

All-breed system extended to genomic evaluations

Long gone are the days when animal breeding could be labeled primarily an “Art.” This phenomenon called “Science” has gnawed away at that perception across time. Historically in dairy genetic improvement, most gains have been supported by the small to modest improvements made in the evaluation technology. The big exception was 10 years ago when selection using genomic data directly was initiated. That breakthrough produced a permanent increase in the rate of genetic improvement, somewhere between 50 and 100 percent.



It is advantageous now to return to the strategy of taking all available opportunities – even though they might be smaller – to continue to improve the evaluation technology. While small changes may not be as exciting as the genomic breakthrough, stacking up numerous small improvements will produce significant advances. Much of the leadership for developing such recent improvements has come from Paul VanRaden of USDA’s Animal Genomic and Improvement Laboratory (AGIL) in Beltsville, Md.

A significant improvement will come in April 2018, when the **all-breed system** initiated for traditional evaluations in 2007 **will also be applied to genomic evaluations**. This new strategy will combine and analyze together the records for animals of all breeds expressed on the same scale. The separate marker effects for each breed will still be computed. Parent averages (PA) will now be calculated using the entire pedigree across breeds. All relatives - regardless of breed - will now contribute to each animal’s parent average and thereby impact directly its genomic evaluation. Said another way, in the past the genetic estimate for individuals whose ancestors included an animal of a different breed were not predicted as accurately as possible. Previously, the genetic value assigned to the ancestor of another breed was substituted with the mean of unknown parents. As of April 2018, genomic evaluations are now calculated on an all-breed genetic base and then are converted back to within-breed bases before official release.

How Will Evaluations be Impacted?

The resulting PTA differences (compared to earlier evaluations) will be larger for those animals with a second breed in their pedigree. Likewise, breeds that have a higher percentage of animals with other breeds in their background will show more changes. In particular, the Jersey and Ayrshire breeds have a higher proportion of animals with some percentage of other-breed genetics in their current population, so these breeds are likely to see more large changes due to the implementation of the all-breed evaluation system.

Nevertheless, since animals are connected, all animals are expected to vary more than usual this run. In the future, because of the improved accuracy of the prediction, there should be less variation for animals with other breed ancestors; the monthly and tri-annual evaluations are expected to be more stable.

Will Crossbred Animals Receive an Evaluation?

Many crossbred animals still will not receive an evaluation, as has been the practice. However, implementation of the all-breed system is a step toward obtaining crossbred evaluations for many more animals. This work is currently in the research phase with application expected in the future.

Other related changes were made alongside implementation of the all-breed system.

- 1) Foreign dam information is now included when its reliability (R) is higher than the U.S. domestic R (it previously had to be at least 5% higher).
- 2) Predicted Transmitting Abilities (PTA) for bulls with from 1 to 9 daughters are now used in the reference population. Previously, PAs for those bulls were used as their PTAs were not published.
- 3) Heterosis was redefined for Ayrshires. The Swedish Reds (SR), Norwegian Reds (NR) and Red European (RE) breeds are now considered to be the same breed as Ayrshires in the males. Previously the logic was only applied for the females. Removing the benefits of heterosis will cause the PTA to be lower for many animals that have European bulls in their pedigrees.

In the Guernsey breed, the strategy for assigning unknown parent grouping was not executed as intended, and April PTAs are inflated for a number of Guernsey animals with incomplete pedigrees. The impact on Guernsey evaluations is still under investigation, and more details will be provided in due time.

In Summary

Genomic evaluations for purebreds are impacted slightly with the implementation of the all-breed system in April 2018, whereas the changes are greater for animals containing pedigrees from other breeds. Because of the improved accuracy of the prediction, there should be less variation for animals with other breed ancestors in evaluations post-April 2018. Research and development continues for crossbred evaluations, and genomic evaluations for additional crossbred animals are expected in the future.