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Technical Session 1
ICAR / Interbull joint session on "Advances in Genetics and Phenotyping"

Limits to selection in U.S. dairy cattle after several generations of genomic evaluation

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Genomic evaluations were introduced in the United States in 2009, and the generation interval for US Holsteins is now 2.2 y, implying approximately 7 generations of selection have now passed. It is not clear how decreasing generation intervals and increasing selection intensities affect limits to selection.

Lower and upper bounds of selection limits were calculated for 19 traits in US Ayrshire (AY; n = 20,373), Brown Swiss (BS; n = 89,136), Guernsey (GU; n = 11,407), Holstein (HO; n = 9,119,871), and Jersey (JE; n = 928,883) cattle. Traits evaluated were milk, fat, and protein yield; productive life; somatic cell score; daughter pregnancy rate; heifer and cow conception rates; heifer and cow livabilities; early first calving; gestation length; and six health traits (BS, HO, and JE only): hypocalcemia (milk fever), displaced abomasum, ketosis, clinical mastitis, metritis, and retained placenta. Genotypes were imputed to a set of 69,200 SNP used for routine genomic evaluation and haplotypes were phased with Findhap v. 3. Lower bounds (SLL) were predicted by selecting the 29 individual autosomes with the largest direct genomic values (DGV) for each breed-trait combination. Upper bounds (SLU) were calculated by summing the alleles at each locus with the largest allele substitution effects. SLL and SLU were also compared to the largest observed DGV (DGVmax) for each breed-trait combination.

SLL was generally 2 to 4 times larger than DGVmax across breeds and traits, while SLU typically ranged from 5 to15 times larger than DGVmax. For example, SLL and SLU for HO milk were 2.59 and 9.44 times as large as the maximum observed DGV (5,037.86). In some cases, predicted selection limits were very small (e.g., AY, GU) compared to others (e.g., BS, HO, JE), which may be due to the limited number of genotyped animals in some breeds, but these patterns were not consistent across traits. Selection limits were greater than DGVmax in all breeds studied, although in some cases they were very similar; e.g., in AY early first calving, SLL was 5.90 while DGVmax was 5.88. This situation likely reflects the small size of the genotyped AY population. These results suggest, despite the decrease in generation intervals and increase in selection intensity over several generations, that substantial opportunity for genetic progress remains in the US dairy cattle population.

Genetic associations between methane emission and other economically important traits

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Genetic selection for reduced methane (CH4) emissions offers a promising strategy to improve the environmental sustainability of dairy production. However, before implementing a new trait in the breeding program, it is essential to understand its genetic relationship with other economically important traits. This study aimed to estimate genetic associations between daily CH4 emission and traits currently included in the routine genetic evaluation of Norwegian Red dairy cows.

In Norway, large-scale phenotyping of methane emissions and feed intake of Norwegian Red cows is conducted across 14 commercial dairy herds. Methane measures are obtained using the GreenFeed system (www.c-lockinc.com). This study included a total of 548,116 daily CH4 records from 2,387 cows collected from 2019 to 2025. Given the limited number of animals with CH4 phenotypes, correlations between estimated breeding values (EBV) were used as an approximation for genetic correlations. Methane EBV for cows with CH4 records were predicted with a linear animal repeatability model using the DMU software. The trait analysed was daily CH4 emission (grams per day), calculated as the average of the cows' GreenFeed visits per day. Official GEBVs for all traits included in the current routine genetic evaluation were available from Geno. Methane EBVs were standardized to an index with a mean of 100 and a standard deviation of 10, and multiplied by -1 so that higher index values indicate lower CH4 emissions, which are considered favorable. Correlations between EBVs for CH4 and other traits range between -0.25 and 0.21. The strongest unfavorable correlations were to body conformation traits related to cow size (angularity, body depth, and stature) and to milk production traits (protein yield and fat yield). Favorable correlations were found with several fertility, health, and calving traits, most notably to the fertility trait "number of inseminations to conception" with a correlation of 0.20, but also to direct calf size, calving ease, and stillbirth. These results provide insight into the strength and direction of the underlying genetic correlations between traits. Understanding genetic relationships between key traits is essential when developing strategies aimed at breeding a feed-efficient, climate-friendly cow for the future.

BWYPEX: Discovery, Approval and Management of Genetic Abnormalities in Cattle

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Genetic abnormalities in cattle continue to challenge animal welfare, reproductive efficiency, and the long-term sustainability of breeding programs. Advances in genomic technologies have significantly improved the ability to detect and manage deleterious variants. However, effective control depends not only on scientific discovery but also on robust reporting systems, clear governance structures, and coordinated industry engagement. Developed as part of the ICAR Brian Wickham Young Persons Exchange Program (BWYPEX), this report integrates perspectives from North America, Europe, and Oceania to examine how genetic abnormalities are identified, analysed, validated, and managed within cattle populations.

The review summarises current methods to detect defects, including phenotype-based reporting and genotype-based surveillance, and evaluates how information flows from farms into national or breed-level analytical systems. Evidence across regions demonstrates that successful systems are characterized by clearly assigned stakeholder responsibilities and transparent industry-wide communication. The report further describes the scientific and procedural steps required to establish a newly identified genetic abnormality, including evaluation of supporting scientific evidence, cost-effective research strategies, development of standardized nomenclature, establishment of biobanks, and the design of gene tests and/or haplotype-based diagnostics to facilitate population-level control. Key management considerations, such as intellectual property frameworks, biobanking strategies, and long-term monitoring, are highlighted as critical determinants of effective implementation.

Despite differences across countries, shared principles emerge, including centralized or clearly mandated authority, supportive environments for reporting, integration of causal variant testing into routine genotyping platforms, and proactive communication strategies. Collectively, these findings provide a structured roadmap for developing national systems to record and identify genetic abnormalities while strengthening international collaboration in their management.

Digital Innovation at the Service of Breeders: The Synergy Portal and Mobile App for Real-Time Genetic Decision Support

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Modern dairy and beef cattle farming requires a paradigm shift where centralized genetic and productive data become strategic tools for daily management. The objective of the Synergy Portal and its dedicated App is to provide breeders with a "data-driven" decision support system, allowing them to manage complex information—such as inbreeding levels and genetic indices—autonomously and directly in the barn. The Synergy platform integrates data from various breed associations (17 breeds) into a single interface. Accessible via web and smartphone (iOS and Android), the tool synchronizes with the National Database (BDN) and breed association records. A key feature is the "Parentele" (Relationships) tool, which utilizes both pedigree information and genomic data to calculate precise levels of similarity between animals. This allows for a more accurate assessment of consanguinity compared to traditional probabilistic pedigree calculations.

Through the mobile app, breeders can now select bulls for mating in real-time. By selecting specific bulls and testing them against their herd, the app provides an immediate table showing the degree of relationship for each individual cow. Breeders can use advanced filters to identify cows with relationship values below a specific threshold, effectively preventing inbreeding and the risk of hereditary defects. This digital integration allows for the optimization of mating strategies, better planning of semen doses, and the preservation of genetic variability, even for smaller or endangered breeds.

The Synergy tools transform a massive amount of raw data into actionable knowledge. By making genetic management "pocket-sized," the platform enhances farm sustainability and competitiveness. It empowers breeders to move from "reacting" to "predicting," ensuring that every mating decision contributes to the long-term genetic health and productivity of the herd.

Novel approach to develop robust artificial neural network for FT-MIR prediction of enteric methane emissions in dairy cows

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Previous studies have demonstrated the potential of milk Fourier-transform mid-infrared (FT-MIR) spectroscopy to predict indicators related to enteric CH4 emissions in dairy cows. Early models mainly relied on PLS regression, a method well suited to smaller datasets with highly collinear variables. However, sufficient accuracy of CH4 reference measurements to reliably capture the underlying population trend requires many observations. The acquisition of such data is limited by financial, practical, and confidentiality constraints. Transfer learning strategies, particularly federated learning (FL), offer a promising solution. FL enables a neural network trained by one research group to be transferred to another without sharing raw data. The second group can further train the model on its own data and share the updated network, preserving data privacy while improving predictive performance. The development of a robust artificial neural network is therefore essential.

The objective of this study was to compare PLS regression with multilayer perceptrons (MLP) and convolutional artificial neural networks (cANN). A dataset of 1,089 records was used, with a subset reserved for external validation. A total of 289 spectral variables were selected and preprocessed using a first derivative, followed by regression on second-order Legendre polynomials according to days in milk. Three MLP architectures (one to three hidden layers) and three cANN models were evaluated, the latter using spectral data reshaped into 3 × 289 images.

Cross-validation performances were consistent with expectations (R^2 between 0.60 and 0.80; mean error around 51 g CH4/day). The MLP with two hidden layers achieved the best results. Neural networks slightly outperformed PLS and, more importantly, open new perspectives for implementing FL frameworks to improve CH4 prediction models without sharing sensitive data.

Using milk mid-infrared spectra from dairy cows to predict methane measured by sniffers and GreenFeed

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Milk mid-infrared (MIR) spectra are of interest to predict enteric methane (CH4) emissions to be used as a widely available phenotype for genetic selection on lower emissions. However, the accuracy of MIR predictions can vary greatly depending on the sample type and the calibration model used. To date, prediction models for CH4 have successfully been created using CH4 measurements from GreenFeed, respiration chambers and SF6. However, increasingly large numbers of individual cows are recorded with cost-effective but less accurate "sniffers", which are used to measure CH4 concentrations in the cow's breath in the feed bin of milking robots. Therefore, our aim was to test the effectiveness of a MIR prediction model tested on CH4 recorded by either GreenFeed or sniffer in Holstein cows in the Netherlands.

In total, 3,015 GreenFeed records (g CH4/day; C-Lock Inc., Rapid city, USA) were available from 1,209 animals on 13 farms, and 40,184 sniffer records (as concentration in ppm) from 9,311 animals on 73 farms. The GreenFeed and sniffer recorded CH4 were analysed as two separate datasets. The CH4 records represented a 13-day average centred on the day of MIR spectrum measurement. In preliminary analyses, a partial least squares analysis was used to model the relationship between the CH4 phenotypes and MIR spectra, by splitting the datasets into calibration and validation sets. Prediction accuracy was assessed via Monte Carlo cross-validation with 100 iterations, using a random animal-level data split (80% calibration, 20% validation). Separate models were fitted including only the GreenFeed data or the sniffer data.

The coefficients of determination of validation (R2) were 0.27 for GreenFeed recorded CH4 (RMSE = 97), and 0.09 for sniffer recorded CH4 (RMSE =227). The first results suggest that CH4 phenotypes can be predicted from MIR spectra with low to moderate accuracy. Next steps will focus on improving the prediction models by incorporating information on parity and days in milk, and performing leave-one-farm-out cross validation to investigate the usefulness for practical application.

Prediction of methane emissions based on milk fatty acid profiles shows similar performance to milk MIR spectra

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This study aimed to predict methane (CH4) emissions measured using the GreenFeed system from milk mid-infrared (MIR) spectra collected on 16 commercial Austrian dairy farms.

All farms used similar feeding systems based on grass and maize silage with varying levels of concentrate supplementation and no grazing. The dataset consisted of 807 records from 604 cows. Two partial least squares regression models were developed: one based on milk MIR spectra and another using milk components, including 14 individual fatty acids (FA), fat%, protein%, and lactose%. Milk yield, lactation stage and parity were included as additional predictors. Model performance was evaluated using 5-fold and leave-one-farm-out cross validation.

In 5-fold cross-validation, the MIR-based model showed moderate predictive ability ($r = 0.52$, $R^2 = 0.27$), outperforming the FA-based model ($r = 0.42$, $R^2 = 0.18$). Combining FA with fat%, protein%, and lactose% improved accuracy ($r = 0.44$, $R^2 = 0.20$). Including milk yield, parity, and lactation stage further increased accuracy for both MIR-based ($r = 0.61$, $R^2 = 0.38$) and FA-based models (0.61, $R^2 = 0.37$). Leave-one-farm-out validation resulted in slightly lower accuracies and revealed substantial variability among farms. Models using all predictors performed best (MIR-based: $r = 0.56$, $R^2 = 0.33$ / FA-based: $r = 0.58$, $R^2 = 0.35$). Overall, milk MIR spectra and FA explained only part of the variation in CH4 emissions, mainly capturing metabolic signals related to energy status. Improving prediction accuracy will require additional predictors and advanced modeling approaches to better capture the complex biological, nutritional and environmental drivers of CH4 emissions. Additional analyses are planned using combine

Comparing Methodologies for Deriving Methane Phenotypes from Laser Methane Detector Data in Small Ruminants

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The Laser Methane Detector (LMD) has been applied to enteric methane phenotyping in livestock since 2008, yet published studies differ markedly in how raw LMD time-series data are processed and converted into methane phenotypes limiting comparability across experiments. To address this, the present study systematically evaluated published LMD data-analysis methodologies by applying them to a single, large field dataset of Ethiopian sheep kept under extensive smallholder conditions.

Methane concentrations were recorded at 0.5-s intervals in 720 indigenous sheep, with repeated measurements collected over three days and recording durations ranging from 5 to 30 minutes. Inspection of the raw LMD time series revealed two distinct signal components: respiration-related methane, characterised by low-amplitude, regular oscillations, and eructation-related methane, characterised by intermittent, high-amplitude peaks originating from rumen gas expulsion. Based on this signal structure, multiple LMD data-analysis methodologies reported in the literature were implemented, including (i) all-values summary approaches using the full signal, (ii) simple peak-based methods, (iii) automated multi-scale peak detection, and (iv) classification of respiration- and eructation-related peaks using published threshold criteria. Methodologies were evaluated based on agreement between phenotypes using Pearson and Spearman correlations, repeatability across days using linear mixed models with animal as a random effect, sensitivity to biological factors (e.g., body weight and sex) and management conditions (e.g., feeding status, year and location).

Results showed that both methodology choice and recording length substantially influenced estimated methane phenotypes. Peak-based and classified phenotypes showed greater sensitivity to biological drivers, while longer recording windows improved repeatability and reduced within-animal variability. In contrast, simple summary measures were more stable across window lengths but less discriminative. These findings indicate that, at present, it is not possible to recommend a single standardized methodology for analysing LMD raw data. Further work, including external validation, calibration against reference methods, and assessment of genetic relevance (e.g., repeatability and impact on animal ranking for selection), is required before harmonised analytical protocols for LMD-based methane phenotyping can be established.

ORAL

Technical Session 2
Validation related to the Use and Usability of Data

A new ICAR test facility to validate sniffer devices that measure methane output of dairy cows

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Governments worldwide have committed to decrease greenhouse gas (GHG) emissions by 2050. Animal breeding is identified as an important mitigation tool to reduce the environmental footprint of livestock because it is cost-effective, permanent and cumulative over generations. The impact t of animal breeding, however, depends highly on the scale of GHG recording. Sniffers are widely recognized instruments for large-scale measurements of methane (CH4) and carbon dioxide (CO2) concentrations in the cow's breath. Even though sniffers are widely used nowadays, there is a lack of (1) comparability between sniffers of different manufacturers, and (2) protocols, the methods to calibrate and utilize the equipment at farm level to increase the repeatability. Therefore, in September 2025, a test facility at the Dairy Campus (Leeuwarden, the Netherlands) was established to evaluate the performance of four different sniffer devices. This is a part of the Global Methane Genetics initiative, which supports international harmonization and standardization of CH4 recording.

A measuring tube was installed in the feed bin of the milking robot, and all four sniffers were connected to this measuring tube, ensuring all four sniffers measure the same air sample at the same time. Sixty cows visit this milking robot several times during the day. Once per month, a reference method is performed where the same air that is analyzed by each sniffer is also sampled in a 10 liter Nalophan sampling bag inserted in a closed vessel. These bags with air are then analyzed in the laboratory with a gas chromatograph (GC). he average CH4 and CO2 concentrations recorded by each sniffer are compared to the CH4 and CO2 concentrations from the GC, sampled in the same timeframe. A GreenFeed (c-lock inc.) is installed near the milking robot, and the cows can visit it freely, providing CH4 production measures of the same cows on the same day. In total, the sniffers will be tested for one year, with monthly references. Spearman rank correlations are calculated to compare the ranking of cows for CH4 with all four devices. The correlations are high (0.92-0.98) among the sniffers themselves and are ~0.33 with the GreenFeed for all sniffers. The International Committee of Animal Recording (ICAR, Utrecht, the Netherlands) has made this an official service for sniffer manufacturers as of January 2026.

Comparison of Enteric Methane Repeatability Estimates Using GreenFeed and Agscent Measurement Devices

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GreenFeed Emissions Monitoring units and Agscent Air sensors both quantify enteric methane emissions. GreenFeed uses an active gas-flux approach and reports methane as g/day, whereas Agscent passively samples air and reports methane concentration. While GreenFeed is being used to generate genomic reference data globally, the Agscent, when paired with an Optiweigh unit, is not yet widely used for that purpose. This study used available data to estimate repeatability to compare the systems.

GreenFeed data were limited to Angus, Charolais, Hereford, Shorthorn, and Wagyu cattle. Data were analysed separately for males (feedlot; n=2947) and heifers (paddock; n=1598), spanning multiple seasons and locations in NSW, Australia. Agscent data were collected in a single paddock system in the southeastern United States on mature cows (≥450 kg; n=49) and their nursing calves (<450 kg; n=32). Only animals with ≥5 samples were considered. Each visit, or spot-sample, to the measurement unit can be used as a record of methane emission. However, given the impact of diet and diurnal pattern on methane production, average production over 1-, 5-, 7-, or 10-day periods were also considered as phenotypes. A random-effects model with animal as the sole effect was used. Repeatability was calculated as variance explained by the animal effect relative to the total variance. For GreenFeed, repeatability increased as the averaging window increased from 0.21 (feedlot) and 0.28 (paddock) for spot-samples to 0.49 (feedlot) and 0.65 (paddock) when methane production was averaged over 10-days. Agscent repeatability showed the same pattern. The lowest repeatability estimates were 0.17 (calves) and 0.23 (cows) for spot-samples while the highest estimates were 0.27 (calves) and 0.45 (cows) for the 10-day average. We also analysed total-animal repeatability of the GreenFeed data with the fixed effects of breed, days of age at time of record, and contemporary group. For spot-samples and 10-day averages repeatability was reduced to 0.13 and 0.35 for feedlot animals and 0.10 to 0.31 for paddock animals, respectively. This implies some variance previously attributed to animal effect was captured by breed and group effects.

Overall, results support the further evaluation of Agscent in large scale genomic reference capture initiatives as a methane recording and ranking tool for grazing animals.

A scalable, automated data pipeline and interactive dashboard for high-throughput methane phenotyping

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Nation-wide collection of high-frequency methane data from sniffers installed on commercial farms poses a significant challenge. Key issues include intermittent connectivity, data fragmentation, limited on-site technical oversight, number of sniffers, and daily volume of data to monitor. We present a robust, automated pipeline designed to streamline the collection and monitoring of data from MooLogger sniffers (Tecnosens S.p.A., Brescia, Italy).

The infrastructure utilizes a VPN mesh to establish secure, persistent remote access to sniffers. A Python core executes automated routines, enforcing data completeness prior to ingestion into a SQL database. Quality control employs multi-tiered alerting: temporal consistency checks, bilateral range validation for gas concentrations, and sniffer-specific rolling baselines to detect sensor drift. An RShiny dashboard serves as the pipeline command centre. It provides visualization of gases, airflow, and live uptime monitoring. The interface integrates a log system to track events, such as calibrations, and parts maintenance, directly linking hardware status to data quality. Furthermore, an automated synchronization module facilitates seamless data sharing with external collaborators. Scalability was demonstrated through the deployment of independent, self-contained instances of the software stack for major international organizations. In Canada, Lactanet manages a national fleet of 59 sniffers (51 Holstein, 6 Jersey and 2 Ayrshire). Sniffers have been deployed across four provinces: 10 sniffers (4 farms) in Alberta, 10 (2 farms) in British Columbia, 26 (15 farms) in Quebec (Methane Quebec Project), and 13 (5 farms) in Ontario, in collaboration with the University of Guelph (Net-Zero Dairy Genome Project). A separate instance supports Qualitas AG (Switzerland) in complex study designs. Project CH4COW monitors 64 sniffers (30 Holstein, 34 Brown Swiss) over a continuous 2.5-year period. The EMBRACE-BS (Global Methane Genetics) project maximizes throughput via synchronized 4-5 months rotations, managing 8 sniffers across two stages: initially split between Austria and Switzerland (48 farms), then consolidated in Germany (24 farms).

This scalable, automated data pipeline and interactive dashboard accelerate the translation of raw sensor streams into reliable phenotypes for global genetic evaluation.

A comparison of data-processing pipelines for methane concentration measurements from sniffers

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Reducing methane emissions from dairy production is an important component of global greenhouse gas mitigation efforts. Genetic selection offers a promising long-term strategy for lowering emissions, but it requires large-scale and reliable methane phenotyping. In dairy systems, methane concentrations (CH_4c) are recorded using breath analyzers, commonly known as “sniffers,” installed in automatic milking systems (AMS). These devices collect gas samples every second or every five seconds, depending on the manufacturer, throughout a milking session that typically lasts five to ten minutes. Sniffers also measure carbon dioxide concentrations (CO_2c). Because sniffers do not include animal identification capabilities, measurements must be linked to individual cows by aligning sniffer timestamps with AMS milking timestamps. However, due to the large volume of data collected and the differences between timestamp systems, this approach is challenging in practice. As a result, several research groups have developed different pipelines and software tools to align, clean, and process CH_4 and CO_2 data. There is an increasing interest in comparing the performance of these pipelines, yet no such comparison has been conducted to date. In this study, we compare two pipelines and a software program used to process CH4 and CO2 measurements in terms of alignment and editing steps.

The first pipeline (P1) was developed at Wageningen University and Research, the Netherlands, in Python. The second approach is the published GEDA program (P2), developed at Aarhus University, Denmark. The third pipeline (P3), originally written in Java, is used by different research groups (including INIA, Spain) but has not been formally published. All three pipelines process raw sniffer data to derive visit-level mean values that represent the average gas concentration recorded during each milking event. Only farms with a repeatability higher than 10 percent for both gases were retained for analysis. Repeatability was estimated by fitting a mixed model with cow as a random effect, using only cows with at least three daily records, and calculating the proportion of variation attributable to differences between cows. In total, data from 23 Dutch dairy farms were used, comprising records collected in 2022 of 2,009 cows and resulting in 49,951 daily observations, with gas concentrations sampled every five seconds during milking. Pearson correlations between the CH4c phenotypes produced by the different pipelines (P1 and P2) ranged from 0.56 to 0.86, depending on the farm. Results from the comparisons of the three pipelines will be presented and discussed at the conference.

The unified framework for processing and storing large-scale sniffers-based emission data

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Accurate quantification of CH4 and CO_2 emissions is essential for evaluating environmental impacts and developing mitigation strategies. In this context, sniffers play substantial role. The quality of such records is a well-known challenge and is critical to address. This study presents the framework dedicated for storing and processing a sniffers-based emission data. It integrates the GEDA pipeline for processing raw measurements within HPC environment and database storage.

The pipeline is based on a stochastic model that represents noisy gas emission signals as a function of automatic milking system's (AMS) data. This formulation enables the workflow that integrates data quality control, errors correction, synchronization of AMS and sniffers data following reliability assessment. The background concentrations are estimated through a weighted regression model following data corrections. Emission phenotypes are estimated as mean concentrations or emission intensities at visit or daily scales. The phenotypes quality is evaluated using linear mixed models to derive local repeatability indicator. GEDA enables workflow that integrates data quality control, errors correction, synchronization of AMS and sniffers data following reliability assessment. The background concentrations are estimated through a weighted regression model following data corrections. Emission phenotypes are estimated as mean concentrations or emission intensities at visit or daily scales. The phenotypes quality is evaluated using linear mixed models to derive local repeatability indicator. The storage system implements a four-tier architecture that covers data ingestion, storage, application logic, and a user interface. There are two distinct pipelines. The staging pipeline automatically ingests raw data into a PostgreSQL/TimescaleDB staging schema with full provenance metadata and idempotent loading. The curated pipeline then exports validated staging data for GEDA processing. A FastAPI backend serves curated data through RESTful APIs with role-based access control, while a frontend provides interactive dashboards and a data explorer with filtering, visualizations, and data export capabilities.

A study, using the four-year data from 38 commercial farms (the number of unique cows is 15335, the average number of observations per cow is 148.45, and the total number of observations is 2276528), assessed the pipeline's efficiency and quality. The estimated heritability values for daily averaged phenotypes are in the range of 0.13-0.16, and the repeatability values are in the range of 0.32-0.41. GEDA provides a novel data pipeline for large-scale processing of sniffer-based emission data. By systematically addressing data heterogeneity, noise, and misalignment, the pipeline produces high-quality emission phenotypes. Its HPC and storage integration represents the unified framework that supports more accurate genetic evaluations and strengthens research targeting mitigation of greenhouse gas emissions in dairy cattle. Overall, GEDA provides a novel, theoretically grounded automated pipeline for large-scale processing of sniffer-based gas emission data. By systematically addressing data heterogeneity, noise, and misalignment, the pipeline produces aligned datasets and high-quality emission phenotypes. Its HPC and storage integration represents the unified framework that supports more accurate genetic evaluations and strengthens research targeting mitigation of greenhouse gas emissions in dairy cattle.

Automating Data Unification, Governance, and Analytics in Animal Science: A Cloud-Native, AI-Assisted Framework

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Metabolism experiments typically use structured or partially controlled conditions and produce large, complex datasets covering animal characteristics, nutrient intake, digestibility, gas emissions, feeding behavior, and production traits. These datasets have grown more complex as researchers routinely collect high-resolution phenotypes and rely more on indirect-calorimetry technologies like respiration chamber and GreenFeed system. Yet inconsistencies in data structure and metadata limit the use of these measurements as reliable phenotypes for genetic analysis and decision support. This creates major bottlenecks when trying to clean, validate, and combine data across studies.

We developed a standardized Excel workbook and a fully automated, cloud-based pipeline for data ingestion, validation, and analysis. Our work was driven by the GEMS project (Accurate Gas Emissions Measures from Cattle with the GreenFeed System), which integrates methane emission, feed intake, and metabolism data from roughly 150 studies worldwide to support the generation of consistent, high-quality methane phenotypes. The workflow runs on Microsoft tools and handles automated ingestion via Microsoft Teams to Azure Blob Storage, through rule-based validation in Microsoft Azure Databricks. We use structured information from study-level data user agreements to define which variables and datasets should be included, allowing the system to check delivered data against what was promised and send notifications when corrections are needed or elements are missing. Once validated, the data are merged with external gas-measurement outputs and organized into analysis-ready tables. Researchers can access these curated datasets in a secure Databricks Clean Room using Python, R, or natural-language AI tools for analysis and modeling, including applications in methane phenotype evaluation, genetic studies, and feed-efficiency research.

While built for GEMS, the modular design can be applied broadly to animal metabolism, greenhouse gas and genetic studies. It reduces manual data handling, improves reproducibility, and accelerates the generation of reliable methane and intake phenotypes for management and genetic analysis.

Whole-genome ICAR parentage verification certification

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Parentage verification certification in dairy cattle currently relies on the standardized 195-SNP ISAG parentage verification (ISAG PV) panel. In this study, we evaluate and compare the performance of the ISAG panel with a whole-genome SNP–based approach. Specifically, we assess the robustness of the ISAG panel across a wide range of contemporary genotyping scenarios, including diverse SNP platforms and marker densities, and examine the potential benefits of extending parentage verification certification to genome-wide SNP datasets. The objective of this work is to propose a complementary parentage certification methodology, applicable when whole-genome SNP data are available, for potential inclusion in the ICAR guidelines.

Genotypic data representing five dairy breeds available at the Council on Dairy Cattle Breeding (CDCB, USA) were analyzed using large subsets of known parent–offspring pairs and unrelated animal pairs (100,000 comparsions for each dataset). Mendelian inheritance was tested using all available ISAG PV SNPs and all autosomal SNPs only, applying only basic quality control filters to exclude SNP and arrays with known poor genotyping performance (e.g. poor clustering and probe performance). An empirical threshold was determined to identify ACCEPTED, DOUBTFUL and REJECTED samples.

The results demonstrate that whole-genome SNP comparisons provide discriminatory power to accurately identify true parentage relationships, even in datasets combining multiple chip types and marker densities. The findings also show that the current ISAG panel exhibits substantially lower sensitivity and specificity compared with the whole-genome SNP approach. Most importantly, nearly one out of four comparisons in our dataset failed to meet the ICAR minimum call-rate requirements when using the ISAG panel, thereby precluding parentage verification. We conclude that, when available, whole-genome SNP comparisons should be preferred over the ISAG panel and recommend their inclusion in the current ICAR guidelines.

Monitoring milk meters: the French experience with this practice, between innovation and user feedback

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Computerized monitoring of milk meters is a statistical method based on production data to verify compliance with accepted accuracy tolerances. Two monitoring methods are recognized in ICAR guidelines. The first applies to farms with milking parlors using milk meters. It compares the milk yield of a given milking with an expected volume calculated from the previous five milkings. This is repeated for all cows to determine the average deviation of each meter. By analyzing all milkings over one month, compliance of the installation can be assessed. The second method applies to single-stall robotic installations. It compares the total milk volume delivered to the bulk tank with the volume collected by the dairy over one month to verify that the meter remains within accepted tolerances.

Three prerequisites are required:

- A data exchange gateway between the robot and the advisory company's database. In France, DataHUB360 fulfills this role and connects all manufacturers.
- Confirmation that all necessary data are available through this gateway (transferable data library).
- Access to dairy collection data via agreements with farmers, plus a manual entry option if automatic retrieval is unavailable.

These systems enable large-scale monitoring. Beyond extending meter validity, they ensure that devices used daily for herd management (feeding, culling, etc.) remain reliable. Farm visits are triggered only when analysis confirms a drift, improving efficiency. This approach supports the rapid growth of milking robots in France, where 9 out of 10 new installations are robotic.

However, the method is currently limited to single-stall farms, while more than 55% of French farms have multiple stalls. After three years of research and field trials, Eliance and IDELE combined a stall-to-stall deviation test with the tank comparison method to extend the service to farms equipped with two robotic milking stalls.

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Technical Session 3
Validation related to the Use and Usability of Data

Australia's National Livestock Identification Systems (NLIS) * invertito con Possenti

Bradley Elizabeth*[1]

[1] Integrity Systems Company

Provide an understanding of the operational aspects of Australia's National Livestock Identification System (NLIS) so that key functionalities and solutions could be reviewed for potential use in the attendee's relevant countries.

The National Livestock Identification System (NLIS) is Australia's system for the identification and traceability of cattle, sheep and goats. NLIS is endorsed by major producer, feedlot, agent, saleyard, and processor bodies, and is also underpinned by State/Territory legislation that forms the regulatory framework for the system. National Livestock Traceability Performance Standards set the timeframes which livestock need to be traced, during an emergency disease outbreak and sit above the Cattle Traceability Standards and the Sheep and Goat Traceability Standards. The Cattle Traceability Standards and the Sheep and Goat Traceability Standards, specify the minimum standards that when adhered to, will ensure the traceability of livestock for disease control and food safety purposes. These standards represent minimum mandatory requirements needed to ensure compliance with the National Livestock Traceability Performance Standards (NLIS Standards - Integrity Systems, n.d.). In November 2020, Integrity Systems Company (ISC) migrated the NLIS Database's data infrastructure from its existing on-premises data centre to Amazon Web Services (AWS). The National Livestock Identification System (NLIS) database is housed within the Australian region within Amazon. This guarantees that the data will be kept physically in Australia. Elizabeth Bradley, Integrity Systems Company Manager - Quality, Policy and Compliance, will be providing an online presentation on the functionality of the NLIS Database so attendees can gain an understanding of the operational aspects of the NLIS.

Italy’s Banca Dati Nazionale (BDN) * invertito con Bradley

Possenti Luigi*[1]

[1] Tecnologie dell’Informazione e della Comunicazione - ICT

Provide an understanding of the operational aspects of Italy’s BDN so that key functionalities and solutions can be reviewed for potential use in the attendees’ relevant countries.

The Italian national livestock identification system was created in the early 2000s by the Ministry of Health in accordance with the new EU regulation on animal identification and registration. It is managed by the IZS of Teramo through the BDN (Banca Dati Nazionale), the National Animal Identification Database, available on the Veterinary Information System Portal (Vetinfo). The BDN registers cattle, buffalo, pigs, sheep and goats, horses, poultry, bees, and other minor species; the system also tracks movements, births, deaths, slaughters and health data for traceability, animal health, and food safety. The traceability system is essentially a certification system that tracks all animal movements from birth to slaughter. Different types of users access the National Database (BDN) via the Vetinfo Portal to update and consult data based on their role. The farmer, operator under EU regulations, is responsible for registering animals in the system and ensuring their traceability. The National Database provides a unique identification for each farm (farms, markets, slaughterhouses) and for large animals such as cattle, buffalo, pigs, sheep, goats, and horses. Collective identification is also permitted for lambs, slaughter pigs, and groups of small animals. Accepted identification methods include electronic identifiers, ear tags, and tattoos. All identification methods must comply with EU regulations. The system is essential for monitoring epidemics and ensuring the safety of Italian food products. An overview of the National Database will be presented to participants by Luigi Possenti, Head of the Information and Communication Technologies Laboratory at IZS of Teramo. Luigi Possenti is an expert in Information Systems for Animal Identification and Registration, Animal Health, and Food Safety, with over twenty years of experience developing complex information systems in the field of veterinary public health, as well as designing web applications and distributed web-based systems.

Advancing national livestock traceability: development and rollout of Rwanda’s first cattle identification and registration

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[1] RAB, [2] RJAHS, [3] PAN Livestock Services

The overall objective of the initiative was to design and operationalize a centralized, web-based national cattle database capable of supporting traceability, performance monitoring, and sector-wide analytics. More specifically, the system was intended to enable comprehensive farm and individual animal identification, record lifecycle events including reproduction, health, production, and ownership movements, and generate automated fertility and productivity indicators for both management and policy purposes.

The National Cattle Identification and Registration System was developed through collaboration between Rwanda Agriculture and Animal Resources Development Board, Royal Jersey Agriculture and Horticulture Society, and PAN Livestock Services Ltd. Functional specifications were aligned with Rwanda’s livestock systems, administrative hierarchy, and diverse ownership models. Built on SQL Server architecture and customized from established livestock recording platforms, the centralized, internet-based database supports real-time multi-user access. Field data are entered via smartphones, tablets, or computers and synchronized to a secure cloud server hosted within Rwanda, ensuring data sovereignty. The system integrates four modules: (1) farm registration with unique premises IDs and GPS coordinates; (2) animal identification using unique ear tags (RFID-ready), recording breed, sex, birth date, pedigree, ownership, and full lifecycle traceability; (3) configurable event recording for reproduction, health, and production data; and (4) embedded analytics with automated KPIs (e.g., age at first calving, conception rate, milk yield, growth, disease incidence) plus rule-based alerts linking insemination, pregnancy diagnosis, and calving projections. Rolled out nationally from October 2021 following multi-zone piloting, implementation included training IT staff, national trainers, and over 1,000 enumerators to standardize digital data capture. To date, 1,417,328 cattle have been registered. Females comprise 78.5%, reflecting Rwanda’s dairy orientation. Breed data were recorded for 766,288 animals: 61% Holstein-Friesian and crosses, 17% indigenous breeds, 12% Jersey and crosses, 3% Sahiwal and crosses, 3% Jersey × Friesian, and small proportions of Brown Swiss, Fleckvieh, and Brahman. Dairy bloodlines represent about 77% of recorded breeds, indicating strong genetic upgrading. Strategically, the platform strengthens traceability, disease surveillance, AI monitoring, movement control, and market regulation. Priorities include complete lifecycle updating, improved breed data, sustainable financing, multi-species expansion, and alignment with international recording standards. The system establishes a scalable foundation for genetic improvement, productivity growth, and evidence-based livestock governance.

Mexico's Sistema Nacional de Identificación Individual de Ganado (SINIIGA) (National System of Individual Livestock Identification)

Reynoso Othón*[1]

[1] SINIIGA – SINIDA / CNOG

Provide an understanding of the operational aspects of SINIIGA so that key functionalities and solutions could be reviewed for potential use in the attendee's relevant countries.

The National Confederation of Livestock Organizations (CNOG) with the committed involvement of organized farmers in the country, implemented and launched SINIIGA, as a basic tool in the process of identifying the origin and traceability. In general, the system uses plastic ear tags with barcodes and, to a lesser extent, RFID devices to manage the health, traceability, and movement of animals, primarily cattle. It is compatible with the National Livestock Registry (PGN) and the Electronic Movement Registry (REEMO) to monitor animal movement, health, and production. The national system has been expanded to provide comprehensive livestock tracking and is working on integrating new technologies. SINIIGA depends of the the Ministry of Agriculture and Rural Development (SADER) through SENASICA and is operated by the CNOG. CNOG has 1,000 offices across the 32 states, assisting producers with PGN updates, registrations, and the distribution of SINIIGA–SINIDA identifiers. Additionally, more than 2,100 offices for th

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Technical Session 4
Heat stress, health and welfare: genetics and management

Novel approaches to breeding for climate-smart dairy cattle

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Climate change remains a significant challenge for dairy production, increasing heat stress on cows and adding pressure to reduce environmental impacts like greenhouse gas emissions. Selective breeding offers a long-term strategy to improve both environmental sustainability and resilience, alongside existing economic goals. However, the relationships among traits related to productivity, heat tolerance, and methane emissions are not fully understood. This project evaluates how breeding for improved heat tolerance influences profitability, animal health, production efficiency, and environmental sustainability. Specifically, it 1) quantifies the impact of heat stress on production, fertility, health, and emissions and 2) investigates the genetic relationships of methane emissions, body maintenance requirements, and feed efficiency, with the ability of cows to maintain performance under heat stress.

Preliminary findings indicate that fat yield is the trait most sensitive to heat stress effects while methane production is only impacted under severe pressure. Additionally, results indicate that higher milk production under normal conditions may be associated with reduced resilience to heat stress, highlighting a potential trade-off between productivity and robustness. Importantly, selection for reduced methane emissions appears unlikely to negatively affect heat tolerance. These results emphasize the importance of balanced breeding strategies that simultaneously improve productivity, environmental sustainability, and resilience.

The culmination of this project will inform the development of breeding programs and indexes to breed climate-smart dairy capable of sustaining profitability while adapting to a changing climate.

Genomic prediction of heat tolerance from rumen sensor data in Australian Holstein cows

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Heat stress negatively impacts livestock by reducing growth, milk production, and fertility performance. Genetic selection for heat tolerance in dairy cattle was first proposed using the rate of decline of milk production under heat stress as a phenotype. This method has been applied in several countries and was included in the national genetic evaluations in Australia. However, the uptake of this breeding value by farmers has been slow due to producer concerns that selecting for heat tolerance will reduce the performance of dairy cattle. Measuring other heat stress adaptations at scale has become possible with wearable sensors, like collars and rumen boluses, addition to farm management. The data being recorded and stored by these devices in turn provides the opportunity to access phenotypes that have been too labor intensive to measure. This study aims to investigate rumen temperature as a novel phenotype for genetic selection of heat tolerance in dairy cattle.

Weather data from the nearest weather station was retrieved from the Australian Bureau of Meteorology and used to calculate daily temperature-humidity index. Hourly rumen temperature data from 2019 to 2023 was retrieved for 920 Holstein cows across two farms in Victoria, Australia. Rumen temperature was corrected for water intake events and will be merged with production and performance data to investigate the relation between them. Cows (n=891) were genotyped for SNP positions on the Illumina BovineSNP50 panel using target capture sequencing. The genotypes were imputed to the custom XST74K SNP panel that is used for the standard genetic evaluations of Australian dairy cattle. Genetic parameters and variance components are being calculated using ASReml software.

The maximum difference within a cow for daily average rumen temperature was 3.6 °C. Across all cows, average daily temperatures ranged from 37.99 °C to 42.15 °C within the experimental period. This is a sizable difference given that even a 0.1 °C increase in body temperature can reduce fertility. The genetic estimates will be evaluated for their potential to predict heat tolerance in Australian Holsteins by comparing them to the current breeding values for heat tolerance included in the genetic evaluations. Exploring novel phenotypes, made accessible by wearable sensors, can help identify heat tolerant cows in ways that are less related to milk yield.

Detecting heat stress in dairy cattle using milk composition data

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Heat stress is a major challenge for dairy cattle health, welfare and productivity, and its intensity is expected to increase with climate change. The RobuST project, conducted in the Auvergne–Rhône-Alpes region (France) and funded by the Regional Council, aimed to assess whether routinely collected milk composition data could detect heat stress in dairy herds and support reactive management.

Heat stress exposure was first estimated using the Temperature–Humidity Index (THI), calculated from meteorological data for more than 4,000 dairy herds located within 5 km of a weather station. Milk yield and detailed milk composition data, including fatty acids, were analysed across THI classes during summer periods, using data from two contrasting years (2021 and 2022). In a second phase, on-farm data were collected during 100 visits in 50 dairy herds during summers 2024 and 2025. Visits were conducted during the warmest part of the day. THI was measured directly in the cows' living environment, and animal-based indicators of heat stress (respiratory rate and skin temperature) were recorded. Herds were classified into three heat stress risk categories. Variations in bulk tank milk composition between three days before the visit and the visit day were analysed. Decision trees were developed to discriminate herd heat stress risk based on milk composition changes.

No clear variation in milk composition was observed when herds were classified solely according to THI derived from daily meteorological averages. In contrast, THI measured directly in the living environment revealed moderate to severe heat stress conditions that were not captured by daily averages. Herd classification based on animal-based indicators showed a significant decrease in milk protein content and an increase in milk urea content with increasing heat stress risk, while milk fat content and fatty acid profiles remained unchanged. Decision trees based primarily on short-term changes in milk protein content allowed discrimination of herd heat stress risk with sensitivities of 67–70% and specificities of 77–100%. These results demonstrate that milk composition data, when combined with animal-based indicators of heat stress (such as respiratory rate and skin temperature), can contribute to data-driven tools for alerting heat stress at herd level.

Prediction of dairy cows' heat stress response from milk mid-infrared spectra for detection and genetic selection

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The heat stress (HS) response of dairy cows remains difficult to record reliably at large-scale because physiological data are scarce and production traits lack specificity. An alternative is to develop a prediction equation based on mid-infrared (MIR) spectra, which are routinely collected and may contain a more specific signature of the HS response than production traits. The objectives were thus to develop this prediction (MIR-HS) and validate it using external data.

Surface body temperatures were recorded during official milk recording visits on 399 Holstein cows from 5 farms in summer 2024. MIR-HS was developed by combining two equations: (1) a partial least square (PLS) regression on surface body temperature and (2) a random forest classification of the HS response based on surface body temperature and milk trait residuals. MIR-HS was then applied to historical milk recording data for validation. This included assessing its response to temperature and humidity index (THI) and identifying the characteristics of the most affected cows. A genetic analysis was also performed to estimate MIR-HS heritability and genetic correlations with routine traits, as well as to identify genomic regions of interest through a genome wide association study (GWAS).

Equation (1) reached a validation R2 of 0.67 with an RMSE of 0.64°C, and equation (2) classified with an accuracy of 61%. Once applied to external data, the resulting MIR-HS reacted as expected to THI. The most affected cows were multiparous, in early lactation, and with high milk yield which is consistent with the literature. Similarly, an expected heritability (0.10) was obtained and the global profile of genetic correlations was favorable. Concerning the GWAS, most of the regions highlighted overlapped with traits related to energy balance, which is consistent as HS is considered a form of negative energy balance. In conclusion, MIR-HS, a routinely available new indicator of HS response in dairy cows shows strong potential for detecting heat-stressed cows and supporting genetic selection for heat tolerance.

Actionable output developed from milk fatty acids to assess rumen health, negative energy balance and production loss in dairy cows

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Metabolic health is crucial for production performance, good fertility and longevity in dairy cows. Early detection of excessive fat mobilization and poor rumen function enables farmers to suitably intervene both at group and individual cow level to prevent milk losses and optimize fertility. Current tools often lack sensitivity and do not offer farmers and advisors direct guidance on how to act. Milk fatty acids (MFA) vary across lactation stage, parity, breed and season, and are therefore not actionable as such. The goal of this study was to develop actionable output based on the MFA profile, incorporating variations with the aforementioned covariates.

The MFA profile, predicted from mid-infrared spectra, was acquired from 181,794 milk samples collected through the national herd milk recording (MR) program at 52 farms over a time period of 4 years (2021-2024). These data, originating from 14,261 unique lactations, were combined with cow auxiliary data, daily milk yield records, and herd MR information (fat and protein yield). We developed 3 metrics to predict the risk on poor rumen functioning (days in milk, DIM 0-450), negative energy balance (DIM0-100), and early lactation milk losses (DIM0-42). The latter was assessed on production losses in the first 150 days of lactation. Each risk metric was classified as ‘low’, ‘medium’ or ‘high’ risk. Odds ratios were calculated to assess the difference in milk losses between these classes, and risks were compared with the current ketosis alerts based on ketones. Milk losses and farmer experiences were evaluated during a second validation study on 27 farms in ‘25-‘26.

On average, cows with a high risk MFA profile were up to 3 times more frequently in the worst 20% quantile for milk losses than cows with a low risk. Contrarily, cows with a low risk MFA profile were up to 3.5 times more likely to experience low (lowest 20%) milk losses as compared to cows with a high risk profile. The MFA based risk metrics were more sensitive than the current ketosis alerts. The second validation study showed that cows with high risk for both energy balance and rumen function had on average 0.6kg/d, corresponding to 74% more milk loss than cows with low risk. MFA risks helps farmers to optimize their ration at group level and to identify cows that need extra attention to prevent milk losses.

Does the automation level of a dairy farm affect animal welfare?

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The number of automation technologies for dairy cattle farming has increased significantly in Germany in recent years, with most technologies focusing on labor-saving and providing relief from physically strenuous labor for farmers. Thereby, automatic milking and feeding systems as well as automatic manure removal and bedding technologies are now commercially available. The influence of these technologies on individual aspects of animal welfare has already been investigated to a certain extent, but there is still a lack of knowledge about the impact of increasing farm automation through various combinations of these technologies. Therefore, the aim of this study was to examine whether the degree of automation on a dairy farm affect welfare indicators of dairy cows from the Welfare Quality® Assessment protocol.

To achieve this aim, 32 trial farms in Northern and Central Germany were categorized into varying automation degrees using a newly developed classification system. The Welfare Quality® Assessment protocol for dairy cows was used to conduct welfare assessments on all participating farms by one trained person. Using analysis of variance (ANOVA), overall welfare scores and individual measures from the protocol were compared across farms with differing automation degrees.

No significant differences were observed in overall welfare scores, suggesting that the influence of automation does not exceed other farm-related factors influencing animal wellbeing, such as housing environment or management methods. However, significant effects of milking, feeding, and bedding systems on the appropriate behavior of cattle were observed. Thereby, higher degrees of automation had a positively affect the human–animal relationship and led to positive emotional states, as cows in highly automated farms are less disturbed and experience greater freedom. Moreover, farms with higher automation degrees had significantly lower scores for the prevalence of severe lameness and dirtiness of lower legs. It could be concluded that a higher degree of automation could help to improve animal welfare on dairy farms. The developed classification system was well-suited to reach the aim of this study and can be utilized for further research related to automation in dairy farming.

Q Index: A nationwide welfare index based on DHI and cattle register data

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Q Check is an established animal welfare monitoring system in Germany, built on routinely recorded data from Dairy Herd Improvement (DHI) and the national system for animal identification and registration (HI-Tier). Covering around 85% of German dairy cows, DHI enables nationwide assessment and comparable analyses based on reliable on-farm data collection. In total 16 Q Check indicators combine complementary information from udder health, metabolic health as well as longevity and animal losses. Building on this framework, the Q Index project was initiated as a methodological extension to aggregate the indicators into three subindices (udder health; metabolic/digestive health; longevity/mortality) and one overall index. The aim was to develop a user-friendly system enabling transparent benchmarking and both horizontal and vertical analyses, with potential to support risk-based audit frequency control for quality assurance systems.

Nationwide DHI and cattle register data from 2021 to 2024 with quarterly resolution were available for index construction and application. Given that most indicators are percentages characterized by skewness, heterogeneous variances, and regional and structural confounding, a robust rank-based methodology was applied: All indicators were transformed into directed percentile ranks (0–100; higher = better). Subindices were calculated as the mean of ranked indicators within each group, and the overall Q Index as the mean of the three subindices. In the initial implementation, percentile thresholds were fixed based on the 2022 national monitoring dataset, ensuring vertical comparability over time.

The Q Index provides a standardized, nationwide animal welfare assessment based on routinely collected and reliable data from DHI. A rank-based approach reduces skewness and structural differences, resulting in stable, herd-size independent values. Interpretability is enhanced through its hierarchical design: the overall index provides a good overview, subindices reflect a summarized assessment within the indicator groups, and the underlying indicators enable targeted diagnostics. This rank-based construction enables intuitive visualization and simple between-farm and longitudinal analyses. By condensing multiple indicators into a structured and easily interpretable index system, farm-level evaluation is simplified and data-driven quality assurance strengthened.

Leveraging herd management, genetics, and DHI by integrating all three data types into a new transition cow decision tool

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Many single measurements can monitor a herd's transition cow program like milk yield, gestation length, dry period length, calving ease, abortions, fresh cow mastitis, etc. However, combining all these into a single, easy to understand measure is more efficient, informative and easier to track over time. The new Fresh Cow Index (FCI) is a single measure that was developed by Dr. Albert DeVries at University of Florida in collaboration with Dairy Records Management Systems (DRMS).

FCI is the Actual Energy Corrected Milk (ECM) on first testday divided by the Predicted ECM times 100. FCI is calculated for cows with a first testday between 5 and 40 days in milk. The predicted ECM is calculated using 25 different cow variables that cover genetic, production, udder health and reproduction data. Data used to calculate FCI is obtained from DHIA milk testing, the Council on Dairy Cattle Breeding (CDCB), and DRMS data.

Analysis of 1 million first parity cows broken out by FCI ranges of 10 FCI starting at <70 up to >=130 show that 305 d completed lactation production ranges from 9560 kg ECM (FCI<70) up to 12400 kg ECM (FCI>=130). Similarly, culling rates expressed as cow being sold or died in that lactation went down from 33% (FCI<70) to 18.1% (FCI>=130). Similar trends were observed in second lactation cows. A secondary analysis evaluated repeatability of lactation performance. Specifically, the likelihood cows who underperform (FCI<100) in a previous lactation would repeat and underperform in the next lactation, as compared to those who performed as expected (FCI>=100) and perform as expected in the next lactation. Data showed that poor performance 1st lactation cows (FCI<70) in their first lactation had a 54.1% likelihood they would underperform (FCI<95) in the second lactation while cows that had an FCI>=130 had only a 33.6% likelihood they would underperform in the second lactation. Additional analysis for health events showed similar trends with low FCI cows experiencing more health events later in lactation while cows with higher FCI values experiencing fewer health events. FCI can be a valuable measurement to evaluate a herd's transition cow program over time by bringing together multiple sources of data into one single measure.

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Technical Session 5
From Milk Analysis to Decision Support: Unlocking Insights for Sustainable dairy management

Intra- and cross-laboratory monitoring framework for MIR-integrated milk laboratory data

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Mid-infrared (MIR) spectrometry of milk has increasingly evolved from a method for the determination of main milk components to a technique used for large-scale prediction of metabolic, efficiency, and emission-related phenotypes. The rapid growth of predictive applications and routinely collected MIR spectra requires harmonized quality assurance across laboratories and instruments. However, operational cross-laboratory monitoring frameworks under real-world recording conditions are lacking. This study presents an interactive dashboard enabling the monitoring of routine laboratory data, including MIR spectra and derived traits, across multiple laboratories since 2021, supporting data governance within the milk recording infrastructure.

Routine milk recording data from eight German milk laboratories of vit DHI member organizations, currently comprising 19 FOSS instruments and up to 90,000 analyses per working day, are automatically aggregated and processed the same day. After linkage to animal-related data, spectra undergo the vit-standardization, a recently introduced statistical framework allowing daily harmonization across instruments under routine conditions. Within the data processing pipeline, it is possible, and also expandable, to insert models that enable the prediction of both milk components and innovative phenotypes. The dashboard provides laboratory- and instrument-specific monitoring of data completeness, main milk components, and model-derived phenotypes. Spectral drift can be evaluated via temporal bias analysis using pilot samples with certified reference values, based on the comparison of routine laboratory results and re-predictions from raw and standardized spectra.

The system establishes a scalable intra- and cross-laboratory quality control infrastructure within milk recording. Multi-year visualizations enable first longitudinal assessment of both standard and novel phenotypes under practical conditions. Drift monitoring supports early detection of instrument-related anomalies and improved traceability of technical events. Although primarily descriptive, the framework substantially enhances transparency, harmonization, and reliability of MIR-derived data streams. This approach strengthens quality assurance in milk recording, supports methodological innovation, and contributes to robust phenotype delivery for farm management and breeding applications.

Extramir spectral proficiency test: comparison of spectral standardisation methods

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The interest of using FT-MIR analysis of milk to predict a large variety of phenotypes (e.g. fine milk quality, health status or environmental impact of cows) is worldwide growing. Such FT-MIR models are tedious and expensive to develop and there is a clear interest in sharing predictive models among organisations of different geographic locations. However, spectral differences between instruments or within instruments across time hinder the sharing and use of common MIR models. To overcome this issue, spectral standardisation methods were developed to harmonise spectral responses of instruments over different networks. The aim of this work was to compare the performances of 4 different spectral standardisation methodologies (Foss, CRAW/EMR, Lactanet and VIT).

Each methodology involved around 10 instruments in the test. Identical sets of 10 milks were distributed by ICAR and analysed by all the spectrometers involved (N=44) to compare their spectral information. A total of 10 FT-MIR models predicting a wide range of phenotypes were applied to all raw and standardised spectra. All these models were developed using spectra standardised with the CRAW/EMR methodology. For each methodology, the spectral and prediction homogeneity across instruments, before and after standardisation, were assessed through the standard deviation of absorbance intensities per wavenumber and the standard deviation of predictions across instruments.

Results highlight the spectral differences between instruments without standardisation and the resulting heterogeneity between predictions of different spectrometers. Overall, the predictions were improved after standardisation for each method in comparison to before standardisation. The 4 standardisation methodologies show different performances in improving the spectral homogeneity between instruments and among spectral regions. Therefore, the performances in harmonising the predictions homogeneity were also different according to methods and models. Finally, the results suggest that differences in spectral standardisation across methodologies may constrain model transferability between networks (i.e. sharing models may require standardising spectra to the same reference to build the model and for predictions). This highlights the need for further research to better understand and potentially overcome these limitations.

Kinetic assessment of the impact of a linseed-rich diet on a milk FT-MIR-based herbage intake indicator

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Using pasture is a sustainable strategy for cattle feeding that provides environmental, economic, and social benefits. Currently, grazing calendars and on-farm controls are the main tools available to the dairy sector to assess the effective use of pasture for milk production; however, these methods are time-consuming and costly. An indicator based on milk Fourier-transform mid-infrared (FT-MIR) spectral analysis could therefore offer advantages in terms of time efficiency, repeatability, and cost-effectiveness. In a previous study, we developed an indicator derived from milk component predictions (e.g. fatty acids, proteins, acidity-related traits) obtained from bulk tank FT-MIR spectra and linked it to the proportion of herbage in the diet, ranging from 0 to 1. In the present study, we further evaluated the potential of this indicator by investigating its annual kinetics across eight farms during 2023–2024 and by presenting preliminary results from this analysis.

A total of 2,445 bulk tank milk analyses were available. Milk was collected every 1 to 3 days and aggregated monthly to match the temporal resolution of grazing calendars. Grazing patterns for each farm were visually assessed and compared with the corresponding calendars.

The proposed indicator showed higher values during grazing periods, with an average increase of 0.17 ± 0.03 (n = 148 aggregated samples). Linseed supplementation did not visually mask the grazing signal but increased the indicator values throughout the supplementation period. When data were available for the same farm, an increase of 0.12 ± 0.01 (n = 31 aggregated samples) was estimated between periods with linseed supplementation without grazing and periods with grazing without linseed. Overall, supplemented diets, particularly linseed-rich feeds, do not appear to mask grazing-related kinetics associated with herbage consumption but rather shift the indicator level during supplementation. The indicator's kinetics therefore appear promising for identifying grazing periods even in the presence of dietary supplementation, although a threshold-based detection approach seems unsuitable due to farm-specific patterns.

Modular Open-Source Framework for Spectral Phenotyping Using Neighbourhood-Adaptive PLSR to Predict Nitrogen Use Efficiency in a Dairy Herd

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Mid-infrared (MIR) milk spectra are widely used for routine phenotyping in the dairy industry, yet predictive modelling approaches remain difficult to implement in practice due to technical and reproducibility barriers. Conventional calibration models, most commonly partial least squares regression (PLSR), are favoured for their mechanistic interpretability. However, global PLSR models are driven by the dominant covariance structure of the calibration datasets, predicting best for samples at the population centre. Peripheral samples are often poorly represented by a global calibration and consequently predicted with greater error, despite being of greatest biological and management interest, motivating local models built with spectrally similar observations. This study presents an open-source modelling framework to lower technical barriers to spectral phenotyping that aims to enhance translation of milk spectral data into actionable decision-support insights and introduces a promising novel neighbourhood-adaptive local PLSR approach.

We introduce the Spectral Phenotyping Prediction Framework (SPPF), a modular open-source Python package integrating spectral preprocessing, model training, and validation within a reproducible workflow. It supports both global and local modelling strategies. Neighbourhood-Adaptive PLSR (NA-PLSR) constructs sample-specific calibration subsets based on spectral similarity, optimising neighbourhood structure alongside PLS hyperparameters. The framework was applied to MIR milk spectra to predict nitrogen use efficiency (NUE), a key sustainability indicator in dairy systems.

NA-PLSR delivered modest overall gains (R2test=0.66 vs 0.63), but showed its strongest advantage at peripheral NUE ranges, reducing RMSE for outlying samples by up to 18.6%. Distributional fidelity analyses also indicate NA-PLSR predictions are closer aligned with measured NUE distributions, with 6–10% improvements across KS, Jensen-Shannon, and Wasserstein metrics. Locally adaptive spectral modelling improved prediction of a complex trait compared to a conventional global model, particularly for samples poorly represented in global calibration models. The open-source SPPF enables reproducible model development and wider adoption of advanced spectral phenotyping, supporting improved use of routine milk spectral data.

Does MIR-based information contribute to practical decision-making on the farm?

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Mid-infrared (MIR) milk analysis has become an important technological development in modern dairy management. However, a critical question remains: do dairy farmers truly value MIR-based information, and does it contribute to practical decision-making on the farm? This presentation investigates the real-world relevance of MIR analysis from a farmer-oriented perspective, focusing on its application in metabolic monitoring and herd health management. Our main objective was to underline the technical evaluation of MIR predictive models with practical feedback from dairy producers to assess usability and impact.

Over the past decade, tools such as the KetoMIR system based on EMR standardised MIR spectral data have been implemented in routine to predict if animals are in danger based on an ample system. The preprocessing of the MIR spectral data, the KetoMIR model and the satistics for the predictions have been made in R with the help of GLMNET, pls, ChemometricsWithR and caret packages.

Due to wide spread extreme negative energy balance after calving and the demand for early detection of ketosis signs, KetoMIR is routinely used on the monthly collected milk samples at MROs LKV Baden-Württemberg, LKV Austria, LKV Nordrhein-Westfalen and LKV- Schleswig-Holstein. After 10 years of using KetoMIR, the results demonstrate that MIR-based indicators provide early and actionable insights into metabolic disorders, enabling farmers to adjust feeding strategies, reduce disease prevalence, and improve overall herd performance. Analysis of long-term data shows clear associations between KetoMIR classifications and key production parameters such as milk yield, fertility, and incidence of ketosis-related diseases. A farmer survey further reveals that while not all producers actively engage with detailed data, a majority recognize the practical benefits of MIR-derived information when presented in an understandable and farm-relevant format. The findings confirm that MIR analysis is most valuable when translated into simple, decision-support tools rather than complex technical reports. Overall, 10 years of experience indicate that MIR technology, when properly integrated into advisory systems, offers meaningful support for improving dairy cow health and farm efficiency.

Decoding lipolysis through individual free fatty FT-MIR model: Enhancing predictive accuracy through real-sample enrichment and advanced algorithms

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Lipolysis is a longstanding and topic of interest within the dairy industry. Having been extensively researched throughout the twentieth century, lipolysis is often prematurely dismissed as a settled or outdated field of study. In recent years, the advent of robotic milking systems and their related increase of milking frequencies have led to a rise in lipolysis levels, sparking renewed interest in monitoring milk quality. For individual cows, this monitoring could help to select cows who could resist to lipolysis and/or highlight bad farming practices. Predicting lipolysis more effectively relies on the analysis of free fatty acid (FFA) concentrations.

Recent research has demonstrated the feasibility of quantifying individual free fatty acids in milk; specifically, the use of Fourier Transform mid-infrared (FT-MIR) spectroscopy on milk has shown promising results in predicting these traits. But this research has several limitations such as the use of unofficial reference analysis and the use of artificial lipolysis samples to gain in variability. To overcome these limitations, individual FFA models developed previously have been used to select, through the Walloon milk recording, 165 samples with a predicted high lipolysis level. Moreover, 41 samples were collected at the local farm of the CRA-W. All samples have been analyzed using the official reference analysis. FFA FT-MIR models built using Partial Least squares (PLS) regression and only the new dataset give the same performance than the literature. To improve the prediction performances as non-linear relationships can exist, advanced machine learning algorithms were tested using the full dataset (N=1004).

PLS regression, Kernel Ridge Regression (KRR), Gaussian process regression (GPR) and Support vector machine Regression (SVR) give better performance than other literature models with R^2CV of 0.72, 0.5 and 0.45 for Short Chain FFA, Mid Chain FFA and Long chain FFA respectively. Adding real lipolysis samples lead to a more robust models without changing the performances. This refinement of lipolysis has resulted in improved oversight of agricultural practices and enhanced valorization of milk for the purpose of its transformation.

Considerations for the Establishment of Practical Accuracy Limits for On-Farm Milk Analysers for Official Milk Recording

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On-farm milk analysers are increasingly used in dairy production systems, yet their integration into official herd improvement and recording schemes remains limited. A key constraint is that existing accuracy limits and testing frameworks are not fully aligned with the primary objective of herd improvement programmes. Farmers make a variety of decisions from milk data: some related to long term performance over a lactation or longer, and some related to recent performance or even today's performance. In contrast, herd improvement schemes are oriented around overall (lifetime) cow performance rather than short-term production fluctuations. The current and proposed ICAR accuracy limits for on-farm milk analysers for use in official milk recording were derived from laboratory reference methods coupled with the goal of detecting significant day-to-day production changes. This approach does not reflect the requirements of herd improvement programmes. In conventional milk recording systems based on laboratory testing of milk samples, overall accuracy is mainly affected by biological day-to-day variation, sampling frequency and on farm handling and sampling factors, rather than laboratory analytical precision. On farm milk analysers produce many repeated measurements for each cow, which makes them much less sensitive to these sources of error. Because of this, setting accuracy requirements for on-farm milk analysers based on the accuracy of laboratory instruments is inappropriate. To set practical and meaningful accuracy limits for on farm milk analysers, evaluation frameworks need to focus on outcomes that matter for herd improvement. Defining accuracy limits in terms of system-level measurement of cow-average or cow-total performance would align the evaluation process with the goal of herd improvement and remove the unhelpful requirement for highly precise individual test accuracy while preserving confidence in official recording data from on-farm milk analysers.

Closing the Utilisation Gap: Converting Routine Milk Analysis Data into Decision Support for More Sustainable Dairy Farming

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The dairy sector often calls for new innovations to improve sustainability, yet a major near-term opportunity lies in using existing milk recording tools far more effectively. This study investigates how the carbon footprint of milk production can be reduced by better utilising routine Dairy Herd Improvement (DHI) indicators already available to most dairy farmers.

We analysed test-day records from Denmark and Thuringia, Germany, focusing on somatic cell count (SCC), differential SCC, milk β-hydroxybutyrate (BHB), and urea. Comparative analyses and mixed-effects models were applied to quantify the yield impacts of health and feeding deviations and to translate avoidable milk losses into greenhouse-gas (GHG) consequences.

Cows with SCC between 250,000 and 1,000,000 cells/mL (15% of test days) produced 3 kg/day less milk than cows below 250,000 cells/mL, while cows above 1,000,000 cells/mL (5%) produced 6 kg/day less. These avoidable losses correspond to approximately 60 t CO_2e per 100,000 cows per day. Ketosis-risk cows (high BHB; 30% of test days) also showed clear yield penalties versus low-risk cows. Furthermore, 20% of samples had elevated urea levels, indicating protein oversupply and substantial opportunities to improve nitrogen efficiency. Overall, the results highlight a utilisation gap: efficient milk testing and data analysis systems already exist, but their decision-support potential is not fully realised in daily herd management. Bridging this gap—rather than waiting for entirely new measurement technologies—offers an immediate and practical pathway to more sustainable dairy farming

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Technical Session 6
Milk Recording in a Technology World: Providing Value Added Services and Data Exchange solutions for Farms with Robots and Sensors

ICAR ADE as an Enabler for Inclusive Data Integration: A Cloud-Based Herd Management Case Study from Catalonia

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The increasing use of automatic milking systems, sensors and digital farm tools has transformed data availability on dairy farms, but has also intensified challenges related to data fragmentation and interoperability. These challenges threaten the central role of milk recording organisations, while also limiting access to advanced decision-support tools for farms with lower levels of technological adoption. The objective of this project was to demonstrate how standardized data exchange based on ICAR Animal Data Exchange (ADE) standards can position milk recording organisations as data integrators and service providers in a technology-driven dairy sector.

Within a European subsidised partnership, the Catalonian Holstein Friesian Federation (FEFRIC) and UNIFORM-Agri jointly developed UNICAT, a cloud-based herd management platform for dairy farms in Catalonia. UNICAT integrates official milk recording and herdbook data, animal identification and registration data from the national GTR database, and on-farm data from milking parlours, automatic milking systems and sensor technologies. Data exchange between FEFRIC systems and the UNIFORM-Agri platform was implemented through an application programming interface (API) fully aligned with ICAR ADE standards, enabling automated, secure and bidirectional data flows. System performance was evaluated using descriptive statistical analyses focusing on data completeness, consistency and timeliness across sources.

The implementation will result in improved data coherence between official and on-farm records, reduced manual data entry and faster availability of milk recording results and animal status updates. Importantly, the platform provides farms with limited on-farm technology access to standardized analytical tools for herd performance monitoring, narrowing the digital divide between highly automated and more conventional dairy farms. The integrated data environment also enables the development of new value-added services based on combined datasets from milk recording, animal identification, and sensor systems. This case study provides a concrete example of how ICAR ADE-based data exchange can strengthen the strategic position of milk recording organizations in an increasingly digital landscape. By combining standardization, interoperability, and inclusiveness, and by ensuring high-quality, reliable, and consistent final data, milk recording can remain a cornerstone of data-driven dairy management. This approach empowers dairy farms with integrated systems to make well-informed decisions based on robust and trustworthy data, while simultaneously supporting innovation across diverse farming models.

{farm-twin}: An Open-Source ICAR ADE–Aligned Farm-Scale Digital Twin

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Digital Twin (DT) technology can synchronise cyber-physical systems through continuous data exchange and real-time analytics, but agriculture is limited by fragmented, proprietary data that hinders interoperability and reduces the value to farms. {farm-twin} aims to provide an open-source, farm-scale digital twin aligned with the ICAR Animal Data Exchange (ADE) standard to support near real-time decision-making in dairy and livestock systems. The specific objectives are to implement an ICAR-compliant data backbone, demonstrate a modular architecture, and show that this design can support scalable, near real-time farm monitoring and integration of advanced analytics.

{farm-twin} implements a three-layer system. The data ingestion layer aggregates streams from animal wearables, environmental sensors, machinery telemetry, and farm management systems, mapping inputs to the ICAR ADE for livestock entities. The core engine layer uses a web framework and database to maintain current and historical farm state and exposes a secure API as a single source of truth, containerised for deployment at edge or cloud. A service layer hosts visualisation, analytics, and automation modules that consume the API for "what-if" simulations, alerts, and closed-loop control. Performance and scalability were explored using a realistic dairy-farm load profile with concurrent API access and measurement ingestion; descriptive performance metrics were used to assess near real-time suitability.

Under the dairy-farm scenario, {farm-twin} provided low-latency access to read/write endpoints and absorbed high-rate measurement streams without compromising responsiveness, supporting near real-time human-in-the-loop use while maintaining fidelity of the virtual farm. The main technical limitation observed was database write saturation at extreme ingestion rates, indicating clear optimisation paths such as sharding or complementary time-series storage. Keeping analytics and simulation outside the core, and enforcing ICAR ADE semantics at the ingestion layer, proved effective for interoperability and extensibility, allowing AI/ML modules (for example, health alerts, greenhouse gas indicators) to be deployed as independent services. Overall, {farm-twin} operationalises ICAR ADE as the backbone of a live digital twin and offers an open, extensible foundation for predictive, prescriptive and federated livestock applications.

LiveStack: An open-source framework for creating livestock data pipelines

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The increased installment of data systems across livestock operations creates a critical need for standardized data orchestration. While ICAR's ADE guidelines establish the foundational architecture and protocols for global interoperability, a practical gap remains in orchestrating diverse on-farm data sources into unified, compliant pipelines.

LiveStack addresses this gap as an open-source, Python-based framework leveraging Apache Airflow and Docker to automate complex data flows. Designed for deployment by technical consultants, it utilizes a declarative approach in which the users describe the data processing and infrastructure they need, while the system handles container orchestration, ETL tasks, and robust monitoring. By leveraging open-source tools for container orchestration, LiveStack can provide centralized user authentication and coordinated access to distributed container environments. The architecture is modular, featuring sub-packages for specialized data cleaning and a plugin system for extensibility, such as integrating Agrifood Data Canada's Semantic Engine for automated data verification. This modular design allows the core functionality to remain agnostic to livestock species. To ensure resilience in rural environments and support data sovereignty, LiveStack is designed to allow for edge, cloud, or hybrid deployments, utilizing local caching to mitigate connectivity issues. A central feature is a standardized API module that outputs data in compliance with ICAR ADE standards. By serving a provider-agnostic data stream, LiveStack lowers the barrier for third-party developers to deploy precision tools by removing the burden of implementing custom ingestion overhead.

LiveStack aims to provide a robust, open-source foundation for an interoperable and scalable livestock data ecosystem. By remaining open-source, LiveStack allows the community to develop and maintain integrations that the entire livestock industry can benefit from.

Stakeholder Role Differences in the Use of Precision Livestock Farming Technologies in Europe

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This study aimed to examine whether and how stakeholder roles shape the adoption, configuration, and governance perceptions of precision livestock farming (PLF) technologies in Europe. Specifically, we investigated role-based differences in technology types, monitored indicators, usage priorities, and data governance perceptions to better understand structural alignment within emerging PLF systems.

Precision livestock farming (PLF) technologies are increasingly understood not as isolated farm tools but as components of broader digital infrastructures and multi-actor socio-technical systems. In such systems, stakeholders occupy different structural positions that may shape technology configuration and data governance. Within the Horizon Europe project Digi4Live, we surveyed 92 stakeholders (farmers 33.7%; non-farmers 66.3%) across EU member states to examine role-based differences in current PLF deployment. Technology type differed significantly by role ($p<0.001$), with on-animal sensors dominating overall and reported almost exclusively by farmers, whereas non-farmers described more diversified portfolios including off-animal and integrated systems. Technology type was also associated with species ($p=0.02$), with on-animal and integrated systems aligned with cattle production and off-animal systems more prevalent in pig production. Usage patterns showed both convergence and differentiation: activity and motion were the most frequently reported indicators across roles, while first ranked primary objectives differed ($p=0.01$), with farmers prioritising reproduction management and non-farmers prioritising health monitoring. Despite these differences in system configuration and intended use, performance evaluations were broadly consistent. Data accuracy satisfaction ($M=3.75\pm0.87$), overall perceived effectiveness ($M=3.60\pm1.05$) and validation realism ($M=3.61\pm0.91$) were significantly rated above neutral (all $p<0.001$) with no role differences (all $p>0.05$), indicating shared confidence in technical performance. By contrast, divergence emerged in governance perceptions: farmers more often reported uncertainty about validation procedures ($p<0.001$) and indicated no barriers to data sharing ($p=0.03$), whereas non-farmers more frequently cited formal validation routes and identified privacy and ownership as constraints. Although respondents perceived a positive ROI overall ($M=3.96 \pm 0.82$, $p<0.001$; no role difference, $p=0.8$), high cost remained the leading concern for wider adoption. Overall, while monitoring architectures and priorities vary by stakeholder role, confidence in technical performance is shared, and differences emerge primarily in governance transparency. Keywords: Precision Livestock Farming, Multi-actor, Technology configuration, Data governance

Generative AI for Dairy Life Trajectory Modeling: Transforming Milk Recording and Sensor Data into Actionable Farm Intelligence

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The objectives of this presentation are to demonstrate methods to leverage generative AI by integrating many different data sources (historical records and real-time data) to provide actionable information to dairy producers.

There is a common challenge in the U.S. dairy industry: farmers need to decide which heifers to raise for better profitability based on limited early-life information, and these early management decisions impact both individual cow and overall farm profitability years into the future. A wealth of data is available to help a farm make better decisions, but most of this information is used retrospectively, after a decision has been made. A research project is underway to develop a novel AI approach using large language models (LLMs) to predict dairy cattle lifetime profitability from early-life indicators. This project adapts autoregressive transformer architectures—proven successful for temporal event modeling in healthcare and finance—to process cow life trajectories as sequences of timestamped events. Our approach treats each cow's life as a "sentence" where events like birth weight, illness, and breeding are "words" that the model learns to interpret in context. The transformer architecture captures long-range dependencies (e.g., calf pneumonia affecting milk production years later) while incorporating temporal dynamics through specialized encoding mechanisms. Beyond prediction, the model generates synthetic life trajectories for data augmentation. This feature could allow small farms with limited historical data to benefit from insights derived from large-scale datasets. The model provides probabilistic profitability predictions and simulates management interventions, transforming reactive decisions into proactive optimization. Training of the model relies on parlor sensor data, health, genetic, and breeding records from Dairy Records Management Systems (DRMS). Here we demonstrate two simple examples 1) the probability of cow termination (culling or death) within the next 180 days, and 2) the probability of major health events (including mastitis, lameness, ketosis, and fever) within the next 90 days. These predictions are probabilistic rather than deterministic, reflecting biological variability and management uncertainty. Outcomes from this work have the potential to significantly shift livestock management by synthesizing millions of life experiences into actionable intelligence accessible to every farmer, regardless of operation size. Predicting future performance can lead to proactive intervention strategies improving profitability measured by limiting losses of animals and improved health.

An accurate machine learning approach to predict fat, protein and milk yield before and during lactation from test-day records

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Lactation models that accurately predict the milk, fat, and protein yield of individual cows over time are important inputs for many farm and dairy processing use cases. For example, they serve as the basis for cow-comparison key figures such as net returns and the lactation index, for herd planning and insemination decisions, and for production planning of dairy plants.

We developed a machine learning model that accurately predicts milk, fat, and protein yields of individual dairy cows up to 500 days in lactation, both at the start of the lactation and after newly incoming milk recording measurements. It uses features based on genetic information, herd and animal levels as compared to population-wide standard curves, pregnancy status, and cow auxiliary data such as parity, calving season, and age. The model is trained and tested on herd-milk recording data from 1.9 million lactations from 8,981 Dutch farms.

For daily predictions of the first 305d of lactation before the lactation has started, the model has a median absolute error (MEDAE) of 3.64, 0.13, and 0.16 kg for milk, protein, and fat yield respectively, and an average percentage error of respectively 15.3, 14.6, and 15.3%. The predictions for later lactation days are slightly poorer (MEDAE of 3.55, 0.14, 0.17 respectively), mainly because the pregnancy status is unknown, and cannot be included in the model at the moment of prediction when done before or at the start of lactation. Once the lactation has started and new milk recordings are included, the median absolute error decreases to respectively 2.45, 0.10, and 0.13 kg, corresponding with a percentage error of 11.3, 11.7, and 12.5% for milk, protein, and fat yield. The predictions at calving provide a reference to compare true performance with the cow's expected performance. The updated predictions, when new measurements come in or when pregnancy is confirmed, can be used as an input to estimate e.g. the dry-off milk yield and the cumulative (305d) milk, fat and protein yield of an animal, herd or parity group. Since the model predicts ongoing as well as future lactations, it can be used for predicting total expected yield of an entire herd or group of herds for horizons up to >1 year.

Machine Learning Approach for Early Prediction of 305-Day Standard Lactation

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Accurate prediction of standardized 305-day lactation yield at various days in lactation enables early performance assessments. This study develops and validates an XGBoost regression model to predict standardized total lactation yield using partial lactation data in Fleckvieh dual purpose cattle. The objective was to develop a machine learning model for 305-day standard lactation milk yield prediction from intermediate records and to compare the approach against a linear regression method.

We engineered a feature set combining production measurements (latest test day milk yield, cumulative yield to date, herd average yield), genetic predictors (estimated breeding values for milk yield and persistency), somatic cell counts, and cyclical features (sine/cosine transformations for test day). Additionally, lag features representing prior milk yields and somatic cell counts were generated to incorporate animal-specific historical trends. A year/lactation level data splitting prevented leakage between training and validation sets. Model validation included metrics at multiple lactation stages and overall animal-level performance stratification.

Over the full test-set (overall performance) the XGBoost model achieved R^2 = 0.94 and a mean absolute error of 330 kg (305-day yield), demonstrating competitive performance with traditional regression baselines (R^2 = 0.94, MAE = 334 kg). Sensitivity testing showed cumulative yield, current milk production and herd average yield, combined with the specific day of lactation as dominant predictors. Error analysis stratified by lactation number highlighted that the model maintains stability across different animal ages. This XGBoost model provides accurate, interpretable 305-day lactation yield predictions from intermediate measurements, providing a robust alternative to traditional lactational yield prediction methods. Future work will focus on daily milk yield prediction and lactation curve forecasting.
Keywords: Dairy cattle, machine learning, lactation yield prediction, XGBoost

Reconstructing representative daily Fourier transform mid-infrared milk spectra from partial milking robot samples using machine learning

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Automated milking systems (AMS) are increasingly adopted on European dairy farms to improve herd monitoring through automatically collected measurements. However, obtaining a representative daily milk sample for milk recording from those systems remains challenging because milk composition varies throughout the day and cows are milked voluntarily. In 2002, Peeters and Galesloot developed an ICAR-certified method to estimate daily fat content (%FAT24h), but not to reconstruct a representative Fourier-transform mid-infrared (FT-MIR) spectrum (SPECT24h) suitable for predicting multiple milk components. So, this study aimed to develop models allowing the estimation of %FAT24h and SPECT24h from partial milkings.

Two datasets were included: one with 49,631 historical records from five farms, three being independent and 2 being included in the experiment, and a validation dataset with 2,230 records from 746 cows across seven Belgian farms where every milking was sampled. Two sampling protocols were evaluated: RZ (one milking) and RM (two milkings), using three estimation methods: M1 (based on Peeters and Galesloot), M2 (weighted average), and M3 (linear regression).

For the RZ protocol, M1 provided the most accurate %FAT24h estimates (RMSE = 0.275%). For RM, accuracy improved (RMSE = 0.193%). Optimal performance was observed when sampled milkings represented 40–60% of daily milk volume. M2 became the most accurate when this proportion exceeded 60% (RMSE = 0.190%), while M3 did not outperform the other methods. Instead of predicting %FAT24h, the second step focuses on reconstructing a FT-MIR spectrum that should be representative of the day. From this spectrum, any prediction equation is applicable, but this study presents the performances for the prediction of fat content. Daily spectra reconstructed from partial milking samples enabled %FAT24h prediction with accuracy equal to or greater than traditional methods. For M1, RMSE was 0.272% (RZ) and 0.193% (RM). For M2, reconstructed spectra slightly improved accuracy (RMSE = 0.182%). These results demonstrate the feasibility of reconstructing SPECT24h from partial milkings and using it to predict milk fat content, potentially enabling the full usage of milk recording FT-MIR spectra for management and monitoring in farms using AMS.

ORAL

Technical Session 7
New Developments in Sheep, Goats and Camelids within ICAR

Assessing the adoption of genomic tools in sheep and goat breeding: patterns, challenges, and perspectives

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Genomic selection has become the reference approach for genetic improvement in many livestock species and is now the standard in dairy and beef cattle breeding, increasing accuracy, shortening generation intervals, and accelerating genetic gain. In small ruminants, adoption remains more heterogeneous. Some breeds, although implemented later than in cattle, have implemented structured genomic selection programs, whereas in others, delays reflect the need to build basic breeding infrastructure, including pedigree and performance recording, and organized breeding nuclei, before genomics can be applied. To capture this diversity, a questionnaire survey conducted by the ICAR Sheep, Goats, and Camelids WG was sent to experts from countries with sheep and goat populations.

Responses were received from 13 experts representing 26 breeds across eight European countries. The survey described the current state of genomic implementation across breeds and countries and identified common patterns of operational strategies. Information was collected on population size, recorded traits, pedigree systems, breeding nuclei organization, and genomic applications, including parentage verification, major gene use, genomic evaluation methods, and genetic diversity indices. Results provided a comprehensive overview of diverse breeding contexts and practical realities, allowing breeds and countries to be grouped into three levels of genomic implementation: 1) structured and fully operational schemes, in which genomic tools are routinely applied, mainly involving breeds from countries with well-established breeding schemes (10 breeds, 3 countries); 2) advanced design schemes, characterized by clearly defined genomic strategies that still require refinements in coordination and operational logistics, including both breeds facing organizational constraints and small local populations (5 breeds, 3 countries); and 3) embryonic schemes, marked by sporadic and non-systematic genomic activities, typically associated with poorly structured breeding programs and limited recording systems (14 breeds, 6 countries).

The results support the establishment of a Reference Centre to promote experience and methodology exchange, helping less-structured programs overcome gaps and integrating selection indices that, alongside production traits, also consider the adaptive potential of local breeds.

Towards ICAR guidelines on conformation traits in dairy sheep recording

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Conformation of an animal refers to the combination of structural correctness of feet and legs, muscling and udder conformation. Feet and leg traits may be useful indicator traits for claw health while proper udder conformation directly affects milk production, resistance to mammary gland diseases, and improved machine milkability. Favourable conformation has a direct relationship with the productivity, longevity, animal health, disease resistance, and adaptability. Dairy sheep breeders widely recognize the importance for inclusion of the conformation traits in the breeding program. However, there is no recommendation on conformation traits recording, with precise description of each trait, recommended scale of linear classification, and statistical models for genetic evaluation. Therefore, this study aims to provide an overview of the current state of conformation recording in Mediterranean dairy sheep breeds in order to develop ICAR guidelines for conformation recording.

Hence, a survey was developed, and members of the breeding associations were invited to participate. The survey consisted of basic information's (country and breeding organisation contact), and specific questions (size and details of dairy sheep population in the conformation recording, breeds involved, and information on the traits recorded). Altogether, eight breeding organizations have responded to the survey. The scored traits included 11 frame traits, 7 leg traits, and 9 udder traits.

The most frequently recorded traits were loin strength, rump angle, rump width, body length, chest width as frame traits, foot angle, rear legs set, and fore legs set as leg traits, and teat position, teat length, udder depth, udder attachment, and udder cleft as udder traits. The core set of traits identified in this study will provide a crucial foundation for the international harmonization of conformation recording in dairy sheep breeds, soon available in the section 5 on conformation recording in ICAR guidelines.

How ICAR can help in fostering cooperation across country in breeding programs: the case of the Latxa and Manech dairy sheep breeds

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ICAR, through its different bodies, provides tools to help organisations in carrying on domestic breeding programs, but also in fostering cooperation across countries to set up joint or collaborative breeding programs. It is the case of the Latxa and Manech dairy sheep breeds, each one with their black and red variation, that are similar dairy sheep breeds respectively raised in the Spanish and French Basque country. Even though each country has so far run separately its own breeding program, several projects have aimed, for almost two decades, at getting both programs closer, by building tools and initiative targeting this objective. ARDI2, an Interreg POCTEFA project, followed this purpose through different actions related to ICAR activities and services. The objective of this communication is to show, through three actions, how ICAR tools and bodies have been resourceful in pursuing the aim of bringing closer the Latxa and Manech breeding programs.

The across-country genomic evaluation task has benefited from the expertise of the Interbull Centre for the management of genotypes obtained from various platforms. By the adaptation of the GenoEx platform for sheep (Sheep GenoEx) and the adaptation of existing pipelines for the imputation stage, Interbull, in collaboration with the partners of the projects, has issued a genotype file aligned, cleaned and imputed, ready-to-use for the genomic evaluation development. The second example is the harmonisation of udder appraisal across Latxa and Manech that relies on the ICAR guidelines, whose section on udder conformation is currently being reviewed for dairy sheep. Finally, the ARDI2 project has developed the process to include Spanish milks in the reference population for the prediction of casein and fatty acid profiles from MIR spectra. The reference population initially built with milk samples from French breeds will benefit from samples from Latxa breed that will bring greater milk diversity, in addition to increasing the size of the training population.

This work, done in collaboration of the European Milk Recording standardisation network, relies on the know-how used in the Extra-MIR project covered by ICAR. These three examples illustrate the concrete benefits provided by ICAR and the bridge that can be built across species through the ICAR network.

International collaboration for multinational evaluations in sheep

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The global sheep industry is under pressure to improve sustainability from producers, retailers, governments, and society. This common goal is an opportunity for increasing collaboration between genetics research groups and service providers around the world. As part of the Brian Wickham Young Person Exchange Program, Michael Aldridge investigated how to facilitate joint international genetic evaluations for methane and feed intake, with visits to the following countries: Australia, New Zealand, Uruguay, the United Kingdom, Republic of Ireland, Norway, and France. This paper focuses on the higher-level recommendations for collaboration.

Trait definitions of methane emissions and feed intake between countries are inconsistent, either due to modelling or reporting requirements. The ICAR wiki should provide guidelines and reasoning for those different trait definitions. Each organisation uses different processing steps and data formats. All organisations store the raw measurements, intermediary calculations, final phenotype, and meta data, however a standard protocol on how to store that data and guidelines on what to keep and share are essential to future international evaluations. The longer it takes to develop a common data sharing solution, the larger the roadblock will become. Within each country, methane emissions, feed intake, and individual animal data (phenotypes, pedigree, genotypes) is owned by multiple organisations. In principle, if it can be demonstrated that data sharing is beneficial for the local country's genetic evaluation, permission or licencing can be obtained. Getting permissions after projects are completed becomes difficult as policies change, important personnel relocate, and priorities shift to new projects. Ideally, when new projects for methane and feed intake are developed, a pipeline for international data sharing should be included in the proposal. The largest scientific challenge is the relatively low genetic linkage between countries. The flow of genetic material is often one directional. A framework is needed to help increase linkage. This could begin with convincing industry bodies to allow for a certain number of international sires to be represented in research and reference flocks.

The current global projects for methane emissions and feed intake are the best opportunity for increasing collaboration and developing a full international genetic evaluation. If done well, it could establish a precedent for other traits.

Accelerating Digitalisation in the Dairy Goat and Sheep Sector through an Integrated ICAR ADE-Based Management Platform

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Background and Objectives: Digitalisation in the dairy goat and sheep sector is still at an early stage compared with dairy cattle. On many goat and sheep farms, reproduction and health events are recorded on paper or not recorded structurally at all. Milk recording is applied on only a limited number of farms worldwide, and traceability requirements differ between countries. Where digital systems are used, data are often spread across separate software programs, milking parlours and sensor platforms. As a result, valuable information is underused for performance recording, phenotyping and breeding decisions. This presentation shares a practical example of how digitalisation can be strengthened in dairy goat farming through the development of an integrated management platform using ICAR Animal Data Exchange (ADE) standards.

Approach: A modular platform is currently being developed to bring together kidding data, kid growth, reproduction, buck management, health events, milk production and genetics into one central and validated environment. Goat-specific processes such as seasonal breeding patterns, multiple births and extended lactations, including standardised 350-day production calculations, are incorporated. The system applies ICAR ADE standards to connect milking systems, feeding equipment and sensors, and to enable controlled data sharing with advisors and veterinarians. Challenges and Opportunities: During development, it became clear that certain goat-specific data elements are not yet fully covered within existing ADE structures. This creates an opportunity to further refine and expand ICAR standards, making them more applicable and visible within the goat sector.

Conclusions: This example demonstrates how practical digital integration can improve data quality, performance recording and phenotyping in dairy goats, while contributing to stronger and more widely adopted ICAR standards.

Mid-infrared spectroscopy adapted to sheep milk for flock management, performance recording and milk processing

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Milk-based indicators offer strong potential to support flock management, performance recording and milk processing in the dairy sheep sector. Mid-infrared spectroscopy (MIR) provides a rapid and low-cost approach to derive such indicators but requires species-specific development to ensure reliable routine use in sheep production systems.

Species-specific MIR prediction equations were developed and evaluated through successive and complementary research projects, based on a long-term co-construction approach with relevant stakeholders, such as the National Dairy Sheep Committee (CNBL) and the French Dairy Sheep Interprofessional Organisation (FBL). MIR spectra are routinely collected within the official dairy sheep performance recording scheme and stored in the national dairy sheep information system (SIEOL), providing a large and standardised data flow for model development, validation and application.

Applying bovine MIR equations to sheep milk resulted in a significant loss of prediction accuracy due to species variability. Conversely, equations specifically developed for sheep milk, particularly for milk urea content, achieved accuracy levels comparable to those obtained in cattle, for both individual and bulk tank milk (Albert et al., 2024). Encouraging prediction accuracies were also reported for milk fatty acids and caseins (Gelé et al., 2014 ; Lagriffoul et al., 2019 ; Corbière et al., 2024). Each year, more than 300,000 MIR spectra from over 730 dairy sheep farms are collected, representing a major asset for the large-scale application of species-specific equations. These results demonstrate the strong potential of MIR-based indicators for operational flock management and performance recording in dairy sheep, while further work is needed to strengthen their use for nutritional advice, but also to explore other fine components or complex traits predictions, including promising methane emission proxies.

Standardization of goat milk MIR spectra and fatty acid prediction equations

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Through the European Milk Recording (EMR), routine standardization of cow milk spectra is now largely implemented in Europe (Grelet et al., 2017). To assess whether this approach could be applied to goat milk, two standardization sets were compared. In addition, two sets of existing fatty acid (FA) prediction models were evaluated: one specific to cow's milk developed within the EMR network (updated from Soyeurt et al., 2011, by CRA-W/ULiège), and a second set derived from the French PhénoFinlait program (Ferrand-Calmels et al., 2014). A new set of goat specific equations was also developed.

Four different prediction models on 20 goat milk samples, analysed with seven instruments and standardized using either cow or goat coefficients were used to evaluate standardization. Differences in prediction accuracy (root means square error - RMSE) between the reference instrument (master) and standardized instruments (slaves) were calculated. 100 goat milk samples were analyzed by gas chromatography (reference method) and used to evaluate existing equations by comparing predicted and reference values. Mean bias, RMSE, and R^2 were calculated. Finally, a new set of equations was developed based on 250 reference analyses covering a wide range of feeding systems and lactation stages. Models were built using partial least squares (PLS) regression and support vector machine (SVM) methods, and their performance was evaluated on an independent validation set.

Results showed that standardization using cow milk provided similar performance to goat milk standardization. Therefore, cow-based standardization coefficients can be used for routine goat milk analysis without loss of accuracy. Significant deviations were observed for most FA with existing sets of equations. For the new set, performances were very good, with 12 equations showing R^2 values above 0.9 (short- and medium-chain saturated FA, total C18:1, C18:1 cis-9, MUFA) and 15 equations with R^2 above 0.8 (C15, C16, C17, individual MUFA, PUFA). In conclusion, goat milk spectra can be routinely standardized using cow milk standardization sets distributed by the EMR/CRA-W and a specific MIR equations for FA composition in goat milk is now available through the Optimir network.

Artificial neural networks outperform partial least squares models for fatty acids estimation using FT-MIR spectrometry on bovine milk: a first step towards transfer learning on small ruminants.

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Fourier transform mid-infrared (FT-MIR) spectrometry in milk can improve production, milk quality and animal welfare among others. Nevertheless, this technology remains underused in dairy ewes and goats, despite it becoming increasingly common in the dairy cattle sector. To reduce the cost of developing equations, transfer learning could be used to adapt FT-MIR models from dairy cattle to dairy sheep and goats. However, this transfer requires artificial neural networks (ANN) but these bovine ANN models do not yet exist. This study aims to develop multi-layers perceptron ANN for fatty acids to see if we can reach at least the same performances as the ones obtained with commonly built partial least squares (PLS) regressions. The ANN models developed for bovine milk were then directly applied to goat milk to evaluate the potential of transductive learning, the simplest transfer learning method.

The database (n=1942) contained 42 individual and groups of fatty acids measured by gas chromatography and their associated standardized bovine milk spectra. A total of 80% was used to train models and 20% used for validation. Validation R^2 values ranged from 0.1223 to 0.9890 for PLS models and from 0.2050 to 0.9886 for ANN models. Compared with PLS models, ANN reduced prediction errors (RMSE) by 0.08 to 47.27% for 39 fatty acids, while an increase in errors ranging from 1.74 to 3.38% was observed for 3 fatty acids. These results highlight an overall improvement in the predictive performance of neural networks compared to PLS models on the validation dataset. After applying the built ANN models on the goat dataset (n=345), only 10 fatty acids have a positive R^2 from 0.1228 to 0.9410, one fatty acid showed an R^2 equal to zero, while the remaining 28 fatty acids have aberrant R^2 values, highlighting the lack of model generalization across species.

In conclusion, these results highlight an overall improvement in the predictive performance of ANN compared to PLS models to estimate fatty acids by FT-MIR spectrometry for dairy cattle. Furthermore, transductive transfer learning confirms that models created specifically for dairy cattle cannot be applied as they are to small ruminants and opens the door to testing more sophisticated transfer learning methods.

Portable NIRS spectrometer for field diagnosis of anemia in sheep infected with Haemonchus contortus

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Haemonchus contortus is a hematophagous parasite that causes anemia in sheep, triggering changes in hemoglobin levels detectable by near-infrared spectroscopy (NIRS). This technique is considered sensitive and fast, does not require sample preparation, consumption of reagents and does not generate residues. The objective was to evaluate the field performance of the portable NIRS spectrometer in the prediction of the packed cell volume (PCV) and also as a diagnostic tool for H. contortus infection.

NIR spectra (1350 - 2500 nm) were collected from 344 blood samples of White Dorper, Santa Inês and Texel sheep, in the field and laboratory, using NIRS portable Buchi (ProxiScout). These spectral data were properly concatenated to the respective reference results (PCV by hematocrit and classification between healthy and anemic animals based on PCV plus parasites' egg count per gram of feces - EPG), and used to generate and validate the multivariate models (quantitative modeling (PLS) and classification (PLS-DA).

The results indicated that the spectral acquisition environment (field or laboratory) did not have a substantial impact on the predictive quality of the models. Both models showed good performance for the diagnosis of anemia in sheep: PLS presented greater accuracy (91%) and sensitivity (100%), ensuring that none anemic animal was not identified (absence of false negatives); while PLS-DA was more specific (99%) and accurate (95%), with minimal false positive rate (1%), reducing the chance of mistakenly classifying healthy animals as sick. Thus, the two models offer complementary performance profiles: PLS is more suitable as a screening tool, ensuring the detection of all cases of anemia, while PLS-DA may be preferable in higher prevalence scenarios, when we seek to maximize the reliability of the positive diagnosis. As both models generate results concomitantly in the system, vets have immediate access to both quantitative prediction of PCV (via PLS) and categorical diagnosis of clinical status (via PLS-DA). This complementarity extends the diagnostic reliability and offers greater flexibility to support fast and assertive decisions for sheep anthelmintic treatment under real field conditions.

Goat colostrum immunological quality: on-farm evaluation

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Goat dairy farms are often characterized by highly variable management practices and production systems. Kid mortality has not been identified as a priority issue in recent breeding programs, despite average losses of up to 30% in some regions. As one of the most important nutritional resources for newborn kids, colostrum plays a crucial role in their survival during the first hours of life. In recent years, several studies have been conducted on the use of rapid tools for assessing colostrum quality in order to intervene when necessary (Kessler et al., 2020; Pérez-Marín et al., 2023). The aim of the study is to analyses the animal factor affecting immunological goat colostrum quality. Additional goal is to evaluate results from two different analytical methods to quantify colostrum quality, such as gamma-globulin concentration (mg/mL) through protein electrophoresis and digital Brix refractometer (% Brix).

A total of 238 colostrum samples was collected from 9 Italian dairy farms. The 47.5% of the samples were from Alpine goats, 39.9% from Saanen and 12.6% from other breeds. The management systems were indoor or indoor with occasional use of pasture. Most of the samples were from 3 or more parity goats (40.4%), 20.2% from first parity and 39.4% from second parity. Colostrum samples came from goats with single kid (22.4%), 64.0% two kids and 13.7% 3+ kids. All data were analysed using SAS software (version 9.4). A regression procedure was used to evaluate the efficacy of the digital refractometer as a rapid tool for assessing the immunological quality of colostrum, obtaining a R-square of 0.603. From PROC Means procedure the average colostrum gamma-globulin concentration resulted 32.5±24.5 mg/mL and the Brix from digital refractometer was 19.2±6.86˚Brix. These results are lower than the suggested threshold of 50 mg/ml or 22 ˚Brix (Kessler et al., 2020), indicating problems linked to immunological colostrum quality in the farms included in the study. In some of the previous studies these quality levels were associated with better goat kid health status. Data found in the present study underline a high variability of the colostrum quality due to endogenous and exogenous factors. Log transformation for regression analysis between two measurements was performed. GLM analysis only for Alpine and Saanen data was done; the effects considered in the model: breed (A, S); farm (1-7), Parity (1, 2, 3+), number of kids (1, 2, 3+). All the effects significantly influenced colostrum quality, both as gamma-globulin and Brix (as log10). The best colostrum quality was found for Alpine goats, 3+ parity and animals with 2 kids.

ORAL

Technical Session 8
From Measurement to Genetics: Methane Emission and Feed Efficiency

Cattle Feed InTake – A system to identify cows, measure feed intake and body weight in dairy cattle under commercial settings using 3D cameras

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Despite feed efficiency being a complex and costly trait to measure, it became an important economic parameter incorporated into several breeding programs. However, the amount of available data still makes it difficult to conduct multitrait genetic analysis of related traits to estimate the consequences of selecting for improved feed efficiency. The CFIT system is a 3D camera-based technology that automatically measures body weight when a cow leaves the milking unit and measures individual feed intake at the feed bunk. The system is based on top-down Microsoft Kinnect v2 cameras using “time-of-flight” technology and the feed intake, animal recognition and body weight algorithms are based on AI modelling using Convoluted Neural Network algorithms. Currently the CFIT system is implemented at more than 30 commercial farms in Denmark, Finland, Sweden and Germany, providing continuous data collection from the dairy breeds Holstein, Jersey and Red Dairy Cattle.

The total data of weekly records of daily intake and body weight is currently 1.282.122 from 7158 RDC, 10914 HOL and 7542 JER cows. Mean feed intake and body weight was 61.8 kg and 689 kg for Holstein, 51.3 kg and 480 kg for Jersey and 59.2 kg and 624 kg for Red Dairy Cattle.

The data is used for both management and selection purposes. Numerous examples of using the data for improved management exist, since intake and body weight level and changes influence both efficiency, health and reproduction. Especially changes in dry cow body weight change show huge effect on performance in the following lactation. In many herds cows that either gain or lose 25 kg of body weight in the dry period has more than 10% lower milk production in the following lactation compared to cows that maintain their body weight in the dry period. Weekly averages based on daily feed intake are used for breeding value estimation for saved feed in Denmark, Sweden and Finland. Both feed intake (h2 = 0.30) and body weight (h2 = 0.65) are heritable traits when measured by the CFIT system and shows meaningful correlation to other traits like health, longevity and reproduction. The system continues to be further developed and to include more phenotypes that can be used for improved management and selection.

Recording methane and feed intake internationally

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Sheep producing countries have been measuring methane and feed intake on their national populations for the development of breeding values. There is interest to combine data from across countries into an international evaluation, but that requires the alignment of protocols, to ensure the same trait was measured. As part of the Brian Wickham Young Person Exchange Program (BWYPEX), Michael Aldridge visited: Australia, New Zealand, Uruguay, the United Kingdom, Republic of Ireland, Norway, and France. The objective of this paper was to identify differences and provide recommendations for aligning protocols.

Methane phenotyping of sheep is well standardised across countries, with the use of portable accumulation chambers (PACs), with minor methodological changes due to local management practices. PACs are manufactured locally using Perspex or built by AgResearch with stainless steel and integrated into purpose-built trailers or modified trucks. The main differences between methane protocols include: 1) the feed on offer before measuring, 2) the off-feed duration before recording, either a strict 1 hour or 1 to 4 hours, 3) the selection of animals in runs, either random or designed groups, 4) the number of animals in a run and the number of animals measured during a farm visit, 5) the measurement duration inside of PACs, 6) actions at various gas concentration thresholds, and 7) the air measurement device used. Feed intake measuring in sheep is less standardised. While commercial units are the most common method, they are all purpose built for research sites. Trial periods range between 6 to 10 weeks depending on adaption periods and ethics requirements. The main differences between feed intake protocols include: 1) which animals are selected for trials, 2) indoor or outdoor housing, 3) number of animals within a trial, 4) feed type used in the trial, 5) method and frequency for measuring daily weight gain, and 6) how potentially spurious records are processed.

The differences in methane phenotyping can likely be overcome with additional data processing or corrected for with fixed effects in linear mixed models. While it may not be possible to standardise the methodology of feed intake trials, it is paramount to report any design differences in any future database. Importantly, the countries currently or planning to measure feed intake need to share knowledge and develop guidelines on how to process individual feed intake measurements.

Heritability of feeding behaviour traits and the genetic relationships with dry matter intake in growing dairy bulls

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The objective was to estimate the heritability of six feeding behaviour traits and evaluate their genetic and phenotypic relationships with dry matter intake (DMI) in growing dairy bulls. The study aimed to determine whether feeding behaviour traits could provide meaningful genetic predictors of how much bulls eat.

Data included five years of DMI and methane records from 1,284 growing dairy bulls measured at two facilities (LIC and CRV). Feeding behaviour and individual feed intakes were measured using Hokofarm RIC2Discover Feed Intake bins. Traits evaluated were daily number of meals (NM), feeding duration (FD), feeding rate (FR), meal size (MS), meal duration (MD), and inter-meal interval (IMI). Variance components, heritability, repeatability, and genetic and phenotypic correlations were estimated using pedigree-based univariate and bivariate REML analyses.

All six traits had greater heritability, and repeatability than DMI (0.08 ± 0.02 and 0.38 ± 0.01, respectively). Dry matter intake had a strong positive genetic correlation with FR (0.76 ± 0.15) and a moderate positive genetic correlation with NM (0.36 ± 0.13). The remaining feeding behaviour traits had genetic correlations with DMI that were near zero. Phenotypically, DMI was positively correlated with NM, FD, MS, and FR (0.16–0.35), near zero association with MD (0.01 ± 0.01), and negatively correlated with IMI (−0.23 ± 0.01). The strong antagonism between NM and the MS/MD/IMI block reflects expected feeding-behaviour patterns: bulls that eat more frequently do so in smaller, shorter meals with shorter inter-meal intervals. The strong genetic correlation between DMI and FR, and near zero between DMI and FD suggest that bulls genetically predisposed to eat more tend to achieve this through eating faster, rather than by spending more time eating. Together, these results indicate that although feeding behaviour traits were heritable, only FR strongly related genetically to DMI, showing that most behaviour traits describe how bulls eat rather than providing genetic prediction of how much they eat.

International perspectives on feed intake phenotyping and feed efficiency in cattle

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International interest in incorporating feed efficiency into breeding goals has increased in recent years. To expand the volume and diversity of phenotypes, attention was also directed towards measuring feed intake under commercial herd conditions. Larger phenotype resources lead to a better understanding of the relationship between feed intake and other traits and may prompt re-evaluation of how feed efficiency is defined. Within this context, the Brian Wickham Young Person Exchange Program set out to (1) document practical procedures needed to obtain reliable phenotypes in research and commercial settings, (2) revisit definitions of feed efficiency, and (3) investigate the genetic relationships between feed intake and other traits.

The program entailed visits to the following organizations: University of Guelph (CAN), Lactanet (CAN), Aarhus University (DNK), VikingGenetics (DNK), ICBF (IRL), Teagasc (IRL), ANAFIBJ (ITA), CRV (NLD), Wageningen University and Research (NLD), Geno SA (NOR), NMBU (NOR), SRUC (GBR), University of Wisconsin-Madison (USA), and CDCB (USA). Information on feed intake recording was gathered through expert interviews and farm visits. The results were then complemented by a literature review.

Important steps for obtaining reliable phenotypes include calibration and ongoing maintenance of measurement systems. Implementation varies across farms: some adhere to strict protocols with defined schedules, whereas others calibrate and maintain the system on as-needed basis. Protocols typically include quality-control procedures (e.g., manufacturer-integrated checks or custom algorithms), followed by data editing to remove errors and outliers. Regarding feed efficiency, the predominant definition used in selection indexes is a form of "feed saved", although it is often calculated slightly differently. Genetic correlations between feed intake and other traits showed large variation. For example, the genetic correlation between feed intake and enteric methane production ranged from -0.20 to 0.84. Overall, robust protocols to ensure reliable feed intake phenotypes exist across countries. Because feed efficiency remains a complex trait, deeper understanding of its genetic relationships with other traits is essential for sustainable genetic improvement.

Tech comparison of methane measurements devices and alternative predictors in dairy cows

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This study compares methane measurement approaches used for phenotyping in dairy systems across countries and describes their implementation and use in national breeding programmes.

As part of the Brian Wickham Young Professional Exchange (BWYPEX) program I conducted a comparative review of methane measurement options in dairy cows via site visits and technical meetings in North America, Europe, and Oceania, plus virtual meetings with European scientists. Evidence from demonstrations, interviews and documents was assessed. Across programmes, there was no single method universally adopted. Appropriateness depended on infrastructure, climate, staffing, and tolerance for operational disruption.

- Sniffer sensors run under a standardised quality-control pipeline and aggregated to weekly traits in automatic milking systems or herringbone parlours delivered repeatable, genetics-grade phenotypes and have been implemented at multi-herd scale.
- Milk MIR provided a scalable population proxy when anchored to a reference group and standardised across laboratories.
- GreenFeed and Respiration Chamber are best retained as anchors and for targeted cohorts rather than broad deployment.
- The SF_6 and Portable Accumulation Chamber can yield valid phenotypes in structured campaigns, but both are operationally demanding.
- Laser methane detector can support field phenotyping in low-infrastructure settings when measurements are repeated under standardised protocols.
- Wearable methane-sensing devices (e.g. ZELP and other systems under development) and rumen-microbiome predictors are currently under validation and are being evaluated in pilot implementations alongside established reference methods.

Across countries, different methane metrics are used for breeding and management purposes: emphasis is on production-independent traits (e.g. efficiency or residual measures), and total methane production (g/day) and intensity (CH_4 per kg milk) are generally the most interpretable measures. Overall, current international implementations demonstrate multiple viable pathways for methane phenotyping in commercial dairy systems. The choice of method reflects national infrastructure, breeding objectives, validation status, and cost structure rather than a single universally preferred approach.

breed4green: First results from a dataset on methane emissions in commercial farms for genetic studies

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In the project breed4green, the genetic potential for reducing methane emissions and enhancing feed efficiency is investigated in Fleckvieh and Brown Swiss cattle.

Given the limited population size of these breeds, indirect traits are of special interest. Additional to the use of data from research stations, a comprehensive data recording concept was developed to measure methane emissions on commercial farms. Data from precision livestock farming systems, like daily milk yield, animal-based sensor data or feeding data are collected. The GreenFeed system and scales are moved between farms for measuring methane and body weight over two 6-week periods on each farm. Weekly milk recordings form the basis for mid-infrared predicted proxies for methane. Body condition, lameness, blood ketone tests, animal health records, hoof trimming data and detailed information on the rations fed are recorded throughout the study. Data recording on 30 farms will continue until 2027. Currently, analyses are available for 681 animals from 16 farms. Cows had a mean body weight of 717 kg and a daily milk yield of 30.8 kg. The mean methane emission measured in 76,982 GreenFeed visits was 431 g per cow per day. To encourage farmer participation, continuous feedback is provided, including reports on methane emissions, feed efficiency, body condition score, lameness score, and benchmarking analyses. The comprehensive dataset is used to investigate genetic relationships between feed efficiency, methane and carbon dioxide emissions, and additional selection traits. Indirect traits to predict methane production, energy balance, and feed intake suitable for integration in breeding programs are developed and validated, focusing on the potential of MIR-based estimators to reduce methane emissions and improve feed efficiency. The study shows that recording methane emissions using the GreenFeed system is feasible on commercial farms. Preliminary genetic analyses for methane emissions in Fleckvieh cattle, including variability between cows, trait correlations and heritability estimates, show promising results. Initial genetic analyses of the indirect traits estimated feed intake and residual carbon dioxide in Fleckvieh cattle suggest that the heritability is moderate. They also show promising correlations with actual and residual feed intake.

Building a Global Integrated Methane Data Ecosystem: Harmonizing Measurement, MIR, and Genomic Data to Accelerate Livestock Methane Mitigation

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Enteric methane mitigation in dairy and beef systems requires accurate measurement, scalable prediction tools, and coordinated global collaboration. However, current research efforts remain fragmented across measurement technologies, biological layers, and institutions, leading to duplication of work and inefficient use of resources. Our ongoing initiative builds on the foundation of the GEMS project (Accurate Gas Emissions Measures from Cattle with the GreenFeed System) by creating an integrated, international data consortium that harmonizes methane phenotypes with complementary biological and management datasets. The core objective is to (1) harmonize international methane measurement datasets to improve methodological standards and data comparability; (2) integrate mid-infrared (MIR) milk spectra and genomic data alongside methane phenotypes; and (3) develop standardized analytical pipelines that enhance predictive modeling and support genetic and nutritional mitigation strategies.

We are building a centralized, FAIR-compliant data infrastructure that aggregates high-resolution methane data measured using GreenFeed, respiration chambers, and SF6, together with animal performance, diet, MIR spectra, and genotypes. Standardized Data Usage Agreements (DUA), harmonized metadata templates, automated validation pipelines, and shared governance structures ensure secure and interoperable data exchange. About 50 organizations worldwide have expressed interest in contributing data. Within the first month of formal data collection, 10 organizations have signed the DUA, and around 50 studies are actively flowing into the data pipeline. Preliminary results demonstrate the feasibility of coordinated global data integration and reveal heterogeneity in measurement protocols, reinforcing the need for standardized processing guidelines. Early harmonization efforts have improved cross-study comparability and enabled expansion toward scalable methane prediction using MIR and genomic information.

Together, a unified global methane data ecosystem strengthens statistical power, reduces redundant research, and accelerates the development of dependable monitoring, prediction, and mitigation tools. This provides a scalable pathway to support evidence-based methane reduction strategies and long-term genetic improvement in livestock systems.

ORAL

Technical Session 10
Adoption and Incentives to Breed for Methane Mitigation

Challenges and options around incentivisation of genetic approaches to mitigation of methane emissions from ruminants

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Challenges and options around incentivisation of genetic approaches to mitigation of methane emissions from ruminants Genetic improvement offers a cost-effective, cumulative and permanent means of reducing methane emissions from ruminants. As with any other approach, such as anti-methanogenic compounds, achieving any change requires some form of practice change by farmers. For genetic approaches, the change is to breed and/or retain animals with superior genetic merit for methane emission. In modern breeding practice, decisions to select and/or retain animals are based on a breeding objective, where the relative weighting of traits in a selection index are usually determined by the expected economic impact of the trait improvement on system profitability. That implies a price can be applied to the estimate of genetic merit for the trait, with that price being the expected impact on income and or cost, ideally across the entire value chain at some point in the future. This is problematic because there is currently no widely accepted price on carbon. Accordingly, there is no clear incentive for farmers, including breeders, to account for methane in selection or replacement decisions. In the short term, this suggests the need for governmental and philanthropic initiatives, hopefully to reinforce private initiatives aimed at creating future market advantage. A second order challenge is to decide what form and where in the value chain to apply any incentive. Options include subsidisation of semen price, some form of credit to the farmer for methane-reducing actions, and market premiums for food ingredients or products with reduced methane footprint. Therefore a number of questions must be addressed:

- What value should be placed on lower than average emissions – essentially defining the carbon price?
- How to incentivize adoption - with cash, or some form of credit tradeable for something of value to farmers?
- Where in the value chain from production to retail to incentivise?
- How to determine the size of the incentive and potential incentive mechanisms -what to pay for and how? Building on approaches to these questions, we identify two crucial roles for national or international genetic evaluation services;

1) establishing the language or currency upon which incentives applied in a particular jurisdiction are based, and 2) potentially generating the metrics required as a routine service. Absent these roles, confusion and resulting lack of action seem inev

N/A

Towards guidelines to validate genetic evaluations for enteric methane emissions

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Enteric methane is a major contributor to agricultural greenhouse gas emissions and has become a major trait of interest for animal breeding in ruminants. Genetic selection offers a permanent, cumulative, and cost-effective mitigation pathway for reducing enteric methane emissions in ruminants. Therefore, genetic evaluations for enteric methane emissions are implemented, or will be soon, by organizations worldwide in dairy cattle, beef cattle and small ruminants. However, it is at an early stage, and approaches vary across breeds, species, regions, and production systems. Genetic progress depends on understanding associations between the phenotypic measurements, the genome and environmental factors. Therefore, harmonized protocols are needed to implement and validate genetic evaluations for methane emissions, maximizing the global impact of genetic selection for reducing enteric methane emissions.

Under the umbrella of the Global Methane Genetics (GMG) Initiative, this study aimed to map the current international status of genetic evaluations for enteric methane emissions across the three species. We surveyed five pillars: methane recording methodologies, SNP genotype data, genetic evaluation frameworks, publication rules of estimated breeding values, and statistical validation methods. Additionally, we reviewed state-of-the-art validation techniques applied to methane-related genetic evaluations, highlighting their limitations and proposing tailored adaptations for methane-specific contexts. Finally, we proposed a quantile-based validation approach to demonstrate the impact of genomic selection for reduced methane emissions, offering a clear statistical pathway to prove that the selection of animals with favorable breeding values results in measurably lower enteric methane emissions.

The findings from this GMG Initiative survey and the validation approaches will provide practical guidelines and validation protocols to support organizations in developing and validating genetic evaluations, ensuring genetic gain for reduced enteric methane emissions.

Approaching a crossroads in selecting for methane production: Trait definition and its consequences for breeding programs

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Genetic selection for lower methane emissions in ruminants is among the most promising climate change mitigation strategies in livestock, due to its permanent and cumulative impact. With implementation of large-scale methane recording in cattle and sheep under commercial conditions, robust phenotypic datasets are becoming available, enabling the estimation of breeding values for reduced methane emissions.

Methane production per animal may increase with higher milk or meat yield, because greater production requires higher feed intake. At the same time, methane intensity (e.g. g methane/kg milk or kg meat) typically declines as production increases, indicating improved “methane efficiency” at higher performance levels. These biological relationships create a crossroads for breeding programs: should selection target gross methane production, methane intensity or yield (g methane/kg dry matter intake) (ratio traits), or residual methane (the deviation from expected emissions given production and intake)? Ratio traits such as methane intensity or methane yield are attractive as indicators of environmental efficiency. They are positively perceived by farmers, as emissions are framed relative to productivity or feed use. However, selection on ratio traits is generally less efficient economically than direct selection on their component traits and may lead to unintended responses. Alternatively, selection indices can include linear functions of component traits (e.g. methane production, milk or meat yield, or feed intake) to achieve clearly defined and transparent breeding objectives. Theoretical frameworks exist to predict genetic progress and make adequate choices between these objectives. In this study, conducted within the Global Methane Genetics initiative, we compare alternative methane trait definitions and evaluate their consequences for selection response. Next to the methane trait, milk or meat production and a generalized health trait were included in the breeding goal to reflect producer-oriented efficiency and robustness. We further provide a SWOT analysis of different methane trait definitions, specifically considering their statistical properties, integration into selection indices, MRV readiness, and adoption potential within the sector.

The effect of including methane traits in selection indexes for ruminants

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Sustainable ruminant breeding programs increasingly incorporate methane emission traits into selection indexes. We compare indexes for dairy, beef and sheep.

A critical first step is clearly defining the breeding objective and the perspective from which it is optimised. For example, the global objective is to reduce methane emissions while maintaining a profitable and efficient animal production industry. Therefore, changes in methane emission must be evaluated against changes in output, implying an objective like methane intensity (methane produced per unit of product). Methane intensity is a ratio that can be improved by either decreasing the numerator (methane output) or increasing the denominator (production output). An optimal balance must be found between selecting for reduced methane and selecting for productivity and other economically important traits. Selecting on methane intensity as a ratio trait is undesirable as it complicates optimising economic response. We therefore recommend linear selection indexes that include component traits such as methane production, feed intake and production output. While the economic value of genetic changes in methane emission traits remains unclear due to lack of clear producer incentives, different selection strategies can be compared provided genetic parameters exist, including genetic correlations between methane traits and other breeding objective traits.

Comparing responses to selection on indexes for dairy, beef and sheep demonstrates that reducing methane per head is generally not desirable as it typically results in lower productivity, negatively impacting methane intensity improvement. Much of the improvement in methane intensity is achieved through productivity gains. The trade-off between improving productivity and curbing methane emissions depends strongly on correlations between methane output and productivity traits, which differ somewhat between species and production systems. We present various examples illustrating principles for achieving such balance in typical industry indexes across species.

Enabling adoption of methane-reducing breeding programs through GHG accounting and MRV frameworks

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Methane emissions from ruminants contribute significantly to global greenhouse gas (GHG) emissions. Genetic selection has proven effective in reducing enteric methane emissions, but achieving real-world impact requires widespread adoption. This study evaluates the role of GHG accounting tools and robust Measurement, Reporting, and Verification (MRV) frameworks in enabling methane-reducing breeding programs.

Drawing on expert interviews and a targeted literature review, it provides an overview of existing national and farm-level accounting tools, explores strategies for integrating genetic potential into these tools, reviews examples of MRV-linked incentive mechanisms in the livestock sector, and maps key stakeholder roles and engagement needs.

The study highlights actionable pathways for integrating low-methane genetics into GHG accounting tools, which allow for quantifying impact, identifying emission hotspots, and guiding practical reduction strategies on farm. When paired with MRV systems, these tools provide credible, verifiable estimates that support incentives such as carbon credit payments, supply-chain premiums, and regulatory compliance. At the outset of scaling low-methane breeding, measurable reductions can drive meaningful progress, providing proof of impact and momentum for the ruminant sector toward a low-emissions future.

Integrating Genetic Breeding Values for Enteric Methane Emissions into Carbon Accounting Frameworks

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Enteric methane emissions from ruminants account for 30–40% of global agricultural greenhouse-gas (GHG) emissions, representing a major challenge for livestock sustainability. Genetic selection offers a permanent and cumulative mitigation strategy due to moderate heritability of methane traits and favourable correlations with production efficiency. However, current carbon-accounting systems and IPCC-based calculators rely on population-average emission factors, failing to recognise animal-level genetic variation and thus limiting incentives to breed low-methane animals. This study proposes a methodology for incorporating genetic merit into emissions calculators and auditing systems within IPCC Tier 2 frameworks.

We review methane trait definitions (including gross methane production, methane yield, methane intensity, residual methane, and methane concentration) and evaluate multiple equations and implementation options. Practical considerations such as trait definitions, unit conversions, and adaptation to alternative national or mechanistic models are discussed, highlighting opportunities and challenges for international application. Using Canadian dairy data, we demonstrate the integration of a residual methane breeding value into Tier 2 calculations, showing approximately a 10% variation in estimated emissions across the current population. This framework aligns genetic merit with carbon accounting, enabling verification and incentivisation of genetic mitigation strategies. Broader adoption will require harmonisation of trait definitions, consideration of genotype-by-environment interactions, and compatibility across calculators and national inventories. This approach supports global efforts to integrate genetics into climate policy and provides a pathway for sustainable livestock production.

Economics of breeding schemes for improved methane efficiency in dairy cattle

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The objective of this project is to evaluate the economic and environmental impacts of various breeding schemes that include new methane efficiency traits at the dairy farm level.

Livestock is responsible for ~32% of anthropogenic methane emissions. Given the urgency in cutting methane from all sources, breeding for methane efficiency offers an additive and permanent solution to reduce methane from cattle. An estimated breeding value for methane efficiency in dairy cattle is already available commercially (e.g., in Canada by Semex; in the Netherlands by CRV). However, immediate adoption and uptake of the methane efficiency trait by dairy farmers is not guaranteed, especially because methane doesn't have an obvious economic value. In addition, long term economic impacts of breeding decisions at the farm level that incorporate the methane efficiency trait have not been evaluated. This evaluation is important to support the development of economic mechanisms to increase the emphasis of breeding for this trait by dairy farmers. We will evaluate 6 different breeding scenarios: 1) Maximizing the economic return using an existing economic selection index like Net Merit Dollars (NM$) which currently does not include a methane efficiency trait, 2) Maximum emphasis on a methane efficiency trait, thereby maximizing genetic progress in methane reduction but giving up some economic returns, 3) Four breeding scenarios in which breeding schemes are designed between the two prior extreme scenarios, in search of major progress in methane efficiency without giving up much on economic returns. We are creating a dairy herd simulation model able to calculate the impacts of these 6 breeding schemes on dairy farm profitability and methane production over multiple generations (30 years). From this, we will estimate the reduction in methane emissions at the cow and herd level over time. We will also calculate the cost per ton of methane reduced in each scenario. Genetic and phenotypic correlations between the methane efficiency trait and older traits like milk production and functional traits will be modeled using Semex and CRV data.

These results will support the development of an economic value for the methane efficiency trait to be incorporated in selection indexes, and the development of policies and market-based mechanisms to support adoption of this trait by dairy farmers.

Assessing Breeding Strategies to Mitigate Methane Emissions in Danish Dairy Cows

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Enteric methane from cattle is the largest agricultural greenhouse gas source in Denmark, and methane traits are heritable making selective breeding a potential mitigation strategy. In May 2025, the Nordic cattle evaluation released breeding values for methane for Nordic Holstein bulls, with Jersey and VikingRed indices expected in 2026. However, economic incentives remain unclear ahead of the planned 2030 CO_2 tax on livestock in Denmark. Uncertainty also persists regarding which methane trait to include in the breeding goal and the effect on the Nordic Total Merit (NTM). This study quantified expected methane reductions and correlated NTM responses when selecting alternative methane traits under different economic weights.

We simulated an open nucleus dairy cattle breeding structure with 20,000 cows across 200 herds and continued selection for 15 years. Each year, 2,000 young bulls and 8,000 heifers were genotyped. Genetic evaluation was performed using single-step genomic BLUP, combining phenotypic data from both genotyped and non-genotyped animals, and selection was based on genomic estimated breeding values (GEBVs). We selected 100 bulls (1–4 years old) with the highest GEBV for mating. The top 100 one-year-old females as multiple ovulation and embryo transfer (MOET) donors (elite bull dams) were mated to the selected bulls (5 matings per donor and two offspring per mating). The remaining 9900 females (1–5 years old) across herds were also used for reproduction. The breeding goal included two traits: milk yield expressed in kg energy-corrected milk (ECM) ($h^2 = 0.30$) and two functional trait ($h^2 = 0.04$), with a negative genetic correlation (rg = –0.30) with ECM. We evaluated the inclusion of three methane traits: Methane Production (MeP), residual methane (MeR), and a methane intensity (MeI), defined as CO_2e per kg ECM. Selection for lower MeI reduced methane emissions by up to 0.02 genetic standard deviation (SD) per year, depending on the applied economic weight, while largely maintaining genetic gain in milk yield (0.34-0.37 genetic SD) due to a favorable correlation between MeI and production. Direct selection for reduced MeP yielded a reduction of 0.01- 0.49 genetic SD but caused a marked decline in milk yield, reflecting the strong unfavorable positive genetic correlation (0.6) between MeP and milk yield. Selection on MeR achieved methane reductions like those from MeP selection but with limited impact on milk yield.

In conclusion, targeting MeP in breeding goals may reduce overall climate efficiency. In contrast, results suggest that MeR may be a more balanced and favorable trait for simultaneous improvement of methane emissions and production performance.

ORAL

Technical Session 11
Milk Recording Supporting Sustainability Initiatives

Farm sustainability index using dairy cattle recording data: the case of Slovenia

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Modern livestock farming faces numerous challenges, including rising input costs, climate change adaptation, environmental pollution mitigation, animal welfare concerns, and society's misunderstanding of the sector. These factors increase the need for optimisation and improved efficiency in milk production. Over the past 30 years, we have developed many tools to support various aspects of dairy cow health, production, reproduction, and nutrition to assist farmers. However, tools that directly incorporate sustainability are lacking. Such tools and decision support systems could provide farmers with additional information for decision-making.

We have developed a novel tool to monitor farm-level sustainability, based on data obtained during regular milk recording. All Slovenian farms in milk recording (~2,500 farms with an average of 29 cows per herd) were included in the project. We identified key areas of sustainability and selected appropriate indicators, which indicate: 1) risk of rumen acidosis; 2) risk of negative energy balance; 3) adequacy of nitrogen balance in the rumen; 4) milk production efficiency; 5) protein utilisation efficiency; 6) reproduction efficiency; 7) udder health; 8) percentage of cows culled due to reproductive disorders; 9) dairy cow longevity; 10) intensity of replacement heifer rearing; and 11) calf mortality. A sustainability index (12) combines information from all other indicators. In the next step, we performed a percentile ranking of farms within each indicator (1–11) and then within the sustainability index (12), encompassing all areas. A farm with the best sustainability index, for example, has a low somatic cell count index indicating good udder health condition, a long-lived herd with good fertility, low calf mortality, and a high percentage of protein utilisation efficiency, which indicates optimal herd management practices.

The developed tool supports comprehensive assessment of herd efficiency, enables comparisons between herds, identifies opportunities for improvement, and provides recommendations that adapt to farm results. This approach complements existing information already available to farmers, offers a tool for optimising production in line with sustainable farming practices, and can be applied to other populations under milk recording.

Combining milk recording and other on-farm data to streamline and improve greenhouse gas emissions

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Understanding farm-level emissions and scenarios for their reduction has become increasingly important. This may be due to national regulations and international market access agreements, brand claims of food businesses, or opportunities for farmers to benefit from industry or government incentives. A combination of animal registration and milk recording records and other farm data sources can dramatically reduce compliance effort for farmers and increase reliability of calculations.

Recognised greenhouse gas (GHG) emission calculations, particularly national-scale models, often have insufficient granularity to accurately represent dairy herd management practices, recognise improvements farmers are making, and provide farm-specific insight into mitigation options. Map of Agriculture gained farmer consent and used connected data from milk recording to populate mathematical calculators for GHG emissions, delivering insights to farmers and dairy processors.

This paper compares software, data capture, calculation, and insights activities undertaken for two dairy supply chains in the United Kingdom and Australia. Greater precision from connected data provides assurance for supply chains and can offer farmers insights into changes they may make while retaining profitability and productivity.

Variation of enteric methane intensity predicted from bulk tank milk in commercial dairy herds

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Enteric methane emissions account for approximately half the greenhouse gas emissions in Canadian milk's carbon footprint, highlighting the need to identify their main drivers to support effective mitigation strategies. This study aimed at describing the variation in enteric methane emissions on large scale on commercial dairy farms and identifying farm practices influencing herd-level emissions.

Herds were ranked on methane intensity (g CH_4 per kg of FPCM) predicted from bulk tank milk spectra collected throughout 2025 from 2,296 Quebec dairy herds. Details on the prediction model are presented in an accompanying abstract. Average methane intensity across individual bulk tanks was 14.9 g/kg FPCM (SD 1.40). Herd key performance indicators were extracted as herd averages from Lactanet (Canadian Network for Dairy Excellence) database. Feed records were collected for 402 herds. Datasets were aggregated with the respective yearly methane average. Univariate analyses were used to assess differences in herd performance across three levels of methane emissions, low (<14.0 g), intermediate (14.0-15.8 g) and high emitters (>15.8 g/kg FPCM).

Across the population, methane intensity differed among seasons (14.3 g in summer vs 15.4 g in winter), predominant breed (14.6 g for Jersey, 14.9 g for Holstein, 16.8 g for Ayrshire herds) and herd size (14.6 g for herds of 120 cows and more vs 15.1 g for herds with 60 cows or less). Herd performance was generally more favorable for low as compared to high emitters with, relative to high emitters, improved reproduction performance ($P < 0.001$; 118 vs 129 days open), transition management ($P < 0.001$; 206 vs −186 points on the transition management index), and health ($P < 0.001$; 154 vs 207 cells/μL and 1.2 vs 3.8% cows with BHB > 0.20 mmol/L). Low emitters tended ($P < 0.05$) to feed higher corn silage proportions (+9.7%) and had a higher ratio milk to concentrates (+0.3) than high emitters. Overall, low emitters had a 5 Can$ greater income over feed costs than high emitters. These results suggest that appropriate changes in herd management and best management practices recommendations can be effective in mitigating enteric methane emissions on farm.

Using Bulk tank Milk Spectra to Predict Enteric Methane Emissions from Lactating Cows in Commercial Dairy Herds

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Enteric methane emissions (EME) account for approximately 30% of global methane emissions. As a result, there is growing interest in monitoring EME using practical, scalable approaches to support mitigation strategies. The objective of this study was to predict herd-level EME using bulk tank milk samples.

Twenty-four methane sniffers were installed on 14 commercial dairy farms equipped with automatic milking systems across Quebec, Canada, starting in August 2024. The sniffers recorded CO_2, CH_4, airflow, humidity, and temperature every 1 second (1.102 billion records collected by December 31, 2025). Sniffer measurements were averaged by 10 seconds and matched to individual milkings for each cow and subsequently aggregated at the herd level. Because sniffer outputs were expressed in ppm, a transfer function (Madsen et al., 2010) was applied to convert methane concentrations into daily EME (g/day). To enable comparisons across farms, predicted EME were expressed as grams of CH_4 per kg of FPCM. A support vector machine model was developed using bulk tank milk spectra to predict herd-level EME (R2 0.72 and 0.55 RMSE 1.32 and 1.74 for training and test sets, respectively, RPD 1.6).

The model was applied to all 4,280 dairy herds in Quebec in 2025 (n= 718,184). The average predicted EME was 14.9 g CH_4/kg FPCM, with values ranging from 8.6 to 24.6 g CH_4/kg FPCM. The averages for summer and winter were 14.8 and 15.2, respectively. Hierarchical cluster analysis could discriminate between herds whose EME were predominantly either in the fourth or first quartile relative to the population, demonstrating the model's ability to discriminate between low and high emitting herds.To our knowledge, no previous studies have reported EME at the herd level. Therefore, model outputs were validated indirectly using cow-level estimates, which were consistent with values reported in the literature. The results indicate that the proposed model can effectively rank dairy farms according to their predicted EME. Such rankings may help identify management, nutritional, or environmental factors influencing EME in Canadian dairy herds.

BWYPEX Program Daily methane emission predicted from milk MIR spectra: the time of model comparison

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Since 2011, the potential to estimate individual enteric methane (CH4) emissions based on the milk MIR spectrum of milk has been highlighted. Various methane prediction equations have been developed worldwide by different scientific teams. Most of these models rely on CH_4 reference data collected with the GreenFeed system (C-Lock Inc.) and are generally built using datasets generated within their own countries, often reflecting specific local conditions such as breeds, feeding systems, and management practices. In parallel, one international equation has also been developed through collaborative work aimed at merging reference data across countries; it is based on CH_4 measurements obtained using both the SF_6 tracer technique and respiration chambers, combined with standardized milk MIR spectra (European Milk Recording technique). This equation integrates reference data from seven countries.

In the framework of BWYPEX, it has been possible to meet different research teams measuring CH_4 emissions and having access to milk MIR spectra. These exchanges provided the opportunity to better understand how existing equations have been developed, how future equations are planned to be constructed, and how they are intended to be applied in practice. It became clear from these discussions that prediction equations have been developed using diverse methodological approaches, and that their final objectives and conditions of use vary considerably from country to country. After discussing with the various collaborators, interest has emerged in applying the different CH_4 prediction models available to a strictly identical spectral database. This database will consist of anonymized Holstein milk MIR spectra from different countries. The aim is to investigate the consistency of the predicted CH_4 values across equations, for example whether cows identified as high CH_4 emitters by one model are also classified as high emitters by the other models, and to evaluate the overall agreement and divergence among predictions.

This work is currently underway, and additional collaborators interested in sharing spectral data or in applying their own CH_4 prediction equations to this common database are warmly invited to participate.

Beyond milk collection: Can Indonesian dairy cooperatives lead the sustainable record-keeping transition?

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The study aims to assess cooperatives' capacity to enhance farmers' record-keeping as a pathway to supporting sustainability initiatives in the Indonesian smallholder dairy sector. We identify the cooperatives' roles particularly in record-keeping practices, and explore the challenges encountered. Despite their close relationship and regular interaction with the farmers, Indonesian dairy cooperatives have not yet fully realized their potential to transform record-keeping practices.

The study involved five dairy cooperatives located in Bandung, Bogor, Boyolali, and Malang. Data collection combined a questionnaire survey of 80 farmers, farm observation of 10 farmers, and in-depth interviews with 12 stakeholders representing cooperatives, milk processing industries, farmer associations, government, and universities. Data were analyzed using descriptive statistics, percentages, multiple response analysis, and multinomial logistic regression. Qualitative interview transcripts were coded through thematic analysis. To map its influence in record-keeping practices, cooperatives' positions were classified using a power interest matrix. Building on this classification, fuzzy logic analysis was then implemented to assess stakeholder salience by identifying the relationship between power and interest and illustrating it through a fuzzy logic decision surface.

All cooperatives involved in this study provided record-keeping facilitation for their farmers, but the data collected still focused on bulk milk sales per farm rather than performance data such as milk production per animal or reproduction indicators (insemination dates, pregnancy results, calving records, etc.). Two out of five dairy cooperatives have already implemented digital record-keeping. The results from the power-interest matrix showed that cooperatives are positioned as key players that have high interest and high power. In addition, the fuzzy logic decision surface illustrated that the cooperatives have high power (4.13/5), interest (4.36/5), and salience (4.27/5). Nevertheless, the findings from the thematic analysis revealed that cooperatives face challenges with technical capacity for livestock data management and insufficient infrastructure resources. Realizing this potential, even though cooperatives are well positioned to drive improvement, requires technical capacity building in livestock data management, better infrastructure, and a commitment to reorienting record-keeping practices not only for transactional but also for breeding-oriented data that support farm sustainability.

ORAL

Technical Session 12
M Part 1: From Guidelines to the Barn: Implementing section 2 of ICAR's Milk Recording Guidelines – Updates and Lessons from the Field

Part 2: Buffalo DHI recording

A flexible non-parametric approach to assessing dairy cow performance

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A key data-driven insight supporting farm decision-making is the ability to compare milk-yield performance across individual cows within a herd. To derive meaningful performance measures, milk yield must be adjusted for systematic influences such as age at calving, calving season, lactation stage, and herd-level effects. However, even in large milk-recording datasets, stratifying by these variables often creates pockets of sparse data, making it difficult to derive robust and accurate adjustments across all stratifications. This research aims to develop a flexible, scalable framework that can model lactation curves reliably across both densely and sparsely observed stratifications.

To achieve this, we apply a stochastic variational Gaussian process (SVGP). A SVGP learns underlying lactation curve structure from data-rich regions and balances these with observed data to produce stable predictions in sparsely observed regions. This Bayesian trade-off between data fit and prior patterns generates smooth, biologically grounded lactation curves across all stratifications, supporting fair and interpretable cow-level comparisons. We trained the SVGP on approximately 16 million test-day milk yield records collected over three years from dairy herds across the Netherlands. All the records contained information about age at calving, calving season, lactation stage, and herd-level management metrics. These systematic variables were included as covariates. Model performance was assessed through predictive accuracy on held-out records and by inspecting the stability of this accuracy across regions with varying degrees of data density. We also inspected fitted curves across ages, seasons, and herd-level metrics to verify smoothness, biological plausibility, and stability in data-sparse regions.

The SVGP generated smooth, biologically consistent lactation curves and delivered stable estimates across stratifications with differing levels of data density. The SVGP scales efficiently to large-scale milk-recording datasets and provides a strong foundation for fairly adjusting milk yields.

A unified Python implementation of standardized 305 day yield calculation methods

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The 305 day yield for milk, fat, and protein is a widely used metric in dairy production, and the International Committee for Animal Recording (ICAR) provides guidelines outlining approved methods for its calculation. However, a global survey of milk recording organizations revealed substantial variation in how these methods are implemented. The Test Interval Method is used by 74% of the organizations, reflecting a preference for methodological simplicity, but it comes with trade-offs in estimation accuracy. The use of the other approved methods showed wide variation in correction factors, standard lactation curves, test day definitions, minimum sample requirements, and exclusion criteria. Such inconsistencies can introduce yield variability that complicates comparisons, for example in international breeding value evaluation, and limit the metric's usefulness in universal models, such as decision support tools. Thus, the objective of this work was to reformulate the ICAR guideline section 2, procedure 2, into a unified, transparent, and accessible software implementation to improve standardization, enhance documentation, support continuous development, and increase the accuracy of 305 day yield estimation.

To achieve this, the ICAR guideline was converted into an open source, Python package that serves as the reference implementation for 305 day yield calculation, with lactation curve modelling serving as the core of the package. In addition to the methods described in the original guideline, this work further incorporates 13 lactation curve models, with both frequentist and Bayesian fitting options, and provides tools to derive characteristics such as time to peak, peak yield, cumulative yield, and persistency. These features allow the package to be imported directly into analytical workflows, enabling users to calculate 305-day yields, fit and compare lactation curves, and derive key lactation characteristics, by calling a single function. Ongoing development includes an online validation platform that will allow users to upload lactation data and compare 305 day yield estimates with reference calculations and observed cumulative yield.

Opportunities and challenges in accurate milk recording on farm in the United States

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In this paper we describe the changing dairy landscape in the US, including adoption of new on-farm technologies and the subsequent evolution in milk recording that we are observing.

There is monumental variation in what dairying looks like in the United States. Dairy herds range in size from small family farms (<50 cows) to large enterprises milking 10,000+ cows in multiple locations. They operate in vastly different climate conditions, use different levels of technology, have multiple dairy breeds, are influenced by different subcultures, and farmers are paid on different milk pricing schemes. With such variation in dairy practices, it's challenging to apply a "one size fits all" solution to accurate milk recording while maintaining efficiencies and minimal disruptions to on farm management. Yet, in any system, high quality information services begin with accurate data entry on the farm. In this paper we describe the changing dairy landscape in the US, including adoption of new on-farm technologies and the subsequent evolution in milk recording that we are observing. Serving the diverse needs while at the same time addressing a shortage in labor requires new solutions to facilitate accurate and efficient milk recording on farm. One such solution is in automating data entry on a test day and employing new technologies that minimize the need for manual or handwritten data entry, reducing labor costs and human error while minimizing disruption of farm operations. These automated methods will become increasingly important as herd size in the US continues to increase and we see more complicated milk testing plans emerge – herds that only test part of their herd, or herds that are managed as a group but located across multiple milking sites with different parlor types, or herds that have milking strings that are milked on different frequencies. Education and outreach of farm owners, herd managers, and DHI technicians will remain critical to adapting existing milk recording systems to changing dairy practices.

The Genetic Transformation of the Italian Mediterranean Buffalo: Five Years of Progress and New Frontiers

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The objective of the present study is to describe and analyze the principal structural and methodological changes that have characterized the IMB genetic improvement program over the last five years, highlighting the transition from genetics to genomics and outlining the new frontiers shaping the future of this globally relevant dairy breed.

Over the last five years, the Italian Mediterranean Buffalo (IMB) breeding program has undergone a profound genetic transformation driven by the integration of genomic technologies and the development of new selection indices. The present study describes the structural and methodological changes implemented within the national genetic program. Genetic evaluations transitioned from pedigree-based BLUP models to a single-step genomic BLUP (ssGBLUP) framework, integrating pedigree, phenotypic, and genomic information within a unified evaluation system. The adoption of genomic evaluation improved the reliability of estimated breeding values for production and morphological traits and supported the implementation of the Genomic Italian Mediterranean Buffalo Index. Between 2021 and 2025, the breeding objective was further expanded through the development of 23 additional indices encompassing reproductive efficiency, animal welfare, sustainability, and disease resistance. Heritability estimates for these functional traits ranged from low to moderate, indicating exploitable genetic variability despite the complexity of these phenotypes. This strategic shift reflects a transition from production-centered selection toward an integrated and sustainability-oriented breeding framework. The IMB program now represents one of the most advanced buffalo genetic systems worldwide, demonstrating how genomic integration can accelerate genetic progress while aligning animal production with long-term efficiency, resilience, and environmental responsibility.

Over the last five years, the Italian Mediterranean Buffalo breeding program has undergone a substantial genetic transformation driven by the integration of genomic evaluation into the national selection scheme. The implementation of ssGBLUP improved the reliability of estimated breeding values and enabled the transition from a pedigree-based framework to a genomic-oriented strategy. This methodological advancement supported the development of the Genomic Italian Mediterranean Buffalo Index and strengthened the capacity for early and more accurate selection decisions. The breeding objective was structurally redefined through the introduction of 23 additional indices encompassing reproductive efficiency, animal welfare, environmental sustainability and disease resistance. Although many functional traits exhibit low to moderate heritability, their inclusion within a genomic multi-trait framework allows balanced and cumulative genetic progress. This multidimensional approach positions the Italian Mediterranean Buffalo breeding program among the most advanced buffalo genetic systems worldwide and establishes a forward-looking model aligned with sustainability, resilience, and long-term productivity goals.

Bayesian Modeling of Lactation Curves in Italian Mediterranean Buffalo Using the MilkBot Equation

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Italian Mediterranean buffalo dairy farming is a key component of the agricultural economy of Southern Italy. Although several quantitative approaches have been applied to describe buffalo lactation dynamics, the adoption of biologically interpretable models remains limited. The MilkBot model offers a mechanistic representation of lactation development, but its application to Italian Mediterranean buffalo has been hindered by the lack of species and parity-specific priors. The aim of this study was to derive and validate parity-specific Bayesian priors for the MilkBot model in Italian Mediterranean buffalo using a large-scale field dataset.

Test-day milk yield records collected between 2018 and 2023 from routine milk recording schemes were analyzed, comprising 403191 observations from 92427 animals across 328 herds. Data were stratified into two parity groups: primiparous and pluriparous. The observations were split into 80% training and 20% testing sets using a herd-level partitioning strategy, ensuring that no herd was represented in both subsets and thereby preventing data leakage. A Bayesian framework was implemented to estimate the parameters of the Milkbot lactation model. Informative priors derived from Irish dairy cows were specified for each model parameter and updated using the train data using a Hamiltonian Monte Carlo algorithm. Four parallel chains were run for each parity group and convergence diagnostics indicated adequate mixing and stable posterior distributions. Posterior distributions were used to obtain the most probable values, which were subsequently applied to predict mean lactation curves and evaluate predictive performance on the independent testing set. The fitted curves closely captured milk yield dynamics throughout lactation across all parity groups, with discrepancies observed during the descending phase of lactation in multiparous animals. Model performance metrics indicated high predictive accuracy for both parity groups, with R^2 values ranging from 0.95 to 0.96, RMSE from 2.57 to 3.23 and MSE from 6.63 to 10.47.

These findings demonstrate that, when supported by appropriately informed priors, the MilkBot equation represents a reliable and biologically meaningful tool for modelling lactation curves in Italian Mediterranean buffalo.

Analyzing milk recordings to support better decision-making through AI: a case study in Italian Mediterranean Buffalo

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Nowadays, the modernization of breeding techniques is essential to enhance productivity and management efficiency. Precision Livestock Farming (PLF) represents a key approach for collecting and analysing herd data through Machine Learning (ML) and Artificial Intelligence (AI). While PLF systems are widely implemented in dairy cattle, their application in other species, such as buffalo, remains limited. One of the main barriers to the adoption of advanced PLF technologies is farmers' difficulty in understanding AI driven processes and properly interpreting model outputs. To address this challenge, a case study in the buffalo sector was developed by Logogramma using AI.CODIUM®, a proprietary platform designed to enable effective human–machine interaction.

The system has been already tested on a single buffalo herd within The BufalaCare project, developed under the framework of RESTART and through collaboration with the 5G Academy at the University of Naples Federico II. In this context, the overall system demonstrated suitability for: (i) Collecting human observations and integrating them with data from external sources such as farm sensors, cameras, scales, and tags. This enables the tracking of each buffalo's wellness history, group affiliation, insemination records, or human diagnosis; (ii) Processing natural language requests via a voice assistant, generating context-based responses derived from the knowledge graph; (iii) The platform integrates heterogeneous data into a unified system, giving farmers a reliable decisionsupport tool with a comprehensive overview of production, reproduction, and herd health. Users can query the knowledge graph in natural language and instantly access relevant information in text or visual formats. Starting from this experience, the aim of the study is expanding the system using information on milk yield, milk quality and reproductive information of 329 herds with 130,531 Italian Mediterranean buffaloes and 1,957,430 milk records collected over ten years (2013–2023). All data are structured within a unified knowledge graph powered by AI.CODIUM®, enabling advanced analytics and predictive modelling based on AI and Deep Learning techniques. The system streamlines the consultation and aggregation of data, fostering best practices, reducing observation time for farmers while delivering valuable support to breeder associations and regional stakeholders.

Evaluating the Robustness of Cumulative Milk Yield Estimation Methods under Limited Test-Day Availability in Italian Mediterranean Buffalo

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Buffalo milk recording systems often provide only a limited number of test-day measurements per lactation. In particular, test-day control, in Italy, are performed approximately once per month, for a total of about nine controls per lactation. At same time, it is essential obtain an accurate estimation of total milk yield for herd management and breeding decisions. The aim of the study was evaluated the performance of three approaches: the Test Interval Method (TIM), the Wood model, and the MilkBot model in reconstructing cumulative milk yield up to 270 days in milk (DIM) using a fixed number of evenly spaced test-day observations.

The dataset included 329 herds comprising 130,531 Italian Mediterranean buffaloes and 1,957,430 daily milk records collected over ten years (2013–2023). For each parity group (1, 2, ≥3), observed cumulative milk yield up to 270 DIM was calculated from the full set of daily records as a gold standard. To simulate routine monthly recording, nine test-day points per parity were selected (DIM = 5, 35, 65, 95, 125, 155, 185, 215, 245). These same nine DIM and milk yield records were used for all three methods. TIM reconstructed cumulative milk yield by applying the trapezoid rule between consecutive records, while Wood and MilkBot estimated model parameters using these DIM, with optimization starting values defined by the fitting package. Results showed that TIM slightly overestimated cumulative milk yield at 270 DIM (+2.03 to +1.21%), while Wood and MilkBot tended to underestimate it (−2.13 to −6.57%).

This indicates that, under regularly spaced monthly test-day coverage, TIM can provide reliable cumulative milk yield. Wood and MilkBot, according to parity order, also returned consistent values offering, at same time, additional insight into the shape of the lactation curve (e.g., peak yield, time to peak, persistency). Future work could explore the performance of these methods under alternative test-day recording schemes and more irregular data patterns.

Phenotypic variation of milk antioxidant activity in Italian Mediterranean buffaloes

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This study evaluated the phenotypic variation of milk antioxidant activity in 849 Italian Mediterranean buffaloes using Total Antioxidant Capacity (TAC), and Ferric Reducing Antioxidant Power (FRAP).

Data were collected from 19 farms in Southern Italy, between December 2021 and December 2023. They included animal characteristics, milk quality traits, and the chemical composition of the diets provided to the animals. At each farm, visits were scheduled in advance to ensure that the sampled animals were balanced in terms of DIM and parity. Linear mixed models were applied to assess the effect of parity, sampling season, milk production level, days in milk (DIM) and farm on TAC and FRAP. Since farm significantly contributed to TAC and FRAP variability ($P<0.05$), we investigated whether dietary composition could partially explain this effect. Two Random Forest classification models were developed separately for TAC and FRAP. Animals were ranked according to their phenotypic values of TAC and FRAP, and the 100 highest and 100 lowest individuals for each trait were selected to define high and low antioxidant activity classes, respectively. Chemical dietary variables were then used as predictors in the classification models and variable importance was evaluated using the Mean Decrease Gini (MDG).

Neither TAC nor FRAP differed across parity, sampling season or milk production classes ($P>0.05$). In contrast, DIM significantly affected TAC, which increased from 149 to 163 nmol/Trolox as lactation progressed. Classification accuracy of random forest model was 0.80 for FRAP and 0.78 for TAC. Acid detergent fibre exclusive of ash (ADFom) and cellulose were the most relevant dietary variables influencing both TAC (MDG=2.61 and 2.59) and FRAP (MDG=3.88 and 2.88). Overall, milk antioxidant activity was primarily associated with farm-related effects rather than intrinsic animal characteristics. The variability explained by farm and dietary fibre fractions suggests that TAC and FRAP can be influenced by nutritional and management factors that can be considered as valid approaches to act on the antioxidant capacity in Italian Mediterranean buffaloes.

ORAL

Technical Session 13
Exploring Current and Future Needs for the Livestock Science and Farming Community

How does rate of genetic gain impact economic optimum productive life?

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Understanding the drivers of economic optimum productive life in dairy herds is important. Previous research suggested the increased rate of genetic gain due to genomics has reduced optimal productive life by several months. We hypothesis that given the rate of genetic gain in Australian Holstein herds is up to $142/cow/year (0.8 standard deviations index units; SD index), the impact of genetic gain on optimal productive life may be greater than previously stated. This study aims to test this hypothesis.

Summary statistics of the rate of genetic progress for Australian Holsteins (born 2019-2023) were calculated across and within herds using data obtained from DataGene. Microsoft Excel was used to deterministically model a dairy herd from lactations 1 to 10, alongside key financial inputs. Five-year average farm financial data (n = 1190 herd-years) were compiled and used as model input. Opportunity costs considered were cost of rearing replacements minus cow salvage value, reduced profit of lactation 1 and 2 animals, reduced profit and higher costs in lactations 6+, loss of income from calves needed as replacements. Adjustments reflecting that voluntary culling each lactation increases superiority of older animals and genetic gain increases profit potential of young animals were also modelled. Optimum productive life was the point where profit (earnings before interest and tax, EBIT, $/cow/year) was maximised. Sensitivity analyses were undertaken of key parameters.

Economic optimum productive life occurred at 3.6, 3.4, 3.4, 3.2 and 3.1 lactations at genetic gain of $0, $15, $40, $65 and $100/cow/year, respectively. For all rates of genetic gain, EBIT changed by less than $11/cow/year when voluntary culling was varied ±4% of where optimum productive life occurred. As part of this work, we looked at the individual impact opportunity costs and adjustments had on EBIT. At Australia's average replacement rate (0.24) and genetic gain ($40, 0.22 SD index), genetic gain had most influence on EBIT adjustments. While at $15/cow/year genetic progress, it had the fourth largest influence. While rate of genetic progress and sensitivity analyses of key input influenced optimum productive life, at most ½ lactation variation was seen. This suggests a range of voluntary culling rates for which productive life is nearly optimised. Considering across herd variation, not just national averages, helps ensure conclusions are relevant to widest audience possible.

European Network on Livestock Phenomics (EU-LI-PHE): an international initiative aimed at facilitating the application of phenomics in animal breeding

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Phenomics is an emerging field in applied biology, including animal husbandry and breeding, that aims to comprehensively characterize the phenome, defined as the full set of physical and molecular traits of an animal. It involves diverse methods and technologies to collect, analyze, and use high-dimensional phenotypic data at the whole-animal level. In livestock production, accurate phenotypic data support the definition of breeding goals, improve selection programs, and guide management decisions related to reproduction, health, and welfare. Consequently, phenomics is increasingly viewed as a key driver of sustainable animal production. The scale and complexity of phenotyping data place phenomics within big data science, requiring advanced analytical methods. Precision livestock farming (PLF) technologies have improved monitoring of health, welfare, and performance, though robust farm-ready solutions across species remain challenging. There is strong overlap between PLF and breeding phenotyping approaches. The European Network on Livestock Phenomics (EU-LI-PHE, COST Action CA22112) promotes interdisciplinary collaboration and training through four thematic working groups and one cross-cutting group.

Several key challenges in livestock phenomics research and innovation remain largely unaddressed or only partially resolved. These challenges are organized into four main thematic areas, which correspond to the working group (WG) structure of the EU-LI-PHE COST Action: WG1, Phenotyping technologies; WG2, Genome-to-phenome integration; WG3, Computational resources and data analysis methodologies; WG4, Economic impact, regulation, policy, and societal aspects. In addition to these four technical pillars that form the scientific foundation of the initiative, a fifth working group, WG5 (Stakeholder engagement, communication, and dissemination), plays a cross-cutting role within EU-LI-PHE.

EU-LI-PHE encompasses approximately 500 WG members from over 50 different countries, who are experts in a variety of disciplines. The limited availability of high-quality phenotypic data is a key bottleneck in animal breeding. The European Network on Livestock Phenomics (EU-LI-PHE) brings together multidisciplinary experts to foster collaboration, innovation, and training in this field. It aims to advance phenotyping tools, integrate genomic and phenomic data, develop analytical resources, address ethical aspects, and support sustainable, competitive livestock production.

Developing a Genetic Submodule in the Ruminant Farm System (RuFaS) Model for Enhanced Whole-Farm Representation

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Genetic improvement is a central driver of long-term productivity and sustainability in dairy systems. However, whole-farm models often represent animal performance without explicitly accounting for genetic merit. This study addresses this gap by developing a genetic submodule for the Ruminant Farm System (RuFaS) model. The objective was to link animals' genetic merit with phenotypic performance and herd-level decisions, enabling realistic evaluation of genetics-driven strategies.

The submodule generates biologically consistent phenotypes by integrating true breeding values (TBVs), estimated breeding values (EBVs), and environmental effects. Fat and protein yields (kg per 305-d lactation) were selected as prototype traits. TBVs were simulated from a bivariate normal distribution with nationally reported genetic variances and correlation of 0.59. Permanent (Ep) and temporary (Et) environmental effects were simulated from zero-centered normal distributions. Phenotypes were calculated as $P = \mu + TBV + Ep + Et$, where μ is the farm mean, Ep captures lifetime environmental effects, and Et represents lactation-specific effects. EBVs were generated from TBVs with accuracies updated across life stages (0.75 to 0.90 with genotyping). Genetic transmission to offspring was modeled by averaging parental contributions and incorporating Mendelian sampling variance, enabling simulation of genetic progress over generations.

The integrated genetic submodule will enable the RuFaS model to evaluate genetics-driven management strategies, including selection-based breeding, culling, and beef-on-dairy programs, within a whole-farm framework. By quantifying economic, genetic, and environmental trade-offs, this work is able to address a critical future need in livestock science: moving beyond siloed analyses toward a holistic assessment of how genetic improvement influences long-term farm sustainability and profitability.

ICAR/IDF Sensor Initiative: Guidelines and reference standards for using rumination sensor data in animal health and welfare assessment

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The increasing availability of data from on-farm sensor systems provides new opportunities for genetic evaluation and assessment of animal health and welfare across the dairy value chain, thereby enhancing transparency and sustainability in the dairy sector. The joint ICAR/IDF Sensor Initiative aims to develop harmonized guidelines that facilitate the effective use of sensor-derived data for improving animal health and welfare.

- The initiative brings together experts from the ICAR Functional Traits Working Group and the IDF Standing Committee on Animal Health and Welfare, representing key stakeholders from academia, breeding organizations, and the dairy industry. Its objectives are to develop and reach consensus on:
- Standardized definitions and terminology for health conditions and behavioral traits derived from sensor-based indicators;
- Data exchange standards that support interoperability along the dairy value chain, aligned with recognized ICAR and IDF principles;
- Guidelines for best practices in data collection, processing, and analysis to support genetic evaluations and health and welfare assessments;
- Recommendations and protocols for evaluating and validating sensor performance. To ensure relevance and facilitate implementation, the core group has established a dedicated forum with sensor technology providers.

This platform enables discussion of results, refinement of proposals, and alignment with stakeholder needs. Init

BROMEDIR - PART A: Development of a miniaturized FT-MIR instrument for in-farm milk analysis

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Portable infrared spectroscopic sensing platforms enable rapid, on-site chemical analysis without centralized laboratories. Analysis of individual cow milk samples is used by many milk recording organizations around the world for cow management. However, milk recording is classically organized every 4 to 6 weeks in farms, while to enhance the capacity of analysis to be used for precision livestock farming (e.g. for early detection of diseases…), the frequency of analysis should be increased. A potential solution to achieve such high frequency measurements is to bring the spectroscopic sensing platform directly to the farm to enable daily analyses.

Micro-electromechanical systems (MEMS)-based Fourier Transform Infrared (FTIR) spectrometers show significant promise for portable analytical instrumentation. Existing miniaturized systems face a critical limitation: their operational spectral range remains limited to the near-infrared (NIR) region, with the widest achieved range only marginally reaching the periphery of molecular fingerprint region's in the mid-infrared (MIR). This work addresses this fundamental constraint by presenting a highly miniaturized, fully integrated MEMS-based FTIR device that dramatically expands spectral coverage throughout the MIR molecular fingerprint region, achieving an ultra-wideband range from 5000 to 1000 cm^{-1}. The very broadband spectral range results from an all-silicon MEMS chip design utilizing free-space light propagation, combined with novel light coupling via micro-optical reflective mirrors. This configuration avoids light propagation through absorptive materials, with silicon being nearly transparent across this broadband range.

The developed system significantly expands spectral coverage into the MIR molecular fingerprint region, overcoming a key limitation of existing miniaturized spectrometers. This achieved with remarkably high a signal-to-noise ratio (SNR) exceeding 5000:1 and spectral resolution reaching 42 cm^{-1} in 10 seconds enabling accurate milk parameters predictions. This extended spectral range captures more characteristic absorption features, facilitating precise molecular identification and accurate quantitative analysis for different milk parameters. This approach would open great potential of the MEMS-based FT-MIR milk analysis (e.g. fine milk quality and health of cows, among other) in the farm.

BROMEDIR - PART B : Evaluation of a miniaturized FT-MIR instrument for in-farm milk analysis

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Mid Infrared (MIR) analysis of milk is a powerful technology to predict a wide range of phenotypes related to fine milk composition, cow health, nutrition and environmental footprint. MIR analysis of individual cow milk samples is used by many milk recording organizations around the world for cow management. However, milk recording is classically organized every 4 to 6 weeks in farms, while to enhance the capacity of MIR analysis to be used for precision livestock farming (e.g. for early detection of diseases…), the frequency of analysis should be increased. A potential solution to achieve such high frequency measurements is to bring the MIR spectrometer directly to the farm to enable daily analyses. The BROMEDIR project aims to fill this gap by developing a portable miniaturized spectrometer operating in a very wide spectral range (5000-1000 cm-1), dedicated among other applications to milk analysis. Thanks to the recent technological miniaturization advances, a prototype was developed to meet dairy stakeholders' requirements and affordable cost

The objective of this work is to develop and assess the performance of the miniaturized portable MIR spectrometer in milk application. The instrument is evaluated, among other criteria, based on the general spectral pattern, the practical signal to noise ratio, the repeatability and reproducibility over time of both the spectral response and the main milk components. The accuracy of the spectrometer to predict the main milk components is evaluated against benchtop predictions after the analysis of 50 raw milk samples from individual cows. Finally, the possibility to transfer existing MIR models is assessed through PDS standardization of the BROMEDIR spectrometer against benchtop instruments.

This approach would open great potential by enabling the use of past developments within the FT-MIR milk analysis framework (e.g. fine milk quality and health of cows, among other).

Transforming routine MIR milk data into actionable tools for Dairy Herd Improvement and cheese production

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Cheese-making properties (CMP) strongly depend on milk composition, which is partly genetically determined. The FROM'MIR programme (2015–2019), conducted in the Montbéliarde breed, demonstrated the feasibility of using routine milk mid-infrared (MIR) spectra to predict CMP related to milk coagulation and cheese yield (El Jabri et al., 2020), and to develop associated genomic evaluations (Sanchez et al., 2022). Building on these results, the FROM4ALL project, launched in 2024, extended this approach to eight French dairy breeds. The FromACT project now aims to implement MIR equations and genomic indexes at a large scale to support Dairy Herd Improvement (DHI) and sustainable milk and cheese production systems.

Prediction equations for seven CMP- three cheese yield traits and four coagulation parameters predicted from MIR spectra (two related to soft cheese and two to cooked pressed cheese technologies) - were developed and validated under laboratory conditions. Large-scale MIR datasets from routine milk recording were used to assess robustness across breeds and production contexts. Genetic parameters were estimated using more than 50 million test-day records from 1,699 to 1,141,657 primiparous cows depending on the breed, applying linear mixed repeatability models. In parallel, multi-stakeholder consultations were conducted in four French regions with strong cheese-making traditions to identify field needs and expectations.

Heritabilities of MIR-predicted CMP were moderate to high (0.26–0.49, except for one trait whose equation is much less accurate) and consistent across breeds, confirming their suitability for genomic evaluation. CMP indexes are already integrated into Montbéliarde breeding programmes, while pilot single-step genomic evaluations are under development for seven MIR-predicted CMP. These results illustrate how routine milk spectral data can be transformed into operational indicators for DHI, linking milk production, genetic improvement and cheese processing. Future developments will focus on strengthening information systems and developing advisory and training approaches to facilitate dialogue between farmers, advisors and processors and improve the sustainability, efficiency and competitiveness of dairy production systems and cheese value chains in France.

HerdPlanner: model-based tactical decision support for reproduction and culling

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Farm size restrictions can be physical (e.g. nr. of cubicles) or environmental (e.g. available space in nitrogen, phosphate or CO2 emissions). Optimal utilization of the available space is needed to maximize profitability, for example by having the right balance between youngstock and milk producing cows. Since there is an almost three year delay between the insemination decision and the start of the resulting heifers' lactation, this is a hard to control process. With 'HerdPlanner' we support the farmer in making decisions to optimize the herd composition within spatial and environmental constraints by guiding individual cow insemination and culling decisions.

In three workshops with in total 29 farmers from across the Netherlands and Flanders, topics such as insemination decisions, voluntary/forced culling and herd composition where discussed. Based on these farmers' feedback, a phased development of the 'HerdPlanner' was formulated. In phase one we focus on advising on inseminations, both at individual and at herd level. Individual insemination advice is based on the (expected) performance, lactation stage, expected dry-off yield, health state and genetic makeup of an animal. The advice varies between 'inseminate', 'wait' or 'do not inseminate'. At a herd level, the advice specifies how much to inseminate with sexed, conventional or beef-on-dairy semen in a 21-day period, in order to achieve the number of heifer calves that are needed to keep the herd on level. HerdPlanner advices are provided to farmers via an experimental module 'AI Lab' in CRV's farm management software. AI Lab collects feedback on both contents and presentation form, such that the tool can quickly be optimized to have maximal value for the farmer. In the second phase we will focus on culling advice based on individual-cow (expected) economic performance.

The tool is evaluated with quantitative and qualitative feedback collected at approximately 50 farms over several months. With HerdPlanner, we provide farmers with valuable decision support for optimizing their herd composition.

Reimagining Animal Identification: Ireland's Progress Towards a Fully Genotyped National Herd

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Genotyping calves at birth enhances traditional identification systems by providing a unique biological identifier for each animal and by enabling verification and corrections of parentage, sex, and breed details supplied before the registration is complete. The cumulative benefits of a fully genotyped national herd present a major opportunity for Irish agriculture, with estimated returns of up to 4:1 on investment (AbacusBio, 2022) predominantly as a result of increased productivity due to more informed breeding decisions.

Administered by the Department of Agriculture, Food and the Marine (DAFM), Ireland's Animal Identification and Movement System (AIMS) requires all bovine animals to be tagged with national EID identity tags and registered on the AIMS database within 27 days of birth. Launched in 2023, the National Genotyping Programme (NGP) is a collaborative initiative involving ICBF, DAFM, and industry stakeholders, and participating farmers. The programme operates on a co-funded model, with each the Government, Industry, and farmers contributing €6 per calf (€18 Total). To date, over 18,600 herds representing more than 1 million cows (Half the national herd) have enrolled voluntarily. Since its launch, over 1 million cows and breeding animals in NGP herds have been genotyped at no cost to farmers through government funding, bringing the proportion of the national cow herd genotyped to 55%. All calves born in participating herds are genotyped at birth, with a DNA sample collected as part of the official DAFM Tag. During peak calving season, over 100,000 samples are processed per week, with the full process from date of birth to DNA Registration completed in 13 Days on average. Since January 2024, more than 2 million calf samples have been processed, with over 1 million expected in 2026 alone.

Delivering DNA calf registration presents significant technical and logistical challenges, including large-scale sample processing, system integration across AIMS, ICBF, Tag Companies and farm software platforms, and the rollout of new identification tags that also facilitate DNA and mandatory BVD sampling. This has been achieved with an average laboratory turnaround of 4.5 days, full calf registration by 13 days of age, and sustained processing of over 100,000 samples per week during peak periods.

ORAL

Technical Session 14
Beef Cattle – Genetic Evaluation and Recording

Implementation of genetic evaluation for intramuscular fat in Norwegian beef cattle using ultrasound measurements

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There is an increasing demand from the beef market and breeding programs for reliable selection tools for intramuscular fat (IMF). The objectives of this study were to estimate genetic parameters for IMF and related traits and to establish a robust routine evaluation model for Norwegian beef cattle.

Ultrasound records from 12,748 animals of the Hereford (n=1,928), Charolais (n=4,990), Angus (n=2,489), Limousin (n=2,003) and Simmental (n=1,338) breeds collected between 2008 and 2022 were analyzed. Linear animal models were applied including fixed effects of classification year, breed-sex, ultrasound device, classifier, image interpreter and a regression on age within breed-sex, and random effects of herd or herd-year and animal. Across-breed multivariate analyses showed moderate heritabilities for IMF, fat depth and muscle depth, and a strong genetic correlation between IMF and fat depth (0.94), while correlations with muscle depth were low and negative (-0.15 and -0.04). Increasing the number of herd×year levels reduced the IMF heritability from 0.23 (310 herd levels) to 0.06 (964 herd×year levels), demonstrating strong environmental and data-structure effects. Within-breed heritabilities for IMF were 0.34 (Hereford), 0.13 (Charolais), 0.12 (Angus), 0.09 (Limousin) and 0.22 (Simmental). Corresponding estimates for fat depth were 0.45, 0.18, 0.15, 0.20 and 0.25, and for muscle depth 0.27, 0.37, 0.15, 0.30 and 0.34. Systematic differences between ultrasound devices introduced in 2017 and between image interpreters affected phenotypic means and variances.

Routine breeding values are now published for IMF. To increase accuracy, a bivariate animal model is used where fat depth is included as a correlated trait. (Co)variance components are based on the across-breed analyses, where the model includes herd as the environmental random effect. The results demonstrate that IMF can be evaluated with sufficient accuracy for selection, provided continued standardization of ultrasound interpretation.

Genetic parameters and breeding values for feed intake and feed efficiency traits from the Staur performance test in Norwegian beef cattle

Furre Siri*[1], Wetten Marte[2]

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The Staur performance test is a central component of the Norwegian beef cattle breeding program, providing individual records for roughage intake, concentrate intake and growth over a 147-day test period. The objectives of this study were to estimate genetic parameters for roughage intake (GFO), feed utilization potential (FUP) and growth, evaluate breeding values for tested bulls, and investigate whether field traits can be used for selection.

Data from 935 bulls tested from 2013 onwards in the Hereford (n=162), Charolais (n=303), Angus (n=165), Limousin (n=238) and Simmental (n=159) breeds were analyzed. A multivariate animal model including the fixed effects of breed and year and the random effects of pen within year and animal was applied. Heritability estimates were high for GFO (0.69) and FUP (0.68) and moderate for growth (0.41). The genetic correlation between GFO and FUP was strong and unfavorable (0.91). Correlations between GFO and growth (0.27) and between FUP and growth (-0.10) were favorable but associated with large standard errors. Phenotypic trends showed increasing roughage intake and decreasing (favorable) FUP from 2015 onwards, while genetic trends for GFO and FUP were close to zero. Breeding values were strongly associated with phenotypes within tests, confirming that previous selection based on phenotypes has been effective, however re-ranking of bulls occurred when systematic environmental effects were accounted for. Accuracy of breeding values was high for tested bulls but dropped markedly for relatives. Among 72,673 animals with a sire tested at Staur, only 288 had reliability >0.30 for GFO. Inclusion of 200-day weight increased the number of animals to approximately 3,800, whereas inclusion of carcass traits resulted in <500 animals. Genetic correlations between Staur traits and field traits were low to moderate (e.g. 0.25 between GFO and 200-day weight and 0.55 between growth and carcass weight).

The results show that selection of test bulls should be based on breeding values to increase accuracy. However, the lack of strongly correlated field traits limit selection for feed intake and efficiency outside the test population, highlighting the need for field phenotypes to achieve further genetic progress.

Towards standardised LR protocols for international beef cattle genetic evaluations

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Reliable genetic evaluation depends on high-quality data and suitable models to estimate breeding values (EBVs). Validation techniques are key for assessing prediction accuracy, detecting bias, and measuring dispersion in genetic models. Since the 1990s, the Interbull Centre has applied such methods for international dairy cattle. Due to differences in breeding schemes, applying dairy validation methods directly to beef cattle poses challenges. An adaptation of Interbull Method II has been developed for beef evaluations; however, certain constraints in this approach motivate research on alternative methods. This study aimed to assess the feasibility of linear regression (LR) for validating beef national genetic evaluations, focusing on criteria to define focal individuals.

Phenotypic and pedigree data were obtained from Interbeef evaluations for the breeds Charolais, Limousin, and Simmental from up to nine European countries. Three trait groups were analysed: carcass traits (weight, conformation, fatness), calving traits (birth weight, calving ease), and live weight traits (average weaning weight). The genetic evaluation models for each breed-country-trait combination varied in random and fixed effects. For each breed and sub-trait, two datasets were created to calculate the EBVs: a whole dataset (dataw) including all available records, and a partial dataset (datap) excluding the most recent years to mimic earlier evaluations. For carcass traits, the last five years were removed, while for calving and weaning weight, the last four years were excluded. The LR statistics were calculated for all breed-country-trait combinations. Three alternative approaches defined validation cohorts within the LR framework: bulls with progeny records in dataw but not in datap; increment progeny information per bull; and difference in effective record contribution. Average bias estimates were −0.22 (carcass), −0.003 (calving), and 0.13 (weaning), with near-zero values demonstrating unbiased predictions. Average dispersion values were 0.62 (carcass), 0.74 (calving), and 0.78 (weaning weight).

Overall, our results demonstrate that the LR method is useful for detecting dispersion and bias in national genetic evaluations, supporting it is use as a practical tool for model validation in beef cattle breeding programs.

Genetic parameters for calving traits in Norwegian Beef-on-Dairy crosses

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The use of beef semen in Norwegian dairy herds is increasing, highlighting the need for genetic evaluations of calving traits for beef sires based on their performance in Beef-on-Dairy (BoD) systems. The objective of this study was to estimate variance components, heritabilities, and genetic correlations for key calving traits in crosses between Norwegian Red (NRF) dams and beef sires.

The genetic analysis was based on data from the Norwegian Dairy Herd Recording System recorded between 2016 and 2024. Herds were required to have at least five BoD calves with Charolais, Aberdeen Angus or Limousin sire born per year. The final data included 44,265 crossbred BoD and 205,486 purebred NRF calves born in the same herds and years. Four calving traits were analyzed: Stillbirth was a binary trait coded as 0 for calves alive at birth and 1 for calves dead at birth or within 24 hours. Calving ease was recorded on a three-point scale, where 1 indicated no assistance needed, 2 for moderate difficulty, and 3 for severe difficulty. Calf size was scored 1 for small, 2 for medium, and 3 for large calves. Gestation length was defined as the number of days between successful insemination or mating, and calving. The pedigree used comprised 601,869 animals. Variance components were estimated using the DMU software package, applying a multi-trait animal model. The statistical model included fixed effects of birth month, twinning, herd-year, calf sex, sire breed, and a regression on age of dam within each calf sex–sire breed combination. Heritability ranged from low to high, with estimates ± SE of 0.66 ± 0.006 for gestation length, 0.33 ± 0.007 for calf size, 0.16 ± 0.008 for calving ease, and 0.05 ± 0.003 for stillbirth. Calf size showed positive genetic correlations with gestation length (0.32 ± 0.01) and calving ease (0.27 ± 0.02) and negative genetic correlation with stillbirths (-0.08 ± 0.03). A strong genetic correlation was observed between calving ease and stillbirth (0.94 ± 0.009). Gestation length had weak genetic correlations with calving ease (0.04 ± 0.02) and stillbirths (0.09 ± 0.03).

his study provides essential genetic parameters for establishing a national genetic evaluation system for calving traits in Norwegian beef-on-dairy production and supports the development of breeding values aimed at improving calving performance, animal welfare, and production efficiency.

PHENO3D: 3D phenotyping of beef calves — scaling image processing into edge-AI and extending predictions across breeds

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Initiated to bring beef cattle selection into the era of high-throughput phenotyping, the PHENO3D project aims to operationalize a non-invasive 3D imaging system enabling real-time estimation of body weight and morphological scores at weaning (Bruyas et al., 2022). The objective is to deliver standardized, robust phenotypes integrated into existing genetic evaluation programs, ensuring continuity with historical data while accelerating and harmonizing phenotypic recordings.

The PHENO3D system combines a dismountable gantry equipped with 10 RGB-D cameras, 3D image preprocessing, and predictive models. The scanner was tested in 50 configurations and demonstrated with end users, leading to major improvements toward a user-friendly system. Preprocessing converts the 10 RGB-D images into a single whole-animal 3D mesh, from which phenotypic indicators are extracted to feed machine learning models, as described by Do et al. (2024). Prediction models for Body Weight (BW), Skeletal Development (SKE), and Muscular Development (MUS) were initially developed for the Charolais breed (Dechaux et al., 2024) and have now been extended to 9 French beef breeds using the same methodology. In total, models were trained on more than 8,500 3D images from 5,000 calves, paired with reference body weights and expert linear scores. The preprocessing stage was implemented as a Python pipeline running directly on the 3D scanner, enabling fully on-device computation without cloud dependency. The edge-AI system was evaluated under external field conditions on 92 calves to assess image quality and pipeline completeness.

Using the same evaluation framework as Dechaux et al., models exceeded the targeted Spearman correlation objectives, achieving a Spearman's ρ of 0.76 for both SKE and MUS. BW prediction reached a mean absolute percentage error (MAPE) of 4.5% across animals. Some models' performances variability was observed, likely due to breed and operational effects, and improvement perspectives will be discussed. PHENO3D demonstrates that automated 3D imaging can deliver reliable phenotypes for large-scale beef cattle recording. By reaching an operational level compatible with routine use, this approach supports the integration of precision phenotyping into genetic evaluation systems.

Manufacturers' Technical Session

Advanced In Line Milk Analyzer and Its Applications

Majus Donatas*[1], Andruliene Laima[2], Vizbaras Dominykas[1]

[1] Brolis sensor technology, UAB, [2] Boumatic HerdLine, UAB

The objective of this work is to present the most recent technological, accuracy, and application driven advancements of the Brolis inline tunable laser spectroscopy milk analyzer, commercially known as MilkGenius within the BouMatic ecosystem. Building on results first introduced at the 2023 ICAR conference, this report aims to:

- describe the pathway leading to the analyzer becoming the first inline milk analyzer validated by ICAR;
- summarize the achieved performance improvements, including next generation hardware introduced in 2025;
- demonstrate how the analyzer integrates within different milking system architectures;
- highlight practical applications enabled through BouMatic HerdLine algorithms, ranging from herd level monitoring to automated care of individual animals.

At the 2023 ICAR conference, we presented the first comprehensive infield performance evaluation of our in-line real-time milk composition analyzer utilizing tunable laser spectroscopy, achieving 0.2% RMSEP for fat and 0.1% RMSEP for protein. In 2024, the analyzer became the first ICAR validated inline milk analyzer, completing extensive testing on the BouMatic Gemini robotic milking system with 0.1% RMSEP for both fat and protein. In 2025, a second-generation analyzer was released, offering higher accuracy, improved industrial design, and broader applicability across farm environments. The analyzer can be deployed across multiple milking system types. As a standalone unit, it provides real time fat, protein, and lactose measurements. When integrated with BouMatic HerdLine algorithms, it supports a wide range of herd and cow level applications. Installation specific functionality varies by data availability: discharge line installation offers an economical solution for herd level composition averages, with pen level values possible when milk flow gaps indicate group transitions; partial coverage parlor or rotary setups provide herd and pen averages per day or milking session, along with limited individual cow summaries; full coverage parlors enable complete individual cow tracking with daily weighted averages and long term detection of NEB, milk fat depression (MFD), and acute events; and robotic milking systems provide the most comprehensive data environment, where analyzer measurements are combined with robot derived parameters to generate deeper health insights and enable automated NEB prevention via controlled energy drink dosing and continuous monitoring of individual cows.

GenoCells: individual somatic cell counts of dairy cows by sequencing tank milk

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GenoCells® offer the possibility to determine somatic cells count for each cow by genotyping the bulk tank sample. GenoCells® technology is now accessible via sequencing, making it possible to target larger herds (>1000 cows).

We implemented a GenoCells® deconvolution workflow in a 500-cow herd using Illumina NovaSeq 6000 short-read WGS of tank milk to estimate cow-specific DNA fractions and infer individual SCC. Cows were genotyped with a 50K SNP array and imputed to WGS-density markers using Beagle against a phased reference panel. Tank reads (49x) were mapped with BWA and at each imputed SNP position, reference and alternate allele counts were extracted and converted to B-allele frequencies (BAF). We fitted a weighted least-squares mixture model in which each tank BAF is expressed as a linear combination of cow allele dosages, with per-SNP weights proportional to read depth to account for shallow coverage noise. DNA fractions were constrained to be non-negative and to sum to one. Cow SCC was reconstructed by combining each estimated DNA fraction with routine milk-yield records and the measured tank SCC (SCC_i = SCC_tank * V_tank * f_i / V_i). To quantify the sequencing-depth requirement for large tanks, the 49x dataset was downsampled in 5x steps and benchmarked against SCC reference values.

Predictions remained stable at 5x (R2=0.97 comparable to 50x, demonstrating that moderate coverage is sufficient to resolve contributors even at 500 cows when dense cow genotypes are available. At 1x , accuracy dropped (R2=0.72) and dispersion increased, particularly among low-SCC cows, consistent with higher sampling variance in allele-frequency estimates and reduced leverage of rare or low-coverage SNPs. Nevertheless, the 1x setting still retained useful signal for screening and could trigger targeted confirmatory sampling. Overall, GenoCells® deconvolution turns one tank sample into cow-level SCC phenotypes and ranked alerts for subclinical mastitis. For recording organizations, the approach leverages existing 50K genotyping programs and routine yield/tank SCC measurements to enable higher-frequency monitoring with minimal additional on-farm sampling. In our 500-cow context, a practical operating point is approximately 5x tank coverage on NovaSeq 6000, balancing cost and accuracy while remaining compatible with automated pipelines in routine dairy herds, now.

Potential of on-line SCC in udder health management and herd improvement

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Mastitis detection in automatic milking systems (AMS) has traditionally relied on deviations in electrical conductivity and behavioural indicators presented to farmers through user interfaces or alert lists. Emerging online somatic cell count (oSCC) technologies, such as the DeLaval Online Cell Counter (OCC), offer quantitative, high-resolution monitoring of udder health at cow and herd level and are receiving increasing attention. Reliable and frequent information on udder health is essential for timely decision making that supports animal health, welfare, and milk production. Our aim is to present and discuss new research and implications for application in and beyond herd management.

Scientific evaluations of the DeLaval OCC demonstrate high performance within ICAR defined ranges, and several applications have been explored in a recent industrial PhD project. Mastitis cases identified by OCC typically resolve within three weeks, whereas prolonged elevations indicate chronicity. Furthermore, the relationship between oSCC and milk loss is nonlinear and varies by parity and between herds, suggesting using herd and parity specific thresholds to pinpoint cases where intervention is required. Compared to monthly sampling, frequent oSCC measurements capture daily dynamics, improving the classification of chronic inflammation and thus supporting earlier treatment and culling decisions. These findings highlight the value of consistent, high frequency monitoring and the implementation of farm specific SOPs to reduce the economic impact of mastitis. DeLaval integrates scientific insights and international recommendations — such as the IDF guidelines for sensor-based udder health management from 2021 —into its innovation strategy. This approach guided the development of our next generation oSCC technology, the DeLaval BioSensors Milk Cell Analysis MCA. Newest research and use cases will be discussed. Our results show that oSCC systems are of high value for udder health farm management and beyond, such as for benchmarking, welfare assessment, genetic evaluations and herd improvement. ICAR and IDF are crucial in unlocking the potential of on-farm data through guidelines for technical validation and use of data. Strengthening partnerships among academia, industry, milk recording organizations, and other stakeholders on oSCC and other data will further advance animal welfare and sustainability in the dairy sector.

Field Implementation of an Inline Milk Composition analyzer and Cloud Analytics System in Dairy Herds

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We evaluate the impact of the BouMatic MilkGenius in-line milk analyzer combined with the BouMatic HerdLine cloud analytics platform on management efficiency, labor requirements, recording accuracy, and timely decision-making in modern robotic dairy farms.

An integrated system consisting of the BouMatic MilkGenius in-line milk analyzer and the BouMatic HerdLine cloud platform was implemented on commercial dairy farms in 11 countries across Europe and North America. MilkGenius automatically measured fat, protein, and lactose concentrations at every milking without manual sampling. Measurements were transmitted to a centralized database where longitudinal algorithms analyzed herd, group, and individual cow trends. Milk composition data were interpreted together with complementary information including milk yield, milking frequency, and conductivity. Alerts and recommendations were delivered through web and mobile interfaces accessible to farmers and advisors. Comprehensive monitoring of parameters enabled earlier identification of negative energy balance, milk fat depression, and acute health deviations compared with visual observation. Continuous milk composition monitoring transformed milk recording from periodic measurement into practical decision support.

- Farms reported reduced labor associated with routine cow observation and monitoring for metabolic disorders. In robotic milking installations, detected metabolic risk triggered targeted supplementation and recovery was monitored through subsequent milk measurements.
- Automated sampling reduced missed animals and sampling inconsistencies, improving reliability of herd records and reducing operator-dependent errors.
- Farms identified additional management inefficiencies, including feeding adjustments and discrepancies related to external milk sampling or payment verification.
- Centralized data access through mobile devices allowed herd status to be checked remotely and supported rapid management decisions on site or off farm. The results demonstrate that milk analysis remains a central biological information source in technology-enabled herds and contributes to more efficient and sustainable dairy management.

Real-Time PCR in Mastitis Diagnostics

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Introduction Mastitis remains the most frequent and costly disease of dairy cattle. Accurate, rapid etiological diagnosis is essential for targeted therapy, antimicrobial stewardship, and herd level control. Since June 2010, Finland has implemented routine real-time multiplex PCR (qPCR) for mastitis diagnostics at national scale, replacing most bacteriological culture (BC) and generating a unique, longitudinal dataset to inform udder-health management. This large-scale adoption provides a unique basis for combining diagnostic, milk quality, and antimicrobial use data to evaluate udder health and management outcomes at population level after the radical change.

Material & methods We summarize operational experience from Finland's centralized diagnostic workflow involving Valio Oy's laboratory network, Movet IDEXX, and the University of Helsinki, which collectively process over 130,000 mastitis PCR samples annually, compared with approximately 2,000 bacterial culture (BC) samples analyzed mainly at the University of Helsinki and Movet. Samples include aseptically collected quarter milk samples from clinical and subclinical mastitis cases, taken predominantly by farmers under veterinary guidance. In addition, national Dairy Herd Improvement (DHI) data from over 180,000 cows are analyzed regularly for somatic cell count (SCC), allowing integration of herd-level inflammation and infection trends with PCR pathogen profiles. PCR analyses employ commercial qPCR panels (15 targets including β-lactamase resistance gene). All laboratories follow harmonized procedures for aseptic sampling, DNA extraction, amplification, and automated Ct-value based result interpretation. Antimicrobial use data originate from FINRES-Vet national surveillance, enabling linkage of diagnostic adoption with trends in veterinary antimicrobial consumption.

Results & Discussion Annual qPCR throughput exceeds 130,000 samples, demonstrating the national scale and robustness of Finland's udder-health surveillance system. The median turnaround time decreased from ≥ 48 h for BC (and 6–10 days for Mycoplasma bovis) to same-day reporting (~4 h analytical time). Across multiple Finnish and international studies, qPCR consistently detected mastitis pathogens more frequently than BC and achieved pathogen detection rates of 83–92% in routine diagnostics. Sample quality was acceptable at large scale: ~13% classified as contaminated (> 2 targets), and 12–18% PCR-negative, indicating reliable farmer sampling. National DHI SCC data show a gradual decline in herd-average SCC over the past decade, corresponding with enhanced diagnostic coverage and targeted herd management. Importantly, antimicrobial usage in Finnish dairy herds has decreased steadily since 2010, contrary to initial concerns that PCR adoption would increase prescriptions. According to FINRES-Vet 2022, both overall antimicrobial consumption and resistance indicators declined, supporting improved stewardship outcomes. Conclusion Finland's nationwide qPCR implementation demonstrates that molecular diagnostics can be successfully integrated into large-scale udder-health management without increasing antimicrobial use. The key lessons include:

1. Embedding diagnostics within herd-health strategy - clear sampling indications, guidelines and aseptic quarter-based sampling technique.
2. Combining molecular and production data - integration of PCR results with DHI SCC data enables herd-specific pathogen profiling and longitudinal follow up of the cows and benchmarking.
3. Interpreting Ct-values contextually - Ct data should be routinely reported and evaluated alongside the pathogen information, SCC and clinical findings.
4. Monitoring stewardship metrics - routine PCR use facilitates evidence-based antimicrobial decision-making, reducing unnecessary treatments. Finland's experience shows that qPCR, when combined with systematic SCC monitoring and national antimicrobial surveillance, forms a powerful, objective, and data-driven foundation for precision mastitis management. The Finnish model provides an international benchmark for linking diagnostics, prevention, and responsible medicine use in sustainable dairy production.

POSTER

Technical Session 2
Validation related to the Use and Usability of Data

Preliminary Evaluation of Phytogenic Dry-Off Tablet on Dairy Cow Transition Health and Performance with pH Plus Bolus from smaXtec

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The dry-off period (DO) represents a pivotal transition in the lactation cycle of dairy cows, significantly impacting health and productivity. During this phase, cows undergo substantial physiological adjustments, including metabolic, hormonal, and immune changes, which prepare them for the subsequent lactation. Mismanagement during this critical stage can result in metabolic disorders, compromised immune function, reduced milk yield, and reduced longevity. To improve animal welfare and health outcomes, effective dry-off strategies are essential. Recent advancements in dry-off strategies emphasize the use of dietary interventions and targeted treatments to support metabolic adaptation and minimize negative energy balance. This study evaluates the impact of a novel dry-off tablet (StopLac®, AHV; containing an Allium-derived compound as the active substance) on the key patterns affected by the intervention.

A longitudinal, randomized, double-blinded pilot trial was conducted on a commercial Holstein dairy herd to evaluate behavioral and rumen physiological responses to alternative dry-off strategies using pH Plus Bolus, smaXtec animal care GmbH, Graz, Austria. Forty-five cows from a single farm were randomly allocated to three groups (n=15 per group): (1) a treatment group receiving a novel dry-off (DO) tablet, (2) a negative control group managed with standard gradual dry-off procedures, and (3) a positive control group receiving an oral acidogenic bolus containing calcium chloride, calcium sulfate, and ammonium chloride, as previously described in dry-off studies using acidogenic boluses. Behavioral activity, rumen temperature, and rumen pH were monitored around dry-off and around calving using automated sensor technologies to capture high-resolution temporal patterns. Data were analyzed in JASP, and temporal boxplots were generated to visualize within- and between-group trends over time. Nonparametric Kruskal–Wallis tests were applied at each time point to quantify the magnitude and duration of differences between treatment groups in behavioral and rumen parameters. This pilot study design aligns with previous work on acidogenic boluses and milk cessation methods at dry-off, which have demonstrated effects on cow activity, lying behavior, and udder comfort, and extends these approaches by integrating continuous rumen sensor data in a randomized, double-blind framework. The outcomes of this study will inform the potential of the DO tablet as a data-driven dry-off intervention and provide parameter estimates to power larger trials aimed at optimizing cow comfort, rumen health, and transition management. In this pilot trial, dry-off strategy markedly influenced both the magnitude and duration of rumination depression, while only modestly affecting rumen pH dynamics. Median baseline rumination (Rum(start)) was numerically highest in the Gradual group (567 min/d; IQR 545–589) compared with StopLac (532; 516–548), yet Gradual experienced the largest proportional decline to Rum(low) (357; 293–421), corresponding to a 37% decrease versus 24% for StopLac (403; 370–436). The temporal profile of rumination disturbance differed substantially between groups. Time for rumination to decline to the nadir T(R.decl) was longest in Gradual (123 h; 83–164) and shorter in StopLac (15 h; 10–19).

The extraction, harmonization, and interpretation of the high-frequency rumination and pH sensor data proved technically demanding, requiring extensive manual preprocessing, ad hoc signal cleaning, and repeated contextual validation of apparent patterns. These challenges highlight the inadequacy of current dry-off monitoring metrics and underscore the need to develop novel, data-driven key performance indicators and composite temporal parameters (for example, T(R.decl), T(R.low), T(R.incr), T(R.Total)) that more accurately characterize dry-off dynamics. In addition, the work emphasizes the urgency of implementing new algorithm-based alert rules that can translate complex sensor trajectories into actionable, early warnings for suboptimal dry-off management and emerging health risks at both cow and herd level. References: Florentino, C. C., et al. "A randomized clinical trial evaluating the effects of administration of acidogenic boluses at dry-off on rumination and activity behavior in the 14 subsequent days." JDS communications 4.4 (2023): 293-297. Rajala-Schultz, P. J., et al. "Effect of milk cessation method at dry-off on behavioral activity of dairy cows." Journal of dairy science 101.4 (2018): 3261-3270. Maynou, G., et al. "Effects of oral administration of acidogenic boluses at dry-off on performance and behavior of dairy cattle." Journal of dairy science 101.12 (2018): 11342- 11353

Quality of data collection and its implications for the reliability of large-scale animal science analyses

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The quality of data collection is critical for ensuring that the results obtained in animal science experiments are representative of productive reality. However, data collection processes frequently present biases or insufficient standardization. Considering this, we sought to study the data recording process by the Council on Dairy Cattle Breeding (CDCB) on North American dairy farms.

After cleaning, we ended up with a dataset of 6,729,954 records from 2,630 herds monitored between 2006 and 2017. To explore possible effects of information volume, herds were stratified according to the total number of observations reported: 100–2,000 records (small), 2,000–10,000 records (medium), and more than 10,000 records (big). Herds with fewer than 100 records were excluded. We focused our analysis on the recording process of animal destination categories. Producers had access to eight animal destination categories — retention in the herd, and removals due to dairy purposes, low production, reproductive problems, mastitis, locomotor problems, death, and other causes — and, based on these, we quantified the number of categories effectively used by each herd. All analyses were performed in Python in the Google Colab.

The results indicate that most producers (91.98%) used all available destination categories, including retention in the herd, suggesting a high degree of completeness and consistency in the recording process. This pattern became even more evident when considering that 4.89% of herds reported seven distinct categories, totaling 96.87% of herds with seven or eight recorded destinations. When analyzing the strata by data volume, we found that "big" records herds reported all the eight categories; Within the "medium" records herds, 98.72% of them reported all categories, whereas the rest, 1.28% employed five, six, or seven categories. In contrast, all herds that reported only one to four categories belonged to the "small" records stratum, of which only 77.50% used the eight available categories, demonstrating that lower data volume is associated with a higher risk of underrepresentation. Thus, we can conclude that the data collection conducted by the CDCB appears to be consistent with reality, such that the few producers who seemingly collect data in an unrealistic manner can be excluded without affecting the interpretability of available data.

POSTER

Technical Session 3
Validation related to the Use and Usability of Data

Animal identification in the Bosnia and Herzegovina: current situation and possibilities

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Imrpovement of the animal (dairy cows identification) in the Bosnia and Herzegovina.

An inquire have been conducted on 144 dairy farms.

For many years, the identification of the dairy cattle and domestic animals in general in Bosnia and Herzegovina has been an obstacle for the development of livestock production in this country. Activities towards the improvement of this sector, oftne initiated by breeders, were most often rejected by the competent authorities, as unfounded, on the one hand, on the other hand, there were never clear explanations for the public, why red meat from Bosnia and Herzegovina' farms cannot be exported to the EU. This situation is also the problem when it comes to breeding and selection work. The quality of ear tags is very poor, there is no interest from the competent structures to transfer marking to breeders, as in EU countries, and no solutions are offered. The results of survey on 144 dairy farms by the Dairy Farmers Association of the Republic of Srpska show very poor results in this area.

From Sectoral Traceability to a National Identification Policy: The Role of SISBOV in the Development of Brazil's National Cattle Identification Plan (PNIB)

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[1] Alltags / Tracer

This study aims to analyse the evolution of Brazil's cattle identification system from the SISBOV programme to the National Plan for Identification (PNIB), highlighting how accumulated regulatory and operational experience enabled the transition from a sector-oriented traceability model to a nationally integrated system aligned with international ISO standards.

This study is based on a qualitative and documentary analysis of the regulatory evolution of Brazil's cattle identification framework. Official legislation, normative instructions and institutional documents related to SISBOV (established in 2002) and the National Plan for the Identification of Cattle and Buffaloes (PNIB) were systematically reviewed. The analysis was complemented by an assessment of operational procedures implemented over more than two decades, including certification routines, numerical identification standards and inter-institutional coordination mechanisms. Particular attention was given to the transition from the programme-based 15-digit identification structure (prefix 105) to the nationally unified ISO-aligned standard (prefix 076), examining its regulatory rationale and systemic implications. The study also considers the intersectoral consultation process initiated in 2020, involving federal authorities, state animal health agencies, industry representatives and producers, which contributed to the design of the PNIB framework and its phased implementation schedule (2025–2032). The findings indicate that SISBOV functioned as an institutional and operational foundation for the development of a comprehensive national identification policy. While originally conceived for gradual universal implementation, SISBOV became consolidated as an export-oriented traceability protocol, enabling the establishment of standardized numerical structures, certification procedures and data validation mechanisms. The accumulated experience under SISBOV revealed structural limitations, particularly regarding fragmented state-level systems and limited electronic interoperability. These challenges motivated the creation of PNIB as a unified national framework. A key structural advancement under PNIB is the adoption of a new 15-digit identifier beginning with the ISO country code 076, replacing the programme-linked 105 prefix. This transition represents a shift from a programme-based traceability model to a sovereign national identification system aligned with international standards, enhancing interoperability, governance consistency and long-term scalability. The Brazilian case demonstrates that large-scale national identification systems can evolve from sector-specific schemes through progressive regulatory adaptation, accumulated operational learning and broad stakeholder engagement.

The Brazilian experience demonstrates that the successful implementation of a nationwide cattle identification system is not solely a technological challenge, but primarily an institutional and regulatory process that requires gradual maturation and broad stakeholder alignment. The evolution from SISBOV to PNIB illustrates how a sector-oriented traceability programme can serve as a foundational platform for the development of a comprehensive national identification policy. The accumulated operational experience, standardized identification practices and certification procedures established under SISBOV were instrumental in enabling the transition toward a unified and mandatory national framework. The adoption of an ISO-aligned national identification standard (prefix 076) represents a structural advancement that strengthens international interoperability, enhances data governance and supports long-term scalability. For countries seeking to expand or restructure their identification systems, the Brazilian case suggests that progressive regulatory adaptation, intersectoral dialogue and alignment with international standards are key success factors for transitioning from segmented traceability schemes to integrated national identification systems.

POSTER

Technical Session 4
Heat stress, health and welfare: genetics and management

A Mobile Infrared Thermography System for Precision Phenotyping and Health Monitoring of Dairy Cows under Heat Stress Conditions

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The increasing scale of dairy production systems necessitates efficient and animal-friendly approaches for continuous health monitoring, particularly in subtropical regions characterized by high temperature–humidity index (THI). In Taiwan, prolonged exposure to elevated THI compromises thermoregulation, increases disease susceptibility, and negatively affects animal welfare and productivity. Body temperature is a fundamental physiological trait reflecting health and stress status; however, routine rectal temperature measurement is invasive, labor-intensive, and impractical for large-scale phenotyping. Infrared thermography (IRT) offers a non-invasive method to quantify surface temperature and has been proposed as a precision phenotyping tool for health and welfare traits. This study evaluated a mobile, self-propelled IRT system integrated with radio-frequency identification (RFID) technology for rapid health screening of dairy cows under heat stress conditions.

The study was conducted in a lactating cow barn at the Hsinchu Branch of the Livestock Research Institute, Taiwan, where environmental conditions were typical of high THI dairy housing. A total of 20–26 lactating Holstein cows equipped with RFID tags were monitored weekly for five consecutive weeks. During feeding, cows were restrained at headlocks, and the mobile IRT unit was remotely operated along the feed alley at a distance of approximately 2 m. Individual cow identification was achieved via RFID, and orbital (eye region) temperature was automatically measured using a dual-lens infrared camera. Rectal temperatures were recorded concurrently for validation. An orbital temperature threshold of 37.5°C was applied for real-time health alerting.

The system achieved a 100% success rate in individual identification and orbital region recognition (n = 138 measurements). Mean orbital temperature of healthy cows was 37.0 ± 0.2 °C (n = 112), whereas cows exhibiting fever (rectal temperature 39.8 ± 0.3 °C) showed higher orbital temperatures (37.8 ± 0.3 °C; n = 26). The average acquisition time per cow was less than 5 s, enabling rapid herd-level phenotyping. These results demonstrate that mobile IRT provides a robust, non-invasive phenotyping approach for detecting thermal and health deviations associated with heat stress. The system shows strong potential for integration into precision dairy management strategies aimed at improving health monitoring, animal welfare, and resilience to heat stress.

Effects of Cold Drinking Water on Panting Behavior and Milk Yield in Lactating Dairy Cows During Summer

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This study aimed to evaluate the effects of cold drinking water compared with room-temperature water on panting time, eating time, rumination time, and milk yield in lactating dairy cows during the summer season. We hypothesized that providing cold drinking water would mitigate heat load, reduce panting behavior, and potentially improve milk production under hot environmental conditions.

The experiment was conducted during the summer using an integrated cooling system that included an ice-water chiller, insulated PU piping between the chiller and drinking trough, and a barn environmental monitoring system to ensure consistent water temperatures. Lactating cows were assigned to two treatments: cold drinking water (20.0°C; treatment group) and room-temperature water (28.0°C; control group). Behavioral parameters (panting time, eating time, rumination time) and milk yield were recorded and compared between groups. Water temperature was maintained and monitored automatically. Statistical comparisons between treatment groups were performed to evaluate differences in behavioral and production responses.

The average panting time during summer was slightly lower in the cold water group (101.87 minutes) compared to the room-temperature group (107.16 minutes). Average milk yield was also slightly higher in the cold water group (26.61 kg) compared to the control group (25.35 kg). Although differences in panting time and milk yield were not statistically significant, the cold water treatment showed potential trends toward reduced heat stress and improved productivity. No significant differences were observed in eating or rumination times. These findings suggest that cold drinking water may serve as a practical heat mitigation strategy for improving dairy cow comfort and productivity during hot seasons.

Assessment and prediction of heat tolerance in dairy cows using blood biochemical indicators

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This study was based on the assumption that heat tolerance in dairy cows is a biologically measurable and relatively stable trait that can be reflected by specific blood biochemical indicators. We hypothesized that cows experiencing lower milk yield losses under heat stress conditions would exhibit distinct metabolic and mineral profiles that could serve as predictive biomarkers.

Data were collected from 59 primiparous and 102 multiparous Holstein cows. A temperature humidity index (THI) ≥ 75 was defined as heat stress conditions. Milk yield residuals under HS were calculated using the Wilmink lactation curve model. These residuals represent production losses attributable to heat stress, with larger negative values indicating greater milk yield decline. Based on residual distribution, cows were classified into three groups: heat-tolerant, heat-sensitive, and intermediate. A data-driven dynamic screening approach was applied to evaluate correlations between 20 blood biochemical parameters and milk yield residuals, while also considering consistency across parities.

Three key biomarkers were ultimately identified: serum calcium (Ca), β-hydroxybutyrate (BHBA), and magnesium (Mg). Heat-tolerant cows consistently exhibited higher serum Ca concentrations, and this pattern was stable between primiparous and multiparous cows, suggesting that heat tolerance may represent an individual and repeatable trait. Based on threshold values derived from heat-tolerant primiparous cows (Ca ≥ 7.8 mg/dL, BHBA ≥ 0.8 mmol/L, Mg ≥ 2.3 mg/dL), a stringent binary classification model was established to predict heat tolerance in multiparous cows. Validation results showed an overall prediction accuracy of 77.78%, with particularly strong performance in correctly identifying heat-tolerant cows (91.7%). These findings demonstrate that early prediction of heat tolerance using blood biochemical indicators is feasible and effective. The proposed model provides a practical and science-based tool to support precision breeding and management decisions in dairy production systems under heat stress conditions.

Automated Claw Locomotion Scoring System for Dairy Cows

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Lameness is a major health problem in dairy cows and a leading cause of reduced productivity, compromised animal welfare, and involuntary culling, particularly in intensive dairy systems under hot and humid climates such as Taiwan. Conventional locomotion scoring relies on subjective visual observation, is labor-intensive, and often fails to detect lameness at an early stage. The objective of this study was to develop and evaluate an automated, image-based claw locomotion scoring system for dairy cows using artificial intelligence.

Data were collected from a commercial dairy farm in central Taiwan over a 10-month period (January–October 2025). Holstein dairy cows housed in free-stall barns and fed a total mixed ration were monitored across different stages of lactation. Side-view walking images were recorded twice daily using synchronized 2D and 3D cameras installed along the milking parlor exit alley, yielding 21,334 walking image samples. Locomotion scores were assigned by experienced experts using a five-point scoring system. An automated lameness analysis framework integrating image segmentation and deep learning was developed. Sixteen anatomical skeletal key points were defined and annotated from lateral-view images to characterize posture and limb movement. Gait was classified into three categories—normal, mild lameness, and severe lameness—corresponding to the conventional five-point locomotion scoring system. The proposed model combined a convolutional neural network and a long short-term memory network to capture spatial and temporal gait features. Model performance was evaluated using temporally separated training and testing datasets across ten independent periods.

Across all test datasets, 22,228 labeled lameness samples were analyzed, of which 19,932 were correctly classified, resulting in an overall accuracy of 89.67%. The proposed image-based system demonstrated stable and reliable performance in automated lameness classification. These findings indicate that the system provides an objective, non-invasive, and effective approach for early lameness detection, with strong potential to enhance precision dairy management, improve animal welfare, and reduce involuntary culling in commercial dairy farms.

Impact of Automated Milking Systems on Productivity, Milk Composition, and Udder Health: A Case Study in Subtropical Taiwan

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To quantify changes in productivity, udder-health indicators, and seasonal resilience after adopting an automated milking system (AMS) in a subtropical dairy herd in Taiwan using DHI test-day records.

A single-herd before–after case study was conducted using official DHI test-day records. The farm installed two AMS units (January and July 2020). To ensure stable operation, we compared the pre-AMS year (Jan–Dec 2019; from 210 cows) with a stabilized post-AMS year (Jan–Dec 2022; from 189 cows). Hot season was defined as Jun–Sep and cool season as Dec–Mar (season used as a proxy for heat load). High SCC events were defined as SCC >2.0×10^5 and SCC >5.0×10^5 cells/mL. Milk yield was compared using unpaired two-tailed Student's t-tests, and high-SCC proportions were compared using chi-square tests (two-sided, P<0.05).

Milk yield increased after AMS adoption (25.60±7.82 vs 31.88±9.82 kg/d). Seasonal resilience improved, with hot-season milk-yield depression relative to the cool season decreasing from 12.5% (2019) to 1.6% (2022). However, high-SCC test days increased post-AMS (SCC >2.0×10^5: 16.6% to 23.9%; SCC >5.0×10^5: 6.4% to 11.9%). In this subtropical herd, AMS adoption was associated with higher productivity and a flatter seasonal yield profile, but with more frequent high-SCC episodes, highlighting the need for strengthened udder-health monitoring and protocols during AMS implementation.

POSTER

Technical Session 5
From Milk Analysis to Decision Support: Unlocking Insights for Sustainable dairy management

Optimization of Differential Somatic Cell Count (DSCC) Threshold for Enhanced Early Screening of Escherichia coli mastitis in Dairy Cattle

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The differential somatic cell count (DSCC) is a critical parameter representing the combined proportion of neutrophils and lymphocytes in milk. While the international standard is typically 65%, its sensitivity for acute pathogens like Escherichia coli (E. coli) often requires local optimization to serve as an effective early-warning tool. This study aims to establish a data-driven DSCC threshold, using the clinical somatic cell count (SCC) benchmark of > 200,000 cells/mL to maximize early E. coli detection.

Milk samples (n=100) from commercial farms were analyzed for SCC, DSCC, and bacterial culture. To ensure universal applicability, a likelihood ratio test (LRT) within a linear mixed model (LMM) was first used to confirm that farm-associated management had no significant impact on DSCC variation. Secondly, an LMM investigated the relationship between E. coli bacterial load and DSCC levels. Finally, the optimal threshold was determined via ROC curve analysis, and Fisher's exact test was used to calculate the odds ratio (OR) for infection risk.

The LRT results confirmed minimal farm-to-farm variation (P = 0.595, ICC = 0.02), justifying the pooling of data across environments. Subsequent LMM analysis revealed no significant linear correlation between E. coli load and DSCC (P = 0.392), supporting a "Saturated Immune Response" model where leukocyte recruitment reaches a biological maximum immediately upon pathogen detection. ROC analysis identified an optimal threshold of 59.3%, achieving an exceptional 96.7% sensitivity. Cows exceeding this threshold exhibited 3.12 times higher odds of harboring E. coli (OR = 3.12). In conclusion, the 59.3% threshold establishes DSCC as a highly sensitive alert trigger, enabling precise interventions before E. coli induces acute clinical outbreaks.

Raw milk composition associated with texture profile attributes of low-moisture mozzarella cheese in Taiwan

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To enhance the added value of domestically produced raw milk, Taiwan's dairy sector is undergoing a value-chain transition from commodity milk sales toward higher-value dairy processing. Variability in low-moisture mozzarella cheese texture undermines product consistency, and differences in raw milk composition may contribute to this variation.

This study examined associations between raw milk composition and texture profile analysis (TPA) attributes across seven production batches. Raw milk was characterized using routinely measured components, including fat, protein, lactose, somatic cell count (SCC), acetone, and fatty-acid profiles. Mozzarella texture was evaluated by TPA (hardness, adhesiveness, springiness, cohesiveness, chewiness, resilience). Pearson correlations were computed at the batch level ($n = 7$), and multivariate structure among milk indicators was summarized using principal component analysis (PCA).

Fatty acids were associated with texture: oleic acid (C18:1) was positively associated with cohesiveness ($r = 0.84$, $p < 0.05$) and resilience ($r = 0.87$, $p < 0.05$). Preformed fatty acids were positively associated with chewiness ($r = 0.84$, $p < 0.05$) and hardness ($r = 0.79$, $p < 0.05$), and long-chain fatty acids (LCFA) were positively associated with cohesiveness ($r = 0.78$, $p < 0.05$). In contrast, protein/casein-related indices were negatively associated with springiness (casein: $r = -0.83$, $p < 0.05$; true protein: $r = -0.81$, $p < 0.05$; crude protein: $r = -0.76$, $p < 0.05$). PCA explained 70.8% of the variance in milk indicators using two components (PC1 44.4%, PC2 26.4%), broadly separating a fatty-acid/solids axis from a protein/casein axis. These preliminary findings suggest that routinely available fatty-acid and protein/casein indicators may help anticipate low-moisture mozzarella texture outcomes. Future studies with larger datasets are needed to validate these associations and develop robust predictive models for low-moisture mozzarella-specific milk grading.

A Farm Management Monitor for the Dairy on Bulk Milk Laboratory Testing, a longitudinal case study on a high-level producing Dutch Farm

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Monthly laboratory analyses on bulk milk (presence/absence of antibodies to 14 diseases, presence of the important minerals from the feed in the right ranges, absence/presence of toxins, and the correct levels of pregnancy-indicators) and regular analyses of the drinking water, reveal all necessary basic parameters for Cultivating Trust and Transparancy along the Value chain of Farm to Fork.

Monthly bulk milk samples from farms are subject to milk-serology and milk-fotometry, and laboratory results are studied in longitudinal statistical analyses to reveal upcoming diseases, flaws in feeding efficiency and presence of toxins in the silage, along with pregnancy-indicators and parameters of drinking water-quality.

This presentation shows the results of longitudinal studies of laboratory data on bulk milk derived from a farm before and after deployment of the Dairy-Farm Management Monitor (Dairy-FMM), indicating improved milk-yields (up to 15%), increased average lactation numbers (from 2.5 up to 4.0, and sufficient head-room for even higher lactation numbers), insemination numbers improved from 3.8 to 1.9, and the integral cost went down from keeping 56% of the total animal population on young stock down to 40%. Moreover, the Dairy-FMM gives full insights in the uptake of essential minerals from the feed.

POSTER

Technical Session 7
Milk Recording in a Technology World: Providing Value Added Services and Data Exchange solutions for Farms with Robots and Sensors

Genomic reconstruction of pedigree records: a key step in the revitalization of the critically endangered Istrian goat

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This study addressed the challenges of maintaining accurate genealogical records in the critically endangered Istrian goat, an indigenous breed primarily managed under low-input extensive to semi-extensive systems. In such environments, traditional field data recording is frequently compromised, which threatens to undermine the revitalization efforts essential for this population. To rectify this, genomic tools were employed to validate and reconstruct the pedigree, providing a robust framework for managing genetic diversity and conservation. Genotyping was performed using a medium-density 60K SNP chip for 214 individuals.

The pedigree was analyzed and corrected using the SeekParentsF90 software. A 1.0% Mendelian conflict threshold was applied to exclude incorrect parental assignments.

Among the 184 tested parent-offspring pairs, the analysis revealed substantial inaccuracies in the official herdbook, with paternity and maternity error rates of 11.3% (6/53) and 18.3% (24/131), respectively. By leveraging genomic information and applying a rigorous 0.5% assignment threshold, the study successfully identified and assigned 4 previously unrecorded or misidentified biological sires and 13 dams. These findings support the hypothesis that extensive rearing conditions carry a high risk of parental misidentification during the kidding season, despite breeder efforts. The integration of genomic corrections significantly improves the reliability of the herdbook, providing a solid basis for the precise estimation of genetic parameters and the implementation of effective mating schemes. Ultimately, this research confirms that genomic-based pedigree validation is not merely an auxiliary tool, but a fundamental requirement for the sustainable conservation and genetic management of the Istrian goat.

Assessing income-based economic efficiency in PDO Manchega sheep breed dairy farms: preliminary results

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Dairy sheep farming in Mediterranean regions operates under structural, climatic, and market constraints that shape production strategies and economic outcomes. In Castilla-La Mancha (Spain), the Manchega breed constitutes the basis of the PDO Manchego cheese supply chain, in which milk payments are directly linked to compositional quality and technological suitability for cheesemaking. In this context, competitiveness cannot be assessed solely in terms of milk yield, as revenue depends on the interaction among flock size, milk composition, price, and management practices. Due to the lack of consistent and comparable cost records across farms, milk sales revenue was used as a direct indicator of economic performance. In regulated PDO systems, where prices are closely tied to quality parameters, revenue-based approaches provide a coherent framework for assessing relative efficiency.

The study analysed 737 monthly observations (2019-2024) from 11 farms participating in the official breeding and technical-economic programme managed by AGRAMA. Milk revenue was modelled using Cobb-Douglas and translog production functions as a function of flock size and fat-and-protein-corrected yield per ewe (FPC). A deterministic frontier approach was applied to estimate efficiency, and panel Tobit models were used to identify determinants of inefficiency. The translog model showed superior goodness of fit ($R^2 = 0.809$). FPC per ewe exhibited the highest elasticity, exceeding that of flock size, confirming that technological milk quality is the main driver of revenue under PDO payment schemes. Although increasing returns to scale were identified, herd expansion alone does not guarantee higher efficiency. Inefficiency was primarily associated with management factors affecting milk quality, particularly elevated somatic cell counts, prolonged milking times, and suboptimal milking routines. Overall, the findings indicate that improving cheese yield potential and strengthening sanitary and managerial performance are more decisive for competitiveness than merely increasing production scale.

Animal Genetic Banking in Georgia: Conservation and DNA/RNA Sequencing of Capra caucasica and Capra cylindrica

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The main objective of this initiative is to establish a reliable scientific foundation for the long-term conservation of Georgia's unique wild goat species by creating a structured animal genetic bank. The project aims to secure and preserve the DNA and RNA of Capra caucasica and Capra cylindrica, ensuring that their genetic diversity is fully documented and safeguarded for future research and restoration programs. Another key objective is to strengthen international scientific cooperation through collaboration with China Agricultural University, enabling advanced genomic analysis that supports conservation, breeding strategies, and the development of future gene banking systems. Ultimately, the project seeks to provide Georgia with a modern framework for protecting its valuable genetic resources and contribute to national and regional biodiversity conservation efforts.

The experimental work for this initiative followed internationally recognized genetic conservation protocols to ensure the accuracy, purity, and long-term usefulness of the collected material. Field specialists conducted controlled sampling of biological materials from Capra caucasica and Capra cylindrica populations in their natural habitats. Tissue, hair follicle, and blood samples were collected using sterile procedures to prevent contamination and to maintain the integrity of the genetic material. Samples were immediately preserved under regulated cold-chain conditions and transported to the partnering laboratory at China Agricultural University. In the laboratory, DNA and RNA were extracted using standardized molecular biology methods, including automated purification systems and high-fidelity extraction kits suitable for wild species. The quality and concentration of nucleic acids were evaluated through spectrophotometric measurement and gel electrophoresis. High-throughput sequencing technologies were employed to obtain whole-genome and transcriptome data, providing a detailed overview of genetic variability, population structure, and unique adaptive traits. The sequencing workflow included library preparation, fragment selection, amplification, and sequencing on next-generation sequencing platforms. Statistical analyses were performed using bioinformatics pipelines designed for wildlife genomics. Raw data underwent quality control, trimming, and alignment to reference sequences. Population genetic analyses—including heterozygosity estimates, genetic distance measurements, and phylogenetic assessments—were conducted using software such as STRUCTURE, MEGA, and R-based statistical tools. These analyses allowed researchers to identify genetic patterns, assess variation within and between populations, and evaluate the overall health and resilience of the species' gene pools. The results form the scientific foundation for future conservation strategies and the establishment of a national gene bank with strong genetic integrity.

The preliminary results of the genetic banking initiative demonstrate that the collected samples of Capra caucasica and Capra cylindrica were of high quality and suitable for full DNA and RNA sequencing. Laboratory analyses confirmed strong nucleic acid integrity, allowing for successful extraction, purification, and preparation of genomic libraries. The sequencing process generated a comprehensive dataset that reveals the presence of distinct genetic markers, adaptive traits, and population-level variations within both species. These findings provide valuable insight into the evolutionary relationships, genetic resilience, and potential vulnerabilities of Georgia's wild goat populations. Genetic diversity assessments indicate that both species retain significant levels of variability, which is essential for long-term survival, adaptation, and resistance to environmental pressures. The results also suggest meaningful differences between regional populations, emphasizing the need for targeted conservation measures. The bioinformatic analyses have enabled the identification of unique gene regions that may be relevant for future breeding, restoration, or reintroduction programs, as well as for the establishment of a national and regional animal gene bank. In conclusion, the project successfully demonstrated that Georgia's wild goat species possess strong and distinctive genetic characteristics that merit priority conservation. The collaboration with China Agricultural University provided high-quality genomic data that will play a critical role in shaping future biodiversity strategies. The findings confirm that the creation of an animal genetic bank is both feasible and scientifically justified, offering a secure foundation for future research, conservation planning, and long-term protection of Georgia's genetic heritage.

POSTER

Technical Session 11
Milk Recording Supporting Sustainability Initiatives

Automated Bottom-Reading Identification of Sample Vials to Ensure 100% Traceability in Robotic Milking Systems (Patent Pending)

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Reliable correspondence between milk samples and individual cows is critical for milk recording and decision support in robotic milking farms. Current workflows often rely on manual labeling and positional matching, which are time-consuming and prone to human error, potentially compromising data integrity. This work presents and validates an automated vial identification system that reads unique identifiers located on the bottom of sample vials integrated within robotic milk samplers. Vials are identified using either optical codes (QR/barcode) or RFID. The system records timestamp and physical position for each sample and synchronizes these data with milking robot records via API or data file import. Matching algorithms associate vial ID, milking time, and sampling sequence to confirm cow-sample correspondence.

Field tests in commercial dairy farms in Spain and France were conducted to evaluate reliability, error reduction, and operational efficiency. Performance indicators included identification success rate, duplicate detection, and time required for sample-to-cow association. The system incorporated cycle-start detection and pneumatic pulse sensing to track sampler movement and avoid false readings. Duplicate or inconsistent reads triggered operator alerts directly on their phone.

Results demonstrated near-complete elimination of mislabeling risk and a significant reduction in labor time compared to manual processes. Automated validation ensured consistent traceability even when vials were later rearranged. This approach establishes a new standard for sample traceability in automated milking, improving data quality for genetic evaluation, health monitoring, and management decisions. Adoption of automated identification can enhance confidence in milk recording data and support the sustainability and digitalization of dairy herd improvement programs.

POSTER

Technical Session 12
M Part 1: From Guidelines to the Barn: Implementing section 2 of ICAR's Milk Recording Guidelines - Updates and Lessons from the Field - Part 2: Buffalo DHI recording

A comparative evaluation of conventional and automatic milking systems on performance and behaviour of dairy buffaloes

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Automatic milking systems (AMS) have transformed dairy farming by allowing individual control of milking frequency, reducing labour, and potentially improving milk yield (MY) and animal welfare. Although widely adopted in dairy cows, their use in dairy Mediterranean buffaloes remains limited due to concerns about adaptability, anatomical differences, and potential effects on milk quality. This study evaluated the response of lactating primiparous Mediterranean buffaloes to AMS, examining MY, milk quality, and feeding behaviour throughout lactation.

The trial was conducted on a commercial farm located in central Italy, comparing a conventional tandem milking parlour (CMS; 6+6, DeLaval, Sweden) with an AMS (DeLaval, Sweden) from 50 to 310 days in milk (DIM). Sixteen clinically healthy primiparous buffaloes were selected and subdivided equally between AMS and CMS. Both groups received the same total mixed ration and were housed in separate sections of the same barn. The two groups were balanced for MY and DIM, with MY of 9.28±0.24 kg/day for AMS and 10.61±1.39 kg/day for CMS, and average DIM of 55 and 59, respectively. Milk yield was recorded automatically, with CMS milked twice daily and AMS milked voluntarily. Individual milk samples were collected six times between March and June to assess quality. Each buffalo was equipped with an ear tag (DeLaval, Sweden) to record daily eating and rumination times. Data were analysed using a mixed linear model, with milking system as a fixed effect, animal nested within group as a random effect, and DIM as a covariate.. Mean MY did not differ between groups (7.34 vs. 7.82 kg/day; SEM = 0.45, respectively for CMS and AMS), although DIM had a significant effect. AMS milk showed differences in coagulation properties (rennet coagulation time: 21.6 vs. 18.8 min; curd firming: 3.95 vs. 3.28 min; curd firmness: 30.3 vs. 38.2 mm, AMS vs. CMS). AMS buffaloes spent more time ruminating (430.56 vs. 337.23 min/day, $P < 0.01$, AMS vs. CMS), while eating time was similar (337.23 vs. 346.15 min/day, $P > 0.05$, AMS vs. CMS).

In conclusion, AMS did not affect MY in primiparous buffaloes but influenced milk coagulation properties. Additionally, it affected feeding behaviour, increasing rumination time and suggesting a potential improvement in animal welfare. Future studies, including a larger number of animals and investigations on multiparous buffaloes, are needed to confirm these effects

Modeling Lactation Curves Using Daily Yield and Milking Interval to Identify Efficient Cows in Automatic Milking Systems: A Case Study in Taiwan

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In automatic milking systems (AMS), cows milk voluntarily, resulting in variable milking intervals (MI) that introduce new parameters for evaluating lactation curves. This study aimed to model lactation curves based on daily milk yield (DMY) and milking interval data, and to explore their use in identifying “efficient” dairy cows within AMS herds.

This study analyzed a total of 541,810 automated milking records from five different farms. Cows were categorized into groups based on the medians of DMY and milking interval. Subsequently, an Incomplete Gamma Function combined with the Wood model was employed to fit the lactation curves. Analysis of Variance (ANOVA) was then used to evaluate the significant effects of different efficiency groups on parameters such as production at peak of lactation (Ppeak), days to peak (Dpeak) and 305-day cumulative milk yield (305-d MY). While AMS settings may vary across farms, this study employed the within-farm median as the classification threshold for MI and DMY to ensure that all comparisons were conducted within a consistent managerial context. Furthermore, the inclusion of a random cow effect (u) in the model accounted for individual random deviations. Combined with the stratified analysis of primiparous and multiparous cows, the potential biases arising from differing equipment configurations have been statistically mitigated.

Results showed that cows were classified into groups using medians of DMY and MI. In terms of herd composition, the proportion of cows classified as high DMY/long MI was 34.0% among multiparous cows and 34.8% among primiparous cows, whereas low DMY/short MI cows accounted for only 8.4% and 8.2%, respectively. The findings of this study suggest that DMY and MI may serve as useful indicators for assessing milking efficiency in AMS-managed herds. Adjusting the herd composition—specifically by focusing on the patterns associated with high DMY/long MI and low DMY/short MI—could potentially enhance AMS operational efficiency. By monitoring these metrics, farms may be able to refine herd management strategies to support improved system performance and equipment utilization.

Difference of lactation curve in 305-day milk yield between automatic and conventional milking system

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Automatic milking systems (AMS) have been increasingly adopted worldwide. Compared with conventional milking systems (CMS), AMS allows greater milking frequency, which may influence lactation dynamics and milk production. The objective of this study was to quantify differences in lactation curve characteristics between AMS and CMS and to better understand lactation performance variability in primiparous and multiparous dairy cows using a unified lactation curve model.

In this study, 50 primiparous and 50 multiparous cows were randomly selected from both CMS and AMS, totaling four experimental groups. The incomplete gamma function (Wood's model) was used to analyze lactation curve parameters, including initial milk yield, rate of increase, rate of decline, time to peak yield, peak milk yield, and 305-day milk yield (305-D MY). Data were analyzed using analysis of variance (ANOVA) followed by Tukey's HSD post-hoc test to determine differences among the four groups. Statistical significance was defined as $P < 0.05$.

Results showed that there were no significant differences in initial milk yield between AMS and CMS in both primiparous and multiparous cows. Otherwise, AMS cows had a higher rate of increase and decline than CMS cows across parities, indicating a faster increase in milk yield during early lactation as well as a higher rate of decline. Furthermore, AMS cows maintained longer peak yield and achieved higher peak milk yields than CMS cows in both primiparous and multiparous groups. These findings suggest that increased milking frequency and flexible management under AMS may contribute to extend and enhanced peak milk production. Overall, the present study suggested that differences in milk production between AMS and CMS may contribute to the dynamic structure of the lactation curve induced by the milking system, rather than from differences in milk yield at a specific day in milk (DIM).

POSTER

Technical Session 13
Exploring Current and Future Needs for the Livestock Science and Farming Community

The phytogenic active ingredient AHV9 drives dose-dependent methane mitigation in vitro

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Introduction: Livestock agriculture, particularly ruminant production, is a significant contributor to global greenhouse gas emissions. While this presents a huge environmental concern, it also represents an energetic loss for the animal. Consequently, mitigation strategies that reduce enteric emissions while maintaining or supporting animal productivity and health are critical for sustainable livestock systems. One such mitigation strategy has been the dietary supplementation of herb and plant derivatives termed phytogenic feed additives. These plant-derived compounds contain a wide range of bioactive compounds that can modify microbial populations within the rumen ecosystem. While many studies have sought to understand how these compounds can influence rumen fermentation parameters, microbiome, animal health and enteric methane output, results have been varied. In this study, we sought to assess the impact of commercial phytogenic feed additives, produced by AHV International, a global leader in animal health innovation, on ruminal fermentation and methane mitigation in dairy livestock.

Five AHV phytogenic compounds, including three commercial end products (1, 2 and 6) and two of their core ingredients (9 and 10), as detailed in Table 1, were used in batch fermentation experiments, modified from Yu et al. (2023), to assess their impact on methane emissions. Freeze-dried grass silage (milled to 1mm), soybean and maize meal were combined (6000:1163:2837) to produce the total mixed ration (TMR) to be used as the diet substrate. AHV products and TMR (1.6g) were added to 100ml Wheaton glass serum bottle. Rumen contents (n=5 animals) were strained through four layers of cheesecloth, combined in equal proportions before being mixed (50:50) with a saliva mimic buffer (Goering and Van Soest, 1970). This was then added to each bottle (60ml) containing the phytogenic compounds in a dose-response design, comprised of the commercially administered dose (1x), a double (2x) and a triple (3x) dose, under continuous CO2 flushing, sealed, and incubated at 39°C. At each timepoint (0h, 4h, and 24h), pH was recorded, and 1.5 mL samples were collected for subsequent VFA, NH3, and 16S rRNA gene analysis. Headspace gas pressure was recorded at 4h and 24h, and a 20ml sample was taken for CH4 quantification by Gas chromatography mass spectrometry. The experiment was performed in four independent biological replicates, each comprising three technical replicates. Statistical analyses were conducted in R, utilising its base stats functions, and visualised using ggplot2. The car package was used to assess the homogeneity of variance. Outliers were identified and removed, and normality and variance were assessed before performing a two-way ANOVA with Bonferroni and Holm corrections for multiple comparisons. AHV product number Product type 1 End-product (commercially used additive) 2 End-product (commercially used additive) 6 End-product (commercially used additive) 9 Core ingredient of end-product 1 10 Core ingredient of end-product 2 Table 1: Test compounds provided by AHV. Above details which of the test compounds are commercially available end products and which are core ingredients of these end products. Results: AHV 9 demonstrated the most significant decrease in methane at the double (44.4%, $p<0.001$) and triple (39.5%, $p<0.001$) doses at the 24-hour timepoint. Ongoing analysis on VFA, NH3 and 16S metataxonomic analysis will shed more light on the potential of AHV phytogenics to improve both animal health and productivity whilst mitigating emissions.

This study demonstrates that AHV 9, a phytogenic active ingredient of a commercial feed additive, exerts a dose-dependent anti-methanogenic effect in vitro. This methane reduction is likely driven by shifts in microbial metabolism, and investigating microbiome changes through planned 16S rRNA gene analysis may provide further insights into these mechanisms. These findings highlight the potential to optimise methane mitigation through reformulation or targeted dosage strategies while maintaining established benefits for dairy productivity and animal health.

ICAR IDF initiative on sensor data for functional traits: reference standards and guidelines to quantify rumination for health and animal welfare recording

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The increasing adoption of sensor technologies and precision farming tools in the dairy cattle sector is revolutionizing the continuous, real-time monitoring of animal health, welfare, and productivity. These digital advancements provide high-frequency, objective, and large-scale data that is essential for proactive herd management. Despite technological proliferation, a significant scientific gap remains in the validation of these commercial sensors. Specifically, a lack of standardized and rigorous protocols often leaves the accuracy and reliability of the generated data undetermined. The overall aim of the joint ICAR and IDF initiative is to develop guidelines to support the adoption of novel technologies and use of sensor data for improving animal health and welfare.

The joint initiative establishes a common agreement on definitions and terminology for health conditions and behaviors measured with sensor systems. In accordance and in collaboration with other working groups, the project develops standards to facilitate the exchange of data and information across different farms and sensor technologies. Making guidelines based on best practices for data collection, handling, and analysis for different use, e.g. genetics, health and welfare monitoring. Generating recommendations and protocols for testing the performance of sensor systems. Sensor-based rumination data was selected as the primary use case due to its high adoption rate and critical value as a health indicator. Despite its popularity, the field currently lacks standardized definitions and independent validation, often leaving the true impact on animal welfare and production unverified. Preliminary results and recommendations on use of rumination data for health and welfare assessment, sensor key performance indicators, and preferred reference standards will be presented.

Irrespective of the use of sensor data, validation and standardization are key to ensure that sensor data from diverse sources remain reliable and comparable, building the trust necessary for data-driven health and welfare decisions. Close collaboration between ICAR and IDF with relevant stakeholders and manufacturers leads to the development of unified guidelines, which will promote global adoption of the use of sensor data in herd management, animal health, and welfare assessment.

POSTER

Technical Session 14
Beef Cattle – Genetic Evaluation and Recording

Drivers of Mobile App Adoption in Extensive Beef Cattle Farms: preliminary results

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Digitalisation is increasingly recognised as essential for improving efficiency, traceability, and sustainability in extensive cattle production systems. Mobile herd management applications offer practical tools for reproductive control, health monitoring, and on-farm decision-making. However, adoption rates remain limited, especially in low-input, pasture-based production systems in Spain, suggesting that behavioural factors play a decisive role in shaping farmers' willingness to adopt these technologies.

This study analyses the intention of low-input cattle farmers to adopt mobile livestock management applications using Partial Least Squares Structural Equation Modelling (PLS-SEM), grounded in the Technology Acceptance Model (TAM). The conceptual framework incorporates perceived ease of use, perceived usefulness, attitude towards technology, and behavioural intention to adopt. A structured questionnaire was administered to farmers operating under extensive conditions. PLS-SEM was employed due to its suitability for predictive research models involving latent constructs and complex interrelationships. The reliability and validity of the measurement model were assessed through factor loadings, composite reliability, and average variance extracted, while structural relationships were evaluated using bootstrapping procedures. The results indicate that farmers' intention to adopt mobile livestock management applications is primarily driven by perceived ease of use ($\beta = 0.715$), with the model explaining a substantial proportion of variance in behavioural intention ($R^2 = 0.870$). Perceived usefulness did not exert a direct effect on intention; however, it had an indirect effect through its positive influence on perceived ease of use ($\beta = 0.465$). Farming experience played only a marginal role, showing a negligible direct association with intention ($\beta = 0.037$) and a slight negative relationship with perceived ease of use ($\beta = -0.098$). Socio-economic characteristics (age, proportion of income derived from livestock, farm size, and prior knowledge of digital technologies) were also included as control variables. Overall, the findings suggest that accelerating digital adoption in Spanish low-input, pasture-based cattle systems requires intuitive, user-friendly, and practice-oriented applications, supported by targeted advisory services and structured training strategies.

Animal Welfare Assessment in Extensive Avileña-Negra Ibérica and Asturiana de los Valles Beef Cattle Farms

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The objective of this study was to evaluate animal welfare (AW) in extensive beef cattle systems of Avileña-Negra Ibérica and Asturiana de los Valles breeds in Spain. Twelve Avileña and sixteen Asturiana farms were assessed in spring 2023 using an adapted Welfare Quality®-based protocol designed for extensive conditions. In winter 2025, complementary animal-based assessments were conducted in 9 Avileña and 10 Asturiana farms. Statistical analyses included Student's t-test (Statistica 14.0.0.15) and descriptive analysis.

Four welfare principles (good feeding, housing, health and appropriate behaviour) were evaluated through ten criteria combining resource- and animal-based indicators. Body condition and rumen fill scores confirmed adequate nutrition in both breeds across seasons. Water availability and cleanliness were satisfactory, though regional differences in water sources were observed. Resting comfort was generally high, with minimal dirtiness, lesions, lameness or ectoparasites. Mortality rates were very low (≤0.04%) and no relevant respiratory or digestive disorders were detected. Hoof condition and locomotion scores indicated negligible lameness prevalence. Climatic variability was greater in Avileña farms, yet Temperature-Humidity Index values did not indicate thermal stress risk. Stocking densities (4.8 vs. 2.7 ha/LSU in Avileña and Asturiana, respectively) ensured freedom of movement. Agonistic behaviours were infrequent. However, flight distance was significantly greater in Avileña cattle, suggesting improvement potential in handling systems and human-animal interactions. Overall, both systems showed high welfare standards, particularly in feeding, housing and health. Raising farmers' awareness that investing in improved handling facilities enhances not only animal welfare but also the efficiency of sanitary campaigns, vaccinations, deworming and reproductive management (e.g., artificial insemination and pregnancy diagnosis) will strengthen economic sustainability and social acceptance, as consumers increasingly favour products from high-welfare systems. These studies were carried out within the framework of the BOVIEX 4.0 project.