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**0945 (T043) Determination of single nucleotide polymorphisms associated with subclinical ketosis in Jersey cattle.** R. T. Fugate<sup>\*1</sup>, L. H. Dauten<sup>2</sup>, G. R. Wiggans<sup>3</sup>, and H. M. White<sup>4</sup>, <sup>1</sup>University of WI, Madison, <sup>2</sup>University of Connecticut, Storrs, <sup>3</sup>Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, <sup>4</sup>Dep. of Dairy Science University of Wisconsin, Madison.

Subclinical ketosis is a fresh cow disorder that is costly in terms of lost milk production and treatment cost. Although treatment and prevention strategies are available, prevention requires targeting animals that are likely to develop the disease. Whole-herd genotyping is becoming more common with commercial dairies, and identification of markers for ketosis predisposition would provide a valuable tool to producers. The objective of this study was to identify single nucleotide polymorphisms (SNP) that are associated with subclinical ketosis in Jersey cattle. Ketotic cows were identified by cowside test using the Precision Xtra meter. Blood and hair samples were collected from 54 Jerseys (ketotic and healthy herdmates on the same day) with < 30 d in milk on New England dairy farms. Mean parity of cows was 2.8, with no difference ( $P > 0.05$ ) between healthy and ketotic cows; no difference ( $P > 0.05$ ) also was found for milk yield, 305-d mature-equivalent milk yield (ME<sub>305</sub>), or ME<sub>305</sub> from the previous parity. Blood serum was analyzed for concentration of nonesterified fatty acid (NEFA) and  $\beta$ -hydroxybutyrate (BHBA). Hair samples were submitted to the American Jersey Cattle Association for genotyping with the BovineSNP50 BeadChip. Concentrations of NEFA and BHBA were analyzed using the SAS 9.2 PROC MIXED; differences in SNP frequency by ketosis status (healthy or ketotic) was analyzed using the  $\chi^2$  test from the SAS 9.2 FREQ procedure. As expected, BHBA concentrations were greater ( $P \leq 0.05$ ) for ketotic cows compared with healthy herdmates (1.63 vs.  $0.91 \pm 0.17$  mmol/L). For NEFA, concentrations tended to be greater ( $P \leq 0.01$ ) in ketotic cows compared with healthy cows (0.45 vs.  $0.33 \pm 0.05$  mmol/L). Of the 54,609 SNP analyzed for each genotype, 1685 were different ( $P \leq 0.05$ ) and 1862 tended to differ ( $0.05 < P \leq 0.1$ ) between ketotic and healthy cows. These data suggest that genotypes from the BovineSNP50 BeadChip could be useful in predicting predisposition for ketosis in Jerseys, but examination of a larger data set is necessary to validate the predictive ability of the identified SNP.

**Key Words:** ketosis, Jersey, SNP

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**0946 (T044) Multi-trait, multi-breed conception rate evaluations.** P. M. VanRaden<sup>1</sup>, J. R. Wright<sup>\*1</sup>, C. Sun<sup>2</sup>, J. L. Hutchison<sup>1</sup>, and M. E. Tooker<sup>1</sup>, <sup>1</sup>Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD, <sup>2</sup>National Association of Animal Breeders, Columbia, MO.

Heifer and cow conception rates (HCR and CCR) were evaluated with multi-trait, multi-breed models including crossbred cows instead of the previous single-trait, single-breed models. Fertility traits benefit from multi-trait processing because of high genetic correlations and many missing observations, with 4 million HCR and 14 million CCR lactation records stored since 2003 vs. 66 million daughter pregnancy rate (DPR) records since 1960. Conception rates were previously modeled using multiple binary success records per parity (such as no, no, yes) that are now pre-adjusted for environmental effects and combined into lactation records for simpler multi-trait analysis with the continuous trait DPR. Genetic correlation estimates were 0.45 for HCR with CCR, 0.86 for CCR with DPR, and 0.36 for HCR with DPR. Inbreeding depression per 1% inbreeding was -0.21 for HCR, -0.10 for CCR, and -0.13 for DPR. Heterosis was 1.3 for HCR, 3.2 for CCR, and 1.4 for DPR. Crossbred cows get the combined effects of heterosis and no inbreeding compared to purebreds that may average 6%. Genetic differences among breeds were fairly consistent with phenotypic differences. Holsteins had the highest phenotypic and genetic averages for HCR, while Jerseys were highest for CCR. Evaluations from the new and previous models were correlated by > 0.95 for both HCR and CCR for recent Holstein bulls with > 50% reliability, but were less correlated in other breeds because of additional crossbred daughters and contemporaries. For Holstein sires with > 90% reliability, correlations between single-breed and multi-breed evaluations were 0.986 for HCR and 0.992 for CCR, indicating little change in rank when adding the other breeds. Genetic trend for CCR was more negative with multi-trait processing because of the correlation with DPR. Genetic trends were validated using Interbull tests 1 and 3. The genetic correlations with other countries estimated by Interbull changed little for Holsteins, averaging 0.02 higher for HCR and 0.02 lower for CCR, but were more variable for other breeds. The new model implemented in December 2013 combines data from all breeds and uses DPR as a correlated trait to improve HCR and CCR evaluations.

**Key Words:** conception, evaluation, multi-trait