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 and 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.*

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