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