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 associ-