

tion, a cohort study was performed on 225 calves from 8 herds in the province of New Brunswick. Preweaning records on calf management and disease events were collected from 2014 to 2015. Adult production records were collected on these calves from their first lactation to 2020. Estimated breeding values (EBV) will be used to determine each calf's genetic potential for production, health, and longevity. Phenotypic and EBV correlations for longevity and production traits will be estimated. Multivariate regression will be performed to identify any calthood environmental and health factors that interfere with a calf's ability to reach its genetic potential for production and longevity traits. Understanding the impact of these factors can help to optimize health management practices on farms, improve profitability, and enhance the genetic potential for increased longevity.

Key Words: calf, health management, genetics

302 Genomic evaluations for Feed Saved in Holsteins. K. L. Parker Gaddis*¹, P. M. VanRaden², R. J. Tempelman³, K. A. Weigel⁴, H. M. White⁴, F. Peñagaricano⁴, J. E. Koltes⁵, J. E. P. Santos⁶, R. L. Baldwin², J. F. Burchard¹, J. W. Dürr¹, and M. J. VandeHaar³, ¹*Council on Dairy Cattle Breeding, Bowie, MD*, ²*Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD*, ³*Michigan State University, East Lansing, MI*, ⁴*University of Wisconsin, Madison, WI*, ⁵*Iowa State University, Ames, IA*, ⁶*University of Florida, Gainesville, FL*.

Official predicted transmitting abilities (PTA) for Feed Saved in Holsteins were released by the Council on Dairy Cattle Breeding (CDCB; Bowie, MD) in December 2020. Feed intake was measured mid-lactation (50 to 200 d in milk) for 4 to 6 wk in 9 US research herds. As of the December 2020 evaluation, 6,221 phenotypes of residual feed intake (RFI) were included from 5,023 Holsteins born from 1999 to 2017. A phenotypic measure of RFI was estimated by fitting dry matter intake as a linear function of milk energy, metabolic body weight, change in body weight, and cohort effects including parity and days in milk. RFI phenotypes were used to estimate traditional PTAs in an animal repeatability model including effects of herd management group, age by parity group, trial date, herd-sire interaction, and permanent environment. Regressions on genomic evaluations for energy-corrected milk and body weight composite (BWC) were also included in the model to remove genomic correlations that were present after removing phenotypic correlations. Genomic PTAs for RFI were calculated from deregressed traditional PTA using 79,060 SNP for 3.65 million genotyped Holsteins. Feed Saved PTA are provided to the industry and calculated as a combination of RFI PTA and BWC PTA (138 pounds dry matter annual intake per unit BWC PTA) to provide expected pounds of feed saved per lactation. Genomic evaluations of Feed Saved have an average PTA of approximately 10 pounds dry matter saved per lactation, ranging from -738 to 613 pounds among all genotyped animals. Young genomic bulls have an average Feed Saved reliability (REL) of 28%, while progeny-tested bulls average 38%, where REL is calculated as 35% BWC REL and 65% RFI REL. Given the limited reference population, collection of additional phenotypes is a primary goal. Studies are continuing that add data to the CDCB feed efficiency database, and international collaborations also will increase the number of available phenotypes. Feed Saved is currently provided to the industry as an individual trait evaluation, along with a proposal to incorporate it into an economic selection index.

Key Words: feed efficiency, genomic evaluation, Holstein

303 Multiple-trait random regression modeling of feed efficiency in dairy cattle. P. Khanal*¹, K. L. Parker Gaddis², P. M. VanRaden³, K. A. Weigel⁴, H. M. White⁴, F. Peñagaricano⁴, J. E. Koltes⁵, J. E. P. Santos⁶, R. L. Baldwin³, J. F. Burchard², J. W. Dürr², M. J. VandeHaar¹, and R. J. Tempelman¹, ¹*Michigan State University, East Lansing, MI*, ²*Council on Dairy Cattle Breeding, Bowie, MD*, ³*Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD*, ⁴*University of Wisconsin, Madison, WI*, ⁵*Iowa State University, Ames, IA*, ⁶*University of Florida, Gainesville, FL*.

Genetic improvement of feed efficiency (FE) is an increasing priority in dairy cattle breeding programs. Currently, popular traits to characterize FE include residual feed intake (RFI) and feed saved (FS). These traits are often measured or defined over short and fixed intervals of 4 or 6 weeks at various day in milk (DIM). Random regression (RR) models flexibly allow recording intervals of variable lengths at various stages of lactation which may genetically differ from each other. Multiple-trait extensions to RR models to jointly model dry matter intake (DMI), milk energy (MILKE) and metabolic body weight (MBW) facilitate estimation of genetic parameters that are specific to DIM not only for these 3 traits but also indirectly for change in body weight (dBW), RFI, and FS. We adapted a Bayesian multiple-trait random regression approach using 17,633 weekly records from 50 to 150 DIM on 1,756 cows from 5 different research herds to more flexibly model genetic parameters for FE component traits across DIM. For computational tractability, only pedigree information, rather than genomic data, was used to specify genetic relationships. The heritability estimates of MBW, DMI, MILKE, genetic RFI and genetic FS ranged within the respective intervals of [0.59, 0.72], [0.22, 0.30], [0.17, 0.38], [0.16, 0.20], and [0.25, 0.31] across DIM whereas the estimated heritability of dBW never exceeded 0.0005. Across DIM, the estimated genetic regressions of DMI on MBW and MILKE ranged within [0.09, 0.14 kg/kg^{0.75}] and [0.21, 0.39 kg/Mcal], respectively, whereas the corresponding phenotypic regressions ranged within [0.10, 0.13 kg/kg^{0.75}] and [0.30, 0.40 kg/Mcal], respectively. Based on this small study, we conclude that there is generally moderate heterogeneity in the genetic parameters characterizing FE across 50 to 150 DIM. We resolve to continue to address the computational challenges of this model using genomic information on our much larger reference population of over 5,000 cows.

Key Words: feed efficiency, multiple-trait analysis, random regression

304 Use of milk spectral data as set of environmental covariates to inform genomic predictions in Canadian Holstein. F. Tiezzi*¹, A. Fleming², and F. Malchiodi³, ¹*Department of Animal Science, North Carolina State University, Raleigh, NC*, ²*Lactanet Canada, Guelph, ON, Canada*, ³*The Semex Alliance, Guelph, ON, Canada*.

Genomic selection models aim at predicting the phenotypic performance of a new, unobserved genotype. In animal breeding, these models are seldom tested for their ability to predict new genotypes' performance under different environmental conditions, despite of the changes in management and diet that the industry undergoes. In this study, milk spectral information was included into genomic prediction models as a set of environmental covariates. The first step involved extracting the environmental component out of the milk spectral wavenumbers (1,060 wavenumbers recorded for 1,540,935 records) by fitting a linear mixed model that included the fixed effects herd-year-season, lactation number and lactation stage as well as the additive genetic, permanent environmental and residual random effects. Variance components estimates