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