CDCB Extends Genomic Evaluations to Crossbreds

By George Wiggans and Ezequiel Nicolazzi[1]

Thanks to the collaboration between USDA-AGIL[2] and CDCB, dairy farmers will be able to receive accurate genomic evaluations for crossbred animals in April. These evaluations are based on a weighted combination of solutions estimated from the purebred populations, and the U.S. is the first country applying this approach to evaluate crossbred animals. Although these estimates for crossbreds are slightly less reliable than those for purebreds, they provide a means for all genotyped animals to receive the best possible estimate of their genetic value, irrespective of their breed composition.

Well-researched Process

Cutting-edge research and a complex development process led to this implementation to provide U.S. producers with this innovative tool. The foundation was set in 2007, with the implementation of an all-breed traditional evaluation system. In that system, records from all breeds (including crossbreds) are combined in a single evaluation. Evaluations are subsequently converted to individual breed bases before publication.

A next step was implemented in 2016, with the publication of Breed Base Representation (BBR) values – which are only provided through the U.S. system as of today. BBR is an estimate of the proportions of Ayrshire, Brown Swiss, Guernsey, Holstein and Jersey genetics in each individual animal. We have made some improvements in the BBR calculations after two years of experience. Breed proportions less than 2% are rolled into the remaining breeds and calculations have been updated using the new 80,000 set of markers implemented in December 2018. Consequently, all animals will receive new BBR values in April 2019. In the future, animals will receive updated values if there is a significant change, most likely caused by genotyping at a higher density, changes in sire/dam, and the inclusion of genotyped close relatives.

The next step was taken in April 2018, when the calculation of genomic evaluations changed to the all-breed base following methodology for traditional evaluations since 2007. By using traditional evaluations uncorrected for the different breed bases, the genomic evaluations can be combined across breed. As in traditional evaluations, genomic evaluations are also adjusted to individual breed bases before publication.

Evaluation Details

The implementation of evaluations for crossbred animals includes slight changes for the purebred evaluations too. Until this April, a SNP-based breed test was used to make the decision to include/exclude animals from the evaluation. CDCB will now use the more accurate BBR estimate to identify which animals receive evaluations using single breed (>90% BBR) or blended solutions. This means that some animals that previously received single-breed solutions will now receive blended solutions. Furthermore, to reduce the effect of other breeds on the breed SNP estimates, only animals with BBR 94% or greater will contribute data to the reference population (the population of animals with phenotypes used to obtain the SNP solutions for that breed). The blending process is not applied to conformation, calving or health traits. Conformation traits are not on the same base across breed, and breeds may have different definition of the traits. Calving and health traits are not calculated for all breeds. For those cases, the single breed evaluation of the evaluation breed is reported.

Crossbred animals will be reported on the breed base with the highest BBR value. A new check for consistency between BBR values and breed code in the animal ID has been implemented. Animals that are close to being a purebred of a different breed will not receive an evaluation until the breed is corrected. For F1 animals, the breed code of the animal ID will be used even if the BBR value is only the second-highest value (restrictions apply).

In a recent test run, nearly 65,000 animals received evaluations based on blended solutions. Of these, nearly half had not received evaluations previously. Those animals that had previously received evaluations are expected to have more accurate evaluations now that their multi-breed composition is considered.

The evaluation of crossbreds does pose some questions. For example, single-breed evaluations are adjusted for inbreeding of future progeny so that the expected inbreeding depression is considered. For crossbreds, the adjustment will be for the expected inbreeding from mating to animals of the breed of evaluation. Future research may discover a better way to adjust these evaluations.

USDA-AGIL and CDCB have made a substantial effort to extend the benefits of genomic evaluations to crossbreds, enabling producers to increase the value of genotyping, particularly when applied to the whole herd. With this enhancement of the U.S. genomic evaluations, more animals will now receive evaluations. Crossbred animals that have been receiving evaluations should have more accurate evaluations now that their multi-breed composition is considered. Also, evaluations of purebreds will be improved slightly by removing mixed-breed animals from the group of animals used to estimate the SNP effects.

Authors
[1]**George Wiggans** served as Research Geneticist at USDA[2] for more than 38 years and since retirement in mid-2016 has continued to contribute expertise as CDCB Technical Advisor. In 2017, he was among an illustrious group of researchers in the inaugural JDS Club 100, having authored or coauthored 100 or more papers in the Journal of Dairy Science®.

Ezequiel Nicolazzi is CDCB Technical Director with previous experience at Italian Holstein Association, the Italian Consortium for Research and Experimentation in Animal Breeding and at PTP Science Park in Lodi, Italy.

[2]United States Department of Agriculture, Animal Genomics and Improvement Laboratory