Breeding and Genetics Symposium: Joint ADSA/Interbull Session: Data Pipelines for Implementation of Genomic Evaluation of Novel Traits

171 International collaborations for breeding for novel traits. Y. de Haas*, Animal Breeding and Genomics of Wageningen University and Research, Wageningen, the Netherlands.

With the successful incorporation of genomic information into breeding schemes the reliance on very large populations of phenotyped animals is relaxed. However, a reference population of several thousand animals is still required to estimate the contribution of each genomic region to expression of the phenotype under investigation. For novel traits, like feed efficiency and enteric methane emissions of dairy cattle, a reference population of this size cannot be easily established within a country, but requires international collaboration. METHAGENE and the Global Dry Matter Initiative (gDMI) are 2 examples of such intensive and successful collaborations. METHAGENE showed that even when enteric methane emissions of individual animals was recorded with different sensors and with different protocols, there are ways to combine the data for joint analyses, so that partners can take advantage of each other. METHAGENE not only looked at direct records of enteric methane, but also at proxies for methane related to (1) ingestion, (2) rumen, (3) milk composition, (4) hindgut, and (5) the animal itself. No single proxy was found to accurately predict enteric methane emissions, while combinations of 2 or more proxies are likely to be a better solution. Combining proxies can increase the accuracy of predictions, mainly because different proxies describe independent sources of variation in enteric methane emissions and one proxy can correct for shortcomings in the other(s). In gDMI, we demonstrated that using dairy cattle dry matter intake (DMI) phenotypes and genotypes from multiple populations increase the accuracy of genomic breeding values (gEBVs) for this important trait, provided a multi-trait approach is used. Data from research herds in Europe, North America, and Australasia were combined to estimate the accuracy of genomic prediction for DMI using multi-trait models. The mean accuracy of prediction was 0.44, ranging from 0.37 (Denmark) to 0.54 (the Netherlands). Overall, for novel traits, there is benefit of collaboration, as phenotypic information from other countries can be used to augment the accuracy of genomic evaluations of individual countries.

Key Words: feed efficiency, multiple trait analysis, selection index

172 Genetic relationships between different measures of feed efficiency and the implications for dairy cattle selection indexes. R. J. Tempelman*1 and Y. Lu2, 1Michigan State University, East Lansing, MI, 2Axio Research, Seattle, WA.

Dairy profit selection indexes have increasingly incorporated one of the various measures of feed efficiency (FE) as a key component trait. Definitions of FE traits range from DMI to residual feed intake (RFI), noting that RFI is effectively DMI adjusted for various energy sink traits such as body weight (BW) and milk energy (MILKE). Other definitions of FE fall between these 2 extremes such as feed saved (FS), which combines RFI and the portion of DMI required to maintain BW. The use of different FE traits can create confusion as to how to meaningfully compare their heritabilities or estimated breeding values (EBV) and their corresponding accuracies, or even how to differentially incorporate these EBV into selection indexes. If RFI and FS are merely linear functions of DMI, BW, and MILKE with known genetic variances and covariances between the 3 traits, there is no need to directly compute RFI or FS phenotypes to determine their heritabilities, genetic correlations, EBV and their respective accuracies. We demonstrate how the estimated aggregate genetic merits and corresponding accuracies are invariant to the specification of a FE trait within a selection index. That is, economic weights for a selection index involving one particular measure of FE readily convert into the economic weights for a selection index involving a different measure of FE. We use these different specifications of FE to provide insight as to the impact of the degree of missingness (i.e., paucity of DMI or BW relative to milk yield records) on the EBV accuracies of the various derivative FE traits. We particularly highlight that the generally observed higher EBV accuracies for DMI, then for FS, and lastly for RFI are partly driven by the typically greater genetic relative to residual correlations between DMI with RFI and FS and by the higher genetic correlations of DMI with BW and MILKE. Finally, we advocate a genetic regression approach to deriving FS and RFI recognizing that genetic versus residual relationships between FE component traits may differ substantially from each other.

Key Words: hoof lesions, genomic evaluation, dairy profit selection index

173 Multiple-trait single-step genomic evaluation for hoof health. F. Malchiodi*1,2, J. Jamrozik1,2, A.-M. Christen3, A. Fleming3, G. J. Kistemaker1, C. Richardson4, V. Daniel4, D. F. Kelton1, F. S. Schenkel1, and F. Miglior2, 1Semex Alliance, Guelph, ON, Canada, 2Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, 3Canadian Dairy Network, Guelph, ON, Canada, 4Valacta, Sainte-Anne-De-Bellevue, QC, Canada, 5School of Applied Systems Biology, La Trobe University, Bundoora, VIC, Australia, 6Vic’s Custom Clips, Arva, ON, Canada, 7Department of Population Medicine, OVC, University of Guelph, Guelph, ON, Canada.

Hoof lesions represent an important issue in modern dairy herds, with prevalence reported in different countries ranging from 25 to 80%. This high prevalence of hoof lesions has both economic and social consequences, resulting in increased labor expenses while decreasing animal production, longevity, reproduction, health, and welfare. Therefore, a key goal of dairy herds is to reduce the incidence of hoof lesions, which can be achieved both by improving management practices and through genetic selection. In Canada, a hoof health sub index has recently been released based on a national genetic evaluation program for hoof health, which was achieved by the creation of a centralized data collection system that routinely transfers data recorded by hoof trimmers into a coherent and sustainable national database. The 8 most prevalent lesions in Holsteins (digital dermatitis, interdigital dermatitis, interdigital hyperplasia, heel horn erosion, sole hemorrhage, sole ulcer, toe ulcer, and white line lesion) are analyzed with a multiple-trait model using single-step GLMUP method. Estimated genomic breeding values for each lesion are then combined into a sub-index (Hoof Health) according to their economic value and prevalence. In addition, data recorded within this system are used to create an interactive management report for dairy producers by Canadian DHI, including the prevalence of lesions on farm, their trends over time, and benchmarks with provincial and national averages.

Key Words: hoof lesions, genomic evaluation, dairy profit selection index

174 Intra-cohort relationships of selection index components. S. Moltke1,2, A. Madsen1, and J. R. Thompson3, 1 Danish Dairy Network, Guelph, ON, Canada, 2Axio Research, Seattle, WA, 3Department of Animal Sciences, University of Wisconsin, Madison, WI.

Traditionally, the components of a breeding index are not allowed to correlate, which can result in invariant economic weights for the components. Here we present a method that allows for intra-cohort (within selection index) relationships. Maximum likelihood equations are used to predict the breeding values for the index and its components. The key difference from standard methods is that the component breeding values are not constraints to be estimated. This allows for the estimation of relationships between components and the component indexes can be corrected for. We demonstrate the use of these relationships in a selection index and show how they must be used to correctly interpret the index breeding values.
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


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. T. Nguyen1, P. J. Bowman1,2, M. Haile-Mariam1, B. J. Hayes3, and J. E. Pryce*,1,2, 1Agriculture Victoria, Bundoora, VIC, Australia, 2La Trobe University, Bundoora, VIC, Australia, 3University 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