# Production, Management, and the Environment: The DairyUp Project— Attacking Major Challenges for Dairy in a Multidisciplinary Project; Posters

**2442 Genetic diversity of bovine rotavirus in dairy calves with and without diarrhea in New South Wales, Australia.** Y. Kida[1,4], Z. U. Abedien[1,4], I. J. Lean[2,4], and B. P. Brito*[3,4], [1]*Australian Institute for Microbiology & Infection, University of Technology Sydney, Ultimo, NSW, Australia,* [2]*Scibus, Camden, NSW, Australia,* [3]*New South Wales Department of Primary Industries and Regional Development (DPIRD), Elizabeth Macarthur Agricultural Institute, Menangle, NSW, Australia,* [4]*Dairy UP Program, Camden, NSW, Australia.*

Bovine rotavirus (BRV) is a major cause of diarrhea in calves, resulting in significant economic losses in the livestock industry. To comprehensively assess the diversity of BRV circulating in New South Wales (NSW), we conducted a large-scale study to identify both dominant and less common genotypes and evaluate their association with disease status and age. A total of 593 rectal samples were collected from calves on 72 farms across NSW. Rectal swabs from 349 healthy calves, 154 with diarrhea, 42 with respiratory issues, 11 with both symptoms, 30 with nonspecific symptoms, and 7 with unknown status. Total RNA sequencing was performed with a mean sequencing depth of 19 gigabases using an Illumina platform. The transcriptome was assembled de novo using SPAdes genome assembler v3.13.0, and the contigs were taxonomically classified using NCBI BLASTn. The transcriptome was mapped to the assembled contigs using Kallisto v0.5.1.1. To assess statistical differences between the contigs mapped to transcriptomes of calves with and without diarrhea, we used DESeq2 v1.44.0. Genotypes were predicted using an online Rotavirus A Genotyping tool developed by the National Institute for Public Health and the Environment, Netherlands. The most common genotypes were G10&6-P[5&11]-I2-R2-C2-M2-A3&13-N2-T6-E2-H3, with the most abundant combinations being G6P[5] and G10P[11]. Less frequent genotypes, such as G24 and P[33], as well as Rotavirus B, were also identified in at least 2 farms. Notably, almost all farms had at least one BRV-positive calf. While G10 was detected in 44 farms, G6 was found in only 25 farms. G24 was found in 2 farms, P[33] was observed in one farm, and Rotavirus B was detected in 5 farms. Multiple co-infections involving different genotype combinations were also observed, with G10 and G6 in 9 farms, as well as P[11] and P[5] in 4 farms. The abundance of the nonstructural protein 3 gene showed a strong, significant association with diarrhea, as did viral protein 7 genotypes G10 and G6. Our findings highlight the high prevalence of 2 dominant genotypes of BRV in calves with clinical and subclinical infections.

**Key Words:** rotavirus, diarrhea, metagenome

**2443 Greenhouse gas emissions of confinement and pasture-based dairy farms: Implications for mitigation.** M. F. Dida*[1,2], S. C. Garcia[1,2], and L. A. Gonzalez[1,2], [1]*School of Life and Environmental Sciences, Faculty of Science, and Sydney Institute of Agriculture, The University of Sydney, Camden, NSW, Australia,* [2]*Dairy UP Program, Camden, NSW, Australia.*

Despite extensive research on the environmental impacts of dairy farming, comparative greenhouse gas (GHG) emissions from confinement and pasture-based systems are still unclear due to inconsistent results from previous studies, which also did not account for carbon (C) sequestration by trees. The present study aimed to compare the GHG emissions of 2 Australian milk production systems (confinement and pasture-based, with 5 farms in each system) using a life cycle assessment approach that incorporates C sequestration by trees. The confinement system used a total mixed ration, whereas the grass-based system primarily relied on grazed forage with concentrate supplementation. The Australian Dairy Carbon Calculator, a Tier 3 tool, was employed to predict the total GHG emissions and emission intensity for milk production. This calculator incorporates emission factors and methodologies from the National Greenhouse Gas Inventory and Intergovernmental Panel for Climate Change, as reported to the United Nations Framework Convention on Climate Change. The tool calculates the emission intensity of a milk production system in terms of $CO_2$ equivalents ($CO_{2eq}$), with emissions allocated to both milk and meat. Animal emissions dominated both systems, representing 85% (54% from enteric $CH_4$ and 31% from manure) of total emissions in the confinement system and 71% (58% from enteric $CH_4$ and 13% from manure) in the pasture-based system. Notably, the confinement system had 13% lower enteric $CH_4$ intensity and 88% lower prefarm embedded intensity (kg $CO_{2eq}$/kg FPCM) compared with the pasture-based system. However, manure-related GHG emission intensity was 129% higher in the confinement. The confinement and pasture-based systems had similar emission intensity for milk (1.02 ± 0.038 vs. 1.07 ± 0.069 kg $CO_{2eq}$/kg FPCM) and meat (5.51 ± 0.779 vs. 6.76 ± 0.868 kg $CO_{2eq}$/kg liveweight). Targeted mitigation strategies should be implemented for each production system to reduce emissions from manure in confinement systems but pre-embedded and fertilizer emissions in pasture-based systems, but enteric $CH_4$ is predominant in both systems.

**Key Words:** dairy, methane, nitrous oxide

**2444 Dairy farming system and land use influence soil organic carbon stocks.** M. F. Dida*[1,3], B. Minasny[2], S. C. Garcia[1,3], and L. A. Gonzalez[1,3], [1]*School of Life and Environmental Sciences, Faculty of Science, and Sydney Institute of Agriculture, The University of Sydney, Camden, NSW, Australia,* [2]*Sydney Institute of Agriculture, School of Life and Environmental Sciences, Faculty of Science, The University of Sydney, NSW, Australia,* [3]*Dairy UP Program, Camden, NSW, Australia.*

The intensification of agricultural practices has profound ecological implications, including adverse effects on carbon (C) sequestration and biodiversity. In dairy farming, intensification drives changes in land use toward more cropping, which can alter soil properties and soil organic C (SOC). Given these impacts, understanding the interplay between dairy farm farming system, land use, and soil characteristics is essential for developing sustainable on-farm land uses that enhance C storage and potentially offset greenhouse gas (GHG) emissions. Consequently, the present study aimed to examine SOC and other soil physicochemical properties across 6 common land use practices on confinement and pasture-based commercial dairy farms: improved pasture (IP), natural pasture (NP), mixed pasture-cropping (MPC), continuous forage cropping (CFC), tree areas (TA), and built-up areas (BA) with no grazing or cropping. A total of 810 soil samples were collected from 9 commercial dairy farms in New South Wales, Australia, at a depth of 0–30 cm. A mixed-effects model was used to assess the effects of land use type and farming system on soil physicochemical properties. SOC stock was highest in NP, followed by TA, IP, MPC, and CFC, with the lowest values in BA ($P < 0.001$). Land use type influenced total nitrogen stock ($P < 0.001$), but total phosphorus was not affected ($P > 0.05$). Pasture-based systems had higher ($P < 0.05$) SOC (105.0 ± 6.26 vs. 60.0 ± 7.00 Mg

C ha$^{-1}$) and total nitrogen stock (8.73 ± 0.654 vs. 5.30 ± 0.731 Mg N ha$^{-1}$), whereas total phosphorus stock (0.56 ± 0.118 vs. 0.15 ± 0.105 Mg P ha$^{-1}$) was greater ($P < 0.05$) in confinement systems. Overall, the NP, IP, and TA land use types, along with pasture-based dairy farming systems, showed greater SOC stocks. These results suggest that both farming systems and land use types could play a role in offsetting GHG emissions and contribute to climate change mitigation. However, further studies are needed to assess annual C sequestration rates for each farming system and land use type to quantify their potential for offsetting GHG emissions within dairy farms.

**Key Words:** dairy, confinement, pasture

**2445     Factors influencing lactose production in dairy cows.** J. I. Gargiulo*[1,4], S. C. Garcia[2,4], and R. C. Hovey[3,4], [1]*New South Wales Department of Primary Industries and Regional Development, Menangle, NSW, Australia,* [2]*Dairy Science Group, School of Life and Environmental Sciences, Faculty of Science, The University of Sydney, Camden, NSW, Australia,* [3]*Department of Animal Science, University of California–Davis, Davis, CA,* [4]*Dairy UP Program, Camden, NSW, Australia.*

Lactose is the primary carbohydrate in bovine milk and determines milk volume by influencing its water content. The concentration of lactose, along with other milk solids, varies across species and cow breeds. However, large-scale data on lactose are scarce, and no studies have examined the factors influencing its variability and production in Australia. We analyzed 393,772 herd test records from 33,280 cows across 85 farms in New South Wales (2008–2022), to assess the relationship between lactose output and milk yield (MY), composition and quality, genetics, and environmental factors. We used Pearson correlations and linear mixed modeling to examine the effects of parity, lactation stage, breed, year, season, climate, heritability, as well as differences between the overall population and cows consistently producing higher milk solids yield (MSY, fat yield + protein yield) per unit of lactose yield (LY). LY, lactose percentage (LP), and MSY varied significantly by breed, parity, lactation stage and season. Both LY and LP peaked in early lactation and declined as lactation progressed, consistent with the traditional MY curve. LY increased with parity number while LP decreased. Lactose yield was negatively correlated with milk fat and protein percentages and environmental factors such as the temperature-humidity index, whereas LP was negatively associated with SCC. Holsteins had the highest daily LY (1.24 kg) and MSY (1.80 kg) but the lowest LP (4.95%), while Jerseys produced the lowest LY (0.93 kg) and MSY (1.57 kg) and had the highest MSY:LY. Heritability estimates suggested a moderate genetic influence on LY, LP, and MSY:LY (0.24–0.33). Cows with higher MSY:LY produced 18% less LY and 15% less MY but maintained similar MSY. These cows were primarily Jerseys, Holsteins, and crosses, and were overrepresented as progeny of 13 sires. These findings highlight key factors influencing lactose production and identify cows that produce lower milk volumes while maintaining MSY, a trait aligned with local milk payment systems. Identifying these cows and their genetic backgrounds offers opportunities for targeted breeding programs to enhance milk production efficiency and composition while reducing environmental impact.

**Key Words:** lactose, variability, productivity

**2446     Microbial diversity using meta-transcriptomics in dairy calves: An insight of the resistome and virulome in health and enteric disease.** Z. U. Abedien[1,4], S. P. Djordjevic[1], I. J. Lean[2,4], J. Webster[3], and B. P. Brito*[3,4], [1]*Australian Institute for Microbiology*

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Microbial communities in dairy calves significantly impact their health, influencing the occurrence of enteric and respiratory diseases. A deeper understanding of microbial diversity in health and disease is critical for improving diagnostic and treatment approaches. This study aimed to explore the microbial diversity and gene expression patterns of various virulence and antimicrobial factors in rectal samples from dairy calves with varying health conditions and 4 different age groups sampled across 72 farms in New South Wales, Australia. A total of 593 rectal samples including 168 from calves with diarrhea were analyzed using high-throughput RNA sequencing. Bacterial taxonomy was assessed using MetaPhlAn 4, calculating α (Shannon and Simpson indices) and β (Bray–Curtis dissimilarity) diversity. Virulence factors and antimicrobial resistance gene expression were also assessed within each age group and disease status. The analysis revealed a complex microbial landscape characterized by approximately 1,000 distinct bacterial genera with top genera including *Anaerovibrio*, *Prevotella*, and *Segatella*. Healthy calves had significantly higher diversity compared with symptomatic calves. Differential expression analyses showed that although antimicrobial resistance genes (e.g., cfxA, Sul2, TetQ, dfrA-12, and aph(6)-la) were present across different age groups, they were significantly greater in calves with diarrhea compared with the healthy calves. Similarly, virulence factors such as afaE VIII, espB, espD, ompA 28, and PorA were distinctly elevated in symptomatic calves compared with asymptomatic calves. This study highlights the diversity of bacterial communities in dairy calves and their association with disease status in relation to virulence factors and antimicrobial resistance genes providing important insights that may inform future strategies for improving calf health and antimicrobial stewardship in the dairy industry.

**Key Words:** metatranscriptomics, virulence factor, enteric disease

**2447     Potential of HSP70 as a noninvasive biomarker for detecting heat stress in dairy cow.** M. R. H. Rakib*[1,5], V. Messina[1,5], J. I. Gargiulo[2,5], J. Nguyen[1,5], N. A. Lyons[3], I. N. Pathirana[4], and S. C. Garcia[1,5], [1]*Dairy Science Group, School of Life and Environmental Sciences, Faculty of Science, The University of Sydney, Camden, NSW, Australia,* [2]*NSW Department of Primary Industries and Regional Development, Menangle, NSW, Australia,* [3]*DairyNZ, Hamilton, New Zealand,* [4]*Department of Animal Science, Faculty of Agriculture, University of Ruhuna, Kamburupitiya, Sri Lanka,* [5]*Dairy UP Program, Camden, NSW, Australia.*

Heat stress (HS) negatively impacts dairy cows, leading to reduced milk production, impaired reproduction, and compromised welfare. Recently, the presence of heat shock protein 70 (HSP70) in bovine milk has been identified as a potential noninvasive biomarker for detecting HS in cows. This study aims to evaluate various methods for detecting HS in dairy cows, with a particular focus on assessing the effectiveness of HSP70 as an indicator. Data from 25 Holstein Friesian cows (third parity, 114 ± 8.3 DIM) in a pasture-based system were collected every 2 d over a 7-wk period at The University of Sydney's Dairy Farm, NSW, Australia. Variables included rectal temperature (RT), infrared thermography (IRT), milk HSP70 concentration (by competitive ELISA, sensitivity: 7.82–4,000 ng/mL), milk yield (L/day) and composition (protein, fat, SNF, lactose). Per-minute reticulorumen temperature (RRT) via bolus sensor and meteorological data from the nearest weather station were also collected over the period of the study. Pearson correlation analyses