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203 Simulating the underlying variation in fertility: Combining physiology and genetics. N.A. Dennis*[1], K. Stachowicz[1], B. Visser[1], F. S. Hely[1], D. K. Berg[3], N. C. Friggens[2], P. R. Amer[1], S. Meier[4], and C. R. Burke[4], [1]*AbacusBio Ltd., Dunedin, New Zealand,* [2]*AgroParisTech, Paris, France,* [3]*AgResearch Ltd., Hamilton, New Zealand,* [4]*DairyNZ Ltd., Hamilton, New Zealand.*

Mathematical modeling can combine a wide range of information sources and facilitate the research of scenarios that would not be feasible to evaluate empirically. We have developed a stochastic model using genetic and physiological data from over 70 published reports on aspects of fertility in dairy cows. The model simulates cow pedigree, random mating allocation, correlated breeding values and interacting phenotypic variables. It was used to generate a large (200,000 cows replicated 100 times) data set of herd records for up to 5 parities within a seasonal dairy production system. From these data, a genetic evaluation of sires based on genetic merit for lifetime reproductive success (LRS) and the impact of high-LRS (Hi-LRS) or low-LRS (Lo-LRS) sires were investigated. LRS was defined as the number of times, during her lifetime, a cow calved within the first 42 d of the calving season. The proportion of daughters which calved (calving rate) in the 2nd parity was the strongest predictor of sire genetic merit for LRS ($R^2 = 0.81$). When 2nd parity calving date was included, the power of the prediction increased substantially ($R^2 = 0.97$). Reasonable predictions could also be made from 1st parity records. A predictive model containing 1st parity records for overall calving rate, and calving rate within the first 21 d, provided a good ($R^2 = 0.76$) LRS estimation when growth rate from weaning until first estrus was also included. Comparison of simulated daughters from widespread industry use (1000 daughters/bull) of sires with high (n = 100, $\mu = +0.70$) and low (n = 100, $\mu = -0.73$) breeding values for LRS, indicated that 12 of the 14 underlying genetic traits were divergent between the sire lines. Phenotypically, the daughters from the Hi-LRS sires displayed first estrus 34.1 d younger than their Lo-LRS contemporaries. Hi-LRS cows calved ~15 d younger at each parity and, despite producing less milk per season (−155L) than Lo-LRS cows, produced more milk over their lifetime (+33%) owing to additional lactations before culling. In summary, this simulation model suggests that lifetime reproductive success contributes substantially to cow productivity, and can be accurately predicted at a young age.

Key Words: breeding, reproduction, modelling

204 Estimating epistatic and dominance genetic variances for fertility and reproduction traits in Canadian Holstein cattle. K. Alves*[1], M. Sargolzaei[1,2], C. Baes[1], A. Robinson[1], and F. Schenkel[1], [1]*Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada,* [2]*The Semex Alliance, Guelph, ON, Canada.*

Non-additive genetic effects are usually ignored in animal breeding programs due to data structure (e.g., incomplete pedigree), computational limitations, and over parameterization of the model. However, non-additive genetic effects may play an important role in the expression of complex traits in livestock species, such as reproduction and fertility traits. We assessed the use of pedigree and SNP-marker-based models to estimate additive and non-additive genetic variances for reproduction and fertility traits in Canadian Holstein heifers (n = 5,825) and cows (n = 6,090). Four traits were analyzed including age at first service for heifers (AFS), calving to first service interval for cows (CTFS), and 56-d non-return rate for heifers and cows (NRR). Four linear models were used (1) additive genetic model (MA); (2) a model including both additive and epistatic (additive by additive) genetic effects (MAE); (3) a model including both additive and dominance effects (MAD); and (4) a full model including additive, epistatic, and dominance genetic effects (MAED). The models which included non-additive genetic effects for AFS and CTFS indicated that epistasis, dominance, or a combination thereof, are as important as additive effects, and sometimes contribute a larger proportion to the total phenotypic variance than the contribution of the additive effects. The partitioning of variance components resulted in a re-ranking of animals in the top 10% based exclusively on the additive genetic effects between models. The change in rank indicates that adjusting for non-additive genetic effects could change selection decisions made in dairy cattle breeding programs. These results suggest that non-additive genetic effects play an important role in some reproduction and fertility traits in Canadian Holsteins and their inclusion in genetic evaluations may improve accuracy of selection based on additive genetic effects.

Key Words: Holstein cattle, low-heritability trait, non-additive genetic effect

205 Discovery of a haplotype affecting fertility in Ayrshire dairy cattle and identification of a putative causal variant. D. J. Null*[1], J. L. Hutchison[1], D. M. Bickhart[2], P. M. VanRaden[1], and J. B. Cole[1], [1]*Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD,* [2]*U.S. Dairy Forage Research Center, ARS, USDA, Madison, WI.*

The goal of this research was to identify the causal variant associated with a haplotype affecting fertility in Ayrshire cattle. The US dairy population is routinely monitored to identify cases where homozygotes for a minor allele are expected, but never observed, which can indicate the presence of a genetic defect causing embryonic death. Such a haplotype was identified on chromosome 17 in January 2013. A second haplotype reached the threshold for statistical significance (7 expected homozygotes and none observed) in October 2013. Sire conception rate was 6.1% lower for matings of carrier sires to cows with carrier maternal grandsires, but the effect was not significant. As of December 2016, 23.5 homozygotes were expected but none had been observed. Most carriers trace back to OAK-RIDGE FLASHY KELLOGG (AYUSA000000125168), born in 1961, but many Canadian carriers only trace back as far as WOODLAND VIEW PARDNER ET (AYCAN000000811799), born in 1994. These bulls share an ungenotyped ancestor in OAK-RIDGE LIGHTNING (AYUSA000000120135), born in 1958. This haplotype has been designated Ayrshire haplotype 2 (AH2), and its frequency has increased from 6% in animals born in 1990 to 21.7% for animals born since 2008. Whole-genome sequence data ranging from 9 × to 13 × read-depth for 8 Ayrshire bulls, 3 carriers and 5 non-carriers, was used to search for the causal variant. The analysis used a short-read sequence data analysis pipeline including BWA (v. 0.7.10) and Samtools (v. 1.3). Likely false positive variants and variants with small predicted functional effects were removed after annotation with SNPeFF (v. 4.3). A splice acceptor variant at 51,267,548 bp in the RNA Polymerase 2 Associated Protein (RPAP2) gene was the most likely causal variant in the haplotype. RPAP2 is an essential component of the RNA polymerase 2 holoenzyme necessary for transcription of snRNA species. Experiments with mouse knockouts also found a deficiency of homozygotes, suggesting that RPAP2 is necessary for embryonic development. These findings provide strong evidence for the existence of a new, lethal recessive in Ayrshire cattle. AH2 carrier status should be reported to the industry routinely and its effect on fertility confirmed.

Key Words: Ayrshire, fertility, genetic disorder

206 Predictions for workability and reproductive traits using two-step and single-step genomic BLUP in Canadian Holsteins.