Breeding and Genetics

118 Association between lifetime selection index predictions and lifetime performance. B. Fessenden1, D. Weigel2, J. Osterstock3, D. Galligan1, and F. Di Croce*.1 Zoetis Genetics, Kalamazoo, MI, 2Zoetis Outcomes Research, Kalamazoo, MI, 3University of Pennsylvania School of Veterinary Medicine, New Bolton Center, Kennett Square, PA.

Selection indexes are critical to genetic improvement as they combine values for many traits into a single value that can be used to rank animals and inform breeding decisions. In 2016, Zoetis Genetics developed the Dairy Wellness Profit Index (DWP$) to estimate the genetic potential for lifetime profit in US Holsteins. This study’s goal was to evaluate if selection index genomically enhanced predicted transmitting abilities had the capability to predict observed lifetime profit in US Holstein animals. Five large herds (n = 2,175 enrolled cows) in the United States were chosen for this study because they had: 1) genomic predictions from females born in 2011, 2) recorded production, reproduction and health events to accurately estimate profit per cow, and 3) at least 200 animals born in 2011. Selection index predictions from 2012 were used to rank the 2,175 animals within herd and assign cows to percentile-based DWP$ groups (genetic groups: Worst 25%, 26–50%, 51–75%, and Best 25%). Herd records were used to calculate lifetime energy-corrected milk, income over feed cost, and lifetime days in milk based on the actual performance from first freshening through when they left the herd; for cows that were still in the herd, current totals were used. Analysis results indicated that DWP$ predictions were associated with differences in phenotypic lifetime energy-corrected milk, income over feed cost, and lifetime days in milk between the worst and best genetic groups. The difference between the worst and best genetic groups was 9004 kg lifetime energy-corrected milk (P < 0.01), $1,607 income over feed cost (P < 0.01), and 202 d in milk (P < 0.01). These results demonstrate that a lifetime selection index can in fact predict differences in actual lifetime profit potential of individuals. These results indicate that DWP$ predictions of young calves and heifers can be used to make informed predictions of future lifetime performance.

Key Words: selection indexes, genomics, lifetime profit

119 Conformation traits of Holstein cows and their association with the Pro$ selection index. L. Alcantara*1, C. Baes2, G. Oliveira Junior1, and F. Schenkel1, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland.

Breeding programs across the globe are shifting their selection goals from production-driven to more balanced indexes that include traits of direct and indirect economic significance, such as conformation, fertility and health. In Canada, for instance, changes were made to better reflect producers and market needs in the wake of improved accuracy of genetic and genomic evaluations and national efforts regarding data recordings. In 2015 a new national profit index, Pro$, was introduced to maximize production yields, while maintaining functional and conformation traits, taking into consideration the accumulated profit to 6 years of age of proven sire’s daughters. The Canadian classification system comprises several linear and nonlinear descriptive traits and defective characteristics that are taken into account to calculate points, which are distributed in 4 different scorecard sections: Mammary System (MS), Feet & Legs, Dairy Strength (DS) and Rump. Understanding the contribution of each of these traits to a monetary index, such as Pro$, would help producers make culling and mating decisions ultimately resulting in more profitable herds. Therefore, the present study used statistical regression and principal component analysis to look at the overall and individual contribution of 23 classification traits to the Pro$ index using deregressed Estimated Breeding Values from 9,292 proven bulls (Lactanet). The total variance explained by the full model was 0.66, and out of the traits included in the model, Dairy Capacity contributed the most to the increase in Pro$.

Stepwise backward regression analysis indicated that all traits should remain in the full model. Principal component analysis showed that the vast majority of traits contributed positively to Pro$ values. Traits from the MS contributed the most to the increase in Pro$ values, whereas Thurl Placement and Rump Angle did not seem to have a sizeable impact on Pro$.

Key Words: conformation traits, Pro$, Holstein

120 Opportunity costs in beef-on-dairy breeding strategies. A. De Vries*, University of Florida, Gainesville, FL.

The use of beef-on-dairy is growing, but the most profitable breeding strategy is often not clear. The objectives were to (1) quantify the value of breeding strategies, (2) discover most profitable, but sometimes complex breeding strategies, and (3) determine the opportunity costs from more constrained or simpler breeding strategies. A daily Markov Chain model including heifers and at least 5 parities of cows was developed. The distribution of predicted transmitting abilities for an economic selection index within the herd depended on genetic reliabilities, genetic trend and genetic variances. Unrestricted breeding opportunities allowed for any combination of sexed, conventional and beef semen. Inputs regarding reproduction, milk production, forced culling, and prices mimicked an average herd and allowed for a calculation of profit/milking cow per yr. A nonlinear solver optimized breeding strategies subject to constraints such as the number of dairy heifer calves to be at least equal to the number needed to replace culled cows. Surplus dairy heifer calves with the lowest predicted transmitting abilities were sold. Using genomic reliabilities and typical market prices of calves, the optimal breeding strategy used a combination of sexed, conventional, and beef semen throughout the herd. Older cows received less sexed semen and more beef semen. Crossbred calves were 34% of all calves born. This strategy made 16% surplus dairy heifer calves. Limiting surplus to 0% reduced profit by $13/milking cow per yr. Limiting surplus to 0% and not using conventional semen reduced profit by $24/milking cow per yr. Use of only conventional semen reduced profit by $63/milking cow per yr. This value is partitioned as $64 greater operational net revenues, $15 lower semen costs, $61 greater genetic lag costs, $50 lower calf sales, and $1 lower genomic testing costs. Opportunity costs for simple strategies ranged from $36 to $72/milking cow per yr. Use of traditional reliabilities resulted in lower opportunity costs for non-optimal strategies. In conclusion, optimal beef-on-dairy breeding strategies can be complex and opportunity costs from simpler strategies may be substantial.

Key Words: beef-on-dairy, opportunity cost, genetic lag

121 The effect of synchronized breeding on genetic evaluations of fertility traits in dairy cattle: Preliminary analysis. C. Lynch*, G. A. Oliveira Junior1, F. S. Schenkel1, and C. F. Baes1,2, 1Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, 2Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland.

Hormonal synchronization alleviates the pressure of estrus detection by affecting the estrous cycle, allowing for higher rates of conception even for naturally low fertile animals. This leads to genetically inferior cows’ performance becoming masked and potentially resulting in similar performance to that of naturally fertile animals. As genetic programs rely on the collection of accurate phenotypic data, phenotypes recorded on treated animals likely affect the genetic evaluations. This study analyzed the traits calving to first service (CTFS), first service to conception and days open in 419,102 cows from 1122 herds with 1,811,394 breeding and fertility records across 3 scenarios. Scenario 1 compared records that included any type of hormone treatment (HORM) against all other records. Scenario 2 compared HORM vs heat detection protocol (HD) records. Scenario 3 compared hormonal synchronization protocol (FTAI) records vs HD. Available data for each trait was characterized based on the use
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

### Implementation of national health trait evaluations in Jersey


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 ≥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

### Breeding dairy cattle for the future: Where is the Canadian industry headed?

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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.