

174 Pooling data for international evaluations for feed intake and efficiency. J. Lassen*, *Viking Genetics, Randers, Denmark.*

Genetic evaluation of feed intake and efficiency is a hot topic worldwide. Lack of data to make genetic evaluation for feed intake and efficiency is an equally hot topic worldwide. Therefore, many initiatives have been made to exchange data. As an example the Efficient Dairy Genome Project led by University of Guelph and University of Alberta institutions from several countries have put up data on feed intake, methane and related traits to exploit the opportunities to make national genetic evaluations. One of the main ideas behind the data sharing in this project is that institutions that contribute data have full access to all the data that is uploaded. For a country to be able to publish breeding values, having access to the data that is the foundation of the estimation is essential. If an institution does not upload data on a specific trait, the institution does not have access to the data from the other institutions on this trait. Each country has their own protocol to make phenotypic and genomic registrations of data. This can be a challenge for setting up an appropriate genomic evaluation. Phenotypes are not measured in the same way between countries and genotypes are from very different panels. In addition, the genetic background of the populations in the participating countries can be very different. For a trait like feed intake where relatively huge genotype by environment interactions are expected, this is a big challenge when number of animals as well as number of records are limited. An alternative would be to avoid having genomic evaluations in such a case; however, this is not an option. New methods to measure feed intake in commercial farms are needed for several reasons: 1) to be able to use individual feed intake as an on-farm management tool, 2) to get more data from cows that are not in experiments and genetically close to the current reference group, 3) to be able to actually demonstrate that selection has an effect. Therefore, more effort should be put into developing tools and technologies that are profitable to farmers.

Key Words: data pooling, feed intake, feed efficiency

175 Development, implementation, and future perspectives of health evaluations in the United States. K. L. Parker Gaddis*¹, P. M. VanRaden², J. B. Cole², E. Nicolazzi¹, and J. W. Dürr¹, ¹*Council on Dairy Cattle Breeding, Bowie, MD*, ²*Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

The rate at which new traits are being developed is increasing, leading to an expanding number of evaluations provided to producers, especially for functional traits. The objectives of this presentation include discussion of development and implementation of health evaluations in the US, as well as potential future work. Beginning in April 2018, routine official genomic evaluations for 6 direct health traits were made available to US producers from the Council on Dairy Cattle Breeding (Bowie, MD). Traits include resistance to milk fever, displaced abomasum, ketosis, mastitis, metritis, and retained placenta. These health traits were incorporated into net merit indices beginning in August 2018 with a total weight of approximately 2%. Previously, improvement of cow health was primarily made through changes to management practices or selection on indicator traits, such as somatic cell score (SCS) and

productive life. Widespread genomic testing now allows for improvement of traits with low heritabilities such as health; however, phenotypes remain essential to the success of genomic evaluations. Establishment and maintenance of data pipelines is a critical component of health trait evaluations, as well as appropriate data quality control standards. Data standardization is a necessary process when multiple sources are involved. Model refinement continues, including implementation of variance adjustments beginning with the April 2019 evaluation. Mastitis evaluations were submitted to Interbull along with SCS for international evaluation of udder health. Possible future developments include multiple-trait models, evaluation of other breeds, and evaluations for additional functional traits such as calf health, feed efficiency, locomotion, or lameness. Future developments will require new and continued cooperation among numerous industry stakeholders. Producers and the dairy industry as a whole must decide how to handle similar evaluations from multiple sources, including proprietary traits from private companies. There is more information available than ever before with which to make better selection decisions; however, this also makes it increasingly important to discern accurate and unbiased information.

Key Words: functional trait, genetic evaluation, health trait

176 Implementation of genomic selection for heat tolerance. T. T. Nguyen¹, P. J. Bowman^{1,2}, M. Haile-Mariam¹, B. J. Hayes³, and J. E. Pryce*^{1,2}, ¹*Agriculture Victoria, Bundoora, VIC, Australia*, ²*La Trobe University, Bundoora, VIC, Australia*, ³*University of Queensland, Brisbane, QLD, Australia.*

Heat stress is an issue of growing concern for many livestock production systems worldwide affecting not only animal welfare, but also farm profitability. In December 2017, genomic estimated breeding values for heat tolerance in dairy cattle were released for the first time in Australia. The data set was constructed by merging herd-test production records with weather station data. Heat tolerance phenotypes were defined as the rates of decline in milk, fat and protein yield after a heat stress event (i.e., temperature-humidity index exceeds 60), and were estimated using a reaction norm model. The genomic prediction equation was developed from a reference population of 2,236 sires (with heat tolerance phenotypes on daughters) + 11,853 cows for Holsteins and 506 sires + 4,268 cows for Jerseys. These sires and cows were genotyped with 46,276 SNP. Each component of heat tolerance (genomically predicted decline in fat, protein, and milk) is weighted by its economic value, which is assumed to be the same as their weights in the Australian selection indices. The genomic breeding values are then standardised within breed to have a mean of 100 and standard deviation of 5. Although the reliability of this new trait is moderate (on average around 38%), it is expected that this will improve as the reference populations are increased. The genetic trend for heat tolerance has worsened, which is consistent with the correlation with the Australian national selection index (Balanced Performance Index; BPI) which is -0.20. Heat tolerance is currently not part of the BPI, however, its inclusion will be considered as part of the next review of the index.

Key Words: heat tolerance, genomic selection