

Information from the Council on Dairy Cattle Breeding (CDCB) Regarding the April 2018 Genetic Evaluations



There have been questions regarding some of the fluctuations in PTAs observed with the April 2018 genetic evaluations. The following information has been provided by CDCB via the **CDCB Connection** e-newsletter, which anyone can sign up to receive at www.uscdcb.com.

There were no changes to the Total Performance Index[®] (TPI[®]) formula in April 2018. More information on TPI can be found here: www.holsteinusa.com/genetic_evaluations/ss_tpi_formula.html

Variability in Fertility Evaluations

For fertility traits, a larger-than-expected variation has been observed with the April 2018 evaluations. This variation was mainly due to changes in bulls' traditional PTAs (Predicted Transmitting Abilities). Across the industry, an undesirable seasonal variation has been observed for the fertility evaluations.

In previous runs, the most recent top animals often had unexplained increases or decreases averaging about 0.5, but the variation reached 1.5 for some top recently-proven bulls in April. Younger animals appear to have larger variations, likely due to extrapolation of the SNP effects. Despite the shift in the mean for recent years, when comparing April to December, the individual animal rankings are fairly stable with high correlations.

CDCB and AGIL* staff are investigating the cause of this undesirable variation and expect a solution to improve the evaluation stability before the August release.

**USDA AGIL = United States Department of Agriculture, Animal Genomics and Improvement Laboratory*

New Multi-Trait Productive Life Genomic Model

The multiple-trait Productive Life (PL) processing for incoming Interbull data was completely revised to prevent the emergency actions taken in April and August 2017. The new system no longer tries to forward the differences between single and multiple-trait PL from one generation to the next, as this logic tended to inflate the resulting evaluation, primarily for foreign bulls. Since foreign bull evaluations were inflated, SNP effects used to estimate genomic evaluations were affected, extending the inflation to the general population.

The inflation was more evident in breeds dominated by foreign bulls, such as Ayrshire and Brown Swiss, but outlier cases were observed in all breeds. The new multi-trait PL

genomic model prevents the inflation and the new system aligns better with the Interbull evaluations for foreign bulls.

A correlation of 96% was found between the previous and new systems when comparing December 2017 PL evaluations with the new methodology, indicating some degree of variation for bulls. Considering that PL has a significant weight in the indexes, this enhancement will impact the Net (and other) Merits of animals.

All-Breed System Extended to Genomic Evaluations

The all-breed system (initiated for traditional evaluations in 2007) was extended to genomic evaluations in April 2018, allowing records from animals of all breeds to be analyzed together on the same scale. Marker effects for each breed are still computed and used within breed.

Relatives - regardless of breed composition - now contribute to every animal's parent average and impact directly its genomic evaluation. Genomic evaluations for purebreds were impacted slightly with the implementation of the all-breed system, 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 future evaluations. Many crossbred animals still do not receive an evaluation. Research continues to develop crossbred evaluations, and genomic evaluations for additional crossbred animals are expected in the future.

A more in-depth article on this topic can be found here: https://www.uscdcb.com/wp-content/uploads/2018/03/All-breed-system-extended-to-genomic-evaluations-04_2018-1.pdf