

of hormone treatment, for example CTFS was split whereby one subset included only FTAI records while the second data set included only HD records. Preliminary statistics are presented in Table 1. By conducting a bivariate analysis the results of this study will identify potential genetic and non genetic differences between the fertility phenotypes recorded under the different scenarios. In addition, this will provide a novel basis in assessing the impact of hormonal synchronization protocols on the accuracy of genetic evaluations for fertility traits in dairy cattle.

**Key Words:** fertility traits, hormonal synchronization, genetic evaluations

**122 Implementation of national health trait evaluations in Jersey.** K. L. Parker Gaddis<sup>1</sup>, L. M. Jensen<sup>2</sup>, P. M. VanRaden<sup>3</sup>, J. H. Megonigal Jr.<sup>1</sup>, E. L. Nicolazzi<sup>1</sup>, H. D. Norman<sup>1</sup>, and C. W. Wolfe<sup>4</sup>, <sup>1</sup>*Council on Dairy Cattle Breeding, Bowie, MD*, <sup>2</sup>*University of Florida, Gainesville, FL*, <sup>3</sup>*Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD*, <sup>4</sup>*American Jersey Cattle Association, Reynoldsburg, OH*.

Health evaluations for 6 traits (resistance to milk fever, displaced abomasum, ketosis, mastitis, metritis, retained placenta) have been available for Holstein animals from the Council on Dairy Cattle Breeding (CDCB; Bowie, MD) since April 2018. Recent research indicated that expanding these evaluations to include Jersey animals was feasible. Concurrently, there was a 112% increase in the total number of usable Jersey health records submitted to CDCB in the span of one year beginning in January 2019. Total number of available phenotypic records by trait as of January 2020 ranged from 85,417 for ketosis to 168,342 for mastitis. Overall incidence ranged from 1.2% for milk fever up to 10.4% for mastitis, similar to those found in Holstein. Heritabilities were assumed to be equivalent to those in Holstein, ranging from 0.6 to 3.1%. The same pipelines as those currently used for CDCB Holstein health evaluations were expanded to include Jersey data. Phenotypes are pre-adjusted for unequal variance before evaluation. Traditional PTA are estimated using a univariate BLUP repeatability animal model accounting for year-season, age-parity, herd-year, and permanent environmental effects, as well as a regression on inbreeding and heterosis. Genomic PTA are calculated with 79,294 markers used in CDCB routine genomic evaluations. Resulting PTA are presented as percentage points above or below the breed's average resistance with more positive values being favorable. Average traditional reliabilities for bulls born since 1990 with  $\geq 90\%$  net merit (NMS) reliability ranged from 17 to 32%, depending on trait. Average

genomic reliabilities for those bulls ranged from 29 to 49%, gaining 12 to 17 percentage points from the inclusion of genomic data. Maximum PTA reliability was 98% for mastitis. Correlations between health PTA and PTA of other routinely evaluated traits were calculated. Significant ( $P < 0.05$ ) correlations ranged from  $-0.52$  between mastitis and milk up to 0.33 between displaced abomasum and livability. Beginning with the April 2020 CDCB evaluations, Jersey animals will receive evaluations for all 6 health traits. The 6 health traits in NMS will receive 2% emphasis.

**Key Words:** health, Jersey, national evaluation

**123 Breeding dairy cattle for the future: Where is the Canadian industry headed?** S. Larmer\*, *Semex Alliance, Arthur, ON, Canada*.

Recent uptake of both genomic technology, improved herd fertility, and advanced reproductive technologies including IVF and sexed semen have drastically shifted the focus of dairy cattle breeders globally. This session will explore how these technologies can be used in tandem both in Canadian dairy herds and globally to maximize the potential productivity and efficiency of dairy cattle on commercial dairy farms. Specifically, we will explore the future of breeding cattle with a focus on the productivity of those animals, rather than a focus specifically on the additive genetic potential of the next generation. This includes the estimation and use of higher order genetic terms and better methods of genomic inbreeding to maximize expected production in the next generation. In the Canadian industry, as is seen globally, we see a clear shift away from the traditional model of data sharing between producer and the public evaluation provider, often stemming from a perception that milk recording systems do not provide enough proportional value to the farm. This is especially driven by the rapid growth in robotic milking systems, where production and other performance metrics are available to the farm on a 24x7 basis. This provides an exceptional challenge for the overall industry to maintain and enhance genetic and genomic predictions for economically important traits. The future will need to adapt to this growing reality, including a shift towards accessing, standardizing and utilizing data from these robotic systems, as well as designing new traits where reference populations can be established to effectively and accurately measure data on a smaller, representative group of animals ("closer to biology" traits). Finally, we will look at the future of indexes that drive profitability on farm, and the impact that creating the right index for a specific production system can have for the productivity and profitability of a dairy producer, using examples from Canada and globally.