

Breeding and Genetics Platform Session: 42nd Discover Conference: Managing Genetic Diversity for Future Dairy and Livestock Breeding

1117 Single-step genomic evaluation of crossbred dairy cattle in the US. A. Cesarani¹, D. Lourenco*¹, S. Tsuruta¹, A. Legarra², E. L. Nicolazzi³, P. M. VanRaden⁴, and I. Misztal¹, ¹*Department of Animal and Dairy Science, University of Georgia, Athens, GA*, ²*INRA, UMR¹³⁸⁸ GenPhySE, Castanet-Tolosan, France*, ³*Council on Dairy Cattle Breeding, Bowie, MD*, ⁴*Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD*.

Dairy cattle evaluations are progressively moving to single-step GBLUP (ssGBLUP). We recently investigated the performance of ssGBLUP for US Holstein and multibreed genomic evaluations in the US. However, the latter comprised data from Ayrshire, Brown Swiss, Guernsey, Holstein (HO), and Jersey (JE) without crossbred data. Because many crossbred animals have been genotyped, the focus is now on including this information in genomic evaluations. Thus, this work aimed to explore a ssGBLUP model considering purebred and crossbred data from the Council of Dairy Cattle Breeding (CDCB). Only phenotypes and genotypes of purebred Holstein, Jersey, and their crosses were considered. A total of 49M records (of which 580k were from crosses) of complete lactations with milk, fat, and protein yields were obtained from January 2000 to August 2021; incomplete lactations by August 2021 were projected. The pedigree contained 89M animals; genotypes at 79,294 selected SNPs were available for about 5M animals, of which 4.48M, 589k, and 39k were pure HO, pure JE, and crosses, respectively. Missing SNPs were imputed within each breed except that parent genotypes were included with the crossbreds. Predictive abilities of BLUP and ssGBLUP were evaluated based on 2 different runs: i) FULL, with all data in the model; ii) TRUNCATED, in which the last 4 years of data were removed from the model. Validation for cows was based on correlations between adjusted phenotypes (FULL) and (G)EBV (TRUNCATED), whereas for bulls on the regression of daughter yield deviations (DYD, in FULL) on (G)EBV (TRUNCATED). Validation animals were divided into purebreds and crossbreds, and the latter were split into groups depending on the breed proportion. Predictivities for purebreds were compared with those from single- and multibreed models. Predictivity from ssGBLUP was similar between purebred and multi-breed evaluations in earlier studies; therefore, including genotypes for crossbred animals should not undermine genomic predictions for purebred animals and should provide more accurate GEBV for crossbreds than the calculations based on breed proportion.

Key Words: ssGBLUP, genomic evaluation, across-breed predictions

1118 Do historically popular sires still capture the genetic composition of the recent US Holstein generation? Y. Steyn*, R. Abdollahi-Arpanahi, D. Lourenco, and I. Misztal, *University of Georgia, Athens, GA*.

The dairy industry is known for its extensive use of reproductive biotechnology, which resulted in a population where most animals can be traced back to only a few sires. Due to their relatedness to the population, historically popular sires could still capture the relevant independent chromosome segments (ICS) of the recent generation. However, due to many recombination events and new epistatic effects, shared haplotypes may be shorter and substitution effects may differ. The objective of this study was to investigate whether old, popular sires are still relevant. The

accuracy of genomic predictions when using different animals as core for the Algorithm of Proven and Young (APY) is an indication of ICS captured by the selected animals. The 100 most used sires born within different rolling time periods of 10 years were used as core. The validation population was 10,153 females born after 2010. Traits investigated were stature (stat) and fore udder attachment (FUA). The accuracies for all time periods ranged from 0.54 to 0.69 for stat, and 0.47 to 0.61 for FUA. The highest accuracies for both traits were achieved with sires born from 2005 to 2014, while the lowest was achieved with those born before 1981. A core size of 2,150 animals (equal to the number of eigenvalues explaining 80% of the variance in the genomic relationship matrix) was tested for different scenarios – random selection (random), males with known parents but no progeny (LPM), animals with the most progeny (MPA), and most popular sires born within 3 different time periods - before 1995 (Time1), 1995 to 2004 (Time2), or 2005 to 2014 (Time3). Using a random core or Time3 resulted in the highest accuracy (0.90 for stature and 0.85 for FUA), while Time3 gave the lowest accuracy (0.86 for stature and 0.79 for FUA). Results show that historically popular sires still capture ICS. However, more is captured by more recently used sires.

Key Words: independent chromosome segments, algorithm for proven and young, accuracy

1119 Reasons for disposal and cull cow value of Holstein and crossbred dairy cattle. S. L. Portner* and B. J. Heins, *Department of Animal Science, University of Minnesota, St. Paul, MN*.

Dairy cull cows account for close to 10% of the US beef market yet little research has classified cull cows by breed or provided detailed information of the cull cow value for dairy farmers. Therefore, the objective of this study was to compare reasons for disposal and cull cow value of Holstein cows (n = 219) with 1964 genetic control Holsteins cows (n = 160), GrazeCross crossbred cows (n = 280) composed of the Normande, Jersey, and Viking Red breeds and ProCROSS crossbred cows (n = 442) composed of the Montbéliarde, Viking Red, and Holstein breeds. Records spanned from January 2010 to December 2021. Cull cow records and receipts were from the University of Minnesota West Central Research and Outreach Center, Morris, Minnesota dairy. Reasons for disposal were recorded in PC Dart Software, and cull value and body weight was from invoices from livestock cull markets. The primary reason for disposal across all cows was 10.8% for died, 5.9% for low production, 19.3% for mastitis or SCC, 48.5% for reproduction and 15.5% for other reasons. Cows that died were not included in the analysis of bodyweight and cull value. Mean bodyweight at culling was 519 kg for 1964 Holsteins, 570 kg for Holsteins, 489 kg for GrazeCross, and 560 kg for ProCross cattle. Independent variables for statistical analysis of cull value with PROC Mixed of SAS were the fixed effects of body weight, year (2010 to 2021), season (spring, summer, autumn, winter), parity (1, 2, 3, 4, 5+), DIM at culling, primary reason for culling, breed group and sire breed group nested within breed group. The Holstein cows (\$694.02) had lower ($P < 0.01$) carcass value compared with 1964 Holsteins (\$784.83), GrazeCross crossbreds (\$741.03), and ProCross (\$723.36) crossbreds. Dairy producers may receive greater cull value from crossbred cows compared with Holstein cows.

Key Words: crossbreeding, cull value, Holstein