

Exploring dairy farmer well-being in the context of animal health and welfare: A One Welfare perspective

A. Le Heiget¹, H. Tambadou¹, B. Zwick¹, V. Fraser-Celin², B. Hagen², A. Jones², J. Kinley¹, E. Pajor³, J.C. Plaizier¹, K. Ominski¹, and M. King¹.
¹University of Manitoba; ²University of Guelph; ³University of Calgary; meagan.king@umanitoba.ca

Dairy farmers are faced with many challenges that come with caring for animals, a phenomenon of interest to the growing concern for the mental health of farmers. To adequately address the needs of dairy and livestock farmers, a deeper understanding of the interconnections between farmer well-being, technology, and animal health and welfare is needed. The objective of this study was to explore dairy farmer well-being in the context of animal health and welfare. An interview guide was created in collaboration with industry stakeholders, academics, and dairy farmers, and was used by the lead author (ALH) to conduct semi-structured interviews with 30 dairy farmers from Western Canada and Ontario. Farmers were selected to represent various age groups, genders, housing systems, and milking systems. The average length of interviews was 77 minutes. The topics discussed included relationships and labour, technology, well-being, animal health, mental health resources, and coping. Interviews transcripts were open-coded by 4 authors (ALH, BH, AJ, VFC) to create a codebook. Preliminary themes indicate that dairy farmer well-being is interconnected with the herd health/welfare and macro- and micro-environments. For example, when farmer well-being is put on the 'backburner' to care for animals, the farmers' physical health and mental health may be negatively impacted; thus, if they are not able to function at their full capacity, this may lead to compromised animal care, further posing risks to animal health and welfare, which is directly linked to production.

Take home message: Emphasis is often placed on the animals within food systems rather than the farmers' that care for them. This study highlights a need for targeted approaches to bring awareness to the well-being of dairy and livestock farmers, and to ensure there are resources available with adequate (agri)cultural competency to support the farmers who produce our food.

A comprehensive evaluation of the genetic background of rumination time in first-lactation dairy cows

L. Lopes¹, F. Schenkel¹, D. Tulpan¹, C. Baes^{1,2}

¹Centre for Genetic Improvement of Livestock, University of Guelph, 50 Stone Road E, N1G 2W1, Guelph, Ontario, Canada, ²Institute of Genetics, Department of Clinical Research and Veterinary Public Health, University of Bern, Bern, 3001, Switzerland e-mail: llopes@uoguelph.ca

The Canadian dairy cattle industry is committed to reducing greenhouse gas emissions. Rumination time (RT) has shown potential as a proxy for several traits, including enteric methane emission (ME) of dairy cattle. However, despite its relevance, little is known about the genetic background of RT. Moderate heritability estimates for RT support further investigation of its genetic architecture. Therefore, our objectives were to: (1) conduct a Genome Wide Association Study (GWAS), identify candidate genes and carry out Quantitative Trait Locus (QTL) enrichment analysis for RT; (2) assess the combined use of RT and milk mid-infrared spectra (MIR) data in machine learning algorithms for ME predictions. A total of 452 mid-first lactation Canadian Holstein cows were genotyped with a 50K panel. Single Nucleotide Polymorphism (SNP) effects were estimated using single-step genomic BLUP, and significant SNPs were identified after a chromosome-wise modified Bonferroni correction. Thirty-five SNPs and 37 genes were associated with RT, and 167 QTLs were enriched, linking RT to fat synthesis and deposition in milk and muscle. Gene Ontology and Kyoto Encyclopedia of Genes and Genomes terms showed that RT is related to synaptic functions. We also assessed the performance of different data sets for predicting ME using artificial neural networks, combining unprocessed or processed MIR data and RT (N = 423). The inclusion of RT did not increase the prediction ability of alternate data sets with or without the inclusion of MIR data. Our results indicate that RT seems to be a weak predictor of ME in dairy cows, but investigations with larger datasets should be carried out to confirm our results. Nevertheless, our findings offer insights into the genetic architecture of RT and enhance the understanding of its physiology.

Take home message: Rumination time is a polygenic trait that seems associated with milk fat production. However, rumination time seems to be a poor predictor of methane emission in dairy cows.