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

1444 Case definition and metabolic disorders: More accurate phenotypes. I. J. Lean*[1,2], H. M. Golder[1,2], D. Sheedy[1,2], C. Old[3], and A. Lean[4,2], *[1]Scibus, Camden, NSW, Australia, [2]Dairy UP Program, Camden, NSW, Australia, [3]A3 Cattle Company, LeGrand, CA, [4]School of Agricultural, Environmental and Veterinary Sciences and the Gulbali Institute, Charles Sturt University, Wagga Wagga, NSW, Australia.*

Our objective is to more accurately define phenotypes of metabolic disorders. A lack of precision and clarity in defining metabolic disorders results in suboptimal progress in understanding, prevention, and treatment of these. Nondifferential errors in classification for dichotomous disorders result in weaker associations and drive hypotheses toward the null; differential errors result in unpredictable outcomes. For continuous variables, misclassification can result in differential errors; the degree and direction of this varies with the exposure distribution, category definitions, measurement error distribution, and the exposure-disorder relationship. Implications for definitions of feed efficiency (FE), ruminal acidosis, and lameness, and genetic progress are considered. Efficiency of beef and dairy cattle has been estimated by residual feed intake (RFI) based on residual estimates from a model predicting DMI as a function of ADG and $BW^{0.75}$. Residuals derived from the model include true variation in FE, but variation from a latent variable, composition of tissue gain, that is protein, fat, and other reserves that are gained and maintained with different efficiencies. Differences in RFI ranking of beef cattle for this model and others that include estimated change in body composition exist. In dairy cattle, inconsistencies exist between the RFI rank of heifers and cows. Genetic selection based on flawed RFI models raises the risk of selection for less fit genotypes. Ruminal acidosis is a prevalent disorder of cattle, but its temporal nature and the heterogeneity of the rumen both within and between days limits the diagnostic value of pH alone. Definitions not solely based on ruminal pH offer a potential for better phenotypic characterization and selection of more fit genotypes possibly improving production and health. Lameness has a low heritability; however, this is not a single disorder and evaluating these conditions as such raises the potential for differential and nondifferential error. Data provided to assess lameness are characterized by under-reporting and also have temporal challenges. DairyUP structures will and have been designed to address challenges of disorder definition to more accurately define phenotypes.

Key Words: feed efficiency, genotypes, ruminal acidosis

1445 Do cows in total mixed ration systems have old lipid profiles compared with pasture-based cows? D. B. Sheedy*[1,6], H. M. Golder[2,6], S. C. Garcia[1,6], Z. Liu[3], P. Reddy[3,4], P. Moate[5], S. J. Rochfort[3,4], J. E. Pryce[3,4], and I. J. Lean[2,6], *[1]School of Life and Environmental Sciences, Faculty of Science, The University of Sydney, Camden, NSW, Australia, [2]Scibus, Camden, NSW, Australia, [3]Agriculture Victoria Research, AgriBio, Centre for AgriBioscience, Bundoora, VIC, Australia, [4]School of Applied Systems Biology, La Trobe University, Bundoora, VIC, Australia, [5]Melbourne, VIC, Australia, [6]Dairy UP Program, Camden, NSW, Australia.*

Disease and herd removal risks increase with parity, yet the underlying biochemistry of aging in cows is unknown. Feeding system may affect lipid profiles, but the consequences on aging and subsequent health is unknown. The objective of this cross-sectional study was to explore associations of plasma lipids with age, parity, and feeding system (TMR vs. pasture-based [PB]). Plasma was collected from dry (n = 696, ~27 d prepartum), and peak-milk cows (n = 796, ~58 DIM) in a stratified (parity: 1, 2, 3, >3) random sample from 15 PB and 15 TMR farms. A targeted liquid chromatography-MS approach quantified 185 lipid species, including phospholipids, sphingomyelins, and triacylglycerols. Dry and peak-milk cohorts were analyzed separately. Machine learning algorithms identified lipid classes stably associated with age and parity (multiple linear regression, partial least squares [PLS], random forest [RF], support vector machine), and feeding system (sparse logistic regressions, PLS, RF). Older and greater parity cows were associated with low concentrations of phospholipids with the long-chain polyunsaturated omega-3 (n-3) fatty acids (FA) of eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA). Dry PB cows had greater phospholipids containing α-linolenic acid (ALA, 18:3 n-3) and ALA derivatives than TMR cows. Peak-milk TMR cows had increased phospholipids containing linoleic acid (LA, 18:2 n-6) and its derivatives than PB cows. The n-3 FA are linked to improved immune function, cattle health, reproduction, and milk quality, while n-6 FA are pro-inflammatory. Importantly, both ALA and LA are essential FA that cannot be synthesized by the body and must be provided in the diet. These findings suggest that TMR cows experience a comparatively low n-3, high n-6 lipid environment, resembling an older cow lipid profile. We speculate that the different FA profiles of pasture (high ALA, low LA) and maize silage (low ALA, high LA) contribute to this observation. The different contributions of pasture and maize silage in diets of PB and TMR farms could theoretically have unintended consequences on cattle health and longevity.

Key Words: n-3 fatty acids, lipidomics

1446 The enteric and respiratory viral diversity of calves in health and disease—A state-wide metatranscriptomic study. B. P. Brito*[1,4], Z. U. Abedien[2,4], and I. J. Lean[3,4], *[1]New South Wales Department of Primary Industries and Regional Development (DPIRD), Elizabeth Macarthur Agricultural Institute, Menangle, NSW, Australia, [2]Australian Institute for Microbiology and Infection, University of Technology Sydney, Ultimo, NSW, Australia, [3]Scibus, Camden, NSW, Australia, [4]Dairy UP Program, Camden, NSW, Australia.*

Despite extensive diagnostic efforts, many cases of respiratory disease and diarrhea in cattle remain unresolved due to inconclusive etiological findings. Untargeted metagenomics is a powerful approach for pathogen detection, enabling the comprehensive identification of microorganisms. In this study, we estimated the occurrence of viral species and genotypes in dairy farms across New South Wales, Australia. A total of 72 farms were sampled, with a proportional distribution across all dairy regions. Samples were collected from calves younger than 49 d. RNA was extracted from nasal and rectal swabs of 918 calves, and total RNA sequencing was performed on 408 nasal and 593 rectal swabs from calves with varying disease statuses. Additionally, a survey on calf management practices was completed by 52 farms. In total, at least 22 viral species and multiple genotypes were identified. To assess the association between viral presence and disease, transcriptomes were mapped to the identified viral genomes using Kallisto v0.5.1.1, and the relative abundance of viral reads was analyzed using DESeq2 v1.44.0 to compare diseased and healthy calves. The viruses most strongly associated 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 ≥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),