196 Genetic and genomic evaluation of late-term abortion recorded through Dairy Herd Improvement test plans. M. Neupane*, J. L. Hutchison, J. B. Cole, C. P. Van Tassell, and P. M. VanRaden, *Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Late-term abortions cause significant economic loss and are of great concern for dairy herds. Late-term abortions ≥152 d and <251 d of gestation that terminate a lactation or initiate a new lactation have long been recorded in Dairy Herd Improvement (DHI). For 22.7 million DHI lactations, the average recorded incidence of late-term abortions across all years was 1.2%. However, the 1.3% incidence of abortions reported in 2012 has declined to < 1.0% incidence since 2015. Small adjustments were applied among the 82 million daughter pregnancy rate (DPR), 29 million cow conception rate (CCR), and 9 million heifer conception rate (HCR) records to more accurately account for late-term abortions. Fertility credits for CCR and HCR were changed to treat the last breeding as a failure instead of success if the next calving is coded as a late-term abortion. Similarly, when computing DPR, days open is now set to the maximum value of 250 instead of the reported days open if the next reported calving is an abortion. The test of these changes showed very small changes in SD and high correlations (0.997) of adjusted predicted transmitting abilities (PTA) with official PTA from about 20,000 HO bulls born since 2000 with >50% reliability. For late-term fetal survival as a trait, estimated heritability was only 0.001 and PTA had a SD of only 0.1% for recent sires with high reliability (>75%). Young animal genomic PTA have near 50% reliability but range only from −0.5 to +.4 because of the low incidence and heritability. Genetic trend was slightly favorable and late-term fetal survival PTA were correlated favorably by 0.08 with net merit, 0.38 with productive life, 0.32 with livability, −0.23 with daughter stillbirth, −0.25 with daughter calving ease, 0.18 with CCR, 0.12 with DPR, and −0.15 with gestation length. Thus, PTA for late-term abortions should not be needed as a separate fertility trait and instead these minor edit changes should suffice. PTA for earlier abortions would add little value because national evaluations for current fertility traits already accounted for those economic losses.

Key Words: fertility traits, genetic and genomic evaluation, late-term abortions

197 Evaluation of bull fertility in Italian Brown Swiss dairy cattle using cow field data. H. A. Pacheco*[1], M. Battagin[2], A. Rossoni[2], A. Cecchinato[3], and F. Peñagaricano[1], [1]*University of Wisconsin–Madison, Madison, WI,* [2]*Italian Brown Breeders Association, Bussolengo, Verona, Italy,* [3]*University of Padova, Legnaro, Padua, Italy.*

Dairy bull fertility is traditionally evaluated using semen production and quality traits; however, these attributes explain only part of the differences observed in fertility among bulls. Alternatively, bull fertility can be directly evaluated using cow field data. The main objective of this study was to investigate bull fertility in the Italian Brown Swiss dairy cattle population using confirmed pregnancy records. The data set included a total of 420,512 breeding records from 1,260 bulls and 136,403 lactating cows between first and fifth lactation from 2000 to 2019. We first evaluated cow pregnancy success, including factors related to the bull under evaluation, such as bull age, bull inbreeding and AI organization, and also factors associated with the cow that receives the dose of semen, including herd-year-season, cow age, parity, and milk yield. We then estimated sire conception rate, considered as a phenotypic assessment of male fertility, using only factors related to the bull. Model predictive ability was evaluated using 10-fold cross-validation with 10 replicates. Interestingly, our analyses revealed that there is a substantial variation in conception rate among Brown Swiss bulls, with more than 20% conception rate difference between high-fertility and low-fertility bulls. We also showed that the phenotypic prediction of bull fertility is feasible, our cross-validation analyses achieved predictive correlations around 0.31 for sire conception rate. Improving reproduction performance is one of the major challenges of the dairy industry worldwide, and for this, it is essential to have accurate predictions of service sire fertility. This study represents the foundation for the development of novel tools that will allow dairy producers, breeders, and AI companies make accurate management and selection decisions on Brown Swiss male fertility.

Key Words: pregnancy records, service sire fertility, sire conception rate

198 Relationship of β-casein A2 genetics, production, and fertility of organic Holstein dairy cows. B. J. Heins*[1], C. D. Dechow[2], and L. C. Hardie[2], [1]*University of Minnesota, Morris, MN,* [2]*Pennsylvania State University, State College, PA.*

The objective of the study was to determine milk production, fertility, and survival for β-casein A2 genotypes of organic Holstein cows. Holstein cows (n = 1, 982) from 13 dairy herds across the Midwest and Northeast were genomic tested with Clarifide Plus for A2 status. Two-hundred fourteen cows were A1A1 (11%), 848 cows were A1A2 (43%) and 920 cows were A2A2 (46%). In total, 2,249 lactation records were used with 1,025 from first parity and 1,224 from second parity and greater. Daily milk, fat, and protein production and SCS from milk recording were calculated with random regression. A lower limit of 50 d for days open (DO) was applied, and cows with more than 250 d for DO had DO set to 250 d. Independent variables for statistical analysis with PROC MIXED included the fixed effects of herd, parity, milk β-casein genotype (A1A1, A1A2, A2A2), and the interaction of milk β casein genotype and parity. Cow and birth date were random effects in the statistical model. Test-day milk production was not different ($P >$ 0.50) for A1A1 (26.4 kg/d), A1A2 (27.5 kg/d), and A2A2 (27.5 kg/d) cows. Days open was not different ($P > 0.40$) for A1A1 (124 d), A1A2 (136 d), and A2A2 (144 d) cows. Furthermore, the number of times bred was not different ($P > 0.44$) for A1A1 (1.77), A1A2 (1.62), and A2A2 (2.13) cows. Survival to second lactation was 83% for A1A1 cows, 97% for A1A2 cows, and 95% for A2A2 cows. Results indicate no difference in production and fertility with regard to A1 or A2 genotype in organic dairy herds. Survival may be biased against the A1 genotype which is indicated by lower survival rates in first lactation.

Key Words: genetic selection, organic, A2 milk

199 Inheritance of a mutation causing neuropathy with splayed forelimbs in Jersey cattle. A. Al-Khudhair*[1], D.J. Null[1], J. Cole[1], C. W. Wolfe[2], and P. M. VanRaden[1], [1]*USDA, Agricultural Research Service, Animal Genomics and Improvement Laboratory, Beltsville, MD,* [2]*American Jersey Cattle Association, Reynoldsburg, OH.*

A new undesirable genetic factor, known as "neuropathy with splayed forelimbs" (JNS), has been identified recently in the Jersey breed. Calves affected with JNS are unable to stand on splayed forelimbs that exhibit significant extensor rigidity and/or excessive lateral abduction at birth. Affected calves are generally alert at birth but exhibit neurologic symptoms including spasticity of head and neck and convulsive behavior. Other symptoms reported include dislocated shoulders, congenital craniofacial anomalies, and degenerative myelopathy. Inheritance of the undesirable genetic factor was determined from a study of 16 affected

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