

a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Key Words: heritability, fertility, dairy cattle

T102 Selection signature analysis in Holstein cattle identified genes known to affect reproduction. Li Ma¹, Tad, S. Sonstegard², Curtis Van Tassel², John B. Cole², George R. Wiggans², Brian A. Crooker³, F. Abel Ponce de Leon³, and Yang Da^{*3}, ¹*Department of Animal and Avian Sciences, University of Maryland, College Park, MD*, ²*Animal Genomics and Improvement Laboratory, ARS-USDA, Beltsville, MD*, ³*Department of Animal Science, University of Minnesota, Saint Paul, MN*.

Using direct comparison of 45,878 SNPs between a group of Holstein cattle unselected since 1964 and contemporary Holsteins that on average take 30 d longer for successful conception than the 1964 Holsteins, we conducted selection signature analyses to identify genome regions associated with dairy fertility. Several genes known to affect reproduction were located in or near genome regions with strong selection signals. These genes include the fibroblast growth factor 1 gene (*FGF1*) on Chr07; the follicle stimulating hormone receptor gene (*FSHR*) and the luteinizing hormone choriogonadotropin receptor gene (*LHCGR*) on Chr11; the KIT ligand gene (*KITLG* or *KITL*), the fibroblast growth factor 6 and 23 genes (*FGF6* and *FGF23*) and the cyclin D2 gene (*CCND2*) on Chr05; the placental growth factor gene (*PGF* or *PLGF*) and the estrogen-related receptor β gene (*ESRRB*) 2Mb downstream of *PGF* on Chr10; and the prolactin receptor gene (*PRLR*) on Chr20. The selection signal for the region containing *FGF1* was among the strongest selection signals we observed. According to the literature on these genes, *FGF1* is involved in broad mitogenic and cell survival activities including embryonic development, *PGF* plays a key role in embryogenesis, *ESRRB* plays an essential role in placenta development, *FSHR* is necessary for follicular development and is expressed on the granulosa cells that are closely associated with the developing female gamete in the ovary of mammals, and *LHCGR* is necessary for follicular maturation and ovulation. Mouse knockout models showed that *FSHR*, *KITLG*, *CCNG2*, and *PRLR* were involved in female fertility proteins. These known gene functions related to reproduction and the fact that these genes were in or near chromosome regions with strong selection signals indicate that these genes could be involved in the vast difference in fertility between contemporary Holsteins and the 1964 Holsteins.

Key Words: fertility, selection signature, Holstein

T103 Genetic interactions for heat stress and herd yield level: predicting foreign genetic merit from domestic data. Janice R. Wright* and Paul M. VanRaden, *Animal Genomics and Improvement Laboratory, Agricultural Research Service, US Department of Agriculture, Beltsville, MD*.

Genetic-by-environmental interactions were estimated from national data by separately adding random regressions for heat stress (HS) and herd yield level (HL) to the US all-breed animal model to improve predictions of future records and genetic rankings in other climates and production situations. Yield data included 79 million lactation records of 40 million cows; somatic cell score, productive life, and daughter pregnancy rate were also tested but had fewer records. Coefficients for HS were the state's July average temperature-humidity index; coefficients for HL were management-level weighted means for energy-corrected milk (ECM) divided by breed-year mean ECM. Coefficients were standardized to a mean of 0 and variance of 1. Predictions of current

(August 2014) from historical (August 2011) records were tested with a model that included herd management group (absorbed), sire estimated breeding value (EBV), dam EBV, and an interaction term (HS or HL) from the truncated data; records were weighted by lactation length for records in progress and by herd heritability using the same weights as in national evaluations. Estimated regression coefficients for sire EBV and dam EBV were always near their expected values of 0.5 and did not change when HS or HL interactions were added to the model. Estimated regressions for interaction terms, expected to be near 1, were 0.80 to 0.93 for HS and 0.61 to 0.72 for HL in yield traits. Squared correlations increased by < 0.0003 for both HS and HL; increases for nonyield traits were even smaller. An additional test used multitrait across-country EBV to predict rankings of the same bulls in the United States and 14 other countries with somewhat different environments. The HS coefficient was significant ($P < 0.05$) in 9 of 14 countries for milk and protein and in 10 for fat; the HL coefficient was significant in 8 countries for milk, 5 for protein, and 1 for fat. Squared correlations after adding an interaction term increased by < 0.004 for HL and < 0.01 for HS. The small changes in rank and correlation gains when HS and HL interactions were included in national evaluations indicate that current genetic predictions perform very well in a variety of environments.

Key Words: heat stress, environmental interaction, random regression

T104 Application of milk mid-infrared (MIR) spectrometry in the dairy cattle industry in Canada. Saranya Gunasegaram^{*1}, Allison Fleming¹, Astrid Koeck¹, Francesca Malchiodi¹, Mehdi Sargolzaei^{1,2}, Milena Corredig^{3,4}, Flavio Schenkel¹, Bonnie Mallard⁵, Ayesha Ali⁷, and Filippo Miglior^{1,7}, ¹*CGIL, University of Guelph, Guelph, ON, Canada*, ²*Semex Alliance, Guelph, ON, Canada*, ³*Gay Lea, Guelph, ON, Canada*, ⁴*Department of Food Science, University of Guelph, Guelph, ON, Canada*, ⁵*Department of Pathobiology, OVC, University of Guelph, Guelph, ON, Canada*, ⁶*Department of Mathematics and Statistics, University of Guelph, Guelph, ON, Canada*, ⁷*Canadian Dairy Network, Guelph, ON, Canada*.

In Canada, many projects are aiming to integrate milk MIR spectra to develop predictions of milk components and cow status. A proportion of milk spectral data from FOSS MIR machines at Canadian DHI partners, CanWest DHI (Guelph, ON) and Valacta (Sainte-Anne-de-Bellevue, QC), have been saved and transferred to the Canadian Dairy Network, since early 2013. With addition of roughly 60,000 milk spectra every month; from approximately 700,000 cows enrolled in milk recording programs in Canada; the database is nearing 1.8 million. These spectra will be merged with recorded cow reproduction and health events (including hoof health). Currently, University of Guelph is analyzing approximately 2,000 milk samples for their fatty acid profile, milk fat globule and casein micelle size, lactoferrin, calcium, casein, and phospholipid content to use as a reference for developing MIR prediction equations. Genetic and genomic evaluation of Canadian dairy cows and bulls will be done using these MIR predicted milk component traits, with the objective of improving the nutritional value of milk and milk products for human consumption. Use of milk MIR spectra will be incorporated in a pending Canadian project, measuring feed efficiency and methane emissions in dairy cattle as a possible means for prediction. Information available to improve both cow management and genetic evaluation in Canadian dairy industry will be increased with the implementation of MIR prediction of a variety of new milk component and cow traits.

Key Words: milk infrared spectra, genomic, dairy cattle