F. Malchiodi*[1], L. F. Brito[1], A.-M. Christen[2], A. Fleming[1], D. F. Kelton[3], F. S. Schenkel[1], and F. Miglior[1,4], [1]*Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada,* [2]*Valacta, Sainte-Anne-de-Bellevue, QC, Canada,* [3]*Department of Population Medicine, OVC, University of Guelph, Guelph, ON, Canada,* [4]*Canadian Dairy Network, Guelph, ON, Canada.*

Digital dermatitis and sole ulcer represent the most prevalent lesions in Canada, with almost 20% and 8% of cows affected by these lesions, respectively. This study aimed to perform a genome-wide association study (GWAS) and functional analysis to uncover genomic regions associated with digital dermatitis and sole ulcer. Hoof lesions were recorded by 51 hoof trimmers during the routine trimming activity in 1,080 Canadian herds between 2009 and 2016. Hoof lesions were coded as binary traits (0; 1), where 1 was assigned to the presence of a lesion in any claw. The final data set contained 249,709 observations from 105,450 animals, while the pedigree file contained 351,215 animals. Of those animals, 20,188 were genotyped either with 50K SNP panel or a low-density panel and imputed to 50K. The model implemented in the weighted single-step GWAS included the fixed effects of herd-date of hoof trimming, hoof trimmer, parity at trimming, stage of lactation at trimming, and the random additive genetic animal and permanent environmental effects. Important genomic regions associated with digital dermatitis and sole ulcer were identified and a list of functional candidate genes within or next to these regions was created.

Key Words: digital dermatitis, sole ulcer, ssGWAS

E. A. Lozada-Soto*[1], K. Anderson[2], C. Maltecca[1], and F. Tiezzi[1], [1]*Department of Animal Science, North Carolina State University, Raleigh, NC,* [2]*Department of Population Health and Pathobiology, College of Veterinary Medicine, North Carolina State University, Raleigh, NC.*

Genetic selection toward mastitis resistance has not advanced substantially in the past. The detection of new traits that will improve selection is needed. The aim of this study was to examine the feasibility of using threshold concentration values of somatic cells as traits in selection against mastitis susceptibility. Quarter milk samples (n = 965) were collected at d 4 and d 11 post calving from Holstein and Jersey cows reared at the Dairy Education Unit at North Carolina State University. Cell counts for total leucocytes (TLC), neutrophils (N), macrophages (M), and lymphocytes (L) were obtained via differential somatic cell count. Intramammary infection with major and minor pathogens, as well as fungi, was determined via microbiological culturing on duplicate quarter milk samples. Log-transformed scores for the cell counts were calculated. MCMCglmm was used to fit various models for the following dependent variables: TLC, N, M, L, major pathogen presence, minor pathogen presence, fungi presence, and cell count thresholds for major pathogens. The animal and the week of sampling were treated as random, while breed, lactation, sampling day, sampling time, and quarter position were treated as fixed. The variance due to the animal was 0.56, 0.65, 0.47, 0.57, 12.57, 2.38, 10.22, 4.87, 3.84, and 4.41 for the variables TLC, N, M, L, major pathogen presence, minor pathogen presence, fungi presence, TLC threshold, N threshold, M threshold, and L threshold respectively. The variance due to the week of sampling obtained was negligible for all variables considered. The effect of sampling day was significant ($P < 0.001$) for the variables TLC, N, M, L, TLC threshold, N threshold, and M threshold. Lactation was significant for the presence of major pathogens. The effects of breed, sampling day, and quarter position were not significant for any variable. A second model included the additive genetic effect of the cow using pedigree information. Heritability results will be presented.

Key Words: mastitis, differential somatic cell count, genetics.

P. M. VanRaden* and M. E. Tooker, *USDA Animal Genomics and Improvement Laboratory, Beltsville, MD.*

Genetic merits in first vs. later parity with correlations <1 were compared with official repeatability models using 88 million lactation records of 34 million cows for yield traits and fewer records for SCS and 2 cow fertility traits. Estimated genetic correlations of first with later parity ranged from 0.85 for SCS to 0.95 for fertility traits. These estimates were also applied to permanent environmental and herd-by-sire interaction effects that were constants within later parities and correlated with first-parity effects. Previous parity variance adjustments were removed. Computation took twice as many processors and required more iteration because of slightly slower convergence. All-parity merit combined first and later merit with weights of 0.33 and 0.67, respectively; genetic correlations of all-parity merit with either first or later merit ranged from 0.96 to 0.99. For all bulls progeny-tested since 1995, correlations with official evaluations were very high (0.999) for all traits. Correlations for the 2 most recent years of progeny-tested bulls were lower (0.991 for SCS to 0.997 for fat yield) because many of these bulls had only or mostly first-parity daughters. Computed reliabilities of these recent bulls averaged 3 percentage points less than official reliabilities. With the latest 5 yr of data removed, correlations of truncated and current evaluations were compared for the most recently proven US bulls. Correlations for SCS were higher for the new model than for the traditional model for Holsteins (0.875 vs. 0.867) and Brown Swiss (0.800 vs. 0.76) but not for Jerseys (0.822 vs. 0.826). Correlations for yield traits did not improve for any breed. In a separate test, modeling maturity effects using random regressions on parity gave predictions very similar to modeling first vs. later records. Modeling lactations as correlated traits can possibly reduce biases from early daughters and slightly improve stability for SCS when bulls transition from genomic predictions to observed daughter records, but did not improve correlations with future evaluations for other traits.

Key Words: maturity effect, parity, genetic correlation

L. C. Hardie*[1], I. W. Haagen[1], L. Han[1], B. J. Heins[2], D. D. Fitzsimmons[3], and C. D. Dechow[1], [1]*Pennsylvania State University, University Park, PA,* [2]*University of Minnesota, Minneapolis, MN,* [3]*Alfred State University, Alfred, NY.*

The objective of this study was to evaluate the relationship between daughter performance on US organic farms with sire predicted transmitting ability (PTA) estimated through national evaluations. Production and fertility data were collected from 3,002 Holstein cows housed on 9 commercial organic farms across the US. Only records from the year of organic certification through 2017 were used, and for a cow to be included in the data set, her first parturition must have occurred during or after the year of organic certification. Daughters belonged to 513 sires with the most commonly used sire having 185 daughters. We regressed 1,560 daughter records of 305-d mature equivalent (ME305) milk, fat, and protein yield on sire PTA for milk, fat, protein, respectively, and we regressed 1,624 records of average lactation SCS, on sire PTA for