

# CDCB changes to evaluation system (April 2018)

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### New health evaluations for Holsteins officially released

*by Kristen Gaddis, Jay Megonigal, Leigh Walton, Duane Norman, John Cole, Paul VanRaden*

Official genetic and genomic evaluations for resistance to six health events in Holsteins (Hypocalcemia, Displaced abomasum, Ketosis, Mastitis, Metritis, Retained placenta) will be first published in April 2018. These traits are six of the most common and costly health events impacting dairy herds. Preliminary results and test files were shared to the industry in December 2017. Positive predicted transmitting abilities (PTAs) measure resistance to these health disorders. For example, a mastitis PTA of +3 indicates that 3% fewer daughters will get mastitis during each lactation. Data from herds all over the country are included in April. Further research is ongoing to: i) extend health evaluations to other breeds; ii) further improve the evaluation model; iii) include these results in the international exchange of evaluations; iv) increase data consistency and sources. Please note that since this is the very first release of this new evaluation, reliabilities are expected to be

lower than in the future, when more and more records will be included in the database. These traits are not yet included in the lifetime net merit (NM\$) formula. For further information please refer to the [content/uploads/2017/09/CDCB-Health-Traits-FAQs-10\\_2017.pdf](https://old.uscdcb.com/cdcb-health-traits-faqs-10_2017.pdf)

## All-breed system extended to genomic evaluations

*By Paul VanRaden, Gary Fok, Mel Tooker, Lillian Bacheller, Jay Megonigal, Leigh Walton*

The all-breed system used for traditional evaluations since 2007 is now also applied for genomic evaluations starting April 2018. This new system allows records from animals of all breeds to be analyzed together and expressed on the same scale. Relatives, regardless of breed composition, will now contribute to every animal's parent average and its genomic evaluation. Previously, animals with pedigrees including ancestors of a different breed were not correctly accounting for the "out of breed" contribution (a generic unknown parent group was assigned, instead of using the full pedigree). Genomic evaluations are now calculated on an all-breed base and then are converted to within-breed genetic bases for release to the dairy industry. **It is important to underline that crossbred animals will still not receive an evaluation.** Genomic evaluations for purebreds will be slightly impacted (except for the revised PL calculations, see next topic), whereas a greater impact will be seen in animals with pedigrees containing ancestors from other breeds.

## Productive Life (PL) correction

*By Paul VanRaden, Gary Fok, Mel Tooker*

The multiple-trait Productive Life (PL) processing for incoming Interbull data has been 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. This logic tended to inflate the resulting evaluation, affecting primarily foreign bulls. Since foreign bull evaluations were inflated, SNP effects used to estimate genomic evaluations were affected, extending the inflation to the general population (e.g., including domestic animals). The inflation was more evident in breeds dominated by foreign bulls, such as Ayshire and Brown Swiss, but outlier cases were observed in all breeds. The new multi-trait PL genomic model prevents this from happening. The evaluations obtained with the new system fit better to the Interbull evaluations for foreign bulls, as a result, reducing the inflation of SNP effects. To give an indication of the impact, the 1712 PL evaluation with the new methodology yielded an average (standard deviation) reduction in PL PTA from 6.10(2.46) to 4.21(1.66) for elite cows. Although averages in bulls remain fairly similar (-0.28 vs -0.34 for official and all-breed, respectively), standard deviations are lower (3.87 vs. 3.1) and the correlation between both systems is 96%, indicating some degree of variation for bulls.

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