodrop and TapeStation platforms. RNA-sequencing will be carried out using the Novaseq platform at an expected 40 million reads per sample. Genotypes will be determined via SNP genotyping on the Illumina Ovine 50k chip or variant calling from RNA-sequencing data. Following quantification of transcripts for each gene, an eQTL analysis will be performed to determine how many variants significantly impact gene expression.

Results: This study is ongoing. Extracted RNA (n = 102) is high quality (RNA Integrity Number ≥ 9.0) with mean concentration of 188ng/ μ l. Results to date will be presented.

Conclusion: To our knowledge, this is one of the first examples of an eQTL study to investigate immune gene expression in sheep. Further work will use expression signatures from sorted immune cell types to carry out computational deconvolution. This will identify functionally relevant immune variants that can be incorporated in new and existing genotyping technologies to inform breeding decisions.

Acknowledgements: The authors acknowledge funding from BBSRC, EASTBIO, and Roslin Technologies.

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Genetic selection of cattle for reduced bovine tuberculosis transmission

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Application: Genetic selection of cattle with low infectivity, in addition to high resistance, could reduce transmission of bovine tuberculosis.

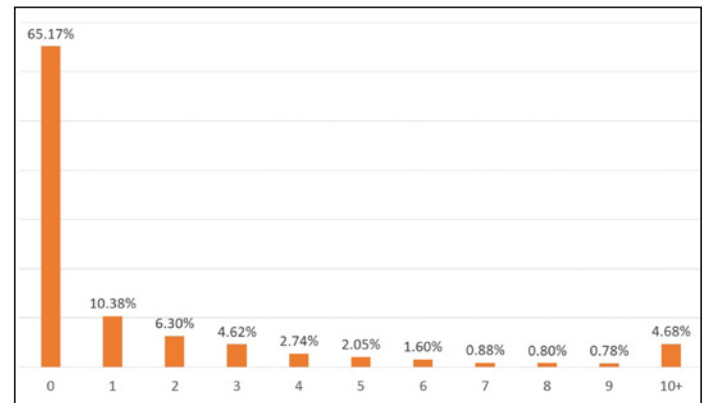
Introduction: Bovine tuberculosis (bTB) has been a persistent cattle disease in the UK. There is abundant evidence that cattle vary genetically in bTB resistance. In 2016, the "TB Advantage" selection index was introduced to the UK dairy industry, allowing farmers to select bulls with enhanced genetic bTB resistance (Banos et al., 2017). Selection for bTB resistance alone may not be sufficiently effective to eradicate the disease. Simulation results show that breeding cattle using both resistance and infectivity can potentially accelerate the impact of genetic bTB control (Tsairidou et al., 2018). However, the genetics of bTB infectivity requires further exploration. The main aim of this study is to assess whether genetic selection of cattle for reduced infectivity in addition to increased resistance to bTB is possible and worthwhile. The first step is to investigate whether detectable genetic variation in cattle infectivity for bTB exists.

Materials and methods: Data consist of 14 tables from the Animal and Plant Health Agency and Edinburgh Genetic Evaluation Services which contain animal, breakdown, herd, and pedigree information. All this information was merged into a unique master table for further analyses. After quality control and consistency checking, the resulting table contains longitudinal records of around 3M animals involved in bTB breakdowns between 1995-2017.

Initially, only breakdowns with a unique index case (i.e. only one animal in the herd tested positive) within a restricted observation period are considered. Given that secondary cases are either infected by the index cases or through external forces (e.g. badgers), Generalised Linear Mixed Models (GLMMs) can be used to determine whether there is significant genetic variation in the number of secondary cases associated with each index case, as a first indication for genetic variation in infectivity.

Results: The dataset considered for the first step analysis contains 67,737 records of animal related to 8,238 breakdowns between 2012 and 2017. Approximately 43% of all breakdowns had only one index case. Amongst these, a large phenotypic variation in the number of secondary cases was found within the first year of the breakdown (Figure 1), which may be partly explained by genetic differences in index case infectivity.

Figure 1: Distribution of breakdowns for secondary cases



Conclusion: GLMMs will be used to identify non-genetic (e.g. herd size, season, duration of breakdown, risk area) and genetic factors that explain a significant proportion of the observed variation in the number of secondary cases within the restricted observation period. If inclusion of genetic effects leads to a significant improvement of the model fit over models without genetic effects, this would indicate that index cases vary in their bTB infectivity.

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Dissecting the pathogenesis of bovine ischaemic teat necrosis

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Application/Introduction: Bovine ischaemic teat necrosis (ITN) is an emerging disease affecting dairy cattle throughout the UK. It causes severe teat lesions that frequently leads to culling and causes welfare and economics issues. Initial data suggested a potential role for digital dermatitis (DD) treponemes (Clegg et al, 2016). Further multidisciplinary investigations were applied to dissect the pathogenesis of ITN including the link between ITN and DD treponemes.

Materials and Methods: Pathological screening: Images of the udder of 46 cows with 70 affected teats from 27 different farms were reviewed to categorise the spectrum of clinical presentations of the disease. Histopathology, including warthin-starry stain and immunohistochemistry (IHC) for DD treponemes were performed on 14 ITN teats as previously described (Crosby-Durrani et al, 2016). Microbiology screening: Samples including swabs of the ante-mortem lesion and tissue obtained post-mortem were screened using nested DD treponeme PCR (Evans et al 2009). DNA extracted from 10 ITN and 10 healthy teats were submitted for Illumina shotgun metagenomic sequencing. Epidemiological screening: A national postal questionnaire was sent to 1855 farmers asking questions on their experience with ITN and more generic questions about their farm.

Results: Pathology: Three different clinical presentations of ITN were defined. Warthin-starry staining and IHC for treponemes detected little involvement of DD treponemes in the lesions whereas an abundance of diverse bacteria could be observed. This contrasts other ruminant treponeme diseases where these techniques detect an abundance of spirochetes within lesions. Microbiology: PCR screening for DD treponemes presented in Table 1.

Table 1. The number of samples (n=137) and percentage that tested positive on nested PCR screening for the different DD treponeme phylogroups.

	Number PCR positive (n=137)
One DD phylogroup detected	29 (21.2%)
Two DD phylogroups detected	3 (2.2%)
Three DD phylogroups detected	8 (5.8%)
Treponema medium	16 (11.7%)
Treponema phagedenis	17 (12.4%)
Treponema pedis	31 (22.6%)

Shotgun metagenomics detected treponemes, although these were more abundant in the control tissue and comprised of less than 1% of the microbiome in ITN lesions. Metagenomic data suggested that ITN has associations with *Acinetobacter* spp. and *Pseudomonas* spp., which requires further investigation. Epidemiology: A farmer survey was conducted and identified potential farm level risk factors included the presence of udder cleft dermatitis (OR: 2.80, 95% CI: 1.54-5.07, P<0.01) and chapped teats (OR: 6.07, CI: 1.96-18.76, P<0.01) within the milking herd. Of note, many farms that reported having ITN did not have DD. Conclusions. We were able to define three different clinical stages of ITN. Taking the current pathological, microbiological and epidemiological data presented here, treponemes do not appear to have a major aetiological role in ITN. Risk factors including presence of udder cleft dermatitis and chapped teats were identified and putative pathogens determined, which should help underpin future control.

Acknowledgements: BBSRC and AHDB dairy for funding this study; farmers for returning questionnaire; allowing use of data and access to farms and animals; ADHB dairy for access to database; veterinary surgeons for submitting samples.

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Sole soft tissue thickness changes over the periparturient period and its association with claw horn disruption lesions in dairy cattle

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Application: These results represent the preliminary findings of a project that aims to further our understanding of the development of lameness causing claw horn disruption lesions (CHDL); this may lead to new prevention strategies and treatment options.

Introduction: Despite their importance, we are yet to elucidate CHDL aetiopathogenesis and the role of the digital cushion/sole soft tissue in their development. This study represents a preliminary analysis of sole soft tissue thickness (SSTT) data which aims to evaluate key factors that underlie the development of CHDL in dairy cows.

Material and Methods From four commercial dairy farms, 2,353 cows and heifers were enrolled 30-60 days before parturition (pre-calving), and then re-examined within 7 days of parturition (fresh), at 50-100 days post-parturition (early lactation) and at 170-200 days post-parturition (late lactation). All cows predicted to calve within the study period were enrolled, until late lactation checks commenced, due to feasibility. At each check the animals were mobility and body condition scored, height was assessed and parity noted. All feet were assessed for infectious and non-infectious foot lesions and these were graded for severity. An image of the digital cushion on the lateral claw, hind left foot was taken using B mode ultrasonography for measurement of SSTT at a later date. Using Image J software, SSTT was measured by a single assessor blinded to cow, farm and stage of lactation. Univariable analysis was undertaken and simple linear regression models were constructed, from which least square means were calculated and Tukey HSD tests undertaken (R Core Team, 2020). Multivariable analysis will be run on the full dataset, once complete. The SSTT was the outcome variable.

Results: The SSTT nadir was shortly after calving, with SSTT increasing throughout lactation ($P < 0.001$). Parity was significant, with lower parity animals having significantly thinner SSTT compared to higher parity animals ($P < 0.001$). There were significant differences in SSTT between farms ($P < 0.001$), and farm by stage of lactation ($P < 0.001$), with the SSTT nadir shortly after calving on two of the farms, and during early lactation on the remaining two farms. An interesting parity by stage of lactation by SU incidence interaction was observed, with first lactation animals who go on to develop a SU during early lactation showing numerically thinner SSTT's compared to heifers which do not go on to develop a SU, this warrants further investigation. This initial analysis has also indicated that taller cows had thicker SSTT's, whilst cows with thinner soles had thicker sole soft tissues.

Conclusions: These results are from a preliminary analysis of the SSTT data from this project. This is the largest study of SSTT measurements collected. Initial results have highlighted that freshly calved animals and heifers have significantly thinner sole soft tissues. Our project adds further evidence that fresh cow management and heifer management are important stages for managing the risk of lameness in the production cycle of dairy cows.

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Milk production and chemical composition from sheep supplemented with pumpkin and chia seeds

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Application: Feeds with high oil content, such as chia seeds, decrease milk yield, but improve milk protein, lactose and total solids without affect fat content, when it is included in the diet. Introduction: The uses of Chia seed (*Salvia hispanica* L.) and Pumpkin seed (*Cucurbita moschata*), could be a good ingredient in supplementation of diets for dairy sheep, as chia seeds contain between 25 to 40% of oil with a polyunsaturated fatty acid (PUFA; specifically alpha-linolenic acid and linoleic acid) content (Schettino et al., 2017) that can be expressed in milk. Therefore, the objective of this study was to determine milk yield production and milk composition in dairy ewes supplemented with Chia (*Salvia hispanica* L.) and Pumpkin (*Cucurbita moschata*) seeds as sources of fatty acids and protein.

Material and methods: Fifteen primiparous Texel ewes (BW 60.5 kg) with 70 ± 5 days in milk were fed three diets distributed in a 3 × 3 Latin square design repeated 5 times, with 3 experimental periods of 20 days each. The amounts of concentrate per sheep per day were 50 g/kg BW^{0.75}, corn silage ad libitum. The soybean meal (SBM, control diet) diet was based on oat hay (100 g/kg DM), sorghum grain (285 g/kg DM), bran wealth (55g/kg DM) soybean oil (15 g/kg DM), soybean meal (160 g/kg DM) and vitamin and mineral premix (35 g/kg DM). Pumpkin seed (PS) and Chia seed (CS) treatments consisted of oat hay (100 g/kg DM), sorghum grain (270 g/kg DM), SBM (270 g/kg DM), CS or PS (87 g/kg DM) in order to replace SBM. Diets were formulated to be isoenergetic and isoproteic (ME, 11.7 MJ/kg DM, 14 % CP). Milk yield (MY, kg/d) was recorded, and individual milk samples (100 mL) were taken on the last 5 days of each experimental period at 16:00h. Milk samples were analyzed in duplicate for total solids (TS), lactose, protein, and fat. Fat-corrected milk (FCM 6.5%, kg/d) and fat-protein corrected milk (FPCM 6.5, 5.8%, kg/d) were determined. Data from the last 5 days of each experimental period were considered for statistical analysis, subjected to a 3x3 Latin square design, SAS software package (2002).

Results: The use of CS or PS seeds did not affect milk fat concentration ($P>0.05$), but increased lactose, protein and total solids ($P<0.05$) in CS-fed dairy ewes. The use of PS or SBM diets increased milk yield (up to 43%) as well as FCM and FPCM ($P<0.05$) compared with CS diet.

Table 1: Milk yield (kg/d) and milk composition (g/100g) from dairy ewes supplemented with SBM, PS, and CS treatments.

Variable	Treatment			SEM	P-value
	PS	CS	SBM		
Dry matter intake, g/kg live weight	2508.8	2512.2	2464.9	56.41	0.806
Silage intake, kg DM	1104.5	1091.8	1078.6	52.57	0.941
Concentrate intake, kg DM	1404.3	1420.4	1386.3	16.87	0.377
Milk yield, kg/d	0.356a	0.212b	0.390a	0.029	0.001
FCM 6.5%, Kg/d	0.342a	0.192b	0.349a	0.026	0.009
FPCM 6.5%, Kg/d	0.335a	0.192b	0.347a	0.026	0.010
Fat, g/100g	6.09	5.43	5.44	0.152	0.132
Lactose, g /100g	4.89ab	5.09a	4.77b	0.068	0.001
Total solids, g//100g	10.70b	11.37a	10.63b	0.142	0.037
Protein, g//100g	5.07b	5.41a	5.03b	0.067	0.016

Conclusion: The results showed that PS and CS significantly change the productive parameters of dairy ewes, in corn silage-based diets. The PS and CP could be used in dairy sheep diets as protein feed alternatives.

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Factors affecting feeding and activity behaviours in healthy pre-weaned artificially reared calves

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Application: An understanding of factors affecting healthy calf behaviour will guide the development of behaviour-based tools for disease detection.

Introduction: Behaviour is increasingly being researched as a tool for early disease detection in artificially reared calves. However, it is important to understand how other factors such as sex, and breed may affect healthy calf behaviour. This is to improve the sensitivity and specificity of behaviour-based tools, as alert accuracy is a major concern for animal keepers when discussing technology-based disease detection.

Material and Methods: One hundred and fourteen dairy bred calves from two herds (herd A= 43 calves, herd B= 71 calves) entered group pens of 12-14 calves at approximately seven days of age and left the study when weaning began at 40 days of age. Calves were bedded on straw with ad-libitum access to racks of straw and concentrate and a single automatic milk feeder with an automated weighing platform (Biocontrol). Seven litres of acidified milk replacer (mixed at a rate of 150g/L) were available

daily. Activity behaviours were recorded using a leg-mounted 3-axis accelerometer (Icecube). Health was scored daily using the Wisconsin calf health score method.

To ensure only days where calves were healthy were included, Data was removed for days when medication was given, health scores were intermediate or high, and for 3 days either side. Calves with at least 10 consecutive healthy days were included and the middle 10 days of the healthy period were taken to achieve a balanced dataset. For parameters with a normal distribution a generalised linear mixed model was constructed using REML in R with animal number nested within group as random effects. Fixed effects tested were live weight, age, sex, herd, season of birth, age of inclusion into the group, dam parity, birth weight and sire breed type (beef or dairy). Model selection was carried out using the Akaike information criterion.

Results: Thirty-one calves were included in the analysis. Live weight, age, sex, herd, season of birth and age of inclusion into the group had significant effects on activity or milk feeding behaviours. Dam parity, birth weight and sire breed type had no significant effects on the behaviours studied. The results of the final models are presented in table 1.

Conclusion: When building behaviour-based disease detection tools, models should account for other calf factors including weight, age, and sex to improve accuracy. While there has been much research into changes in calf behaviour with social housing and greater milk allowances but there is very little literature on other factors that affect behaviour in pre-weaned calves.

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Table 1: Factors affecting behaviour in healthy pre-weaned calves with $p < 0.1$ in the final model.

Behaviour	Fixed effect	Level	Effect size	Confidence interval	P value
Lying bouts /day	Season	Autumn	Reference	Reference	Reference
		Summer	6.8	2.6 - 10.8	0.0187
		Winter	-0.4	-3.4 - 2.7	0.7866
	Herd	B	Reference	Reference	Reference
		A	4.0	1.1 - 6.5	0.0082
	Sex	Female	Reference	Reference	Reference
Male		-3.2	-6.4 - 0.1	0.0711	
Motion index/day	Age		-61.5	-96.2 - -25.8	0.0009
	Sex	Female	Reference	Reference	Reference
		Male	-653.98	-1360.5 - 3.3	0.0652
Motion index units/ standing bout	Age		-3.1	-4.9 - -1.0	0.0014
	Age at inclusion into group pen	-11.2	-18.88 - -2.2	0.0065	
	Weight		0.08	0.02- 0.14	0.0073
Volume milk/ visit	Weight		-5.4	-11.1- -0.3	0.0454
	Birth weight		-19.4	-22.6- 2.0	0.1217

Effects of concentrate supplement on feed intake, growth performance and blood parameters of N'dama calves fed cultivated Napier grass basal diet

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Application: Concentrate supplementation could be utilized to improve the growth performance of N'dama bulls under intensive management system and ensure sustainable cattle production all year round to improve farmers livelihood.

Introduction: Livestock production offers resilient resources of economic as well as social sustenance to most individuals in Ghana. This contributes to improving food security and alleviating poverty. There is a high demand for animal products such as meat and milk in Ghana due to population growth. Intensification of cattle in a well-established pasture/ranch is not commonly practiced in Ghana as most cattle are grazed on natural pasture without concentrate supplementation. The major limitation of this system of production is an acute shortage of feeds and fodder especially during dry season which negatively affects animal growth. This problem can be addressed when a high yielding and nutritious forage like Napier grass is cultivated for feeding cattle with concentrate supplementation for optimum performance. The aim of this study was to assess the effects of concentrate supplement on feed intake, growth performance and blood parameters of N'dama calves fed Napier grass basal diet.

Material and methods: Sixteen N'dama calves with an average age of eight months and weighing 99.06kg were used in a twelve-week experiment. The animals were randomly assigned to one of four dietary treatments in a Completely Randomized Design (CRD) according to their body weight. Treatment diets consisted of (T1) Napier grass only offered at 3% of live weight (LW), (T2) openly grazed plus 1% concentrate of LW, (T3) Napier grass plus 1.5% concentrate of LW, and (T4) Napier grass plus 2.0% concentrate of LW. The grass was harvested after 60 days of re-growth and chopped to a length of 15 cm and fed individually to the calves. The concentrate ingredients were well mixed to ensure uniform consistency and nutritive characteristics for efficient rumen functions. The amounts of concentrate and fresh grass offered to each animal were adjusted weekly. Animals were weighed at the beginning of the experiment and subsequently every two weeks for the duration of the study. At the end of the experiment, blood samples were taken from each animal via jugular vein puncture. All experimental data collected were analyzed as a CRD using SAS (2012). Means that were significantly different were separated using Tukey's test at $p < 0.05$.

Results: The concentrate treatments had a significant ($p < 0.0001$) effect on live weight gain, average daily gain and total dry matter intake but did not adversely affect the levels of blood haematological and biochemical indices of the animals under intensive management (Table 1).

Conclusion: Supplementing Napier grass basal diet with concentrate significantly improved live weight gain, dry matter intake, and average daily gain of N'dama calves under intensive management system compared with the control animal with bulls on 1.5% BW concentrate supplement having the highest performance. In addition, supplemental concentrate had no influence on the levels of blood haematological and biochemical indices of the animals.

Table 1: Effect of concentrate supplement on the growth performance and blood parameters of N'dama bulls fed Napier grass basal diet.

Parameters	Treatments				SEM	p
	T1	T2	T3	T4		
Live weight, kg						
Initial weight	97.75	100.25	98.7	99.55	1.32	0.59
Final weight	133.38 ^b	123.13 ^c	147.05 ^a	146.83 ^a	0.94	<0.0001
Live weight gain (kg)	35.63 ^b	22.88 ^c	48.35 ^a	47.28 ^a	0.89	<0.0001
Average daily gain (g/day)	421.11 ^b	272.32 ^c	575.6 ^a	562.8 ^a	10.63	<0.0001
Total DMI (kg)	258.93 ^d	342.70 ^c	412.00 ^b	451.35 ^a	1.43	<0.0001
Blood parameters						
RBC (M/ μ L)	9.04	9.23	6.92	7.73	0.75	0.1447
Blood glucose (mg/dl)	64.13	73.18	72.5	77.08	3.26	0.0858

abc Values having different superscripts in the same row are significantly different at $p < 0.05$, SEM=Standard error mean; DMI = Dry matter intake T1= Napier grass only, T2= Open grazing+1.0% concentrate, T3= Napier grass+1.5% concentrate, T4= Napier grass+2.0% concentrate

The effect of supplementary milk and creep feeding on post-weaning piglet growth

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Application: Strategies to increase creep intake may be more beneficial to piglet post-weaning performance than increasing supplementary milk intake.

Introduction: Supplementary milk (SM) is known to improve piglet pre-weaning survival (Kobek-Kjeldager et al. 2020), and creep feeding improves piglet adaptation to weaning, with piglets that have consumed creep feed having higher feed intake immediately post-weaning than those that haven't consumed creep feed (Muns and Magowan, 2018). However, the combined effects of SM and creep pre-weaning on piglet growth are less well understood. This is likely due to difficulties in assessing individual piglet usage of SM and/or creep feed. This study recorded individual piglet usage of SM provided from birth, and creep feed offered from day 11 of suckling.

Materials and methods: Twenty-eight litters of piglets were selected across two batches (cohorts) farrowing six weeks apart. Litters were selected to have supernumerary piglets compared to the sow's functional teats (+2 piglets), to effectively model the effect of large litter sizes. Piglets were weighed at birth, d4 and then weekly to weaning (d26). They were assigned a birthweight group: 1: ≤ 1.04 kg; 2: 1.06-1.52 kg; 3: 1.54-1.90 kg; 4: ≥ 1.92 kg. Post-weaning, piglets were weighed at d7, 15, 29

and 54. Supplementary milk (Faramate, Volac International Ltd) was offered from birth, and creep feed from d11, both ad libitum. Usage was measured using the PigTrack® system (Asserva, France), whereby the electronic ID (EID) of each visit to the SM bowl/creep feeder was recorded. Multiple regression was performed using Genstat (20th edition) with the variables: total duration of SM visits (milk du), total duration of creep visits (creep du), weaning weight and grouping factor of birthweight group.

Results: All regression models were simplified to include significant terms ($P < 0.05$) only (Table 1). Milk du was a significant model term relating to piglet ADG from birth-d15 post-weaning. After d7, birthweight group ceased to be a significant factor, whereas weaning weight had a positive effect on ADG from d15-54. Where weaning weight was a significant term, it had the highest contribution to each model, with other terms included having an additive effect. Creep du had a significant positive effect on ADG from weaning until d54, but no effect pre-weaning.

Conclusion: The beneficial effects of creep feeding duration were more persistent than those of SM usage on ADG through to d54 post-weaning.

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Table 1: The effects of SM (milk du) and creep usage (creep du), weaning weight (wn wt) and birthweight group (group) on piglet ADG from birth-d54 post-weaning (pwd54).

Period	Equation	r ²	s.e	P-value
Birth-wean (d26)	$C_{\text{group}}^{\alpha} - 0.007 \text{milk du}$	31.8	47.9	<0.001
Wean-pwd7	$C_{\text{group}}^{\beta} + 0.005 \text{milk du} + 0.016 \text{creep du}$	13.0	94.8	<0.001
Wean-pwd15	$107 + 0.007 \text{milk du} + 0.013 \text{creep du} + 20.2 \text{wn wt}$	17.5	88.5	<0.001
Wean-pwd29	$237 + 0.017 \text{creep du} + 22.8 \text{wn wt}$	23.9	80.6	<0.001
Wean-pwd54	$363 + 0.019 \text{creep du} + 28.6 \text{wn wt}$	30.8	82.4	<0.001

α : C group 1: 230; 2: 269; 3: 309; 4: 322. β : C group 1: 123; 2: 158; 3: 175; 4: 224.
Birthweight group 1: ≤ 1.04 kg; 2: 1.06-1.52 kg; 3: 1.54-1.90 kg; 4: ≥ 1.92 kg.

Estimating individual-level pig growth trajectories from group-level weight measurements

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Application: Being able to track the growth of individual livestock can be beneficial to farmers, however, the cost of RFID systems typically prevents this from being financially feasible. Machine learning approaches can help to alleviate this issue by estimating individual growth trajectories from unknown weight measurements without requiring expensive RFID systems.

Introduction: Despite an increasing number of pig farmers implementing data collection systems to improve farm management, the cost of implementing such systems remains a barrier to many. This is primarily due to the fact that some of the most useful data are on an individual pig level, which requires investment of labour and expense of systems such as RFID tagging (Ruiz-Garcia and Lunadei, 2011). We thus propose an alternative solution, where pen-level weight measurements on pigs, which are significantly cheaper to obtain, are used to estimate individual-level growth trajectories using machine learning models.

Material and methods: A dataset consisting of liveweight and feed intake data for 424 grower-finisher pigs recorded by individual feeding stations (Nedap, Netherlands) was obtained from a commercial UK farm. We emulated group-level weight measurements by sampling from our individual-level weight data. From group-level weight data, we trained a support vector machine algorithm to predict, for each pair of time

points, whether those pairs of points belonged to the same pig or not. The support vector machine was then used to estimate likelihood values for each pair of points within each group-level time series. We then clustered these likelihood values using agglomerative clustering with complete linkage, and the resulting clustering tree was cut to produce a fixed number of clusters with each cluster corresponding to an estimated trajectory for one pig. To estimate the performance of the resulting models, we matched the predicted growth trajectories to the true trajectories using the Jonker-Volgenant algorithm (Crouse, 2016) to minimise the root mean squared error.

Results: In Figure 1 we exemplify the performance of the algorithm on one example group-level time series for 10 pigs. The predictions for this time series resulted in a root mean squared error of 1.40 Kg per pig.

Conclusion: Using this method, it was possible to predict approximate growth trajectories of grower-finisher pigs without using their RFID tag identities. It is, however, currently unclear what the most appropriate metric is for this task, though the exact metric will likely differ depending on how these predictions are utilised. Also, in its current form, this algorithm will likely struggle to generalise between farms and will thus require further work before being applied in commercial settings.

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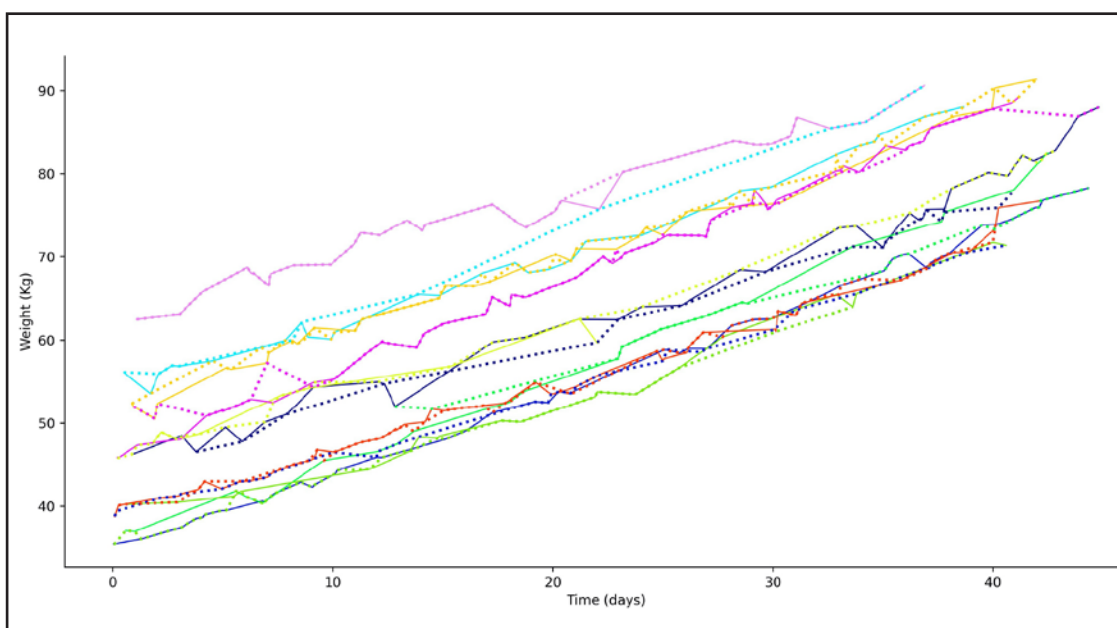


Figure 1: True individual pig growth trajectories using RFID tag identities (solid lines) and predicted growth trajectories obtained from a machine learning algorithm (dotted lines) for 10 grower-finisher pigs. Each colour represents the liveweights for an individual pig.

Modelling growth in Suffolk sheep with insufficient mature weight records for polynomial random regression models

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Application: Mature weight records are rarely recorded in sheep which necessitates novel modelling methods to accurately predict genetic value for growth and optimize high quality food production for a growing human population.

Introduction: Random regression modelling has been used across multiple animal species to model longitudinal data (Schaeffer, 2004). The random regression model accounts for the correlation between measures of the same trait and the wide environmental variability involved in growth, but this requires many weight records. However, mature weight records are often neglected. This study aimed to develop models for growth data in Suffolk sheep that is insufficient for polynomial random regression modeling due to a lack of mature weight records. Two methods were employed. In method A missing mature weight records were predicted for the animals based on their sires and the years in which the lambs were born and then analyzed with random regression models using polynomials or simple linear regression for animal and permanent environmental (PE) effects. Method B used a random linear regression animal model to model animal and PE effects.

Materials and Methods: This project was conducted with a dataset provided by AHDB with records from 14,870 Suffolk sheep. It included multiple weight records for each animal, with a total of 42,244 records. Four weight recordings were identified for the analysis including birth weight, weaning weight (9 weeks), scan weight (21 weeks), and mature weight. There were 89 mature weight records. Method A began with filtering the data in R to include only animals with a mature weight. The sires and birth years of these animals were identified and a prediction model for each of the ten sire groups and each of the year groups was made. The prediction model was: Mat weight = birthweight + weaning weight + scan weight. Mature weights were analyzed in a random regression model with polynomials of order 1 for animal and PE effects. Method B used an animal model with the recorded mature weights alone. A three-generation pedigree was formed in R using a match function and a full pedigree provided by AHDB. A random regression was fitted with a linear age effect. All analyses were done in ASREML, and genetic parameters were estimated.

Results: Models in Method A with polynomials failed to converge but the linear model converged. Method B resulted in an additive genetic variance of 0.016 for birth weight (BW), 13.58 for weaning weight (WW), 68.688 for scan weight (SW), and 990.92 for mature weight (MW). This corresponded to heritabilities of 0.015, 0.487, 0.687, and 0.759 respectively. The correlations were: BW,WW = 0.4603, BW,SW = 0.0151, BW,MW = 0.0040, WW,SW=1.0, WW,MW=1.0, MW,SW = 1.0. The estimates of heritabilities from the method A with linear regressions were slightly higher than method B at: 0.007,0.192,0.539, and 0.947 respectively.

Conclusions: Simple linear regression models resulted in possibly useful genetic parameters for growth but some fine tuning of approach is required.

Acknowledgements:

The authors acknowledge funding from AHDB

Reference: Schaeffer, LR 2004. Livestock Production Science, 86(1-3), 35-45.

Use of machine learning models to predict body condition score in sheep

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Application: The prediction of body condition score (BCS) in ewes provides a means for producers to easily and consistently collect BCS data for their flocks. It provides a reliable comparison both within and between flocks. The prediction of BCS also reduces labour associated with measurement and recording.

Introduction: Body condition score is a subjective measure of the muscle and fat coverage across the vertebrae in the loin region of a ewe (Thompson & Meyer, 1994). It provides a means of assessing fat deposits and therefore energy reserves of sheep. Body condition score is used on farm as a management aid for targeted nutrition and to assess flock performance. Predicting BCS from variables commonly collected on farm reduces the subjective nature, human error, and labour associated with manually scoring. Research shows that there is a significant positive relationship between BCS and weight (Kenyon et al., 2014), therefore it was hypothesised that BCS could be predicted from weight, with the addition of other variables, such as: age; breed; and event or days since last lambing, to improve the accuracy of predictions.

Materials and Methods: Data collected as part of the Agriculture and Horticulture Development Board (AHDB) Challenge Sheep (Challenge Sheep | AHDB, n.d.) project were used to develop machine learning models to predict BCS. Data collected from 7003 ewes across 11 UK farms, over a three year period were

used to build the models. Data were collected on a range of parameters including: ewe weight and BCS at key stages of production; reproductive performance; lamb performance and; mortality. Scorers from each farm underwent BCS training and calibration sessions at the start of the project. The dataset was split into training and test datasets using an 80:20 split to observe model generalisability. Five machine learning models (linear regression, random forest, K- nearest neighbour, support vector machines and gradient boosting) were used to predict ewe BCS from variables: weight; age; days since last lambing and; breed. Body condition score was predicted as a continuous variable, using metrics root mean square error (RMSE) and coefficient of determination (R^2) to evaluate performance. Results: Gradient boosting models were most efficient in predicting BCS from the four predictor variables (Figure 1, training RMSE = 0.38, training R^2 = 0.64), while also performing well on the test dataset.

Conclusion: Body condition score can be predicted using machine learning models and is an effective way to reduce human error associated with manually collecting BCS. Gradient boosting, using variables: weight; ewe age; days since last lambing; and breed was most effective at predicting BCS.

Acknowledgements: The authors acknowledge funding from AHDB Beef and Lamb.

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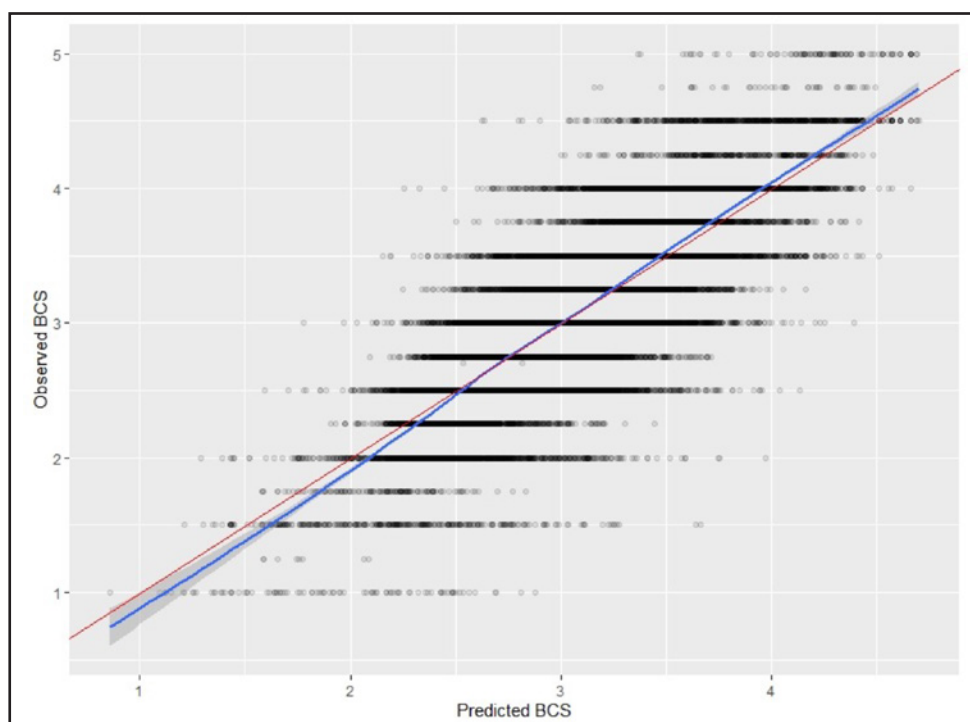


Figure 1: Observed BCS against predicted BCS on training dataset for gradient boosting model.

The impact of environment on the accuracy of beef cattle measurements using video image analysis

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Application: The accuracy of live animal parameters, extracted in real-time from 3-Dimensional (3D) images, can be impacted by external factors such as the environment in which the images are captured.

Introduction: Video image analysis technology can be used to map the morphometrics of cattle to create parameters which can be used with other animal information to predict post-slaughter carcass characteristics. Three-dimensional images measured on-farm were previously found to predict EUROP fat and conformation grades with 54% and 55% accuracy respectively (Miller et al., 2019), indicating the potential for implementation of objective methods for assessing carcass value on farm. The aim of the current work was to assess the impact of the environment on the accuracy of 3D measurements obtained from the live animal.

Materials and Methods: Data were collected from four commercial farms, one research farm and one commercial abattoir, with eight Basler Time-of-Flight near-infrared cameras (Basler inc., Exton, PA) being used to create 3D scans of live beef cattle. The cameras were either (i) suspended 3m above an automated weigh platform (Beef Monitor, Richie Agricultural, Scotland) or (ii) suspended 3m above a raceway in the lairage of a commercial abattoir. As cattle passed under the cameras, a 3D scan was captured and 60 potential predictor variables (widths, lengths, heights, ratios, areas and volumes) were extracted in real time by Innovent Technology Ltd. using Halcon software (MVTech Software GmbH, Munchen, Germany). Univariate statistics was carried out for all variables, however the current work focuses on length measurements. The data from the farm cameras were compared with that of the abattoir cameras, assessing the impact the environment can have on the accuracy of measurements.

Results: A scatter plot (Figure 1) showed that all camera units produced similar total length measurements (LengthToT) of the cattle, suggesting that they were recording this variable consistently. Plots of length measurements of the cattle from the tail head to the widest point of the rear, as a proportion of LengthToT (LengthTR_Prop) (Figure 2a) and length measurements from the widest point of the rear to the widest point of the middle as a proportion of LengthToT (LengthRM_Prop) (Figure 2b) show the measurements of the farms units to be visually different to measurements from the abattoir units. Additional analysis showed this to be a significant difference ($p < 0.05$), with parameters extracted from the abattoir camera

unit having a larger LengthTR, while a smaller LengthRM. Further investigation indicated that the setup in the abattoir was leading to incorrect recordings when identifying the width measurements which determine the different lengths. This was often due to cattle touching the walls of the race, leading to inconsistencies in measurements.

Conclusion: For accurate measures to be extracted from 3D scans of live cattle, the animals must be positioned in a suitable environment, where external factors, such as the walls of a race cannot interfere with automated measurements.

Acknowledgements: Funded by SRUC and AHDB

References: Miller, G.A., Hyslop, J.J., Barclay, D., Edwards, A., Thomson, W., Duthie, C.A., (2019). *Frontiers in Sustainable Food Systems* 3, 30.

Figure 1: Total length measurements (LengthToT) of live beef cattle from abattoir and farm camera units.

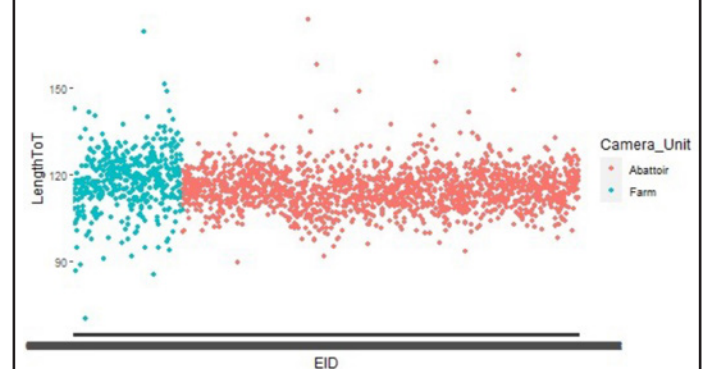


Figure 2a: Length measurements from the tail head to the widest point of the rear of live beef cattle, as a proportion of the total length, from abattoir and farm camera units.

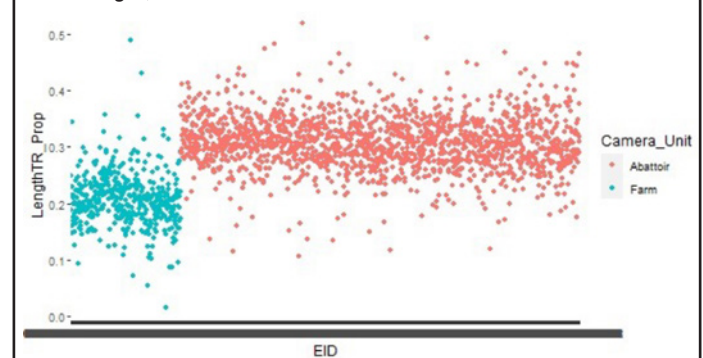
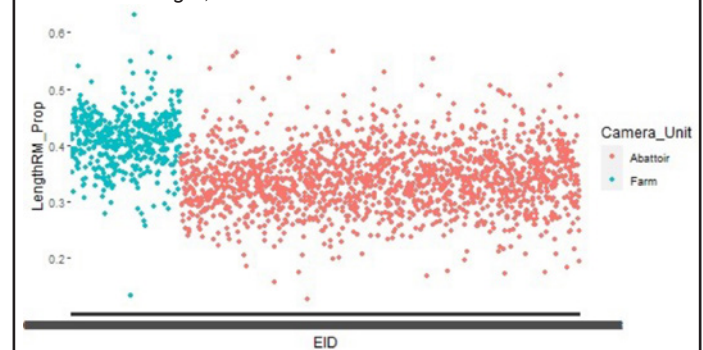


Figure 2b: Length measurements from the widest point of the rear to the widest point of the middle of live beef cattle, as a proportion of the total length, from abattoir and farm camera units.



Development of a novel ethogram for assessing rider performance while performing piaffe in dressage

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Application: Developing a rider ethogram that has the potential to become a valuable tool as an objective grading system in competitions for stewards and officials of the Fédération Equestre Internationale to halt adverse behaviours from escalation, safeguarding the wellbeing of the horse and rider.

Introduction: Evidence shows that rider behaviour and cues have a significant influence on the behaviour of the horse and the quality of equine kinematics. Conflicting, ambiguous cues and head neck positions that limit the horse's respiratory system, locomotion and eyesight vision over a prolonged time can lead to mental or physical discomfort which is detrimental for the welfare. As a response to the discomfort ridden horses may show conflict behaviour which is unfavourable. Consequently, rider actions, the applications of cues, and horse head positioning, inadvertent or otherwise, may have an impact on the horse's movement and their behaviour, including the incidence of conflict behaviours. Research has explored equine biomechanics in piaffe, determinants for performance in dressage have been proposed however rider skills whilst performing piaffe are yet to be determined. Ridden horse ethograms with incorporated conflict behaviours, signs of pain and lameness exist and are utilised to assess the state of the horse exist. An ethogram that incorporates rider performance variables affecting the state horse has not yet been developed and could offer an additional approach to evaluate the state of the combination. This study aimed to develop a novel evidence-based ethogram as a methodology for assessing rider actions in piaffe.

Materials and methods: The ethogram was developed by listing 14 descriptors of the rider's posture and validated through a short survey (N=11) with binary answers to questions on two different video observations of riders in piaffe. Members of staff of Sparsholt's Equine Centre, students and coaches validated the ethogram. With a limited sample of two riders, it was demonstrated that the ethogram could be used accurately with an inter-rater agreement at 75%.

Expert riders from the Olympics 2012 in the Grand Prix were categorised as elite (top ten), lowest-achieving elite (bottom 10 in the class), and non-elite professional riders (n=10) to identify any differences between the levels. Rider positions were compared from photographs of video recordings on angles of body segments and head positioning were assessed with visualisations of "on" and "behind" the vertical and counted. Data were not normally distributed and to find differences between the categories Kruskal Wallis on body segments and Fisher's Exacts tests on head positions were done.

Results: Kruskal Wallis tests found no statistically significant differences between body segments of the different rider categories. There were significant differences (one way ANOVA $F=0.232$, $p=0.022$) in elbow, hip, and knee positioning of the lowest-achieving riders versus the other levels (Table 1). Fisher's exact found statistically significant differences in horse head positions ($p=0.004$) in the lowest-achieving category versus top-rated elite level.

Conclusions: The results suggested differences in the rider levels on rider position in which the lowest-achieving elite level stood out with more variances versus the other levels.

Table 1: Mean and standard deviations of the body segments of different categories of riders (Levene's test).

	Elbow		Shoulder		Hip		Knee	
	M	SD	M	SD	M	SD	M	SD
Level:								
Top elite	118.16	5.17	46.68	59.45	143.97	12.95	92.53	32.76
Lowest achieving elite	108.95	25.64	53.19	45.52	125.94	29.37	71.12	41.60
Non-elite professional	114.20	8.31	23.54	15.44	153.59	15.44	114.20	9.67

UK beef and sheep farmers' barriers to adopting rotational grazing systems

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Application: The results of this work will be used to create a baseline of grazing systems within the UK and allow us to highlight key barriers and enablers to different grazing practices. This will be used to help encourage long-term change to more economically and environmentally sustainable grazing systems.

Introduction: Despite the importance of grassland management in farm economic and environmental performance, little is known about current grassland management practices. Furthermore, it is unknown what farmers' attitudes are to grazing practices that require regular pasture measurement and data input – measures that require additional labour and other costs but can notably improve the efficiency of grass utilisation. The aim of this study is to better understand current grazing management on beef and sheep farms and the barriers to adopting potentially more productive and efficient (e.g., rotationally grazed) systems.

Material and Methods: A survey was developed after a review of literature and in consultation with experts in the relevant fields. Following piloting with 20 farmers, it was published online and advertised via social media channels, farming press, farming levy bodies and unions. Follow-up interviews asked more open-ended questions and gave farmers a chance to express their thoughts and opinions. Frequency tables will be used to show a summary of the categorical data. Pivot tables and cross tabulation will be used to examine relationships between variables, e.g., between farm type and grazing system used. A detailed thematic analysis will be undertaken on the information gathered during the interviews. Codes will be assigned to themes that occur within the data to highlight key patterns and trends.

Results: A total of 231 respondents completed the survey from across the UK, with a mean age of 49 and a diversity in terms of education levels. 60% of respondents defined their land type as lowland, 30% as upland, and 10% as a mixture, with a significant range in farm size. The full (quantitative and qualitative) analysis will be completed in time for a poster presentation at the BSAS conference. Early analysis of the follow-up interviews indicates that key barriers to adopting potentially more productive and efficient grazing systems include cost of investment, lack of knowledge, provision of adequate water and shade, and an unwillingness to change. The key enabler highlighted is access to expert knowledge and advice.

Conclusion: Grazing practices play a vital role in the economic and environmental performance of a farm. Our work creates a baseline of current practices and identifies the key areas that need to be addressed to bring about the transition to potentially more sustainable grazing practises on beef and sheep farms. The results will have relevance given the ongoing changes to agri-policy towards environmental deliverables, and future challenges to the market.

Acknowledgements: The authors acknowledge the KESS 2 programme, Hybu Cig Cymru, the Department for Environment Food & Rural Affairs, and ADAS.

Strategies to reach zero carbon beef and sheep production on Welsh farms

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Application: Understanding baseline farm greenhouse gas emissions and how they may be mitigated requires a validated, standardised carbon accounting tool. This work demonstrates the extent to which efficiency measures can reduce emissions, and the degree of afforestation needed to enhance sequestration to off-set remaining emissions, enabling farms to reach net zero.

Introduction: The Climate Change Committee has recommended a 64% reduction in greenhouse gas emissions from the agriculture and land-use sector to meet the 2050 net zero target in the UK. However, it is still unclear what these changes will look like at a farm level. The aims of this study are: i) to assess the effects of carbon calculator choice on baseline carbon footprints of Welsh beef and sheep farms, and ii) to investigate strategies for these farms to reduce emissions and increase sequestration to achieve net zero. The study will define net zero typologies and assess their effect on production.

Material and Methods: Carbon footprints were calculated for 20 Welsh beef and sheep farms using three carbon accounting tools: Bangor University's Carbon Footprinting Tool, AgRE Calc, and the Farm Carbon Calculator. Tools were compared based on their input requirements, emission estimates and sensitivity to

mitigation options. A hybrid model including emission estimates from AgRE Calc and sequestration calculations from the Bangor Tool were then chosen to calculate baseline emissions. Mitigation scenarios for each farm were created. Mitigation measures and abatement potentials were sourced from the most recent Marginal Abatement Cost Curve. The reduction in emissions achieved and area of woodland needed for offsetting to reach net zero were noted and the effect on production assessed.

Results: Carbon accounting tools have notable differences in emissions estimates (Figure 1) and therefore footprints from different tools are not directly comparable. The application of mitigation measures was projected to reduce emissions by an average of around 30% across all farms. After implementing these measures, the area of farm needed for woodland to off-set (via sequestration) remaining emissions ranged from 15-50%. Therefore, at present, achieving net zero would have a significant effect on production through the reduction in livestock numbers required to 'free' land for offsetting purposes.

Conclusion: Urgent action must be taken to improve livestock farming's contribution to the net zero target due to its critical role in Welsh society and economy. Calculating carbon footprints of farms is a key first step, but a standardised carbon accounting tool is required to understand both baseline farm emissions and the impacts of mitigation measures. However, mitigation measures alone will not sufficiently reduce emissions, therefore enhancing sequestration through afforestation will be needed. The subsequent impacts of this on production capacity will need to be considered.

Acknowledgements: The work was part of the Knowledge Economy Skills Scholarships (KESS 2) supported by the Welsh Government's European Social Fund and part-funded by Hybu Cig Cymru – Meat Promotion Wales.

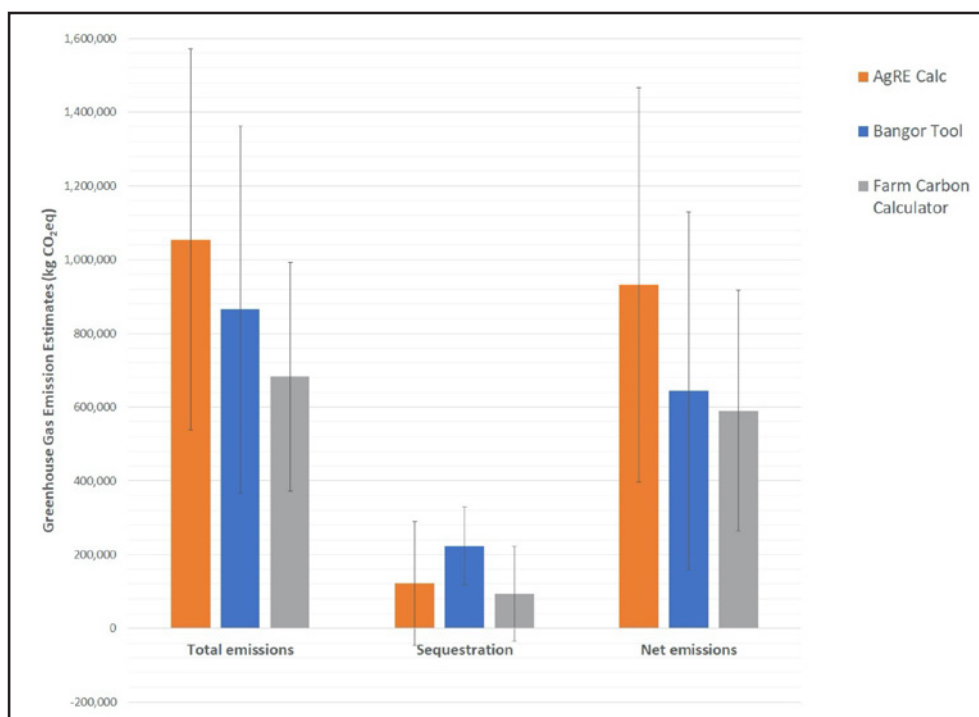


Figure 1: Mean emission estimates \pm standard deviations ($n=20$) for each total emissions, sequestration, and net emission estimate from AgRE Calc, the Bangor Tool and the Farm Carbon Calculator.

Evaluating enteric equations for predicting dairy cattle methane emissions

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Application: Equations used to predict enteric emissions vary considerably and have not been evaluated against a variety of diets. This is important to assess their accuracy in representing the effect of diet on enteric emissions and their suitability for use in whole farm simulation models.

Introduction: Cattle are the highest anthropogenic contributors of methane to the atmosphere (Pinares-Patiño et al., 2016) and enteric fermentation (EF) is the main cause of their emissions (Gilardino et al., 2020). Diet is the main variable that effects EF (Van Gastelen et al., 2019), yet is not considered during the development of enteric equations. The aim of the present study was to compile a set of enteric equations and common UK dairy feeds, to compare their ability to capture the effect of diet composition.

Material and Methods: "Science Direct" was used to find current EF equations, which resulted in 102 international equations. The equations were collated and converted to the same functional unit output of methane as grams per day (CH₄g/day), by dividing emissions in megajoules per day, by 0.05565. The equations were coded into R programming language and a dairy nutritionist formulated seven diets specific to the UK. The equations were grouped into 12 categories based on the number and type of factors included, such as dry matter intake (DMI) and neutral detergent fibre (NDF). The results were then plotted for each equation category created. It was then observationally determined, using a comparative approach, whether the equations were consistent or represented the various diets, by their ranking of most to least emitting.

Results: In general, the equations showed large variation between each other, even within the same diet. Single factor equations, such as the DMI only equations, did not show the effect of dietary composition on the emissions. The equations were consistent in their ranking of the diets, except for those including GEI.

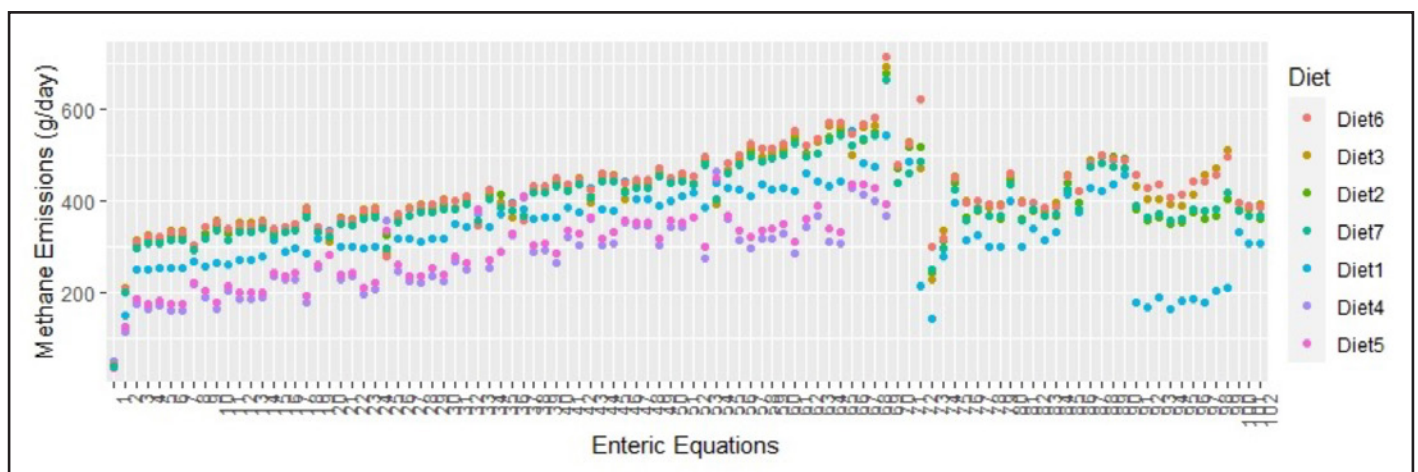
Conclusion: The equations showed large variation in results and some lacked detail to effectively show the differences in the emissions between diets. However, there was consistency between detailed equations (excluding GEI based equations) and the ranking of most to least emitting diets, indicating that these equations are representative for use in models and showing the best to worst emitting diets, even if the predicted CH₄g/day vary. Whilst highlighting a need for further research into enteric emissions and diet to gain more accurate methane predictions.

Acknowledgement: The authors acknowledge funding from the Agriculture and Horticulture Development Board (AHDB) and the AgriFood Charities Partnership (AFCP).

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Figure 1: The predicted methane emissions using 101 enteric equations, against seven diets.



Variability in enteric methane eructation peaks among dairy cows

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Application: Signal processing of CH₄ eructation peaks was used to explore variability of enteric CH₄ emissions in dairy cattle on commercial farms across the UK. Emission and production measures from commercial farms will help inform farm level mitigation options.

Introduction: Enteric CH₄ emissions in dairy cows are known to change due to variations in diet and animal factors (Rotz et al., 2010, Garnsworthy et al., 2012). Few studies have measured CH₄ emissions across several commercial farms with different production systems (e.g. grazing and non-grazing). This study explored variation in enteric CH₄ emissions among a large dataset of commercial dairy cattle in the UK.

Material and methods: A total of 105,701 CH₄ spot measurements were obtained from 2,436 dairy cows using robotic milking stations across 18 farms in the UK. Cows were milked on average 2.5 (s.d. 1.0) times per day. Eleven farms fed a partial mixed ration (PMR) and 7 farms fed a PMR with grazing. Cows were mostly Holstein-Friesian. CH₄ concentrations in breath (ppm) were measured at 1s intervals during milking visits using one infrared CH₄ analyser per milking station (Guardian Plus; Edinburgh Instruments., Livingston, UK). CH₄ data were extracted from the time-series signal using peak analysis tools in MatLab Signal Processing Toolbox (version R2020a; MathWorks, Inc., Natick, USA), with CH₄ emission rate (g/min) derived by maximum peak amplitude (ppm) / [1 - EXP(-(peak rise for amplitude in seconds / 60))] x 60 x 0.706 x 10⁻⁶. Dry matter intake (DMI) of individual cows was predicted from milk yield and live weight using the equation DMI (kg/day) = 0.025 x live weight (kg) + 0.1 x milk yield (kg/day) (MAFF, 1984). A multiple experiment model was used to assess effects of explanatory variables on average CH₄ emissions per cow by using GenStat 20th Edition.

Results: Milk yield averaged 30.4 kg/d and average enteric CH₄ emission rate across the 18 farms was 0.37 g/min (maximum 0.63, minimum 0.20, standard deviation 0.12). CH₄ emissions were affected by parity, week of lactation, and the interaction between diet and DMI (Table 1). CH₄ increased to 0.4 g/min at week 10 of lactation and then was steady until week 70. First and second parity cows had higher emissions (0.38 g/min) than other parities, with emissions declining towards cows in their fifth parity (0.35 g/min). Increasing DMI increased emissions (0.01 g/min per kg DMI) and emissions were higher for grazing cows (0.2 g/min per kg DMI).

Table 1: Variables affecting enteric methane emissions (g/min) by dairy cows on commercial farms.

Variable	F statistic	n.d.f	SED	P value
Parity	10.6	4	0.005	<0.001
Week of lactation	4.2	69	0.018	<0.001
Diet	5.0	1	0.006	0.026
DMI	98.4	1	0.001	<0.001
Diet x DMI	17.8	1	0.002	<0.001

Conclusion: This study confirms that enteric CH₄ emissions increase with increasing DMI. This study suggests that increased longevity of cows and improved diet quality can reduce CH₄ emissions on commercial farms.

Acknowledgements: This research was funded by a PhD studentship from the government of Sultanate of Oman. Collection of original methane data was funded by Defra.

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