of animals based on pedigree accuracy. Dairy data sets are complex, especially with regard to differences in daughter parentage accuracies across bulls. This complexity is difficult to simulate, and uncertain parentage models should be tested because of the potential to mitigate bias differences across bulls.

Key Words: genomic, simulation, single-step genomic BLUP

171 Genomic predictability of single-step GBLUP for production traits in US Holstein. Y. Masuda*[1], I. Misztal[1], P. VanRaden[2], and T. 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 validate genomic predictability of single-step genomic BLUP for 305-d protein yield for US Holsteins. The genomic relationship matrix was created with the Algorithm of Proven and Young (APY) with 18,359 core animals. The full data set consisted of phenotypes collected from 1989 through 2015 and pedigrees limited to 3 generations back from phenotyped or genotyped animals. The predictor data set was created by cutting off the phenotypes, pedigree animals, and genotypes in the last 4 years from the full data set. Genomic predictions (GPTA2011) were calculated for predicted bulls that had no recorded-daughters in 2011 but had at least 50 such daughters in 2015. We calculated the daughter yield deviations with the full data (DYD2015) for the predicted bulls (n = 3,797). We also used the official GPTA published in 2011 with a multi-step method as a comparison, although the official methods have changed since then. Coefficient of determination (R^2) and slope (b_1) were calculated from a linear regression of DYD2015 on GPTA2011. We investigated the effect of different unknown parent groups (UPGs) and a weight (ω) on the inverse of the pedigree relationship matrix for genotyped animals ($\mathbf{A}_{22}^{-1}$) to compensate incomplete pedigree. When applying QP-transformation to $\mathbf{A}^{-1}$, the R^2 was 0.52 with ω = 1 compared with 0.51 from the official GPTA. The b_1 was similar (0.78) to 0.81 from the official GPTA. Using ω = 0.90, the R^2 was still similar (0.50) but the b_1 was greatly improved (0.96). With QP-transformation in $\mathbf{H}^{-1}$, the R^2 was less than 0.4 and the b_1 was smaller regardless of ω. Without any UPGs, the predictability and the inflation showed the same level as the official GPTA. The GPTA of a young animal is equivalent to the direct genomic value when many genotypes are included in the evaluation. Fixed UPGs in $\mathbf{H}^{-1}$ added an extra value to GPTA of young animal but this addition is likely redundant in genomic prediction. We should exclude the UPG contributions from GPTA of young genotyped animals when $\mathbf{H}^{-1}$ is QP-transformed.

Key Words: genomic evaluation, incomplete pedigree, Holstein

172 Implementing SNP-level multiple-trait across country genomic evaluation without genotype sharing. B. Fragomeni*, D. Lourenco, Y. Masuda, and I. Misztal, *The University of Georgia, Athens, GA.*

There is a growing interest of Interbull in releasing a multiple across country genomic evaluation. However, most countries are not able to provide genotypes, and an alternative methodology is required. One strategy called SNP MACE posits a multiple-trait SNP BLUP based on left- and right-hand sides of national SNP BLUP. However, different countries use different sets of SNPs and multiple-trait computations with SNP may be difficult. We propose an alternative model based on reconstructing phenotypes for an independent genotyped population. Each country would submit only SNP effects, the number of reference animals, and average reliabilities of GEBV. This information can be used to create a pseudo-population with pseudo-observations. The combined data can be analyzed by multi-trait GBLUP. Conversion of GEBV would provide SNP effects in scale of every country. Simulations included 30k animals resembling the US Holstein population, with effective population size of 120. Chromosome number and size mimicked the cattle genome. The population was then divided in 3: 2 countries and 1 test population with 10k genotyped animals in each, and a different trait was assigned to each country. For the genotyped animals in the 2 countries, DYD were generated with an average reliability of 0.8. SNP effects were calculated with GBLUP in each one of the 2 countries. With SNP effects from the 2 countries, phenotypes were reconstructed for the test population. A bivariate GBLUP was then fitted, and GEBV/DGV were calculate for the test population for both countries. Accuracies were calculated for the validation population on the scale of 2 countries. When SNP effects of one country were used, the realized accuracy was 0.94 for the same population and 0.69 for the second country. When SNP effects of both countries were used, the accuracy for any country was 0.95. With the use of the APY algorithm, the procedure is computationally viable for any population size and any number of countries. An important issue is creation of pseudo-population that holds the same genomic information as the national population.

Key Words: SNP-MACE, genomic MACE, SNP effect, Interbull

173 Lifetime Net Merit versus annualized net present value as measures of profitability of selection. M. R. Schmitt*[1], P. M. VanRaden[2], and A. De Vries[1], [1]*Department of Animal Sciences, University of Florida, Gainesville, FL,* [2]*USDA-AGIL, Beltsville, MD.*

Current USDA linear selection indexes such as Lifetime Net Merit (NM) estimate lifetime profit given a combination of 13 traits. In these indexes, every animal gets credit for 2.78 lactations of the traits expressed per lactation, independent of its productive life (PL). Selection among animals with different PL is an example of investment in mutually exclusive projects that have unequal duration. Such projects are best compared with the annualized net present value (ANPV) technique. The objective of this study was to compare the ranking and value differences between NM and ANPV for the top 1,539 Holstein sires for NM available in the December 2017 genetic evaluation from the Council on Dairy Cattle Breeding. To calculate the ANPV, economic weights from USDA estimates were multiplied by the PTA of single event traits. Heifer conception rate was recognized at first calving and livability at the end of life. The economic weight of PL was converted from a marginal value of $21 per lactating month depreciated over the standard length of 2.78 lactations, to a replacement cost (−$1500) at the beginning and a salvage value ($800) at the end of life. All other traits were considered lactation dependent, and the economic weights were multiplied by the number of expected lactations (2.78 + PTA PL/10). The values for all 13 traits were discounted and converted to ANPV to compare animals with different investment horizons on the same common horizon. Correlation and rank correlation between NM and ANPV was 0.993 for the group of 1,539 bulls. However, 32% of bulls with the same ANPV had NM deviations greater than $9.90 from the expected NM. Within the highest 300 NM bulls, correlation and rank correlation between NM and ANPV was 0.964 and 0.943, respectively, and the largest changes in ANPV rank from NM rank were −96 and +117. Bulls with a combination of low lactation traits and high PL resulted in the greatest decrease of ANPV rank compared with NM rank. In conclusion, the re-ranking of bulls based on 2 different measures of profitability suggests that further discussion is warranted about construction of selection indexes for genetic selection.

Key Words: investment, profit, genetics