ated with enteric disease were rotavirus and bovine kobuvirus, while bovine rhinitis virus A showed the strongest association with respiratory disease. Additionally, viral infections were significantly associated with specific age categories (0–7, 8–14, 15–42, and >42 d), particularly for some species of caliciviruses and picornaviruses. Viral detection was widespread among the 72 farms sampled, with kobuvirus present in 69 farms and bovine rhinitis virus A in 30 farms. We reconstructed the evolutionary relationships of 15 viral species for phylogenetic analysis, revealing substantial diversity in bovine rhinitis viruses A and B, bovine picornaviruses, and caliciviruses. Viral characterization at the genotype level enables a better understanding of the variants associated with disease. This level of resolution is critical for developing more sensitive diagnostic tools capable of distinguishing pathogenic strains.

Key Words: metagenomics, infectious diseases, calves

1447 Investigating genotype and environment effects on the rumen microbiome. H. M. Golder*[1,2] and I. J. Lean[1,2], *[1]Scibus, Camden, NSW, Australia, [2]Dairy UP Program, Camden, NSW, Australia.*

Currently there is a lack of capacity to rapidly and accurately detect rumen dysbiosis. Our objective is to improve phenotypic definitions of the rumen microbiome and metabolome to better utilize host and environment interactions to rumen challenges to enhance productivity. Our investigations of ruminal acidosis suggest that there would be an incidence of 500 cases over the first 100 DIM per 100 cows. There is marked among animal variation in response to typical and challenge environments. The task is to quantify the distribution of risk over time among cows given the temporal dynamic nature of the rumen environment and its microbiome, especially when perturbed. In a 293-cow multisite and -country GWAS, there was only a tendency for an association with being in the low-risk acidosis category. There were associations between the host and relative abundance of individual bacterial phyla and families and markers or tendencies for markers for acetate, butyrate, iso-butyrate, iso-valerate, and caproate. Others demonstrate some rumen microbes have a heritability of $\geq$0.15. The rumen microbiome has substantial redundancy, which can produce inefficiency but offers protection against perturbation. Ruminants have a host-specific core microbiome, likely critical for basic function and a noncore probably for resilience. Investigation and understanding of the non-core may open greater potential for successful manipulation. Challenges in defining the rumen phenotype include what, where, who, and how often we should measure with high repeatability. We need to know whether some cows have nearly constant perturbation, while others exposed to the same diets are stable. Dairy UP is validating some potential markers and technologies from sensors, sniffers, artificial intelligence, camera surveillance, and bodily fluids at the individual and herd level to quantitate the lagged production responses and recoveries to dysbiosis. In summary if we don't appropriately define phenotypes of the rumen microbiome and metabolome we will not progress the field and optimize health and production.

Key Words: acidosis, dysbiosis, phenotype

1448 The positive associations between calf and lactation performances in dairy cattle. S. W. J. Legge*[1,4], P. C. Thomson[1,3], C. E. F. Clark[1,2], and S. C. García[1,4], *[1]Dairy Science Group, School of Life and Environmental Sciences, Faculty of Science, The University of Sydney, Camden, NSW, Australia, [2]Sydney Institute of Agriculture, The University of Sydney, Camperdown, NSW, Australia, [3]Sydney School of Veterinary Science, Faculty of Science, The University of Sydney, Camden, NSW, Australia, [4]Dairy UP Program, Camden, NSW, Australia.*

Australian dairy farms are increasingly capturing a wealth of data throughout the lifecycle of animals through the deployment of technology. This includes, among other data, details such as the sex of the calf, calving difficulty, health interventions, movement events, calving dates and parity, and milk production quantities. The underutilization of these extensive data presents a significant opportunity to optimize management practices, and drive improvements in productivity. The relationships between birth weight (BWT), weaning weight (WWT), lactation performance, and key production parameters have been explored in efforts to improve dairy cattle management. Our initial study demonstrated that there were potential indicators of high and low performance (measured as WWT) at very early age. Whether WWT relates to future lactation performance, both in terms of milk yield and number of lactations, remains unclear. Here, data from a cohort of 1,440 female Holstein Friesians were used to assess the impact of WWT (proxy for calf-rearing performance) on the number of lactations, milk yield per lactation and total lifetime milk yield. This study assesses how calf-related measurements might affect first lactation, lifetime production and age when animals are removed from production. Our results from modeling reveal that although BWT showed a slight positive linear trend with lactation-specific milk yield and a significant effect, the influence of WWT was far more pronounced with an additional 53.1 ± 8.5 kg milk yield/kg WWT in each lactation. Moreover, WWT exhibited a strong positive effect on lifetime milk yield and the likelihood of completing multiple lactations. Notably, we observed that calf performance at weaning significantly impacted the probability of remaining within the herd, where a calf with a WWT of 50 kg has a probability of 0.17 of attaining 3 or more lactations compared with 0.41 for a calf with a WWT of 100 kg. This has implications for overall lifetime productivity. These findings underscore the importance of early calf management and management decisions in optimizing milk production and herd sustainability.

Key Words: weaning weight (WWT), lactation performance, productivity

1449 Evaluation of the effects of an enzymatic and biological additive on bedding in compost-bedded pack barns in Australia. A. Lean*[1,3], H. M. Golder[2,3], J. Quinn[1], I. J. Lean[2,3], D. Sheedy[2,3], and A. Gunn[1], *[1]School of Agricultural, Environmental and Veterinary Sciences and Gulbali Institute, Charles Sturt University, Wagga Wagga, NSW, Australia, [2]Scibus, Camden, NSW, Australia, [3]Dairy UP Program, Camden, NSW, Australia.*

Bedding management in compost-bedded pack barns (CBPB) can be challenging. Maintaining a low-moisture and high-heat environment within the bedding is key to CBPB management. Manure Pro (Lallemand, Blagnac-Cedex) is a bedding additive we aim to assess for use in CBPB. A 5-wk exposure study was conducted on 40 areas in 5 CBPB in South-Eastern Australia from July 2023 to August 2024. Areas were monitored for bedding temperature at 10 to 25 cm, aerial ammonia (NH_3) and cow numbers within each area every 2 ± 1 d. Daily measures of external temperature, humidity and rainfall were recorded. Three farms were monitored for pack weekly moisture, carbon:nitrogen (C:N) levels and time cultivating the pack. The bedding was divided into treatment and control areas alternating along the bedded pack. Areas were monitored for 1 wk before treatment application at wk 2 and 4. Mean bedding temperatures per farm ranged from 19.29°C (SD 1.76) to 37.93°C (SD 3.42). Outcome means for control and treatment were bedding temperature 30.07°C (SD 7.37) and 30.09°C (SD 7.43), percentage of cows per area 4.99% (SD 4.34) and 5.01% (SD 3.95), moisture 43.36% (SD 6.04) and 43.32% (SD 6.26), NH_3 0.03 ppm (SD 0.24) and 0.01 ppm (SD 0.15) and C:N ratio 12.47 (SD 1.39) and 12.71 (SD 1.59). Mixed models were used to evaluate the effects of treatment over time on bedding temperature, moisture, and cow preference with no changes ($P > 0.05$) being found. Ammonia was detected on 6 monitoring days over 3 farms. The farms evaluated for C:N were below the recommended 30:1, which is expected to cause increased microbial NH_3 production in the bedding and increased aerial NH_3 in the barn but this did not occur. There was no clear benefit of Manure Pro treatment in the study farms. A low C:N ratio may have led to reduced effectiveness in these CBPB. More studies to understand the interactions of Manure Pro with bedding should include cultivation time, moisture, C:N and controlled use of material additions.

Key Words: cow preference, ammonia, bedding temperature

1450 AI for a dairy cattle heat tolerance phenotype.

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Climate change and extreme weather events pose substantial risks to dairy cattle production and welfare, with heat stress being a major disruptor. Current approaches for heat tolerance phenotype selection in dairy cattle primarily use statistical models. To enhance selection of heat-tolerant dairy cattle, we integrate AI with a statistical genetic model that links heat tolerance to declines in milk, fat, and protein yield with temperature-humidity index (THI) rising above 60. This decline is modeled at both herd "population" and individual level, where the individual decline per unit increase in THI is represented by the corresponding random slope with the intercept providing the baseline. For this modeling, 20 yr of climate data were preprocessed and combined with New South Wales dairy cow herd test data for the Holstein breed, covering the same time period and resulting in 1.3 million records. Comparative analysis between the statistical and AI-based models demonstrated that the AI model had a smaller standard deviation of the residuals (3.25 L/d) compared with that for the statistical model (3.37 L/d). A high correlation ($R^2 = 0.90$) was observed between the random slopes estimated by both models, indicating that the models resulted in similar heat tolerance estimates but with a meaningful difference emphasized by the lower modeling error for the AI-based approach. A negative association between estimated random intercepts and slopes was identified, indicating that highly producing animals are less heat tolerant. Further analysis for heritability of the 2 traits (slope and intercept) using each method were done resulting in intercept: 0.354 ± 0.007, and slope: 0.166 ± 0.006 for the AI model, and intercept: 0.362 ± 0.007 and slope: 0.140 ± 0.006 for the statistical model. Our findings highlight the importance of considering both traits to improve the selection for heat tolerance without compromising overall production levels. The proposed model combines the strengths of statistical modeling with the capabilities of AI, resulting in a more accurate and efficient means of identifying heat-tolerant cattle.

Key Words: heat stress, individual cattle level, milk production