Study demonstrates International bull evaluations by genomic BLUP with a prediction population

By Lindsay Pressman

In the past, international genetic evaluations by Interbull were based on daughter yield deviations (DYD) for bulls. It is possible that multiple DYD for each bull were used in a multiple-trait sire-model best linear unbiased predictor (BLUP), where each country was treated as a separate trait. From many countries with the multiple across-country evaluation (MACE), pooling DYD increased reliabilities above those possible using data of any single country. As a result, the evaluations were available only for proven bulls. Under genomic selection, most marketed bulls are young genotyped bulls with no daughters, so there is no DYD information. MACE could be adapted to the genomic information with genomic best linear unbiased predictor (GBLUP) if genotypes were available for bulls. A research paper, published in the *Journal of Dairy Science* by B. Fragomeni et al., entitled "International bull evaluations by genomic BLUP with a prediction population", aimed to determine whether multi-country genomic evaluation can be accomplished by multiple-trait GBLUP without sharing genotypes of important animals.

For 25,000 animals, each with four traits assuming the same genetic variance and 0.8 genetic correlations, phenotypes and genotypes with 40k SNP were stimulated. The population was split into four subpopulations corresponding to four countries. One subpopulation for each trait. A prediction population was formed from genotyped animals that were related to each country's population, but that were not present in the individual countries. Phenotypes were reconstructed for the prediction population based on the SNP effects of a country and the prediction animals' genotypes. Genomic estimated breeding values were also calculated for each country and converted to SNP effects. The prediction population was used as the basis for the

international evaluation. This enabled bull comparisons without sharing genotypes and only sharing SNP effects.

The authors found that the MACE GBLUP is easy to apply as the exiting MACE software because it can be modified by replacing the inverse of the numerator relationship matrix with the inverse of the genomic relationship matrix. To do this, it is possible to use the algorithm for proven and young animals to eliminate restrictions on the number of genotyped animals. Also, the use of GBLUP MACE allows for multi-country genomic evaluation in countries that are not required to submit original genotypes or phenotypes. The method produced less accuracy than with explicitly combined populations, but greater accuracy than with any single country. Computations are minimal and can be done for a large number of countries and animals. However, problems are still relevant, including the creation of within-country reference populations and reasons for reduced accuracies in countries with unequal size. When discussing the research, authors questioned how to create a simple prediction population that has the same genomic information as multiple countries' populations. The predicted population had strong relationships with each country because the last simulated generation was used for prediction. More study needs to be done in this area. An additional question was whether GBLUP MACE would retain good accuracies in complex data structures. If the traits are the same in all populations, with SNP MACE all left- and right-hand sides are added, and the results are the same as with a combined analysis. The same will be true with GBLUP and original data sets, but not necessarily with prediction populations. Overall, while the GBLUP MACE is valuable, more research and further studies are necessary.

This is important because it is now possible to use a prediction population in which the genotypes of the animals is acquired, and their phenotypes can be calculated for each country in

the evaluation, based on the SNP effects. SNP effects are easy to be shared, do not cost money and do not belong to any breed association or artificial insemination company. If the diverse countries are willing to share their data on SNP effects, it is possible to perform an international genomic evaluation using the prediction population. This research is also important because with genomic evaluations it is possible to identify more animals in different populations. With international evaluations we will be able to compare different countries, and select dairy bulls from other places, which can help in increasing the genetic diversity in the United States populations. It can also help United States companies to import their semen from animals in other countries.

"This study shows that we can perform an international genomic evaluation without the need of sharing expensive data. Moreover, it can be done with a somewhat simple methodology and it only depends on the will of countries to share data." – Breno Fragomeni

To view the full article, B. Fragomeni, Y. Masuda, H. L. Bradford, D. A. L. Lourenco, and I. Misztal. (2019) International bull evaluations by genomic BLUP with a prediction population, visit the ***Journal of Dairy Science***, Vol. 102, No. 3, 2019, Pages 2330-2335. https://doi.org/10.3168/jds.2018-15554.