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and are reported since May 2016 for all 1.6 million genotyped dairy animals. Animals with > 94% of any breed were rounded to 100%, and contributions of other breeds were set to 0%. All-breed scale GPTAs were first computed for each pure breed for traits milk, fat, protein, productive life, somatic cell score, daughter pregnancy rate, cow conception rate, livability, and net merit. These estimates included foreign information from multi-trait across-country evaluation (MACE) and foreign dams converted from within-breed to the all-breed base. Then, marker effects for each breed were blended by BBR to compute evaluations for crossbreds (<94% purebred) for those same traits. Conformation traits do not have an all-breed scale, so only the Jersey marker effects were applied to the crossbreds, and results seemed reasonable. Calving traits are not predicted for crossbreds, and instead a common mean was used for all crossbreds as is the current practice for breeds other than Holstein and Brown Swiss. All-breed GPTAs were then converted to within-breed GPTAs. Correlations of GPTAs for purebreds computed on the all-breed vs. current within-breed scales were 0.97 to 0.99 for most traits and breeds. Crossbred GPTAs were then computed for 44,023 crossbreds, 20,367 of which had no previous GPTAs because of breed check edits. The new GPTAs were for 1,822 Jersey × Holstein crossbreds with >40% of both breeds (F1 crosses), 75 Brown Swiss × Holstein F1, 7,237 Holstein backcrosses with >67% and <94% Holstein, 7,820 Jersey backcrosses, 313 Brown Swiss backcrosses, 1,763 other crossbreds of various mixtures, and 1,337 purebreds that had previously failed breed checks. Additional automation and redesign of many downstream programs is required for the new all-breed system to be used in weekly, monthly, and full releases. The new system is expected to provide accurate predictions for crosses among the 5 dairy breeds evaluated.

Key Words: crossbreeding, genomic prediction, breed composition

462 Genetic trends from single-step GBLUP and traditional BLUP for production traits in US Holstein. Y. Masuda*[1], I. Misztal[1], P. M. VanRaden[2], and T. J. Lawlor[3], [1]*University of Georgia, Athens, GA,* [2]*USDA, AGIL, Beltsville MD,* [3]*Holstein Association USA Inc., Brattleboro, VT.*

The objective of this study was to compare genetic trends from a single-step genomic BLUP (ssGBLUP) and the traditional BLUP (tradBLUP) models for milk production traits in US Holstein. We used 764,029 genotyped animals in this study. Phenotypes were 305-d milk, fat, and protein yield from 21,527,040 cows recorded between January, 1990 and August, 2015. The pedigree file included 29,651,623 animals limited to 3 generations back from recorded or genotyped animals. We applied a 3-trait repeatability model with the same genetic parameters used in the US official genetic evaluation. Unknown parent groups were incorporated into the inverse of a relationship matrix (H^{-1} in ssGBLUP and A^{-1} in tradBLUP) with the QP-transformation. In ssGBLUP, 18,359 genotyped animals were randomly chosen as core animals to calculate the inverse of genomic relationship matrix with the APY algorithm. Computations with tradBLUP took 6.5 h and 1.4 GB of memory, and computations with ssGBLUP took 13 h and 115 GB of memory. Estimated breeding values were adjusted to a genetic base on recorded cows born in 2000 in each model and converted to GPTA in ssGBLUP and PTA in tradBLUP. For genotyped sires with at least 50 daughters with phenotype(s) born between 2000 and 2010, the genetic trend of GPTA was always greater than PTA in all traits. The difference in 2 genetic trends was almost constant for the sires born up to 2008 (on average, 11 kg in milk, 0.5 kg in fat, and 0.3 kg in protein yield) and the difference was greater in the last 2 years. The difference between the GPTA means for the bulls born in 2010 was 35 kg for milk, 2.2 kg for fat, and 1.2 kg for protein yield. For genotyped cows with phenotype(s), the GPTA trend was identical to or slightly greater than the PTA trend up to 2006. Two trends started to diverge obviously in 2007 and the GPTA trend kept rising while the PTA trend remained at the same level. The single-step method provides very similar genetic trends to the traditional evaluations except for the last few years. The recent lower PTA trend can be due to a downward bias caused with genomic pre-selection of young animals.

Key Words: genomic evaluation, genetic trend, PTA

463 A Genetic Diversity Index method to improve imputation accuracies of rare variants. A. M. Butty*[1], F. Miglior[1,2], P. Stothard[3], F. S. Schenkel[1], B. Gredler[4], M. Sargolzaei[1,5], and C. F. Baes[1], [1]*Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada,* [2]*Canadian Dairy Network, Guelph, ON, Canada,* [3]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada,* [4]*Qualitas AG, Zug, ZG, Switzerland,* [5]*Semex Alliance, Guelph, ON, Canada.*

Different methods to select animals for sequencing have been developed, which rely on pedigree-based relationship matrices, genomic relationships matrices, or on haplotype frequencies. Relationship-based methods select representative key animals of a population whereas haplotype frequency methods aim for better coverage of rare variants. Good average accuracies of imputation from SNP chip to whole-genome sequence (WGS) for common haplotypes were reached with the relationship-based methods. Imputation of rare variants, however, still needs to be improved, which can possibly be accomplished with a newly developed Genetic Diversity Index (GDI). This algorithm optimizes the count of unique haplotypes present in a group of animals composed of already sequenced individuals and a fixed number of sequencing candidates. Optimization is run iteratively, exchanging one candidate at a time and computing the GDI of the new group. Use of the simulated annealing algorithm defines whether the last individual added to the group should be kept. Simulated annealing has the advantage of searching for a global optimum in a situation where multiple local optima are present. The previously mentioned key ancestor and haplotype-based methods for selecting sequencing candidate were assessed and compared with the GDI algorithm using simulated cattle WGS data. Average squared correlation coefficients were used to assess imputation accuracy. A preliminary study showed that the accuracy was 1.5% higher when using GDI to enlarge the reference population than the second-best method. Application of the different methods of selection in North American Holstein data showed that the GDI algorithm selected animals carrying a higher percentage of rare haplotypes than other methods examined. Principal component analysis of the population showed that the animals selected with all tested methods were similarly distributed over the pool of candidates. When representative animals of a population are already sequenced and good overall imputation accuracies are reached, sequencing of genetically diverse animals improved the accuracy of the imputation of rare variants to the WGS density level.

Key Words: sequencing, simulation, imputation

464 Determination of quantitative trait variants by concordance via application of the a posteriori granddaughter design to the US Holstein population. J. I. Weller*[1,2], D. M. Bickhart[2], G. R. Wiggans[2,3], M. E. Tooker[2], J. R. O'Connell[4], J. Jiang[5], and P. M. VanRaden[2], [1]*Agricultural Research Organization, The Volcani Center, Rishon LeZion, Israel,* [2]*Agricultural Research Service, Beltsville, MD,* [3]*Council on Dairy Cattle Breeding, Bowie, MD,* [4]*University of*