Improving reproductive performance of dairy cattle has become one of the major challenges of the dairy industry worldwide. Most studies have investigated cow fertility while bull fertility has received much less attention. However, there is growing evidence that the service sire represents an important source of variation for conception rate in dairy cattle. As such, the main objective of this study was to perform a comprehensive analysis to reveal the genomic architecture underlying male fertility in dairy cattle. Sire Conception Rate was used as a measure of bull fertility including records in both Holstein and Jersey breeds. The analysis included the application of alternative genome-wide association mapping approaches and the subsequent use of gene set enrichment tools. The association analyses identified several genomic regions strongly associated with bull fertility. Most of these regions harbor genes, such as CCT6A, CKB, IGF1R, KAT8 and TDRD9 with functions related to sperm biology, including sperm development, motility and sperm-egg interaction. Some regions showed marked dominance effects, which provide more evidence for the importance of non-additive effects in fitness traits such as male fertility. Moreover, gene set analyses revealed many significant Gene Ontology and Medical Subject Headings terms, including fertilization, sperm motility, calcium channel regulation, and SNARE proteins. Most of these terms are directly implicated in sperm physiology and male fertility. Our study contributes to the identification of genetic variants and biological pathways responsible for the genetic variation in bull fertility in Holstein and Jersey breeds. Additionally, our findings may provide opportunities for improving dairy bull fertility via marker-assisted selection.

Key Words: sire conception rate, association analysis, gene set enrichment

The use of genomic data has revolutionized the prediction of complex traits in animal breeding in the last decade. Genomic prediction is generally considered as a black box because it ignores any available information about functional features of the genome. However, it is believed that genomic prediction can be more accurate and more persistent by integrating biological information. As such, the main objective of this study was to evaluate alternative models for predicting a complex trait such as bull fertility using both genomic and biological information. Sire conception rate (SCR) was used as a measure of bull fertility. The data set included 8k Holstein bulls with SCR records and 55k single nucleotide polymorphisms (SNPs) spanning the whole genome. Different subsets of SNPs were evaluated, including SNPs within or near genomic regions (n = 26k), SNPs linked to genes in the Gene Ontology (GO) term reproduction (n = 0.9k), SNPs linked to genes that belong to Medical Subject Headings (MeSH) terms related to sperm biology (n = 0.3k), and SNPs that were marginally associated with SCR (n = 18k). Both linear and Gaussian kernels were constructed for each set of SNPs and fitted in the models either separately (single kernel) or simultaneously (multi-kernel). Predictive ability was evaluated by mean-squared error (MSE) and predictive correlation (COR) in 5-fold cross-validation. Interestingly, the entire set of SNPs achieved good SCR predictions in the testing set (MSE = 4.13, COR = 0.35). Neither genomic regions nor GO or MeSH gene sets achieved predictive abilities higher than their counterparts using random sets of SNPs. Notably, kernel models fitting significant SNPs showed better predictive ability (MSE = 4.04 and COR = 0.36) than the whole-genome approach in both single and multi-kernel analyses. Models fitting Gaussian kernels outperformed their counterparts fitting linear kernels irrespective of the set of SNPs. Overall, our findings suggest that genomic prediction of bull fertility is feasible in dairy cattle. Pre-filtering SNPs based on testing marginal associations seems a promising alternative to avoid fitting the whole set of SNPs. The potential inclusion of gene set results into prediction models deserves further research.

Key Words: prediction of complex traits, gene set, functional genomics

The objective of this study was to investigate the development of sexed semen conception rates in the field and compare those to the conception rates of conventional semen over the last 5 years (2012–2016). Conception rates were estimated for conventional and sexed semen using field data from 63 dairy farms. In this period, sex-sorted semen underwent many significant changes with the introduction of SexedULTRA processing as well as improvements through the use of high throughput digital sorting technology. The total numbers of inseminations in the data set were 2,214,246 for conventional and 343,154 for sexed semen from 2,508 Holstein sires. The percentage of sexed semen used in those herds increased from 8% in 2012 to 23% in 2015. A linear mixed model was fitted to the data that included an interaction term between year-month of insemination and semen type, the insemination number (1–3) and the age of the service sire at the time of insemination. Random effects included the service sire and a herd-year-season of insemination effect. The model was fitted separately for heifers and cows, whereas the cow model included the lactation number (1–3) as an additional fixed effect. Least squares means (LSM) on the interaction between year-month and semen type were used to describe the changes in conception rates over time while averaging over the remaining fixed effects. The cow conception rates showed strong seasonality which is consistent over years with any semen type. That seasonality was not observed in heifers. The LSM conception rate in cows in January 2012 was 0.38 while sexed semen reached 0.25. In heifers this difference in conception rates was even more pronounced with 0.58 using conventional and 0.38 with sexed semen. Through the years the technological and biological advances in sexed semen processing that were introduced seems to have improved the conception rates starting in 2013. In June 2014 conventional and sexed semen conception rates were almost at the same level for the first time (0.34 and 0.33). In 2015 the conception rates of sexed semen were stable and at 0.88 and 0.86 of conventional semen conception rates in cows and heifers, respectively.

Key Words: sexed semen, conception rates, fertility
Mathematical modeling can combine a wide range of information sources and facilitate the research of scenarios that would not be feasible to evaluate empirically. We have developed a stochastic model using genetic and physiological data from over 70 published reports on aspects of fertility in dairy cows. The model simulates cow pedigree, random mating allocation, correlated breeding values and interacting phenotypic variables. It was used to generate a large (200,000 cows replicated 100 times) data set of herd records for up to 5 parities within a seasonal dairy production system. From these data, a genetic evaluation of sires based on genetic merit for lifetime reproductive success (LRS) and the impact of high-LRS (Hi-LRS) or low-LRS (Lo-LRS) sires were investigated. LRS was defined as the number of times, during her lifetime, a cow calved within the first 42 d of the calving season. The proportion of daughters which calved (calving rate) in the 2nd parity was the strongest predictor of sire genetic merit for LRS (R² = 0.81). When 2nd parity calving date was included, the power of the predictor increased substantially (R² = 0.97). Reasonable predictions could also be made from 1st parity records. A predictive model containing 1st parity records for overall calving rate, and calving rate within the first 21 d, provided a good (R² = 0.76) LRS estimation when growth rate from weaning until first estrus was also included. Comparison of simulated daughters from widespread industry use (1000 daughters/bull) of sires with high (n = 100, µ = +0.70) and low (n = 100, µ = −0.73) breeding values for LRS, indicated that 12 of the 14 underlying genetic traits were divergent between the sire lines. Phenotypically, the daughters from the Hi-LRS sires displayed first estrus 34.1 d younger than their Lo-LRS contemporaries. Hi-LRS cows calved −15 d younger at each parity and, despite producing less milk per season (−155L) than Lo-LRS cows, produced more milk over their lifetime (+33%) owing to additional lactations before culling. In summary, this simulation model suggests that lifetime reproductive success contributes substantially to cow productivity, and can be accurately predicted at a young age.

Key Words: breeding, reproduction, modelling

Estimating epistatic and dominance genetic variances for fertility and reproduction traits in Canadian Holstein cattle. K. Alves¹, M. Sargolzaei¹,², C. Baes¹, A. Robinson¹, and F. Schenkel¹, ²Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ³The Semex Alliance, Guelph, ON, Canada.

Non-additive genetic effects are usually ignored in animal breeding programs due to data structure (e.g., incomplete pedigree, computational limitations, and over-parameterization of the model. However, non-additive genetic effects may play an important role in the expression of complex traits in livestock species, such as reproduction and fertility traits. We assessed the use of pedigree and SNP-marker-based models to estimate additive and non-additive genetic variances for reproduction and fertility traits in Canadian Holstein heifers (n = 5,825) and cows (n = 6,090). Four traits were analyzed including age at first service for heifers (AFS), calving to first service interval for cows (CTFS), and 56-d non-return rate for heifers and cows (NRR). Four linear models were used (1) additive genetic model (MA); (2) a model including both additive and epistatic (additive by additive) genetic effects (MAE); (3) a model including both additive and dominance effects (MAE); and (4) a full model including additive, epistatic, and dominance genetic effects (MAED). The models which included non-additive genetic effects for AFS and CTFS indicated that epistasis, dominance, or a combination thereof, are as important as additive effects, and sometimes contribute a larger proportion to the total phenotypic variance than the contribution of the additive effects. The partitioning of variance components resulted in a re-ranking of animals in the top 10% based exclusively on the additive genetic effects between models. The change in rank indicates that adjusting for non-additive genetic effects could change selection decisions made in dairy cattle breeding programs. These results suggest that non-additive genetic effects play an important role in some reproduction and fertility traits in Canadian Holsteins and their inclusion in genetic evaluations may improve accuracy of selection based on additive genetic effects.

Key Words: Holstein cattle, low-heritability trait, non-additive genetic effect

Discovery of a haplotype affecting fertility in Ayrshire dairy cattle and identification of a putative causal variant. D. J. Null¹, J. L. Hutchison¹, D. M. Bickhart², P. M. VanRaden¹, and J. B. Cole¹, ¹Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD, ²U.S. Dairy Forage Research Center, ARS, USDA, Madison, WI.

The goal of this research was to identify the causal variant associated with a haplotype affecting fertility in Ayrshire cattle. The US dairy population is routinely monitored to identify cases where homozygotes for a minor allele are expected, but never observed, which can indicate the presence of a genetic defect causing embryonic death. Such a haplotype was identified on chromosome 17 in January 2013. A second haplotype reached the threshold for statistical significance (7 expected homozygotes and none observed) in October 2013. Sire conception rate was 6.1% lower for matings of carrier sires to cows with carrier maternal grandsires, but the effect was not significant. As of December 2016, 23.5 homozygotes were expected but none had been observed. Most carriers trace back to OAK-RIDGE FLASHY KELLOGG (AYUSA000000125168), born in 1961, but many Canadian carriers only trace back as far as WOODLAND VIEW PARDNER ET KELLOGG (AYCAN000000811799), born in 1994. These bulls share an ungenotyped ancestor in OAK-RIDGE LIGHTNING (AYUSA000000120135), born in 1958. This haplotype has been designated Ayrshire haplotype 2 (AH2), and its frequency has increased from 6% in animals born in 1990 to 21.7% for animals born since 2008. Whole-genome sequence data ranging from 9 × to 13 × read-depth for 8 Ayrshire bulls, 3 carriers and 5 non-carriers, was used to search for the causal variant. The analysis used a short-read sequence data analysis pipeline including BWA (v. 0.7.10) and GATK (v. 3.3). Likely false positive variants and variants with small predicted functional effects were removed after annotation with SNPEFF (v. 4.3). A splice acceptor variant at 51,267,548 bp in the RNA Polymerase 2 Associated Protein (RPAP2) gene was the most likely causal variant in the haplotype. RPAP2 is an essential component of the RNA polymerase 2 holoenzyme necessary for transcription of snRNA species. Experiments with mouse knockouts also found a deficiency of homozygotes, suggesting that RPAP2 is necessary for embryonic development. These findings provide strong evidence for the existence of a new, lethal recessive in Ayrshire cattle. AH2 carrier status should be reported to the industry routinely and its effect on fertility confirmed.

Key Words: Ayrshire, fertility, genetic disorder

Predictions for workability and reproductive traits using two-step and single-step genomic BLUP in Canadian Holsteins.
For low heritability traits, large reference populations are required to achieve high reliability of genomic EBV (GEBV). By including genotyped and non-genotyped animals simultaneously in the evaluation, the single-step GBLUP (ssGBLUP) has the potential to yield more accurate and less biased evaluations. The aim of this study was to compare the reliability and bias of genomic predictions for various workability and reproductive traits in Holstein cattle using 2-step GBLUP (tsGBLUP) and ssGBLUP. A total of 33,568 bulls and 6,849 cows were genotyped. Genomic predictions were assessed using genotypes only for bulls or for bulls and cows under different approaches: (1) GEBV estimated by ssGBLUP with a default blending of 5% of the pedigree relationship matrix among genotyped animals (A22) and 95% of the genomic relationship matrix (G); (2) Direct genomic value (DGV) estimated by tsGBLUP where 5% or 20% of A22 was blended into G; (3) GEBVi as an index combining EBV and DGV, where the latter was obtained from tsGBLUP with 5% or 20% blending. Regular BLUP without genomic information were also carried out and EBV served as benchmark for comparisons. Reliabilities were obtained with forward prediction, following the Interbull validation method. Validation bulls had at least 50 daughters in 2014. Including genomic information improved reliability, on average, by 14.5 pts for ssGBLUP and 12 pts for tsGBLUP compared with BLUP. Overall, ssGBLUP predictions had 3.3 pts greater reliabilities and were 0.15 pts less biased compared with tsGBLUP. When a 20% blending was used in ssGBLUP, predictions were less biased, but no differences in reliability were observed compared with a 5% blending. Adding genotypes for cows had a small, positive impact of 1.5 pts in reliability for ssGBLUP and 1.6 pts for tsGBLUP; bias was reduced by 0.002 and 0.023, respectively. When genomic information is available for cows, predictions for both workability and reproductive traits can be slightly improved. Single-step GBLUP leads to more accurate and less biased predictions compared with 2-step GBLUP.

Key Words: genomic EBV, reliability, single-step GBLUP

208 Determining the economic value for efficiency traits. C. Richardson*, G. Guarni, J. Bryant, D. Lourenço, L. Brito, M. Sargolzaei, C. Baes, F. Miglior, M. Olayemi, and J. Bryant, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Department of Animal and Dairy Science, University of Georgia, Athens, GA, 3The Semex Alliance, Guelph, ON, Canada, 4Canadian Dairy Network, Guelph, ON, Canada.

Alterating management practices and production designs to create a more sustainable global system has been highlighted in government policies and corporation objectives. In the dairy market, the inefficient utilization of feed and high production of emissions associated with raising and maintaining cattle are scrutinized for contributing to environmental degradation, and therefore, have become targeted areas for improvement. Feed is a major expense for the Canadian dairy industry, representing over 50% of all production costs. A new prospect for decreasing the environmental footprint of the dairy industry is to increase feed efficiency and decrease methane emissions through the selection of genetically superior animals, as these traits are favorably correlated. Current selection programs have been successful in achieving breeding objectives related to production, health and longevity. It is also important to develop a selection program that includes an aim to increase total system efficiency, thereby, maintaining a viable industry both economically and environmentally. Thus, the economic value of efficiency traits to be used in selection programs must be determined. The methodology introduced below was used to determine the total savings associated with selecting for a decrease in the total dry matter intake of a lactating first parity dairy cow; including the economic value of the reduction in feed-related methane production. The lifespan of a typical Canadian dairy animal was divided into stages based on significant changes in production and maintenance of energy requirements by the animal. Regression coefficients defined as a ratio of the mean total feed intake across production animal life stages relative to a first parity lactating cow, were used to determine the economic effect of decreasing feed intake. The result of these coefficients applied to determine the cost savings associated with the lower output of emissions. Using this approach, the approximate lifetime savings generated by a more feed efficient production animal can be estimated.

Key Words: feed efficiency, methane production, economics
Genomic predictions of transmitting ability (GPTAs) for residual feed intake (RFI) were computed using data from 4,621 42-d and 202 28-d feed intake trials of 3,947 US Holsteins born 1999–2013 in 9 research herds. The 28-d records had 8.5% larger error variance than 42-d records and received less weight (0.92 vs. 1.0) in the evaluation. The RFI averages were already adjusted to remove phenotypic correlations with milk energy output, metabolic body weight, and body weight change and for several environmental effects including other nutrition experiments during the feed intake trials. Traditional breeding values (BVs) for RFI of 74.3 million Holsteins were obtained by an animal model that also included effects for age-parity group, trial date, herd management group, permanent environment, herd-sire interaction, and regressions on inbreeding and on genomic evaluations for milk energy and body weight composite (BWC). The milk energy and BWC terms were specified with the intent to remove positive genetic correlations that remained after the phenotypic correlations were removed. Estimated heritability was 0.17 and repeatability across lactations was 0.42. Genomic BVs for RFI included 60,671 genetic markers for 1.4 million Holsteins and produced calculated genomic reliabilities for young animals averaging 19% compared with traditional reliabilities of 5%. A parallel test using somatic cell score (SCS) records for these same 3,947 cows indicated lower observed than expected genomic reliability (11% vs. 19%). The economic value of RFI is very large and could receive >20% of total genetic gain. However, the low reliability will limit the extra genetic progress to about 4% more than current progress. The RFI predictions were added to the extra feed associated with large BWC and then multiplied by −305 to convert from extra feed eaten per day to feed saved per lactation. Additional feed intake records could make feed saved a very important trait in future selection indexes for dairy cattle.

Key Words: feed intake, genomic evaluation, dairy efficiency

210 Breeding strategies for improving feed efficiency in Holstein cattle using ZPLAN+. K. Houlanan*,1, F. Migliore1,2, C. Maltecca1, B. Gredler1, A. Fleming1, and C. Baes1, 1University of Guelph, Guelph, ON, Canada, 2Canadian Dairy Network, Guelph, ON, Canada, 3North Carolina State University, Raleigh, NC, 4Qualitas AG, Zug, Switzerland.

Feed accounts for over 50% of the total costs on a dairy farm in North America, with feed prices expected to continue to rise in coming years. There is a clear need to improve the feed efficiency of dairy cattle. Studies have shown that there is variation in the amount of feed consumed between animals that have similar production. By exploiting this variation on a genetic level, there is an opportunity for greater and more permanent improvement in feed efficiency. Determining an optimal breeding strategy for improving feed efficiency in dairy cattle would be helpful in reducing feed costs, while maintaining or increasing output. Measuring feed intake can be expensive and time consuming. There are different ways to express feed efficiency, including residual feed intake (RFI) and dry matter intake (DMI). RFI and DMI are genetically correlated with milk yield. Using these genetic correlations, along with phenotypic correlations and heritabilities, an optimal breeding strategy will be created and analyzed using ZPLAN+. ZPLAN+ is a software program that aids in the modeling and calculation of complex breeding scenarios using genomic information. This program will be used to assess the genetic gain, monetary gain, and costs associated with including feed efficiency in a selection index for the Canadian dairy industry. Both RFI and DMI will be simulated as measures of feed efficiency, and the results will be compared with determine which trait is optimal to include in the index. In addition to this work, long-term effects of including feed efficiency in the Canadian selection index on traits of economic interest such as milk yield, fertility and health will be analyzed. The results of this work will provide insight for the Canadian dairy industry as to the best method for including feed efficiency into the existing selection index.

Key Words: feed efficiency, breeding strategies, genetics

211 A comparison of feed intake, production, body condition score, body weight, and frame size of ProCROSS crossbred versus Holstein cows during the first 150 days of first lactation. B. N. Shonka-Martín*,1, B. J. Heins2, and L. B. Hansen1, 1University of Minnesota, St. Paul, MN, 2West-Central Research and Outreach Center, Morris, MN.

Three-breed (Montbéliarde, Viking Red, Holstein) rotational crossbreds (ProCROSS) cows (n = 44) were compared with Holstein cows (n = 41) for feed intake, production, and body traits during the first 150 d of first lactation. Cows calved in the University of Minnesota campus herd from September 2014 to April 2016. A total mixed ration (TMR) was fed twice daily, and refusals were weighed once daily. All cows were individually fed the same TMR on an ad libitum basis. Feed intake was recorded and dry matter intake (DMI) was calculated. Body weights were recorded twice weekly, body condition score (BCS) was evaluated once weekly, and height at both the withers and the hips was measured once a month. Best prediction (BP) was used to estimate production from data collected from routine milk recording. Mean body weight and BCS were calculated for monthly periods. Statistical analysis of total 150-d DMI included the fixed effects of year, age at calving, breed, and the interaction of year and age at calving and the random effect of cow nested within breed. A similar model was used for production traits except age at calving was removed because this variable is adjusted for by BP. Month nested within breed was an additional fixed effect for the body traits. Crossbred cows (2,770 kg) consumed significantly (P < 0.01) less DMI during the first 150 d of lactation than Holstein cows (2,922 kg). Fat plus protein production was not different (P = 0.54) for crossbred (338 kg) and Holstein cows (328 kg), but the crossbreds were numerically higher. Crossbred cows (3.39) had significantly higher (P < 0.01) BCS than Holstein cows (3.16) during the first 150 d of lactation. However, body weight was not different (P = 0.33) between the crossbreds (556 kg) and Holsteins (545 kg). Crossbred cows (136 cm) were shorter (P < 0.01) for height at the withers than Holstein cows (138 cm), but similar (P = 0.51) for height at the hips (143 cm vs. 144 cm, respectively).

Key Words: crossbreeding, feed intake

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