Breeding and Genetics I

M100  Genetic evaluation of gestation length as a trait of the service sire. J. R. Wright* and F. 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 PTA were based on 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. 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. P. Martin*,1, C. Baes1, K. Houlanan1, S. Beard1, C. Richardson1, and F. Miglior1,2, 1University of Guelph, Department of Animal Biosciences, Guelph, ON, Canada, 2Canadian Dairy Network, Guelph, ON, Canada.

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*1, F. Miglior1,2, F. Schenkel1, B. Gredler3, P. Martin1, A. Fleming1, and C. Baes1, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Canadian Dairy Network, Guelph, ON, Canada, 3Qualitas AG, Zug, Switzerland.

Mitigation of methane (CH₄) 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-CO₂ greenhouse gasses contributing to climate change. To date, there have been studies describing the reduction of enteric CH₄ 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 CH₄ to be possible to reduce its emission through selection programs. Determining an optimal breeding strategy for mitigation of CH₄ emissions would help reduce the environmental impact of the Canadian dairy industry. Enteric CH₄ production itself is challenging to measure directly, so selection on correlated traits to indirectly reduce CH₄ may be more cost effective and less labor intensive. Heritabilities along with genetic and phenotypic correlations between CH₄ emission and other traits of interest will be compiled or estimated. ZPLAN+ will be used to simulate and analyze breeding strategies that include CH₄ 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 CH₄ 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 CH₄ emissions.

Key Words: methane, genomics, animal breeding
M103  Genome-wide copy number variant analysis in Holstein cattle reveals variants associated with 10 production traits including residual feed intake and dry matter intake. E. E. Connor1, Y. Zhou1, G. R. Wiggans1, Y. Lu1, R. J. Tempelman2, S. G. Schroeder1, H. Chen1, and G. Liu1, 1Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, 2Canadian Dairy Network, Guelph, ON, Canada, 3Northwest A&F University, Yangling, Shaanxi, China.

Copy number variation (CNV) is an important type of genetic variation contributing to phenotypic differences among mammals and may serve as an alternative molecular marker to single nucleotide polymorphism (SNP) for genome-wide association study (GWAS). Recently, GWAS analysis using CNV has been applied in livestock, although few studies have focused on Holstein cattle. Here, we describe 191 CNV of high confidence that were detected using SNP genotypes generated with the BovineHD Genotyping BeadChip (Illumina, San Diego, CA) among 528 Holstein cows. The CNV were used for GWAS analysis of 10 important production traits of cattle related to feed intake, milk quality, and female fertility, as well as 2 composite traits of net merit and productive life. In total, we detected 57 CNV associated (P < 0.05 after false discovery rate correction) with at least one of the 10 phenotypes. Focusing on feed efficiency and intake-related phenotypes of residual feed intake and dry matter intake, we detected a single CNV (CNV1) associated with both traits which overlaps predicted olfactory receptor gene OR2A2 (LOC787786). Additionally, 2 CNV (CNV32 and CNV66) within the RXFP4 and 2 additional olfactory receptor gene regions, respectively, were associated with residual feed intake. The RXFP4 gene encodes a receptor for an orexigenic peptide, insulin-like peptide 5 produced by intestinal L. cells, which is expressed by enteric neurons. Olfactory receptors are critical for transmitting the effects of odorants, contributing to the sense of smell, and have been implicated in participating in appetite regulation. Our results identify CNV for genomic evaluation in Holstein cattle, and provide candidate genes contributing to variation in feed efficiency and feed intake-related traits.

Key Words: dairy cow, genome-wide association study, copy number variation

M104  Association of residual feed intake with disease indicator traits in Holsteins. D. Haillemariam1, G. Manafizar4, J. Basarab1,2, M. Miglior1,2, G. Plastow1, and Z. Wang1, 1Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, 2Alberta Agriculture and Forestry, Lacombe, Alberta, Canada, 3Canadian Dairy Network, Guelph, ON, Canada, 4CGIL Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada.

The objective of this study was to investigate the association of residual feed intake (RFI) with routinely measured milk components that are indicators of subclinical mastitis and ketosis. Milk somatic cell count (SCC, 103 cells/mL) is commonly used to diagnose subclinical mastitis while β-hydroxybutyrate (BHB, mmol/L) and acetone (ACT, mmol/L) are indicators of ketosis. RFI was phenotyped in 71 lactating Holstein dairy cows at the Dairy Research and Technology Center–University of Alberta with components of metabolic body weight, empty body weight change, and milk production energy requirements over 255 d in milk using random regression and multiple linear regression models. Correspondingly, test-day milk samples were collected twice a week and analyzed at DHI lab by a MIR spectrometer (MilkoScan FT+, Foss, Hillerød, Denmark) during the same period as for RFI prediction. A total of 3,810 test day records for each of the traits; SCC, BHB and ACT were obtained from April to August 2016. The data were analyzed using a MIXED model procedure of SAS with fixed effects of RFI (-RFI and +RFI), lactation number (1, 2 and 3+), milking time (AM and PM), interactions of RFI x lactation, RFI x milking time and random effects of cow. Days in milk was included in the model as a covariate. The result indicated that -RFI and +RFI groups did not differ in SCC (381.01 ± 55.77 vs. 359.47 ± 47.14; P = 0.76), BHB (0.53 ± 0.07 vs. 0.64 ± 0.05; P = 0.25) and ACT (0.30 ± 0.06 vs. 0.32 ± 0.04; P = 0.75). The correlation analysis also showed no evidence of RFI association with SCC (r = 0.01; P = 0.91), BHB (r = 0.17; P = 0.17) and ACT (r = -0.042; P = 0.72). The result suggests that selection for RFI may not be negatively correlated with incidence of subclinical mastitis or ketosis in dairy cattle. Estimation of the genetic correlations of RFI with SCC, BHB, and ACT in a larger sample is warranted to confirm these preliminary results.

Key Words: RFI, mastitis, ketosis

M105  Use of RNA-sequencing technology for detection of microbial species. S. Lam1, F. Miglior1,2, L. L. Guan3, A. Islas-Trejo4, D. Seymour1, V. Asselstine1, L. F. Brito1, J. F. Medrano3, and A. Cánovas1, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Canadian Dairy Network., Guelph, ON, Canada, 3Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada., 4Department of Animal Science, University of California-Davis, Davis, CA.

Evaluation of the bovine transcriptome using RNA-Seq (RNA-Seq) has made substantial impact in assessing functional and structural genomes in cattle. A preliminary study evaluated the metatranscriptome of bovine milk to determine the composition and structure of bacterial populations influencing subclinical mastitis. Differences in bacterial presence in milk between healthy and mastitic quarters were found in Holstein cows using RNA-Seq technology. The objective of this study is to further evaluate the use of RNA-Seq technology to assess the non-mapped milk bacteria genome in dairy cattle. Transcriptomic and metagenomic analysis were performed using RNA-Seq technology and 16S ribosomal sequencing on milk collected from 4 quarters of healthy (n = 4) and mastitic (n = 4) dairy cows. Milk samples were collected 3 h after morning milking to obtain a high percentage of epithelial cells. Cow teats were cleaned with gauze (70% isopropanol) and milk was collected by hand milking directly into sterile 50 mL Falcon tubes or using a 3 cm plastic cannula to collect milk within the teat canal to avoid external contamination. Total RNA was extracted from somatic cells (SC) and milk fat globule (MFG) membrane from both hand milking and cannula milk samples. Using a RNA-seq analysis pipeline, preliminary results revealed that 60 to 75% of reads were categorized as mapped to the bovine reference sequence. All reads not mapping to the bovine genome were annotated for MFG (32% hand milking, 20% cannula) and SC (25% hand milking, 12% cannula). Analysis of SC non-mapped reads identified differences in microbial species present in healthy and mastitic milk. Further analysis will lead to more precise mapping of sequence data and improved understanding of bacterial gene expression, integrating data generated from RNA-Seq and 16S sequencing. Future assessment of the non-mapped reads using RNA-Seq will be performed to study the ability of RNA-Seq technology to capture invasive pathogens in milk and their association to genes differentially expressed in healthy and mastitic quarters. This assessment may lead to a comparative approach to examine the immune response to infection in dairy cattle.

Key Words: genome/host, transcriptomics/metatranscriptomics, RNA-sequencing technology
M106 Genetic trends of linear type traits for validation of genomic evaluation in US Holsteins. S. Tsuruta*,1, T. J. Lawlor1, D. A. L. Lourenco1, Y. Masuda1, and I. Misztal1, 1University of Georgia, Athens, GA, 2Holstein Association USA, Brattleboro, VT.

Proper modeling of genetic evaluations is necessary to obtain accurate forward predictions. Differences in genetic trends for genomic (G)PTA, traditional PTA, parent averages (PA), and daughter yield deviations (DYD) can illustrate a model’s ability to control bias due to genomic preselection and improper parameter choice. Phenotypes for 18 linear type traits and genotypes were provided by Holstein Association USA and USDA-ARS, respectively. The full data consisted of 10,067,745 records up to 2014 calving, 9,730,943 animals in pedigree, and 569,404 genotyped animals with 60K SNP. For validation of young genotyped animals who did not have phenotypes or daughters in 2010, 9,235,355 records and 105,116 genotyped animals were used to estimate genetic trends, comparing with those estimated from the full data set. The BLUP-P90IOD2 program was used to predict GPTA in 2010 and in 2014 with single-step genomic BLUP using the algorithm of proven and young animals. The trends were calculated separately for bulls with at least 50 daughters in 2014 and for cows with records. Assuming that GPTA in 2014 were the most accurate, GPTA in 2010 for more than half of the traits, when no parameter adjustments are made, showed some bias. Traits with directional selection, i.e., body size and udder traits, were overpredicted. Parent averages in 2014 were similar to PTA and DYD in 2014 and lower than GPTA in 2014. Traits with an intermediary optimum, such as rump angle and foot angle, showed little or no bias. Lowering the heritability slightly improved both the accuracy and predictability. Including an adjustment (weight <1.0) to the inverse of the relationship matrix of the genomic tested animals dramatically improved the predictability of the model with a slight decrease in accuracy. Future research is ongoing to fully understand how this adjustment is altering our assumptions in the basic model; e.g., how this adjustment is related to genetic parameters that could be different by generation and why some traits are not overpredicted without any adjustment.

Key Words: genomic evaluation, genetic trend, linear type trait

M107 Sources of variation in minor milk components and their potential prediction using mid-infrared spectroscopy. A. Fleming*,1, F. S. Schenkel1, S. Nayeri1, C. Baes1, R. A. Ali2, M. Corredig1,3, and F. Miglior1,5. 1Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, 2Department of Mathematics and Statistics, University of Guelph, Guelph, ON, Canada, 3Department of Food Science, University of Guelph, Guelph, ON, Canada, 4Gay Lea Foods Co-operative, Mississauga, ON, Canada, 5Canadian Dairy Network, Guelph, ON, Canada.

Variation in minor milk components is of interest to consumers and milk processors but additional knowledge is needed to ascertain its sources. A phenotyping tool such as mid-infrared (MIR) spectroscopy would help future inquiry into these traits on a large-scale routine basis. The objectives of this work were to examine the variation of characteristics and contents of minor milk components and assess the ability to predict them from MIR spectra of the milk. A total of 4,116 milk samples were collected from 421 cows representing 4 dairy breeds coming from 47 Canadian herds. The MIR spectra of the milk samples were obtained through DHI labs. Not all samples were analyzed for all traits, but some overlap occurred. Samples were analyzed for casein micelle size (n = 3,117), total (n = 986) and soluble (n = 937) calcium, lactoferrin (n = 2,054), and α-, β-, and κ-casein proportions (n = 2,067). Milk component traits were examined separately using a linear model including the effects of herd nested within breed, days in milk class, parity, season, and animal. Herd nested within breed, days in milk class, and season had significant effects on all examined traits. Significant differences were noted between breeds for casein micelle size, total calcium, lactoferrin, and casein proportions. Lactoferrin and casein proportions also differed between parities. Moderate and negative Pearson correlation coefficients were found for lactoferrin content with test-day milk, fat, and protein yields (P < 0.001). Moderate and positive Pearson correlation coefficients were found between lactoferrin and somatic cell score as well as total calcium and protein percentage (P < 0.001). Partial least squares regression using a 10-fold random subset cross-validation was used to predict the milk components from the MIR spectra. The average cross-validation R^2 (R^2_cv) values were very low for casein micelle size, total and soluble calcium, and α-, β-, and κ-casein proportions at 0.31, 0.24, 0.16, 0.03, 0.10, and 0.08, respectively. For lactoferrin a R^2_cv of 0.55 was found, which may allow for MIR predicted lactoferrin to serve as a limited indicator of the true lactoferrin content in milk.