calves reported by Jersey breeders across the country. Their pedigrees all traced on both paternal and maternal sides to a common ancestor born in 1995. Genotypes revealed that JNS is attributable to a specific haplotype on *Bos taurus* autosome (BTA) 6, and about 6% of the genotyped Jersey population are now carriers of the haplotype. The region of shared homozygosity was further examined by sequencing, revealing missense variant rs1116058914 at base 60,158,901 of the ARS-UCD1.2 reference map as the most concordant with the genetic condition and most likely cause. The single base substitution (G/A) is in the coding region of the last exon of the ubiquitin C-terminal hydrolase L1 (*UCHL1*) gene that is conserved across species. Mutations in humans and gene knockouts in mice cause similar recessive symptoms and muscular degeneration. Since December 2020, carrier status is tracked with a haplotype and reported for all 303,087 genotyped Jersey animals. With random mating, about 300 affected calves per year would result from the 370,000 US Jersey cows in DHI. Selection and mating programs can reduce the number affected using either the haplotype status or a direct gene test in the future. Breeders should report calf abnormalities to their breed association to help discover new defects such as JNS.

Key Words: genetic defect, lethal recessive, carrier

200 Single-step genomic predictions for yield traits in US Holsteins with unknown parent groups and phenotype-pedigree truncation. D. Lourenco*[1], A. Cesarani[1], Y. Masuda[1], S. Tsuruta[1], E. Nicolazzi[2], P. M. VanRaden[3], and I. Misztal[1], [1]*University of Georgia, Athens, GA,* [2]*Council on Dairy Cattle Breeding, Bowie, MD,* [3]*AGIL-USDA, Beltsville, MD.*

In this study we assessed the reliability and inflation of GEBV from ssGBLUP with unknown parent groups (UPG) only for the pedigree relationship matrix (**A**) and for both **A** and the pedigree relationship matrix among genotyped animals ($\mathbf{A}_{22}$). The first scenario was termed UPG1 and the second was UPG2. Six large phenotype-pedigree truncated Holstein data sets were used. The complete data included 80M records for milk, fat, and protein yield from 31M cows born from 1980 to 2017. Truncation scenarios included pruning of phenotypes for cows born before 1990 and 2000 combined with truncation of pedigree information after 2 or 3 ancestral generations. A total of 861,525 genotyped bulls with progeny and cows with phenotypes were used in the analyses. Reliability and inflation/deflation of GEBV were obtained for 2,710 bulls based on deregressed proofs (DRP), and on 381,779 cows born after 2014 based on adjusted phenotypes (predictivity). Reliabilities ranged from 0.54 to 0.69 for UPG1 and from 0.69 to 0.73 for UPG2. The regression coefficient of bull DRP on GEBV ranged from 0.77 to 0.94 for UPG1 and was 1.00 for UPG2. Cow predictivity ranged from 0.48 to 0.51 for UPG1, and 0.51 to 0.54 for UPG2. The regression coefficient of cow adjusted phenotypes on GEBV was 1.02 for UPG2 with the most extreme truncation. Overall, reliability and predictivity from ssGBLUP with UPG2 were not affected by phenotype-pedigree truncation. Computations with the complete data set took 58h with UPG1 and 23 h with UPG2 because the number of rounds to converge was twice as large in UPG1. Similar computations with truncation before 2000 took 36 h and 15 h. Old phenotypes (before 2000) did not impact the reliability of predictions for young selection candidates, especially in UPG2. Here we used a selected set of 861k genotyped animals, but tests with 3.4M genotypes confirmed the computational feasibility of ssGBLUP without loss in reliability. In ssGBLUP evaluations with missing pedigree, unknown parent groups assigned to both **A** and $\mathbf{A}_{22}$ provided accurate and unbiased evaluations regardless of phenotype-pedigree truncation scenario.

Key Words: large-scale genomic evaluation, unknown parent groups

201 Are indirect genomic predictions a good option as the number of genotypes continues to rise? S. Tsuruta*[1], D. A. L. Lourenco[1], Y. Masuda[1], I. Misztal[1], and T. J. Lawlor[2], [1]*University of Georgia, Athens, GA,* [2]*Holstein Association USA Inc., Brattleboro, VT.*

As the number of genotyped animals continues to grow every year, the computational cost increases. One way to reduce the cost is to remove the older genotyped animals that have been culled and had no progeny nor phenotype. Another option could be indirect genomic predictions (IGP) for genotyped animals that have no progeny nor phenotypes. Assuming that these genotyped animals have no significant impact on the other genotyped animals, it is more practical to predict their genomic performance indirectly. The objective of this study is to conduct IGP for various genotyped animal groups for 18 linear type traits in US Holsteins using 2.3M genotyped animals and to investigate if the IGP are accurate and unbiased. Phenotypic records for 18 linear type traits used in December 2018 genetic evaluation in US Holsteins were provided by Holstein Association USA, and genotypes in December 2018 were provided by the Council on Dairy Cattle Breeding. The full data set consisted of 10.9M records up to 2018 calving, 13.6M animals in the pedigree, and 2.3M genotyped animals with 79K SNP. Genomic prediction was conducted with single-step genomic BLUP, applying the 18 multi-trait animal model to calculate direct genomic predictions (GEBV) for all genotyped animals, and then IGP were calculated for genotyped animals with no progeny nor phenotype by year from 2014 to 2018. To reduce computing costs, IGP were calculated by GEBV from randomly selected genotyped animals from 15K to 60K. R^2 in GEBV = $b_0 + b_1$*IGP ranged from 0.96 to 0.98 for males and from 0.95 to 0.96 for females for 18 traits. The high correlation (0.95) between b_0 and annual genetic gains for 18 traits indicates the bias in IGP due to directional selection, which can be adjustable. For practical genomic evaluation, 25K to 35K randomly selected genotyped animals from GEBV can be used to obtain accurate and unbiased IGP. The result in this study can be a practical solution when conducting a large-scale genomic evaluation and can make more frequent evaluation with lower cost when genotyped animals have no phenotypes nor progeny. Further coordination will be needed to determine how genotyped animals should be selected for IGP.

Key Words: ssGBLUP, indirect genomic predictions, US Holsteins

202 Automatic scaling in single-step genomic BLUP. M. Bermann*, D. Lourenco, and I. Misztal, *The University of Georgia, Athens, GA.*

Single-step genomic BLUP (ssGBLUP) requires compatibility between genomic and pedigree relationships for unbiased and accurate predictions. Scaling the genomic relationship matrix (**G**) to have the same averages as the pedigree relationship matrix (i.e., scaling by averages) is one way to ensure compatibility. This requires computing both relationship matrices, calculating averages, and changing **G**, whereas only the inverses of those matrices are needed in the mixed model equations. Therefore, the compatibility process can add extra computing burden. In the single-step Bayesian Regression (SSBR), the scaling is done by including an average of the breeding values of the genotyped animals (μ_g) as a fixed effect in the model. In this study, such scaling called "automatic" was implemented in ssGBLUP via QP transformation of the inverse of the relationship matrix used in ssGBLUP. Comparisons involved a simulated data set, and the genomic relationship matrix was computed using different allele frequencies either from the current population (i.e., realized allele frequencies), equal among all the loci, or from the base population. For all the scenarios, we computed bias, accuracy, and dispersion. With no scaling, the bias expressed in terms of