

BOOK OF ABSTRACTS

PRE-COFERENCE JDR SESSION

Genome-wide responses to macrocyclic lactone treatments in *Ostertagia ostertagi*

Paul Campbell, Andrew Forbes, Kathryn Ellis, Roz Laing and Jennifer McIntyre

School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow, G12 8QQ

The macrocyclic lactone (ML) drug family is the most widely used class of anthelmintics in animal health. Ivermectin, an avermectin, and moxidectin, a milbemycin, are structurally distinct compounds with similar therapeutic applications. Resistance to both drugs is now widespread among gastrointestinal nematodes of livestock; however, despite their extensive use, the genetic mechanisms underlying ML resistance remain poorly defined. Using newly assembled chromosome-level reference genomes for *Ostertagia ostertagi*, we applied a genome-wide approach to identify signatures of selection following ML treatment in two field populations from Scotland. Faecal egg count reduction tests (FECRTs) were conducted in dairy calves, with larvae collected before and after treatment for pooled, mixed-species whole-genome sequencing. To minimise the effects of interspecific read misalignment, filtering protocols were optimised by aligning simulated reads from both species to each reference genome and to a combined reference assembly. We then identified species-specific treatment-associated changes in allele frequency, nucleotide diversity and genetic differentiation across the genome. Our analysis revealed a shared 15-Mb locus on chromosome 5 in populations treated with either ivermectin or moxidectin (Figure 1). This region contains 709 genes, including 37 with orthologues within a previously identified ML resistance-associated locus in *Teladorsagia circumcincta*. The identification of a common genomic region following selection with two different ML subclasses provides evidence for convergent genomic responses to ML treatment and highlights candidate regions that may contribute to resistance in *O. ostertagi*. These findings provide new insights into the genomic basis and evolution of ML resistance in field populations of *O. ostertagi*.

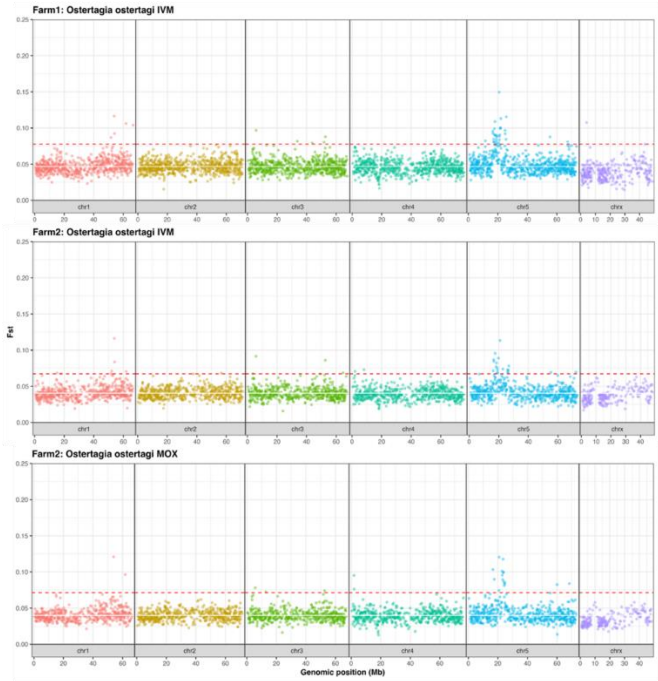


Figure 1. Genome-wide *F*ST analysis of *Ostertagia ostertagi* populations before and after macrocyclic lactone treatment. Genome-wide genetic differentiation between pre- and post-treatment populations across three populations. A pronounced peak on chromosome 5 was consistently observed across all populations. The dashed red line indicates the genome-wide mean *F*ST plus three standard deviations.

Exploring faecal microbiome signatures associated with milk drop syndrome in dairy cattle during suspected mycotoxin exposure

Joana Lima

School of Veterinary Medicine and Biosciences, SRUC, Edinburgh

Milk drop syndrome (MDS) is characterised by reductions in milk yield accompanied by changes in faecal consistency and often attributed to mycotoxin-contaminated feed in dairy cattle. However, individual animals may respond differently under similar farm-level exposure to mycotoxins, potentially reflecting differences in their gut microbiomes. This study investigated whether faecal microbiome composition and functional potential differed between MDS-affected and unaffected dairy cows during a suspected mycotoxin-associated event. Faecal samples were collected from ten dairy cows on a commercial farm, comprising five animals exhibiting MDS and five unaffected animals. Shotgun metagenomic sequencing was performed to characterise microbial taxonomic composition and functional potential (i.e., KEGG orthologous groups). Feed samples (total mixed ration) were analysed for mycotoxin contamination. Multiple mycotoxins were detected in the feed, the most abundant being penicillic acid at 279.5µg/kg. No significant differences in alpha diversity were observed when comparing MDS to unaffected animals at either the genus or functional level. Similarly, PERMANOVA did not identify significant differences in overall microbial community composition or functional profiles, with MDS status explaining approximately 11% and 12% of the variation, respectively. Nevertheless, sparse partial least squares discriminant analysis (sPLS-DA) identified subsets of microbial genera and KEGG orthologues that discriminated between affected and unaffected cows. Genus-level classification achieved a balanced error rate of 0.110, compared with 0.309 for functional profiles. Among the selected genera, *Proteiniphilum* and *Candidatus Merdicola* were associated with MDS-affected animals, whereas *Micromonospora* was more abundant in unaffected animals. Genes identified as important to discriminate between MDS and unaffected animals included e.g., *acpH*, related with lipid transport and metabolism, and *torR*, involved in the two-component system needed for bacteria to adapt to changing environments, both of which were more abundant in unaffected animals. These preliminary findings suggest that specific taxonomic and functional features may be associated with MDS. Despite the absence of an overall effect on the faecal microbiome, there is potential for the identification of microbial biomarkers of MDS or susceptibility to mycotoxin-contaminated feed, which could be explored in the development of a pen-side test to diagnose MDS and to identify the causative mycotoxin.

A study to consider the prevalence of pelvic axial rotation in dairy cows and it's use as an objective indicator of lameness taking into consideration other cow-level and management factors

Victoria Harris[1], Ruth Wonfor[2] and Manod Williams[2]

[1] Institute of Biological, Environmental & Rural Sciences (IBERS), and [2] Department of Life Sciences, Aberystwyth University, Ceredigion, Wales, SY23 3DA

Pelvic axial rotation (PAR) describes asymmetrical positioning of the pelvis around the body's axial skeleton and has received little research attention in dairy cattle. This study investigated the prevalence of PAR and its association with lameness and other cow-level and management factors across eight UK dairy farms. PAR was measured in lactating dairy cattle (n=403) using photogoniometry (Kinovea software) alongside mobility score, body condition score (BCS), parity, days in milk (DIM), pregnancy status and farm management variables. PAR was observed in 80.1% of cows, with a threshold of ≥1° identified as the minimum rotation associated with a measurable distinction between cows with and without rotation. Single variables were first screened for their association through simple linear regression analysis. Multivariable models were then constructed using manual backward stepwise elimination. The degree of PAR was significantly associated with mobility score ≥2 (***β*** = 0.739, 95% CI: 0.055 - 1.424, p = 0.034). No significant associations were identified between PAR and farm management, milking method, BCS, parity, DIM or pregnancy, and no direct association between PAR and milk yield was identified (p>0.05 in all models). The degree of PAR was also significantly associated with an 'imperfect gait' in cows with mobility score ≥1 (β = 0.564, 95% CI: 0.097-1032, p = 0.018). The association between the degree of PAR and cows with either lameness or an imperfect gait suggests that with further research, PAR may have potential to be used as an objective measure for mobility changes. Mobility scoring is widely used to identify lame cows but can be both time consuming and difficult to detect consistently, particularly at an early stage. PAR is an objective measure that, if explored further, could potentially be used to improve intervention timing, welfare, and productivity. Due to a limited number of cows with lameness score ≥2 (7% of sample), further longitudinal research is required to establish whether PAR precedes the development of observable lameness and to determine its suitability for incorporation into on-farm precision livestock monitoring systems for remote or automatic detection.

From assay development to real-sample testing: an extraction-free LAMP-lateral flow workflow for rapid detection of dairy-associated bacteria

Maha Shalaby[1], Iyona Jarvis[2] and Richard J. Dewhurst[1]

[1]Dairy Research & Innovation Centre, School of Veterinary Medicine and Biosciences, SRUC, Dumfries, DG1 3NE, [2]Technical Department, Arla Foods, Lockerbie DG11 1LW

Rapid on-site detection of bacterial contamination could support timely hygiene and quality decisions in dairy processing, but conventional microbiological testing generally requires laboratory-based sample preparation, instrumentation and technical expertise. These limitations create a point-of-need (PON) diagnostic gap. This study aimed to develop a rapid, extraction-free molecular workflow based on loop-mediated isothermal amplification (LAMP) and lateral flow strip (LFS) detection for four dairy-associated bacterial targets: *Bacillus cereus* group, *Clostridium* spp., *Staphylococcus aureus* and *Escherichia coli*. Target-specific single-plex LAMP assays were developed and evaluated using spiked milk and whey samples. A simple 1:10 dilution followed by heat treatment at 95 °C for 10 min enabled direct amplification without conventional DNA extraction. Under thermocycler conditions, single-plex assays showed high analytical specificity, with limits of detection ranging from 10-10^3 and approximately 10^2 CFU/ml in spiked diluted, heat-treated milk and whey, respectively. Translation to LFS detection resulted in target-dependent reductions in analytical sensitivity. Three duplex configurations enabled simultaneous detection of paired targets, although primer competition reduced sensitivity, with limits of detection generally increasing to 10^4-10^5 CFU/ml. The workflow was further evaluated using 52 naturally contaminated industrial whey samples and compared with reference qPCR following DNA extraction, extraction-free LAMP using a thermocycler, and a simplified heat-block/LFS workflow. Comparison with routine microbiological results was limited because these methods primarily assessed viable growth and did not necessarily distinguish vegetative cells from spores. Interpretation was further complicated because DNA-based detection cannot distinguish spore-associated from vegetative-cell-associated target material. Thermocycler LAMP detected 49/52 qPCR-positive *Clostridium* spp. and 20/31 qPCR-positive *B. cereus* group samples, while heat-block/LFS detected 42/52 and 19/31, respectively. For *E. coli* and *S. aureus*, heat-block/LFS detected 25/36 and 14/26 qPCR-positive samples, respectively. Concordance with qPCR was therefore target dependent, with additional losses observed in the simplified heat-block/LFS workflow. Overall, the study demonstrates the feasibility of an extraction-free LAMP-LFS workflow for rapid detection of dairy-associated bacteria while highlighting the challenges of translating analytical performance into robust real-sample and point-of-use testing. The findings establish a technical foundation for rapid hygiene monitoring and identify sample preparation, target-specific optimisation, primer-tag compatibility and LFS signal generation as priorities for further development and validation.

Animal-mounted technologies can reduce GHG emissions intensity on commercial dairy farms

Holly J. Ferguson[1], Louise C. McNicol[1], Holly Nisbet[1], Jenna Bowen[2], Julian Bell[3] and Carol-Anne Duthie[1]

[1] SRUC, West Mains Road, Edinburgh, EH9 3JG, [2] University of Bristol, Langford House, Langford, BS40 5DU, [3] Agrecalc Ltd., West Mains Road, Edinburgh, EH9 3JG.

Precision livestock farming (PLF) technologies are primarily designed to improve livestock management rather than directly mitigate emissions. However, by enhancing production efficiency, these technologies may contribute to progress towards net zero targets in the dairy sector through reductions in greenhouse gas (GHG) emission intensity. The potential environmental benefits of PLF adoption were modelled using data from nine Scottish dairy farms representing a range of dairy production systems found across Europe. Farms were grouped into three system types: high-yielding systems (~10,000 L/cow/year), moderate- to high-yielding systems (~8,500 L/cow/year), and traditional or cross-bred systems (~6,000 L/cow/year), with three farms represented in each group. The analysis examined accelerometer-based fertility and health monitoring technologies and their potential effects on milk yield. Farm-level emissions were calculated using Agrecalc, a UK carbon calculator, by comparing baseline emissions with three modelled scenarios: fertility improvements alone (S1), fertility improvements combined with increased milk yield (S2), and health improvements combined with increased milk yield (S3). Technology impact assumptions were informed by a review of peer-reviewed research and grey literature on PLF technologies for dairy and beef cattle. Modelled technology adoption generally lowered GHG emission intensity, although changes in total farm emissions varied between scenarios and farms. The largest mean reduction in emission intensity occurred under S3 (-6.98%), followed by S2 (-6.33%), while S1 achieved a smaller reduction (-2.04%). In contrast, mean total farm emissions decreased by 1.6% under S1 but increased slightly under S2 (+0.15%) and S3 (+1.15%), despite reductions occurring on individual farms in these latter scenarios. The greatest emission intensity benefits were generally observed in farms with poorer baseline performance, e.g., longer calving intervals and lower milk yields, suggesting that initial production efficiency influences the environmental gains achievable through PLF adoption. These findings indicate that PLF technologies may offer opportunities to reduce the GHG intensity of dairy production, although improvements in emission intensity do not necessarily translate into lower absolute farm emissions and that adoption of technologies should be targeted for each farm's needs. The magnitude of these benefits depends on both the technology scenario and the farm's baseline performance.

MONDAY AFTERNOON

Associations between calf serum total protein concentrations and subsequent survival, milk production and fertility using data from three UK clinical veterinary practices.

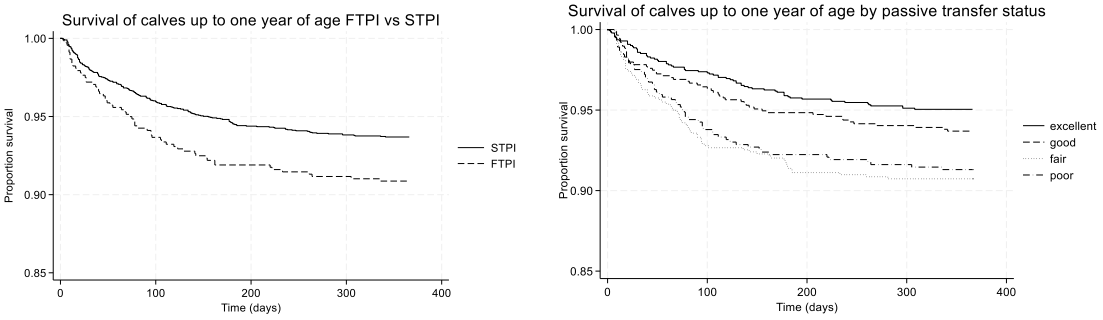
Thomas Jenkins[1,3], Gregor Taylor[2] Andrew Henderson[3], Richard Vazquez[1], Rachel Dean[3], Jenny Stavisky[3] and Katharine S. Denholm[1]

[1]School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow, Glasgow, G61 1QH, [2]Advanced Quantum Architecture Laboratory, EPFL, 2002 Neuchâtel, Switzerland, [3]VetPartners Group, York, YO30 4UZ

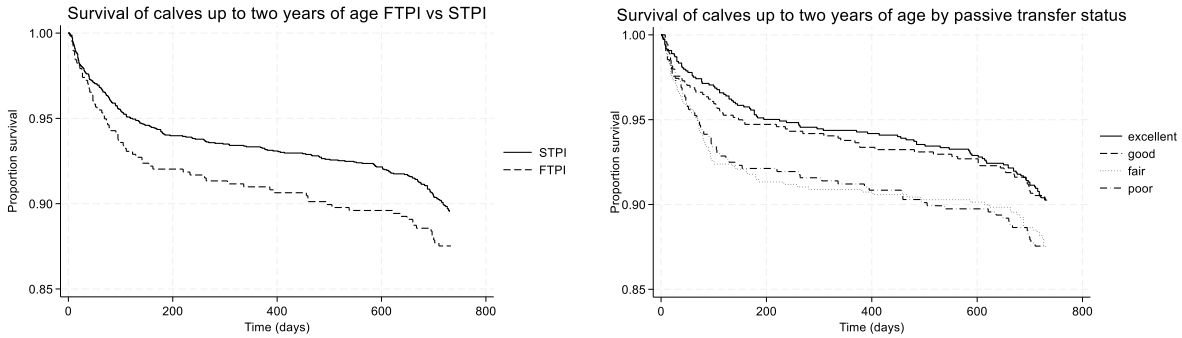
The authors were presented with a convenience sample of 10,370 serum total protein (STP) results collected from calves on 78 farms across three UK veterinary practices. The objective of this study was to measure associations between STP in the first seven days of life and later life performance in terms of survival, milk production and fertility parameters. Data was extracted from the Cattle Tracing Service database and Milk Recording Organisation databases in order to trace the relevant animals to the respective data source and to extract output variables of interest. Mixed effects parametric survival models assessed survival to one and two years. Linear mixed models were constructed for outcome variables of interest including: age at first calving; first calving to conception interval; first lactation 305 day milk yield and fat and protein production. Mixed effects logistic models were constructed for dichotomous outcome variables 'achieved target age of first calving' (target 730 days); 'produced a calf by 24 months of age' and 'produced a calf by 30 months of age'. In each of these models, STP was considered using both the traditional dichotomous pass/fail and the four-category allocation system advocated in recent literature. Survival to 6 months and 12 months was associated with passive transfer status, but survival to 24 months was not. These findings were consistent whether using a dichotomous or four category STP system. Calves with failure of transfer of passive immunity had mortality hazard ratios of 1.74 and 1.41 up to six and 12 months respectively. There was no association between STP and likelihood of producing a calf by 24 months, however calves with high STP were 1.38 times more likely to produce a calf by 30 months of age than those with poor STP when using a four category classification. This association was not significant using a dichotomous STP category system. No association was observed between STP and milk production parameters. Any association between passive transfer status and reproductive or production performance was small or absent. The survival data indicated minimal benefit in categorising calves into STP groups beyond the traditional dichotomous classification system, however reproductive traits suggested advantages to the four category system.

Figure 1. Kaplan-Meier survival curves for calves up to, (a) one year of age (n=3706 dairy heifers, n=36 farms, n=3 UK veterinary practices, animals born between 2020 and 2024), and (b) two years of age (n=3037 dairy heifers, n=36 farms, n=2UK veterinary practices, animals born between 2020 and 2023). Calves are separated by failure to transfer passive immunity (FTPI; serum total protein < 5.2g/dL) and by passive transfer of immunity status using 4 category system (Lombard et al., 2020).

a)



b)



Identification and validation of a microRNA panel for detection of bovine respiratory disease in calves

Stephen Chiweshe, Jennifer Savage, Kayleigh Allen, Mara Rocchi, Bill Golde, Chris Cousens and Thomas Tzelos

Moredun Research Institute, Pentlands Science Park, Bush Loan, EH26 0PZ

Bovine respiratory disease (BRD) is one of the most important health and welfare challenges facing the dairy industry, with substantial impacts on calf morbidity, mortality and subsequent productivity. Current diagnosis relies largely on clinical signs, which may become apparent only after disease has progressed, potentially resulting in unnecessary or untargeted antimicrobial treatment. There is therefore a need for sensitive biomarkers capable of detecting BRD at an earlier stage. MicroRNAs (miRNAs), small non-coding RNA molecules involved in the regulation of gene expression, have emerged as promising biomarkers of disease. This study aimed to identify and validate miRNAs associated with BRD in calves and assess their potential as biomarkers for disease detection. Samples were collected longitudinally from calves monitored for the development of BRD, including blood-derived samples, saliva and nasopharyngeal swabs, alongside clinical assessments and lung ultrasonography. RNA sequencing was performed on white blood cells from a different set of samples collected before and after infection with Pasteurella multocida. Bioinformatic analysis was used to identify miRNAs associated with disease, and candidate biomarkers were subsequently validated using quantitative PCR (qPCR). Several miRNAs showed differential expression in calves developing BRD compared with healthy calves. Following validation and statistical evaluation of eight candidate biomarkers, three miRNAs were identified that, when combined as a biomarker panel, showed strong performance in discriminating diseased from healthy calves. The three-miRNA panel demonstrated greater discriminatory potential than individual biomarkers, supporting the value of combining multiple host-derived markers for disease detection. This study identified a three-miRNA biomarker panel with potential for detecting BRD in calves. Further validation is required to determine whether these biomarkers can be reliably detected in minimally invasive sample types, supporting the development of a practical diagnostic test suitable for field use. Validation in larger and independent calf populations will also be required to establish the robustness and diagnostic performance of the panel under commercial conditions. Ultimately, early detection of BRD could support more targeted intervention, improve calf welfare and contribute to more judicious antimicrobial use.

Discovering antibiotic-producing bacteria in the bovine gut: exploring the potential of *Streptomyces* to manage calf scour

Kaisha Murray-Cleland[1], Lia S McQueary[1], Emily Horsburgh[1], Rheinallt Jones[2] and Rebecca E McHugh[1].

[1]School of Infection and Immunity and [2]School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow, G61 1QH

Antimicrobial resistance is a growing challenge for livestock production, highlighting the need for new approaches to prevent and control infectious disease while reducing reliance on antibiotics. The bovine gastrointestinal tract represents an underexplored reservoir of microbial diversity and potentially beneficial natural products that could help shape the gut microbiome and protect against pathogens. Our research has identified *Streptomyces* bacteria associated with the bovine gut that produce compounds capable of inhibiting important pathogens, including Shiga toxin-producing Escherichia coli (STEC), Salmonella Typhimurium and enterotoxigenic E. coli (ETEC). These findings reveal that antibiotic-producing bacteria are present in the bovine gut and raise exciting questions about their natural role in microbial competition, pathogen exclusion and animal health. Supported by funding from the Hannah Dairy Research Foundation, our project, Streptomyces in the bovine gut to reduce calf scour, will investigate when these bacteria establish within the calf gut microbiome, from birth through to weaning. By understanding their colonisation dynamics and exploring their interactions with other gut microorganisms, we aim to establish whether these bacteria and the compounds they produce could contribute to natural protection against enteric pathogens. Ultimately, this research seeks to uncover an overlooked aspect of bovine gut ecology and explore how naturally occurring beneficial bacteria could inform new strategies for disease prevention. By laying the foundations for microbiome-informed approaches to calf health, this work has the potential to support more responsible antimicrobial use and contribute to the long-term sustainability of dairy farming.

Growth and health of dairy calves fed milk replacer at different feed rates

Jessica S. Cooke[1], Ian E. Watson[1], Steven J. Morrison[2] and Gillian E. Scoley[2]

[1]Volac Milk Replacers Ltd, Cambridgeshire, SG8 5QX, [2]AFBI Hillsborough, Northern Ireland, BT26 6DR

Growing demand for dairy-protein for human consumption is placing pressure on the availability and cost for use in calf milk replacer (CMR). Feeding more milk has been associated with pre-weaning growth and improved first-lactation productivity. But high milk allowances can suppress starter intake and compromise rumen development and growth around weaning. Feeding more CMR increases costs and uses limited high-quality protein without necessarily delivering additional benefits. This experiment evaluated the effect of CMR allowance (6 L/d vs 8 L/d) on calf growth and health. Holstein heifer calves (n=96) were randomly assigned as pairs and fed CMR (22% crude protein (CP), 18% fat) at either up to 6 L/d (900g dry matter (DM)/d) and weaned at d63 or 8 L/d (1200g DM/d) and weaned at d77. Calf starter (CS; 18% CP), chopped forage and water was available ad libitum. Individual CMR intake, paired CS intake and body weight was measured from birth-91d. Faecal and respiratory scores were assessed 3 times/week, and thoracic ultrasound scanning (TUS) was carried out pre and post weaning. Linear mixed models showed calves fed 6L consumed more CS compared to those fed 8L between d15-84 (P<0.05), but there was no difference from 85 – 90d (P=0.163). Calves fed 8L were heavier at 28, 42, 49 and 63d of age (P<0.05) but there was no difference at 77d (6L: 99.6 vs 8L: 101.8 kg, P=0.072). Calves offered 8L gained an average of 110 g/d more than those offered 6L from birth-49d (P<0.05), but between d49-63 and d63-77 calves fed 6L grew faster than 8L calves (P<0.05). Calves offered 6L showed improved feed efficiency parameters between birth and weaning compared to those offered 8L (P<0.05). Average faecal score (d14-20), and respiratory score (d21-27) was higher in 8L calves than those fed 6L (P<0.05). Despite numerical differences, there was no significant effect of CMR level on the probability of calves receiving a TUS score of 1 or more. Under the conditions of this study, feeding an additional 25kg of CMR delivered only a 2kg body-weight advantage at 11 weeks due to impaired starter intake, and provided no health benefit.

Table 1. Feed intake and growth performance (mean ± SEM) of calves fed up to 6L or 8L per day

	Feed Rate		
	6 L/d (900g DM/d)	8 L/d (1200g DM/d)	P-value
Total individual CMR intake (kg DM) d5-weaning (d63 or d77)	43.9 ± 0.1	68.7 ± 0.08	<0.001
Total paired CS intake (kg DM) d5-77	124.9 ± 4.0	74.5 ± 2.5	<0.001
Daily live weight gain (kg/d)			
birth-d49	0.69 ± 0.01	0.80 ± 0.01	<0.001
d49-63	0.91 ± 0.03	0.81 ± 0.03	<0.05
d63-77	1.22 ± 0.05	1.09 ± 0.03	<0.05
birth-d77	0.83 ± 0.01	0.86 ± 0.01	0.072

Commingling intensity is associated with distinct temporal systemic transcriptomic trajectories in weaned Angus × Holstein calves

Farsan S. Rahman[1], Joanna Urbaniec[1], Matthew A. Scott[2], Amelia R. Woolums[3], Noelle Noyes[4] and Joseph Neary[1]

[1] Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Liverpool L69 7ZB, [2]Veterinary Education, Research, and Outreach Center, Texas A&M University and West Texas A&M University, Canyon, TX, USA, [3]Department of Pathobiology and Population Medicine, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS, USA and [4]College of Veterinary Medicine, University of Minnesota, St. Paul, MN, USA

Bovine respiratory disease (BRD) is the leading cause of morbidity and mortality in calves, resulting from immature immunity, stress, and viral exposure. Commingling of unfamiliar calves during transport and pen assignment influences BRD risk. This study evaluated how commingling intensity affects the blood transcriptome of weaned Angus × Holstein calves from 10 commercial farms (SF). Animals were assigned to four mixing groups based on the number and proportion of contributing SF: Control (1 farm, 100%), Low (2 farms, 80%/20%), Medium (2 farms, 50%/50%), and High (5 farms, 20% each). The study enrolled 120 animals, with 30 per mixing group. We performed whole-blood RNA sequencing on blood samples collected on days 0, 1, 3, 7, and 21 post-mixing. Differentially expressed genes (DEGs; adj.P.Val<0.1), specifically from the Day × Mixing interaction, were identified using differential expression for repeated measures (dream). Functional enrichment analyses were performed using g:Profiler (Gene Ontology terms, KEGG and Reactome pathways; adj.P.Val<0.05) and Zenith (Hallmark pathways; adj.P.Val<0.05).

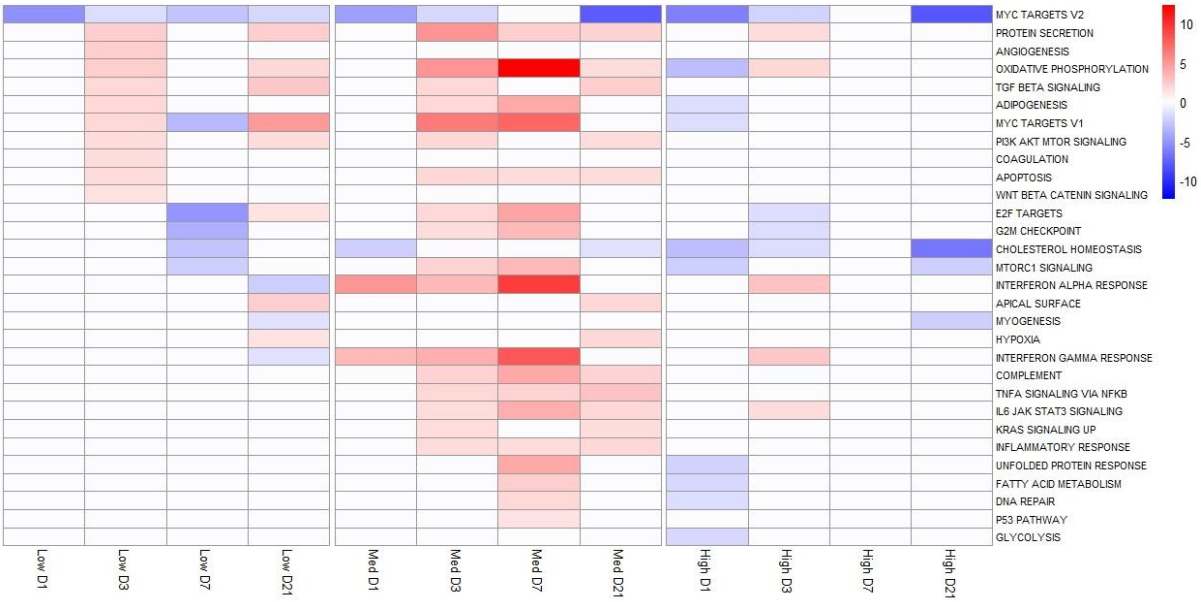


Figure 1: Hallmark pathway enrichment of all differentially expressed genes from Day × Mixing interaction contrasts identified by dream.

Transcriptomic responses varied according to both time and mixing intensity. Low mixing remained broadly similar to Control throughout the study, whereas Medium and High mixing showed early responses followed by distinct temporal trajectories. High mixing was characterised by an early response, with interferon pathway enrichment and suppression of cholesterol/lipid metabolism, MYC-associated programmes and cell-cycle pathways, most of which had attenuated by Day 3 (Figure 1). In contrast, Medium mixing showed early immune changes, partial convergence by Day 7, and renewed

divergence by Day 21. Despite few DEGs at Day 7, pathway-level changes remained evident. Trajectory-based clustering identified gene clusters enriched for interferon regulation, mRNA splicing, cell-cycle/DNA-replication, ribosome biogenesis, steroid biosynthesis and haematopoietic signalling. Together, these patterns indicate coordinated regulation of immune, proliferative, RNA-processing and metabolic programmes, with distinct Medium and High trajectories. These findings indicate that transcriptomic responses were most evident in the Medium and High groups but were not proportional to mixing intensity. Rather, commingling intensity was associated with distinct temporal responses, with High mixing producing a rapid and transient response, whereas Medium mixing showed a non-linear trajectory characterised by early activation, partial convergence, and later re-emergence of immune-associated activity.

Nasal shedding of bovine coronavirus during commingling is associated with reduced average daily gain and lung lesions in weaned seropositive calves

Joanna Urbaniec[1], Alkiviadis Anagnostopoulos[1], Peers Davies[1], Federico G. Hoffmann[2,3], Noelle Noyes[4] and Joseph Neary[1]

[1]Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, [2]Department of Biochemistry, Nutrition and Health Promotion and [3]Institute for Genomics, Biocomputing and Biotechnology, Mississippi State University, Mississippi State, MS, USA, [4]College of Veterinary Medicine, University of Minnesota, USA

Bovine coronavirus (BCV) is a common calf pathogen associated with scours and bovine respiratory disease (BRD), yet its epidemiology and genetic diversity on British farms remain poorly understood. Commingling (mixing) is commonplace in commercial calf-rearing units and increases BRD risk. This study investigated BCV infection in 120 weaned Angus×Holstein calves sourced from 10 British dairy farms (source farms; SFs). Three cohorts of 40 calves were sourced from five SFs per cohort and assigned to commingling pens of varying mixing intensity. Calves remained in their respective pens for 21 days. Deep nasal swabs, faecal samples, and serum were collected throughout the study. Nasal and faecal samples underwent qPCR and Sanger sequencing, while serum was tested for BCV-specific IgG. Calves were monitored daily for clinical BRD, with lung lesions assessed using thoracic ultrasonography. Average daily gain (ADG) was calculated from weights recorded on source farms and at the beginning and end of mixing. High BCV-specific IgG titres were detected at enrolment and declined throughout the study. Seropositivity did not prevent BCV shedding, although overall viral genetic diversity was low (~2%). Distinct genetic variants were identified between source farms and, in one case, within the same animal at different timepoints. Nasal shedding was not associated with clinical BRD within seven days of disease onset. However, high shedders were approximately 4.5 times more likely to have concurrent ultrasonographic lung lesions and had lower ADG (-0.38 kg/day) than non-shedders. The odds of clinical BRD increased with both commingling duration and intensity, while BRD was not meaningfully associated with ADG during the study period. Overall, BCV infection was widespread but largely subclinical in seropositive commingled calves. High levels of viral shedding were associated with poorer production outcomes, whereas BRD risk was primarily influenced by the duration and intensity of commingling.

TUESDAY MORNING

The Grass is Greener: Cow behaviour on and preference for multi-species swards

Laura Shewbridge Carter[1], Marie J. Haskell[2], Holly J. Ferguson[1]and John R. Newbold[1]

[1]*Dairy Research and Innovation Centre, School of Veterinary Medicine and Biosciences, Scotland's Rural College, Dumfries, UK,* [2]*Animal Welfare Group, School of Veterinary Medicine and Biosciences, Scotland's Rural College, Edinburgh, UK*

Regenerative agricultural practices, focusing on soil health, ecosystem function, and delivering farmer and environmental benefits, have gained attention as potential climate change mitigation strategies. Multi-species swards (MSS), containing a range of grasses, forage legumes, and herbs, offer an alternative to conventional perennial ryegrass (PRG) monocultures, but their effects on dairy cow behaviour, feeding preferences, and welfare implications remain poorly understood. This study assessed the effects of sward on behaviour of thirty-two Holstein cows, assigned to graze exclusively on either PRG or MSS for 28 days (Phase 1). Ankle-mounted accelerometers recorded daily step count, lying and standing times, while focal observations assessed grazing behaviour. Following this, cows were managed as a single group with simultaneous access to both swards for 10 days (Phase 2), during which behavioural measurements continued, and camera-based scan sampling was used to assess sward occupancy. Not all species sown persisted in the MSS and, at the time of the study, was dominated by grass, white clover, and red clover (34%, 24%, and 37% of DM, respectively). During Phase 1, daily step count, total lying and standing time, and proportion of time spent grazing did not differ between treatments ($P > 0.05$). However, MSS cows had shorter (82 vs. 93 min/bout; $P = 0.006$) and more frequent lying bouts (7.1 vs. 6.5 bouts/day; $P = 0.046$), more frequent grazing bouts (4.9 vs. 3.6 bouts/5 min; $P = 0.004$), and took fewer steps while grazing (21 vs. 26 steps/5 min; $P = 0.001$) than PRG cows. When given simultaneous access to both swards during Phase 2, cows showed greater occupancy of PRG (estimated proportion = 0.72; $P < 0.001$).Overall, MSS influenced the organisation of grazing and lying behaviour without substantially altering overall daily activity or time budgets, however, welfare implications remain unclear. Greater occupancy of PRG was unexpected given previous evidence that cows select mixed diets, although occupancy does not necessarily reflect dietary selection. Future research combining individual cow location with concurrent behavioural data could clarify whether cows use PRG and MSS differently for grazing, resting, or other activities, and help establish the welfare implication of MSS access.

Routine ELISA histories, hidden infection burden and future Johne's disease risk: evidence from simulated dairy herds

Victoria Heyraud[1], Efstathios-Alexandros Tingas[1], Gemma Charlton[2] and Nick Wheelhouse[3]

[1]School of Computing, Engineering & the Built Environment, Edinburgh Napier University, EH10 5DT, [2]Department of Animal Health, Behaviour and Welfare, Harper Adams University, TF10 8NB, [3]School of Applied Sciences, Edinburgh Napier University, EH11 4BN

Johne's disease is a chronic infectious disease caused by *Mycobacterium avium* subsp. *paratuberculosis* (MAP). It can spread within dairy herds while infected animals remain difficult to identify through routine testing. This limits how confidently farmers can interpret milk-ELISA histories when assessing future infection risk, however, the individual-based modelling provides a framework for representing infection dynamics at the animal level. We examined whether the relationship between adult ELISA results and subsequent Mycobacterium avium subsp. paratuberculosis (MAP) infections changes as a herd epidemic develops, and compared it with the relationship for the true number of infected adults. We analysed 180 independent, 20-year dairy-herd histories generated using a stochastic individual-based MAP transmission model. The model represents infection progression, shedding and environmental contamination. At years 5, 10 and 15, we used 2,092 independently seeded continuations to investigate how current herd states and subsequent stochastic events influence future infection burden. We also compared held-out predictions of year-20 adult infection prevalence based on longitudinal milk-ELISA histories and true adult and young-stock infection information. The proportion of future adult infection-prevalence variation associated with the current herd state was 54.2%, 71.8% and 90.1% at years 5, 10 and 15, respectively. Prediction skill from diagnostic histories increased from 6.3% at year 5 to 51.4% and 71.6%, compared with 45.2%, 69.0% and 88.4% using true-infection information. Additional diagnostic sensitivity analyses showed that improved simulated detection reduced but did not eliminate the early forecasting difference. In these simulated dairy herds, the information conveyed by routine milk-ELISA histories changed substantially with epidemic development. ELISA history provided less predictive information early in the epidemic, when the gap relative to underlying infection burden was greatest. Epidemic stage therefore matters when interpreting routine surveillance in relation to future MAP infection risk. These findings remain conditional on the model and its biological and diagnostic assumptions.

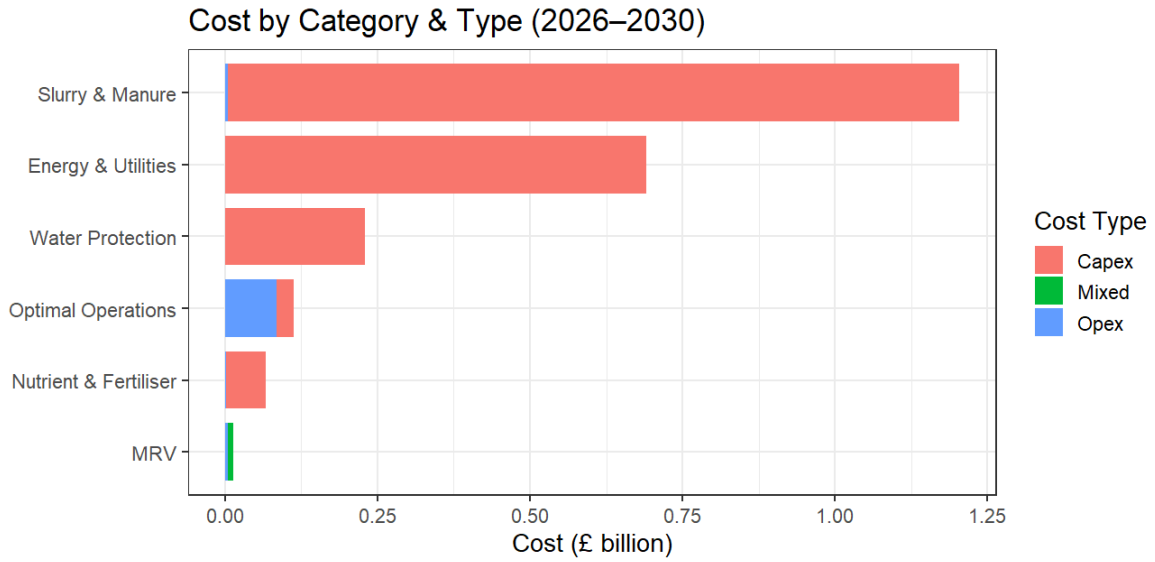
Defining pathways towards sustainable production for the UK dairy sector

John R. Newbold, Richard J. Dewhurst and Margaret D. March

Dairy Research and Innovation Centre, SRUC, Dumfries, DG1 3NE.

The UK dairy sector produces around 15 billion litres of milk annually and is crucial to nutritional security, while also providing multiple foods for the nation, supporting jobs and contributing to rural economies. With 65% of UK milk produced within Science Based Targets initiative-aligned supply chains, the sector is committed to sustainability. Dairy farmers are already enhancing soil health, nutrient management and biodiversity through improved land management, slurry handling and habitat creation, while also focusing on animal health and welfare. The goal is to gather momentum, increase the uptake of mitigation practices to further reduce greenhouse gas emissions, restore biodiversity, improve water and air quality and maintain high standards of animal welfare. To drive, strengthen and develop this sustainability commitment through the Dairy UK Roadmap, a series of actions with associated costs required for progress have been identified (https://dairyroadmap.co.uk/pathway-report/) and by incorporating retailers, processors, industry bodies and farms across all four nations this is a unique opportunity for the dairy sector. To achieve objectives through uptake of activities, a pathway to 2030 has been developed which emphasizes scaling proven measures, investing in infrastructure and technologies, and preparing for emerging innovations and climate change. Key actions include improving herd efficiency, optimizing farm nutrient use, investing in slurry and manure infrastructure, reducing energy-related emissions and exploring methane-reducing technologies. Success depends on collaboration among farmers, processors, retailers, government, finance providers and researchers, with support for knowledge exchange and consistent measurement of environmental impacts. The estimated investment required is around £2.4 billion, with a significant portion allocated to slurry and manure infrastructure, energy systems and water protection. By 2030, the aim is to transition from examples of excellence to consistent progress across the entire UK dairy sector, fostering a more sustainable and resilient industry.

Figure 1. Category transition costs by investment type



Use of a faecal microbiome signature to determine health status and productivity in dairy cattle

Nisha Tucker[1], Nektarios Siachos[2,3], Georgios Oikonomou[2], Lorenzo Viora[4], David Bennett[4], Ana Borsanelli[5], Iveraldo Dutra[6], Arnoud van Vliet[1], Marcello Riggio[7], Martha Betson[1] and Roberto La Ragione[1,8]

[1] School of Veterinary Medicine, Faculty of Health and Medical Sciences, University of Surrey, Guildford GU2 7AL, [2] Department of Livestock and One Health, Institute of Infection, Veterinary & Ecological Sciences, University of Liverpool, Liverpool, [3] School of Veterinary Medicine, SRUC, Aberdeen AB21 9YA; [4] School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow, Glasgow G12 8QQ; [5] Department of Veterinary Medicine, School of Veterinary Medicine and Animal Science, Universidade Federal de Goiás (UFG), Goiânia, Goiás, Brazil; [6] Department of Production and Animal Health, School of Veterinary Medicine, São Paulo State University (UNESP), Araçatuba, São Paulo, Brazil; [7]Dental School, University of Glasgow, Glasgow G2 3JZ; [8] School of Biosciences, Faculty of Health and Medical Sciences, University of Surrey, Guildford GU2 7XH, Surrey

Dairy products remain an important source of nutrition for people worldwide. As farming intensifies, there is a need for innovative strategies to monitor animal health, welfare and productivity. Cattle are completely dependent on their gastrointestinal microbiota for energy and essential nutrients. Therefore, changes in the gut microbiome can impact their metabolism with consequences for disease susceptibility and productivity. This is particularly relevant during the transition period when the cows undergo significant metabolic changes. Direct sampling of the rumen is invasive therefore we used faecal samples as a less invasive alternative. The main aim of the study was to determine whether the faecal microbiome could be used as an indicator of health and productivity in dairy cattle. Seventy-eight Holstein cattle from two commercial herds were enrolled between July 2023 and October 2023. Paired rectal swabs were collected before and after calving (-21 days to +10 days) then processed to isolate DNA for shotgun sequencing. The resulting sequences were filtered to remove low-quality, adaptor, and bovine-associated reads prior to bioinformatic processing to generate microbial profiles for each sample (SqueezeMeta v1.6.3 and SQMtools v1.7.2). These profiles were combined with health and productivity data for analysis (phyloseq v1.56.0). Animals with recorded health events exhibited significant shifts in faecal microbial composition compared to those without recorded disease. Pre-calving Shannon alpha diversity indices were significantly higher in animals with retained foetal membranes (p-value = 0.00763, Wilcoxon test) whilst post-calving Shannon indices were significantly lower in animals with mastitis (p-value = 0.04617, Wilcoxon test). Higher yielding animals had significantly lower Observed and Chao alpha diversity indices than lower yielding animals (p-value$_{Observed}$ = 0.00160, p-value$_{Chao}$ = 0.00158, Wilcoxon tests). In contrast, animals with higher butterfat percentages had higher faecal alpha diversity indices (p-value$_{Observed}$ = 0.0580, p-value$_{Chao}$ = 0.0642, Wilcoxon tests). These results highlight disease-specific shifts in faecal microbial diversity. Variations in production status are also correlated with changes in the faecal microbiome. Whilst further work is needed to elucidate the mechanisms linking microbial community profiles to host phenotype, the ability to detect such microbial changes could pave the way for novel diagnostic tools.

Accuracy of a feed formulation algorithm for predicting milk yield in lactating cows

Mulunji Mtawali, Bettie Kawonga, Liveness Jessica Banda, Fanny Chigwa and Daniel Chiumia

Animal Science Department, Lilongwe University of Agriculture and Natural Resources, Bunda Campus, Lilongwe, Malawi

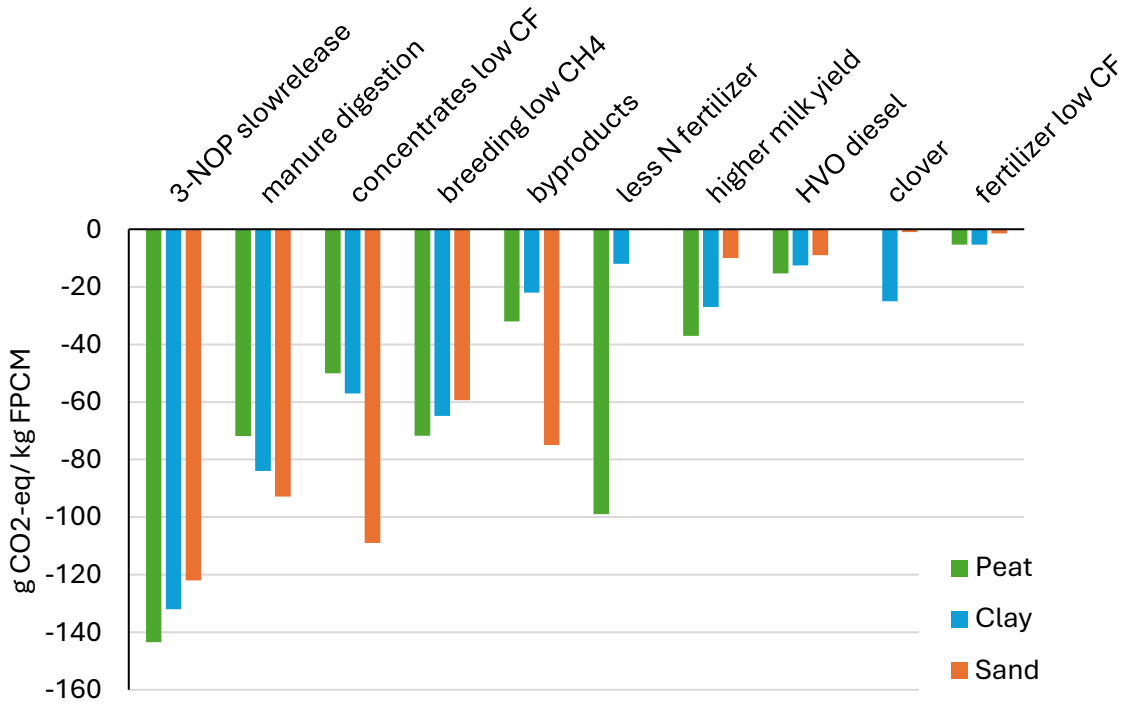
Smallholder dairy farmers face challenges in formulating diets that meet the nutritional requirements of lactating cows while achieving desired production targets. Ration formulation methods based on linear programming provide practical approaches to improving diet formulation but their performance needs to be evaluated under field conditions. This study evaluated the predictive performance of an automated feed formulation algorithm developed for lactating dairy cows in Malawi. Fifteen lactating cows, comprising Holstein Friesian and Holstein Friesian–Zebu crossbreds, were used in a 30-day feeding trial conducted under smallholder farming conditions. The algorithm generated individual feed formulations based on cow characteristics, available feed resources and targeted milk production. Observed milk yield was recorded throughout the trial and compared with formulation targets. Predictive performance was evaluated using the concordance correlation coefficient (CCC), coefficient of determination (R^2), root mean square error (RMSE), mean bias (MB) and mean absolute error (MAE). A generalized linear mixed model was also used to assess factors contributing to variation in observed milk yield. Agreement between predicted targets and observed milk yield improved with increasing temporal aggregation. CCC increased from 0.620 for daily observations to 0.664 and 0.772 for weekly and monthly observations, respectively. Similarly, R^2 increased from 0.586 to 0.687 and 0.899, while RMSE decreased from 4.13 kg/day to 3.65 and 2.69 kg/day. The algorithm generally overestimated observed milk yield, with mean bias of approximately 2.96, 2.74 and 2.65 kg/day for daily, weekly and monthly observations, respectively. Days in milk and feed intake were significant predictors of observed milk yield. The findings demonstrate the potential of the feed formulation algorithm to support diet formulation and production-target setting under smallholder dairy farming conditions. However, the observed systematic over-prediction and moderate predictive accuracy indicate a need for further refinement and validation using larger datasets and longer-term trials under tropical dairy production systems.

Reducing the carbon footprint of milk on Dutch dairy farms: how far can we go?

Akke Kok, Aniek Hilkens and Alfons Beldman

Wageningen Social and Economic Research, Wageningen University & Research, the Netherlands.

Companies within the dairy sector set climate goals to contribute to the Paris agreement. In this 4-year project, two dairy chains aimed to achieve 50% reduction in the carbon footprint of milk by 2030. We analysed the reduction potential and costs of a set of mitigation measures for three Dutch farm types through modelling. Simultaneously, a group of Dutch pilot farmers started a plan-do-check-act cycle implementing reduction measures with specialized advisors. The model Dairywise was used to model reduction measures for three farm types. The model simulates a dairy farm for a one year period with detailed submodules for feed supply, environment, and economics. Farm types were based on Dutch dairy farms in the Farm Accountancy Data Network. They differed in soil type (peat, clay, sand), herd size (88 – 151 cows) and grazing regime (0 – 2,300 hours of grazing per year). Mitigation measures included: feeding byproducts, increasing milk yield, usage of grass-clover swards, reducing artificial N-fertiliser use, manure digestion, breeding for lower emissions, feeding feed additive 3-NOP, and reducing the carbon footprint of inputs. The total set of measures reduced the carbon footprint by 382-489 g CO_2-eq/kg fat-and-protein-corrected milk (FPCM) compared with the baseline footprint of 894-1,097 g CO2-eq/kg FPCM. The economic impact of the set of measures ranged from -€2.51 to -€3.91 per 100 kg of milk among farm types. Measures differed in reduction potential and costs between farm types. The analysed set of measures reduced the carbon footprint of milk by 44%. This is an optimistic figure, as breeding for lower emissions takes time, and not all techniques are readily available. In practice, pilot farmers reduced the carbon footprint of milk by 29-37%. Their reductions were based on a combination of targeted reduction measures and further optimalisation of management. Customized advise, a farm-specific calculation tool and practical learning networks of farmers were crucial for this result.



POSTERS

Genetic variation in resilience to reduced milking frequency in dairy cattle

Rowan Cook and Richard J. Dewhurst

School of Veterinary Medicine and Biosciences, Scotland's Rural College, Edinburgh.

Milking frequency is a key management decision which has been investigated for its impact on animal performance, and economic returns. However, less attention has been given to whether genetic merit influences an animal's resilience to changes in milking frequency. Data were collected from SRUC's Langhill dairy genetics herd, which contains two genetic lines of cattle: one representing the UK national average for milk solids (C) and another selected for increased milk solids (S). This study evaluated the effects of reducing milking frequency from three milkings per day (x3) to two milkings per day (x2), followed by a return to x3 milking. Milk yield, fat concentration, protein concentration, and somatic cell count (SCC) were analysed using linear mixed models including genetic line, milking period, lactation number, and their interactions as fixed effects, with animal fitted as a random effect. Estimated marginal means assessed differences between milking frequences. Significant effects of genetic line, milking period, and their interaction were observed for milk yield ($P < 0.001$). Transition from x3 to x2 milking reduced milk yield in both lines, but losses were greater in C cows than S. During the adaptation phase, yield declined by 3.5 kg in C and 2.1 kg in S, while the full x2 period resulted in reductions of 8.4 and 5.9 kg, respectively ($P < 0.001$, fig. 1). Following the return to x3 milking, yield partially recovered in both lines, with similar recovery between genetic lines. Milk fat concentration increased during the x2 period in both lines ($P < 0.001$). The increase was greater in line C than in line S during the established x2 period (0.33 vs. 0.23 percentage units; $P = 0.006$). Protein concentration also increased under x2 milking (0.20-0.24 percentage units; $P < 0.001$), however the difference between genetic lines was not significant. SCC responses were variable, with no consistent differences between genetic lines. These results demonstrate genetic variation in resilience to reduced milking frequency. Animals selected for increased milk solids experienced smaller milk yield losses during x2 milking, suggesting they may be better suited to production systems that utilise reduced milking frequencies.

Pasture diversity modulates the milk fat microRNA profile in grazing dairy cows

Loubna Abou el Qassim, John Newbold and Richard Dewhurst

Dairy Research & Innovation Centre, SRUC, Dumfries.

Pasture composition and botanical diversity influence the nutritional characteristics of dairy milk, including its fatty acid profile and antioxidant properties. MicroRNAs (miRNAs) are small non-coding RNAs involved in post-transcriptional regulation of gene expression and may respond to nutritional and environmental factors. This study aimed to investigate differences in milk fat miRNA expression between cows grazing multispecies pastures and those grazing low-diversity pastures.
The study was conducted in August 2025 at Barony farm. Thirty-six dairy cows were allocated to two groups (n = 18 per group), balanced for age and lactation stage. One group grazed a multispecies pasture (MP), while the other grazed a low-diversity pasture (LDP) dominated by Italian ryegrass. Milk was collected once weekly over three consecutive weeks during morning milking. For each group, milk samples were pooled to obtain a representative group-level profile. Milk fat was isolated by centrifugation, and total RNA was extracted using the mirVana miRNA Isolation Kit. Small RNA libraries were prepared using the VAHTS Small RNA Library Prep Kit and sequenced on an Illumina NovaSeq X Plus platform. Following read normalisation and filtering, miRNAs with expression levels above 10 reads per million (RPM) were retained. Differential expression analysis was performed using the limma package, voom transformation and empirical Bayes statistics. Multiple testing was controlled using the Benjamini–Hochberg method. The analysis revealed distinct milk fat miRNA expression patterns between cows grazing multispecies pastures (MP) and those grazing low-diversity pastures (LDP). Seventy-four candidate miRNAs met the exploratory selection criteria of an absolute log2 fold change of at least 1 and a nominal p-value below 0.05, with a tendency towards higher miRNA expression in MP. However, none remained statistically significant after correction for multiple testing using the Benjamini–Hochberg method. Exploratory results suggested that a diet based on diverse pastures might induces a positive reprogramming of the milk miRNA profile, likely associated with increased metabolic activity and regulatory functions in the mammary gland. Although they should be interpreted cautiously given the lack of statistically significant results after multiple-testing correction.

Survey of the parasite distribution of an island population of first grazing season dairy youngstock

Simon Kealey, Jake Collyer, Paul Campbell, Kathryn Ellis and Roz Laing

School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow, Glasgow, UK

Gastrointestinal nematode (GIN) infections are ubiquitous in pasture-based grazing systems across the UK. When managed inadequately, these infections can lead to decreased production and fertility, and therefore, economic loss. Many farms in the UK employ whole-group treatment methods often using the macrocyclic lactones class of anthelmintics, including ivermectin and doramectin, to manage GINs. While this is effective at ensuring each individual in the group has some level of protection, it has led to increasing cases and prevalence of anthelmintic resistance. Anthelmintic resistance is becoming an area of increasing concern worldwide, however there is a distinct lack of data regarding dairy cattle in comparison to sheep. Four groups of first grazing season calves from dairy farms on the Isle of Bute were followed from May to July 2026 to collect faecal egg count (FEC) data, detect the presence of bovine lungworm, and to determine the predominant GIN species during the surveyed months on each farm. This study utilized the OvaCyte™ (Indical Bioscience), a novel automated FEC analyzer, to assess GIN burden, as well as using techniques such as coproculture, lungworm Baermann, and PCR to determine L_3 presence and infection trends across the first three months of the grazing season. The FECs for each group of calves were mostly low, regardless of management practices, and the predominant species of GIN present were *Ostertagia ostertagi* and *Cooperia oncophora.* The bovine lungworm, *Dictyocaulus viviparus,* was detected on one farm. This study serves as an initial step towards assessing the current parasite challenge on each of the four surveyed farms, potentially allowing for future targeted treatment plans and individualized recommendations on management strategies to lower the parasite challenge based on the collected data, with aims to reduce production losses due to parasitism and promote responsible anthelmintic use.

Water availability, bedding substrate and surface transfer of environmental mastitis pathogens in a synthetic slurry model

Hollie Leighton, Robert F. Smith and Joseph M. Neary

Department of Livestock and One Health, Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool.

Environmental mastitis remains an important challenge to dairy cow health, but the environmental conditions governing pathogen proliferation and transfer within bedding remain incompletely understood. Bedding hygiene is commonly characterised using total moisture content (MC), although microbial growth also depends on water availability (water activity; a_w), which may differ among bedding substrates at equivalent MC. Investigation of these relationships is complicated by the compositional and microbiological variability of naturally contaminated slurry. We developed and initially evaluated a standardised synthetic slurry formulation (SSF) containing lignocellulosic material, soluble organic nutrients, urea, lactose, and casein hydrolysate as a controlled analogue of faecal, urinary, and milk-associated contamination. *Escherichia coli*, *Klebsiella pneumoniae*, and *Streptococcus uberis* were evaluated independently in SSF and in sawdust and straw under controlled moisture conditions. All three organisms were recoverable from SSF after 24 h. Addition of SSF to sawdust was strongly associated with gravimetric MC (R^2 = 0.987; $P < 0.001$), enabling standardised preparation of 10 to 40% MC treatments. Recovery of *E. coli* and *K. pneumoniae* increased with increasing MC in both bedding substrates. *S. uberis* was recovered from straw (6.55 to 8.48 $\log_{10}$ CFU/g across 10 to 40 % MC; P = 0.011) but was not recovered from sawdust using the culture method employed. Sorption measurements demonstrated marked substrate differences in water availability; at 5 % MC, a_w was 0.76 in straw compared with 0.32 in sawdust. Following removal of contaminated bedding, viable bacteria and residual slurry-associated moisture remained detectable on underlying rubber surfaces, with greater residual contamination at higher bedding MC. These findings demonstrate that equivalent gravimetric MC does not necessarily represent equivalent microbial conditions across bedding substrates. Incorporating water availability and transfer to animal-contact surfaces may improve characterisation of environmental mastitis risk and support more targeted management of dairy cow lying environments.