

Breeding and Genetics IV

407 Genetic aspects of colostrum quality traits including immunoglobulin G in Holstein cows. A. Costa^{*1}, A. Goi¹, G. Visentin², M. De Marchi¹, and M. Penasa¹, ¹University of Padova, Legnaro, Padova, Italy, ²University of Bologna, Bologna, Italy.

Immunoglobulins G (IgG), A (IgA), and M (IgM) account for 80% of total proteins in bovine colostrum and are important for the passive transfer of antibodies from the dam to the calf. The practical difficulties of samples collection and the high cost of gold standard analysis have so far hampered the estimation of genetic parameters of both bovine colostrum and mature milk IgG, IgA, and IgM concentrations (g/L). In the present study, 672 colostrum samples from the same number of Holstein cows were collected within 6 h after calving. The concentration of IgG, IgA, and IgM was determined through radial immunodiffusion. The pedigree included 6,714 animals, i.e., cows with phenotypes and up to 6 generations of ancestors. Linear models were used to estimate variance and covariance components through univariate and bivariate analyses, respectively. The model included the random animal additive genetic effect and the fixed effects of parity (5 levels: 1, 2, 3, 4, and ≥ 5), season of calving (4 levels), year of calving (2 levels), and herd (9 levels). Colostrum IgG, IgA, and IgM averaged 93.24, 4.89, and 5.16 g/L, respectively, and were normally distributed. Heritabilities (\pm standard error) of IgG, IgA, and IgM were 0.14 ± 0.14 , 0.33 ± 0.16 , and 0.19 ± 0.14 , with coefficients of genetic variation of 13.1, 30.8, and 19.7%, respectively. The IgG correlated phenotypically with IgA (0.52 ± 0.04) and IgM (0.59 ± 0.03), and IgA correlated with IgM (0.48 ± 0.04). Overall, genetic correlations were weak (<0.10) except for the association between IgG and IgA (0.37 ± 0.41). Results agreed with the literature and highlighted that the most important colostrum quality trait, i.e., the IgG, tended to be the least heritable Ig. Further efforts will allow to improve data size and variability and will be focused on coupling Ig data with other information to estimate the association between Ig of the colostrum administered to the calf and health and productivity in the subsequent lactations.

Key Words: colostrum quality, dairy cattle, genetic improvement

408 Gene mapping, gene-set analysis, and genomic prediction of postpartum blood calcium in Holstein cows. L. Cavani^{*1}, M. B. Poindexter², H. A. Pacheco¹, C. D. Nelson², J. E. P. Santos², and F. Peñagaricano¹, ¹University of Wisconsin–Madison, Madison, WI, ²University of Florida, Gainesville, FL.

The onset of lactation results in a sudden irreversible loss of calcium for colostrum and milk synthesis. Some cows are unable to quickly adapt to this demand and succumb to clinical hypocalcemia. Our goal was to perform a comprehensive genomic analysis of blood total calcium concentration (Ca) in periparturient Holstein cows. We first performed a genomic scan and a gene-set analysis to identify major genes, pathways and mechanisms affecting postpartum Ca. Then, we assessed the prediction of postpartum Ca using genomic data. Data consisted of 7,691 records of plasma or serum Ca measured in the first, second, and third day after parturition (DAP) of 959 primiparous and 1,615 multiparous cows that calved between Dec-2015 and Jun-2020 in 2 dairy herds. All cows were genotyped with 80k SNPs. The statistical models included lactation (1 to 5+), calf category (male, female, twins), and DAP as fixed effects, and season-treatment-experiment, animal, and permanent environmental as random effects. Model predictive ability was evaluated using 10-fold cross-validation. Heritability and repeatability estimates

were 0.083 (SE = 0.017) and 0.444 (SE = 0.028), respectively. The association mapping identified 2 major regions located on BTA6 and BTA16 that explained 1.2% and 0.7% of additive genetic variance of Ca, respectively. Interestingly, the region on BTA6 harbors the gene GC, which encodes the vitamin D binding protein, and the region on BTA16 harbors LRRC38, which is actively involved in potassium transport. Other sizable peaks were identified on BTA5, BTA2, BTA7, BTA14, and BTA9. These regions harbor genes associated with calcium and potassium channels (*CATSPER4*, *CACNA1S*, *CRACR2A*, *CDKN1B*, *KCNK9*). The gene-set analysis revealed terms related to calcium ion transport, calcium ion binding, and calcium signaling. Genomic predictions of yet-to-be observed Ca yielded predictive correlations equal to 0.73 using both fixed and random effects, and 0.21 using only genomic breeding values. Overall, our results can contribute to the development of novel genomic strategies for reducing periparturient hypocalcemia in dairy cattle.

Key Words: calcium homeostasis, postpartum hypocalcemia, whole-genome scan

409 Estimates of genetic parameters for health traits in US organic Holstein cows. L. C. Hardie^{*1}, I. W. Haagen¹, B. J. Heins², and C. D. Dechow¹, ¹Pennsylvania State University, University Park, PA, ²University of Minnesota, St. Paul, MN.

The objectives of this study were to estimate genetic parameters for health traits measured in US organic Holstein cows and establish genetic relationships with national evaluations for corresponding traits. Data were gathered from 38,949 lactations from 19,139 Holstein cows on 16 USDA certified organic farms. Health traits analyzed on these cows included mastitis, lameness, any metabolic disease (METAB; ketosis, displaced abomasum, and milk fever), any reproductive disease (REPRO; retained placenta and metritis), died, transition cow diseases (defined as any disease occurring ± 21 d of parturition), and any health event. Stayability through a given lactation was also analyzed. All traits were analyzed as binary variables within each lactation (1 = diseased, 0 = otherwise). Genotypes on 2,347 cows with breed representation of at least 87.5% Holstein were combined with a minimum of 4-generation pedigree. Using the BLUPF90 family of programs, multivariate threshold models were employed to estimate genetic parameters with fixed effects of herd and lactation and random effects of herd-year-season of birth (stayability), herd-year-season of calving (health traits), animal, and permanent environment. Heritabilities ranged from 0.03 ± 0.01 (REPRO) to 0.11 ± 0.03 (METAB). Genetic correlations among health traits ranged from -0.42 ± 0.17 (mastitis and METAB) to 0.93 ± 0.03 (transition and any health event). When evaluating traits in terms of resistance to disease, genetic correlations between stayability and health traits ranged from 0.21 ± 0.22 (lameness) to 0.69 ± 0.12 (any health event). Approximate genetic correlations with corresponding national evaluations for health traits were 0.72 for mastitis; 0.42, 0.33, and -0.05 between METAB and displaced abomasum, ketosis, and milk fever, respectively; 0.51 and 0.44 between REPRO and metritis and retained placenta, respectively; and 0.62 between died and livability. In conclusion, there is a heritable component to health traits in US organic cows and a favorable relationship with health traits evaluated nationally, such that organic dairy producers will be able to achieve genetic improvement in the health of their cows.

Key Words: health, organic, genomic