



Genetic Evaluation Update – December 2016

This summary details changes to the Zoetis CLARIFIDE® Plus Wellness Trait genetic evaluation implemented between October and December 2016. In parallel with the release of official results for the Council on Dairy Cattle Breeding (CDCB) genetic evaluation, Zoetis Genetics is releasing a full genetic evaluation for Wellness Traits in December 2016. If you have questions or concerns regarding this information, please contact Fernando Di Croce fernando.dicroce@zoetis.com.

Addition of Phenotypic and Genotypic Data

During the period following the last official genetic evaluation for wellness traits in August 2016, we incorporated 340,000 new phenotypic records and more than 25,000 new genotypes encompassing now a total of 275,000 genotypes into the evaluation. As with any other genetic evaluation, some movement in the standardized transmitting abilities (STA) and indexes are expected. It is important to consider that changes in CDCB predictions may also impact the Dairy Wellness Profit Index™ (DWP\$™) outcomes given that the CDCB core traits are included in the index along with the wellness trait predictions.

Phenotype Editing

In an effort to minimize the potential for overestimation of genetic merit for Wellness Traits attributed to right censoring of recorded data, new procedures for editing of health phenotypes during processing of lactation records were implemented in October 2016. New data editing rules were defined for each wellness trait based upon the proportion of events observed by a given days in lactation at risk for that event. Effectively, the duration of days at risk required to define an animal as “healthy” was increased, particularly for traits typically observed throughout the lactation including mastitis and lameness. Although some movement in the STA and Index predictions were observed, these corrections and adjustments reduce biases and provide a better estimate of future observed disease events relative to prior methods.

APY Algorithm and Estimating Reliabilities

We previously communicated evidence of higher than expected estimated reliabilities for a subset of bulls that have genotyped offspring with no or few milking daughters. As a result of this apparent issue with

the methods for calculating these values, reliabilities were not reported for animals with values greater than expected given available pedigree, genomic and phenotype data.

After extensive internal Zoetis testing and collaboration with The University of Georgia (UGA; Dr. Ignacy Misztal), the APY algorithm (Misztal et al., 2014; Misztal, 2016) was implemented in the Zoetis Genetic Evaluation in November 2016. The APY is a computationally efficient solution to accommodate the large number of genotypes. Also, a new program to calculate reliabilities, compatible with the features of the APY algorithm was implemented. These new features will allow to properly estimate reliabilities for all the animals in the evaluation including the subset of bulls that have genotyped offspring with no or few milking daughters. This is a substantial improvement over previous algorithms that will translate in delivering the most accurate predictions using the latest technology. Genetic evaluations beginning December 2016 will contain reliabilities for all animals including the previously affected subset of bulls reported without reliabilities.

Published Methodologies

We are pleased to communicate that the article “Development of genetic and genomic evaluation for wellness traits in US Holstein cows” has been accepted for the Journal of Dairy Science and it is currently in Press: [http://www.journalofdairyscience.org/article/S0022-0302\(16\)30734-2/fulltext](http://www.journalofdairyscience.org/article/S0022-0302(16)30734-2/fulltext). This manuscript details the methodologies used in the CLARIFIDE Plus genetic evaluation.

Misztal I, Legarra A, Aguilar I. Using recursion to compute the inverse of the genomic relationship matrix. *J. Dairy Sci.* 2014;97(6):3943-3952.
Misztal I. Inexpensive Computation of the Inverse of the Genomic Relationship Matrix in Populations with Small Effective Population Size. *Genetics.* 2016;202(2):401-409.

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