

Breeding and Genetics

153 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 20km 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 THI = 79 for both milk and protein yields, while the first threshold was reached at about a THI = 64–72 for milk yield and THI = 57–64 for protein yield, depending on the province and parity. The expected reduction in milk yield after a THI ~79 was –0.40 kg/d and –0.19kg/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 ~57 was –3.3g/d and –2.6g/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

154 Estimation of genetic parameters for stayability in organic Holsteins. L. C. Hardie*¹, B. J. Heins², and C. D. Dechow¹, 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 sta-

yability 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

Trait	All parities	To parity 1	Parity 1 to 2
Productive life	0.54*	0.33*	0.73*
Livability	0.45*	0.44*	0.64*
Milk yield	0.29*	0.06	0.26*
Daughter pregnancy rate	0.12*	–0.10	0.30*
Heifer conception rate	0.16*	0.12	0.17
Early first calving	0.21*	–0.23*	0.42*

*Differs from 0, $P < 0.05$.

Key Words: organic, herd-life, heritability

155 Genomic evaluation of heifer livability. M. Neupane*, C. P. Van Tassel, 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

156 Genomic evaluation for abortions and twinning in dairy cattle. N. Vukasinovic*, D. Gonzalez-Pena, J. Brooker, C. Przybyla, and S. DeNise, *Zoetis, Kalamazoo, MI.*

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