Breed and Genetics

Assessing the use of public weather station data to investigate the effects of heat stress on milk production in Canadian Holstein cattle. I. Campos*, C. Baes, A. Canovas, and F. Schenkel, University of Guelph, Guelph, ON, Canada.

The objectives of this study were to identify the temperature-humidity index (THI) thresholds where heat load starts to affect production traits (milk, fat, and protein yield) in the first 3 lactations of Holstein cows, and to assess potential differences in heat stress in Quebec and Ontario. A total of 2.1 million test-day records from 167,620 Ontario cows and 3.1 million records from 225,104 Quebec cows spanning an 11-yr period (2008–2018) were used. The climatic data consisted of hourly measurements of ambient temperature and relative humidity. In total 58 weather stations were located within a maximum distance of 20 km from each herd. A k-means cluster analysis was performed within each THI > 75 to exclude herds that may have some type of cooling system. A linear model was fitted to adjust the phenotypes, which were then plotted against the THI levels for each parity. To identify the THI threshold at which milk production starts to decline, a segmented polynomial was used to describe the shape of the curve of the relationship between production and THI values. During the summer, the average THI was 69 and 68 in Ontario and Quebec, respectively. Two heat stress thresholds were identified for milk yield and protein yield, one being associated with a low decline in the yield and the other one associated with sharper decline. For both provinces, the second threshold was reached at about a THI of 79 for both milk and protein yields, while the first threshold was reached at a THI of 64–72 for milk yield and THI of 57–64 for protein yield, depending on the province and parity. The expected reduction in milk yield after a THI of 79 was -0.40 kg/d and -0.19 kg/d in Ontario and Quebec, respectively. The same features for protein yield were -16.2 g/d and -9.7 g/d. For fat yield, the expected reduction in yield after a THI of 57 was -3.3 g/d and -2.6 g/d for Ontario and Quebec, respectively. Therefore, the estimated rate decline differed between the 2 provinces, which may be related to the higher percentage of tie stall barns in Quebec (92%) compared with Ontario (<70%).

Key Words: dairy cow, heat stress, temperature-humidity index

Estimation of genetic parameters for stayability in organic Holsteins. L. C. Hardie*, B. J. Heins², and C. D. Deechow¹, ¹The Pennsylvania State University, University Park, PA, ²University of Minnesota, West Central and Outreach Center, Morris, MN.

The objective of this study was to estimate genetic parameters for stayability of organic Holsteins and determine genetic relationships with other traits. Stayability (1 = remained in herd to a given parity, 0 = left) was generated for parity 1 through 5 for cows from 16 USDA certified organic farms. Animals with a Holstein sire and no other breed for 3 generations were included. All models included fixed herd-year-season of birth and pedigree completeness and the random effect of animal. Heritabilities for parity 1 (n = 27,630 with 66% staying in the herd from birth to parity 1), 2 (82% staying from parity 1 to 2; n = 12,766) and 3 (78% staying from parity 2 to 3; n = 6,978) were estimated using univariate threshold models. Genetic correlations among them were estimated with bivariate linear models. An across-parity analysis used records (n = 101,201 from 27,630 animals) for individual parities up to 5; the fixed effect of parity and random effect of permanent environment were added. Approximate genetic correlations between stayability and nationally evaluated traits were extrapolated from PTA correlations for bulls with accuracy of PTA stayability greater than 0.35. Heritability estimates for stayability to first, second, and third parities were 0.10 ± 0.01, 0.07 ± 0.02, and 0.07 ± 0.03, respectively. The across-parity heritability estimate was 0.12 ± 0.01 and repeatability was 0.61 ± 0.004. The genetic correlations for stayability to parity 1 and 2, 1 and 3, and 2 and 3 were 0.80 ± 0.08, 0.60 ± 0.22, and 0.81 ± 0.19, respectively. Genetic correlations between stayability and most key traits were positive, but less so for heifers (Table 1). In conclusion, there is a genetic component to stayability that remains consistent across parities such that it can serve to mitigate selection bias in genetic analyses with sparse recording of production traits.

Table 1 (Abstr. 154). Approximate genetic correlations with stayability

<table>
<thead>
<tr>
<th>Trait</th>
<th>All parities</th>
<th>To parity 1</th>
<th>Parity 1 to 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Productive life</td>
<td>0.54*</td>
<td>0.33*</td>
<td>0.73*</td>
</tr>
<tr>
<td>Livability</td>
<td>0.45*</td>
<td>0.44*</td>
<td>0.64*</td>
</tr>
<tr>
<td>Milk yield</td>
<td>0.29*</td>
<td>0.06</td>
<td>0.26*</td>
</tr>
<tr>
<td>Daughter pregnancy rate</td>
<td>0.12*</td>
<td>-0.10</td>
<td>0.30*</td>
</tr>
<tr>
<td>Heifer conception rate</td>
<td>0.16*</td>
<td>0.12</td>
<td>0.17</td>
</tr>
<tr>
<td>Early first calving</td>
<td>0.21*</td>
<td>-0.23*</td>
<td>0.42*</td>
</tr>
</tbody>
</table>

*Differs from 0, P < 0.05.

Key Words: organic, herd-life, heritability

Genomic evaluation of heifer livability. M. Neupane*, C. P. Van Tassell, and P. M. VanRaden, Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD.

Differences in breeds and sire lines suggest the presence of a genetic component for heifer livability (HLIV). Genomic evaluation of this trait can increase profitability and improve animal health and welfare. Evaluations for HLIV were examined from 3,360,847 calf data records for heifers of all breeds born from the year 2009–2016. Data were obtained from the national cooperator database maintained by the Council on Dairy Cattle Breeding, USA. The total number of deaths reported was 134,804 (4.01%), which includes the herds with death loss between 1 and 25%. Total death rate from >2 d of age until the heifer left the herd or until a maximum of 18 mo of age was evaluated, but records were not included until 3 years after the birthdate so that live status of contemporaries could be confirmed by a calving date. Deaths observed until 2 d after birth were included in stillbirth rather than HLIV. The scale used for analysis of HLIV was 0 (died) or 100 (live) and the heritability estimate was 0.4% based on sire model REML. Genomic predicted transmitting abilities (GPTA) for Holstein range from −1.5% to +1.5% with a standard deviation of 0.5%, and GPTAs for Jersey range from −0.8% to +0.8% with SD of 0.2% compared with means of about 4% death loss. Reliabilities of genomic predictions for young animals averaged 46% for Holsteins and 30% for Jerseys while corresponding traditional parent average reliabilities averaged 16% and 12%. Correlations of HLIV were 0.44 with productive life, 0.34 to 0.36 with yield traits, 0.37 with calving trait dollars, and 0.36 with early first calving on proven Holstein bulls. The HLIV trait had a favorable genetic trend in recent years, likely because of selection for the correlated traits. The trait HLIV could get 1% of emphasis on net merit index making economic progress of $0.05 million per year. By encouraging more recordings on calf mortality, the reliabilities of evaluations can increase significantly.

Key Words: heifer livability, genomic evaluation, animal welfare


Abortions and twinning are undesirable reproductive outcomes in dairy herds. Both traits are believed to be largely caused by environmental factors. However, studies have shown that there is a substantial genetic component to these conditions. The objective of this study was to develop genetic and genomic evaluation for abortions and twinning in Holstein cattle using single-step genomic BLUP (gBLUP) methodology. Production, reproduction, and pedigree data recorded on farms using herd management
software were available for this study. Abortions (ABRT) were defined as a recorded abortion event between 42 and 260 d after the successful breeding. Twinning (TWIN) was defined as a pregnancy resulting in birth or abortion of twin calves (alive or dead). The traits were analyzed using the univariate threshold animal model with repeated observations. The model included the fixed effect of parity (1–5) and the random effects of animal, herd x year x season of calving, and permanent environment. In addition, the model for ABRT included the fixed effect of the breed composition of the embryo (purebred vs. crossbred), the random effect of service sire, and the covariates of milk yield and days open. The data consisted of 3,848,620 and 5,338,162 records with an overall incidence of 11.0% and 3.0% for ABRT and TWIN, respectively. Genotypes were available on 978,368 animals. The estimated heritabilities were 0.077 and 0.089 for ABRT and TWIN, respectively. Predicted transmitting abilities (PTA) were expressed in percent points as deviations from the average estimated probability of a disorder in the base population, which was defined as all animals with phenotypes born in 2015. The PTA ranged from −8.72 to 12.92 and from −6.98 to 20.39 for ABRT and TWIN, respectively, with higher values representing higher risk of having a disorder. The reliabilities of PTA for young genotyped animals without own phenotypes were on average 0.36 and 0.39 for ABRT and TWIN, respectively. Genetic and genomic selection of animals less prone to abortions and twinning could be a useful tool for improving reproductive performance in dairy herds.

**Key Words:** abortion, twinning, genomic evaluation

157 A feasibility study to implement genetic and genomic evaluations for twinning in Holstein cattle. A. Sewale*, M. McClure, and K. Olson, ABS Global, DeForest, WI.

Twin births are detrimental for dairy producers due to their association with several unfavorable effects, including increased reproductive disorder, culling risk, abortions, and calving interval. The aims of this study were to (A) assess the incidence of twinning and evaluate its risk factors; (B) examine this trait’s association with other traits of economic importance; (C) to develop genetic and genomic evaluations for twinning. The data included Holstein calving records from 2000 to 2019, comprising 1,804 herds with 14M calving records from 25,868 AI sires. The 2018 overall twinning rate was 4.2% which represented a 9.94% increase from 2010. Twinning rate increased with parity with rates of 1.16%, 4.73%, and 7.86% for parities 1, 2, and 3+, respectively, and AI sires’ overall twinning rate ranged from 0 to 13.89%. A genetic evaluation of twinning was carried out using a single-trait linear sire model which included the fixed effects of parity and herd-year-season with random effects of sire and the residual. The sire evaluation results were expressed as an estimated transmitting ability (ETA) representing the expected twinning rate differences among daughters with the average ETA set to 100 and std of 5. The ETAs had a normal distribution ranging from 75 to 115. Traditional evaluation results for twinning were de-regressed and used as pseudo-phenotypes to predict the direct genomic values for animals with 43K SNP genotypes. No markers with large effects were observed. Twinning had statistically significant but low correlations with numerous production and fertility traits which indicate that a direct twinning breeding value is needed to make any significant impact on the trait. In conclusion, this study showed large variation in the predicted twinning breeding values indicating that the implementation of genetic and genomic evaluation for twinning will help producers make breeding decisions to reduce their herd’s economic risk from twin births.

**Key Words:** twinning, genetic and genomic evaluations

158 Identification and validation of candidate genes for heat tolerance in Australian Holstein dairy cattle. E. K. Cheruiyot‡, M. Haile-Mariam, B. G. Cocks, I. MacLeod, and J. E. Pryce, Agriculture Victoria Research, Department of Jobs, Precincts and Regions, Melbourne, Australia; School of Applied Systems Biology, La Trobe University, Melbourne, Australia.

Heat tolerance is the ability of an animal to maintain production and reproduction levels under hot conditions and is now a trait of economic relevance in dairy systems worldwide. Understanding the genetic basis for heat tolerance is an important part of the strategy to breed for cattle adapted to warmer environments. We sought to identify and validate candidate genes involved in heat tolerance in Australian Holstein cattle using 50K SNP chip and imputed whole-genome sequences (WGS) in 2 data sets: cows (n = 20,623) and bulls (n = 1,622). The WGS was imputed using Run 7 of the 1000 Bull Genome Project based on the ARS-UCD1.2 reference genome. After quality checks, approximately 45K and 15 million SNPs remained for analysis from the 50K chip and the WGS, respectively. The heat tolerance phenotypes that were used for this study were derived from test-day milk, protein and fat yield data of cows that calved between 2003 to 2017 and represent the response of cows to heat stress. For the 3 milk traits, the slope which measures change in milk yield due to variability in temperature-humidity index from reaction norm models calculated for individual animals after accounting for known fixed effect was used as phenotype in association analysis using GCTA software. We used cows for discovery and bulls that were not sires of the cows for validation. Our results point to the polygenic nature of heat tolerance, with no variants surpassing a significance threshold of $P < 1.0 \times 10^{-6}$ for 50K SNP data. While we detected some associations when the threshold was set at $P < 1.0 \times 10^{-3}$, there were high false discovery rates. In contrast, we detected multiple variants with $P < 1.0 \times 10^{-4}$ across the genome using WGS, suggesting greater power compared with 50K SNP data. Across our cow and bull validation set, we confirmed several candidate genes, including some that have been reported previously. Our results are preliminary and could be useful to enhance the reliability of heat tolerance genomic breeding values of Australian Holstein cattle which is currently about 38%. This will be investigated in a further study.

**Key Words:** heat tolerance, dairy cattle, whole-genome sequences (WGS)