

# CDCB changes to evaluation system (April 2020)

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### Genetic base change

*By Duane Norman, Paul VanRaden and George Wiggans*

The base for U.S. genetic evaluations will be updated, effective with the April 7, 2020, triannual evaluations. A detailed article on expectations and approximate base change values was published in February and is accessible at [https://uscddb.com/wp-content/uploads/2020/02/Norman-et-al-Genetic-Base-Change-April-2020-FINAL\\_new.pdf](https://uscddb.com/wp-content/uploads/2020/02/Norman-et-al-Genetic-Base-Change-April-2020-FINAL_new.pdf).

**EDIT 2020/04/07:** The values in the article can be considered as final, except for calving and health traits in which changes in the model and edits modified the estimates of genetic trend and the base change values.

CALVING (Hostein and Brown Swiss): Whereas differences between previous and new PTAs for the maternal traits (DCE, DSB) are difficult to estimate because they are affected by year of birth of the sires, SCE and SSB genetic trends were favorable and about -0.6 and -0.3 for Holstein, respectively, causing PTAs to increase by 0.6 and 0.3. The genetic trend and base change were 0 for SCE in Brown Swiss.

HEALTH (Holstein): Updated values are: Resistance to Milk Fever (MFV): 0.0, Resistance to Displaced Abomasum (DAB): 0.13, Resistance to Ketosis (KET): 0.4, Resistance to Mastitis (MAS): 0.73, Resistance to Metritis (MET): 0.45, Resistance to Retained Placenta (RPL): 0.0

## Disease resistance (health) traits for Jersey animals

*By Kristen Gaddis, Laura Jensen, Jay Megonigal and Paul Vanraden*

Disease resistance (health) evaluations for six traits (resistance to milk fever, displaced abomasum, ketosis, mastitis, metritis, retained placenta) have been available for Holstein animals since April 2018. Recent research indicated that expanding these evaluations for Jersey animals was feasible, as there has been a 112% increase in the total number of usable Jersey health records since the initial research was completed.

Total number of available Jersey phenotypic records by trait ranged from 85,417 for ketosis to 168,342 for mastitis, as of January 2020. Overall incidence ranged from 1.2% for milk fever up to 10.4% for mastitis, similar to Holstein findings. Heritabilities were assumed to be equivalent to those in Holstein, ranging from 0.6 to 3.1%.

The same pipelines as currently used for CDCB Holstein health evaluations were expanded to include Jersey data. Phenotypes are pre-adjusted for unequal variance prior to evaluation. Traditional Predicted Transmitting Abilities (PTAs) are estimated using a univariate BLUP repeatability animal model accounting for year-season, age-parity, herd-year and permanent environmental effects, as well as a regression on inbreeding and heterosis.

Resulting PTAs are presented as percentage points above or below the breed's average resistance with more positive values being favorable. Average traditional reliabilities for bulls born since 1990 with  $\geq 90\%$  net merit (NM\$) reliability ranged from 17 to 32%, depending on trait. Average genomic reliabilities for those bulls ranged from 29 to 49%, gaining 12 to 17 percentage points from the inclusion of genomic data. Maximum PTA reliability was 98% for mastitis. Correlations between health PTA and the PTA of other routinely evaluated traits were calculated.

In NM\$, the total weight of the six health traits will be 2%.

## New edits for disease resistance traits

*By Kristen Gaddis, Jay Megonigal and Paul VanRaden*

New editing criteria are now implemented for disease resistance and applied to both Holstein and Jersey populations. The editing criteria includes:

- Implementation of 700 maximum days in milk maximum for usable lactation record. Previously all health records were excluded for some cows with lactations longer than 400 days.



- Implementation of minimum incidence levels for each event at 10% of the current incidence rate for herd-years with over 100 animals. This edit was included to detect herds poorly recording health events.
- Implementation of smoothed heritability estimates by lactation for variance pre-adjustments.
- Because of the inclusion of animals from different breeds in the evaluation, heterosis is now included in the model.

## Health Evaluation Model Upgrade

*By Kristen Gaddis, Ezequiel Nicolazzi and Paul VanRaden*

The April 2020 evaluation for health traits in both Jersey and Holstein breeds included a change in model, in addition to the previously-announced changes in the editing of phenotypic records. During the review of the test run results, it was noted that some bulls were being penalized by the uneven distribution of their daughters (many daughters in a handful of herds). To mitigate this effect, the health evaluations now include a sire by herd interaction effect and more stringent parameters. This change produced the intended effects, both within and across traits. Genetic correlations with other traits such as productive life, somatic cell score, and daughter pregnancy rate improved, which is desirable. More research will follow to study the impact of unbalanced data on the health evaluations.

## Calving traits evaluation updates

*By Stefano Biffani, Francesco Tiezzi and Christian Maltecca.*

A full revision of calving trait evaluations was performed to identify the validity of the assumptions made during original development. Both the phenotypic editing procedure as well as the current models were thoroughly investigated. Several changes to the editing of the data used were implemented to exclude herds only reporting easy calvings (i.e., calving score 1) and to merge extreme categories (calving scores 4 and 5) – because of their low frequency in the data.

On the model side, genetic parameters were re-estimated and will be updated. The assessment on the data entering the evaluation identified a relatively recent trend in the sex ratio of calves, especially in first lactation animals, only partially accounted for. The model introduced in April 2020 will include an interaction effect of parity-sex-birth year of sire and MGS, among other minor changes. These changes were tested and compared with previously published results, and they were validated independently at the two latest Interbull test runs. All validation tests showed a large improvement in correlations with other countries and in the estimation properties of the new model.

Nationally, the calving traits will see a variation in trends as the new model estimated less genetic progress in recent years, largely because of accounting for the recent trend in sex ratio. The resulting animal rankings will be affected, especially in the maternal traits of Daughter Calving Ease (DCE) and Daughter Stillbirth (DSB).

The improvements made to the calving trait evaluations will provide better predictions that more accurately reflect the current dairy industry.

## New SNP set used for genomic evaluations

*By Paul VanRaden, Bingjie Li, Dan Null (AGIL), and George Wiggans (CDCB)*



The SNP set used for April predictions includes new SNPs that better track inheritance in additional breeds and traits. Markers with largest effects were selected from high-density genotypes imputed for five breeds. The selected markers were also provided to genotyping laboratories in September 2019 to allow future improvement of their arrays.

The April list of 79,060 SNPs used includes 4,589 new markers and several additional gene tests. This revision also removed 4,824 of the least informative SNPs from the previous list of 79,294 SNPs to reduce computing time while improving prediction accuracy. Carrier status for some haplotypes is affected by these changes, and more direct gene tests are now used.

Find further summaries of the SNP selection process in these papers:

- VanRaden, P.M., Null, D.J., O'Connell, J.R., Cole, J.B., and Li, B. [Genomic prediction and marker selection using high-density genotypes from 5 dairy breeds](#). J. Dairy Sci. 102(Suppl. 1):400(abstr. 471). 2019.
- Li, B., Fang, L., Null, D.J., Hutchison, J.L., Connor, E.E., VanRaden, P.M., and Cole, J.B. [High-density genome-wide association study for residual feed intake in Holstein dairy cattle](#). J. Dairy Sci. 102(12):11067-11080. 2019.

## **New standard deviations for type traits in non-Holstein breeds**

*By Paul VanRaden*

With the introduction of the new base, some type trait PTAs will have moderate to large standard deviation (SD) changes in breeds other than HO. The base SD set previously used an average SD across all years of data, whereas the new methodology uses only cows born 2013-17 to set the 2020 base SD. Variances increased for most linear trait PTAs of most breeds, but not for HO because their published PTAs are standardized (STAs).

## **Discontinuation of subset format 38 files**

*By Ezequiel Nicolazzi and Jay Megonigal*

Effective the April 2020 evaluation, the following subsets of the format 38 files will no longer be released:

- 38coeff.zip
- 38off.zip
- 38ai.zip
- 38s.zip
- 38i.MYY.xml
- 38i.MYY.xlsx



The above files were created at the time internet connections were slow, as creating subsets of the data avoided downloading large files for only a subset of animals. Since those reasons are no longer valid, only the official format 38 (38alloff.zip) and its traditional counterpart will be published.

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