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# Breeding and Genetics I

**M100 Genetic evaluation of gestation length as a trait of the service sire.** J. R. Wright\* and P. M. VanRaden, *Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

Predicted transmitting abilities (PTA) for gestation length (GL) were developed for all dairy breeds and crossbreds. Initial GL edits gave 20.5 million records of 10.8 million cows and included GL after either heifer or cow inseminations. Preliminary analysis revealed a very negative genetic trend in the last 2 years (toward shorter gestation), causing concerns about effects of unreported embryo transfer (ET) or sexed semen. Further edits required a sex code from the calving ease database and a pedigree record for each calf to determine its ET status. Those edits reduced the data to 12.4 million records of 6.8 cows born since 1990. The model included effects of conception month, age-parity of dam, breed of dam, offspring code, herd-year-season, service sire, permanent environment of dam, and error. PTA were computed for all 73 million animals from their additive relationships to the sires. An animal model for GL as a trait of the calf might provide higher reliability by using maternal genetic relationships for dams, but the focus here was on service sire direct genetic effects, which were nearly 4 d shorter for Holsteins and Jerseys than for Brown Swiss and Guernseys. Heritability estimates computed as 4 times the service sire variance were 0.48 from heifers and 0.44 from all lactations (heifers and cows) based on 5 million Holstein GL records. The GL PTA for recent Holstein bulls (born 1995 or later with 90% or higher reliability) have a minimum of -5.6 and maximum of +6.4 and a SD of about 1.4 d. Jersey and Brown Swiss bulls both had the same SD of about 1.4 after adjustment to within-breed bases but had smaller ranges of values than Holstein due to fewer bulls: -4.2 to +5.0 for Jersey; -3.6 to +5.6 for Brown Swiss. Genomic predictions for Holsteins averaged 65% reliability. Short GL is favorably correlated by about 0.38 with daughter calving ease and by about 0.24 to 0.29 with yield and productive life. Thus, current strong selection for these correlated traits has already decreased GL in recent years. Gestation length (GL) can be useful in mating programs to group all birth dates together in seasonal calving, managing maternity pens, or improving calving ease as a correlated trait. Official GL evaluations are expected in 2017.

**Key Words:** gestation length, genomic prediction, calving management

**M101 Genetic correlations among Canadian selected traits: literature review and completion of the matrix of correlations.**

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In the past few years, several new phenotypes have been recorded in the Canadian dairy industry such as metabolic diseases and hoof health. With the addition of these novel traits, there are now a considerable number of traits considered for selection and over 80 traits are routinely evaluated by CDN. However, this quick increase in the number of traits has been done without a systematic estimation of the genetic correlations among traits. Not taking the genetic correlations into account can lead to a loss in selection efficiency, especially for traits with low heritability for which its relationship with another trait may have a large influence during the selection process. As part of the Efficient Dairy Genome Project (<http://genomedairy.ualberta.ca>) indexes for feed efficiency and methane

emissions are in development, as well as their inclusion in the Canadian composite indexes (LPI and Pro\$). As genetic correlations between these 2 new traits and the already evaluated ones will be needed, this is the proper time to look at the existing correlations among evaluated traits and estimate any missing ones. First, a selection of 35 of the 80 traits was performed. The first level of composite index rather than the individual index was taken for the conformation traits to avoid the multiplication of traits. As well, a few traits were discarded due to their nature of not being suitable for correlation estimation. Then, the Canadian literature was reviewed to fill the matrix of correlations. After this review, we found that correlations among traits within the same type of trait were mostly already calculated. However, there were few reported estimations of correlations between traits belonging to different groups of traits. We also identified some correlations that were calculated too far in the past and need to be re-evaluated. The next step will be the completion of the matrix with new estimations and the calculation of correlations with feed efficiency and methane emissions. This work is an opportunity to complete the knowledge of the Canadian traits, and the use of this new information will improve current and future dairy selection.

**Key Words:** genetic correlations

**M102 Breeding strategies for mitigating enteric methane emissions of dairy cattle using ZPLAN+.** S. Beard\*<sup>1</sup>, F. Miglior<sup>1,2</sup>, F. Schenkel<sup>1</sup>, B. Gredler<sup>3</sup>, P. Martin<sup>1</sup>, A. Fleming<sup>1</sup>, and C. Baes<sup>1</sup>, <sup>1</sup>*Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada,* <sup>2</sup>*Canadian Dairy Network, Guelph, ON, Canada,* <sup>3</sup>*Qualitas AG, Zug, Switzerland.*

Mitigation of methane (CH<sub>4</sub>) emissions in dairy cattle production has become of particular concern in recent years, as it has been identified as being one of the most prevalent non-CO<sub>2</sub> greenhouse gasses contributing to climate change. To date, there have been studies describing the reduction of enteric CH<sub>4</sub> emissions through nutritional and microbial manipulation, though there is potential for greater and more permanent progress using genetic selection. It has been shown that there is sufficient genetic variation in enteric CH<sub>4</sub> to be possible to reduce its emission through selection programs. Determining an optimal breeding strategy for mitigation of CH<sub>4</sub> emissions would help reduce the environmental impact of the Canadian dairy industry. Enteric CH<sub>4</sub> production itself is challenging to measure directly, so selection on correlated traits to indirectly reduce CH<sub>4</sub> may be more cost effective and less labor intensive. Heritabilities along with genetic and phenotypic correlations between CH<sub>4</sub> emission and other traits of interest will be compiled or estimated. ZPLAN+ will be used to simulate and analyze breeding strategies that include CH<sub>4</sub> emission as a novel trait. ZPLAN+ is a software that allows the modeling and calculation of complex animal breeding scenarios using genomic information. The software will be used to model genetic gain, monetary returns, and costs associated with including this trait in the selection index for the Canadian Holstein population. Additionally, long-term effects of the proposed selection index and the correlations between CH<sub>4</sub> emissions and other traits of interest included in the current breeding strategy will be analyzed. Outputs from this project will provide insight for the Canadian dairy industry as how to best include new information into the existing selection index to reduce CH<sub>4</sub> emissions.

**Key Words:** methane, genomics, animal breeding