

# CDCB changes to evaluation system (August 2018)

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### Health traits in Net Merit \$

*By Paul VanRaden, John Cole, and Kristen Parker Gaddis*

The August 2018 NM\$ update includes genetic evaluations for six new direct health traits first introduced in April 2018 for Holsteins: displaced abomasum, hypocalcemia (milk fever), ketosis, mastitis, metritis and retained placenta. In Net Merit, the disease resistance traits are grouped into a health sub-index (HTH\$) that is not published separately, similar to the calving ability sub-index (CA\$).

Economic values of the six new traits were obtained as averages of two recent research studies plus additional yield losses not fully accounted for in published genetic evaluations for yield traits. Some yield losses associated with health conditions are not fully accounted for when 305-day lactation records include adjusted

test days coded as sick or abnormal. The added weight of HTH\$ on NM\$ will lead to nearly the same progress for HTH\$ because NM\$ has been accounting indirectly for health effects for a long time. Addition of these six new traits to the index is counteracted by removal of indirect health costs previously assigned to other traits such as somatic cell score and yield.

Additional NM\$ updates include new economic values for each unit of predicted transmitting ability (PTA) and the relative economic values of traits. Full details of the changes are provided in an updated format that documents the other indexes: <https://aipl.arsusda.gov/reference/nmcalc-2018.htm>.

## Changes in fertility trait modeling

*By Paul VanRaden and Jana Hutchison*

Age-parity adjustment factors for daughter pregnancy rate (DPR) and cow conception rate (CCR) are revised for August to improve the stability of genetic trend estimates. During the April evaluation, recent genetic trends in traditional predicted transmitting ability (PTA) for DPR and CCR decreased when new age-parity groups were added by an automated process scheduled every five years. As a result, the fertility PTAs, NM\$ and breed association indexes for recent animals declined by 1.7 DPR, 1.4 CCR and \$22 NM\$ in April.

Since 1995, age-parity effects for production have been estimated separately within five-year periods. Age and parity effects gradually changed across the decades, and more modern cows reached mature yield sooner ([Norman et al., 1995](#)). Different age-parity groups within each five-year period helped pass Interbull trend validation and had large effects on estimated genetic trend. These adjustments performed well for production, so were also used for SCS and fertility traits. However, because time groups are based on fresh dates, when the latest fertility group was formed, the least fertile daughters were partitioned into the new group whereas the most fertile daughters remained in the earlier group. To prevent abrupt changes in the future when new time groups are formed, the five-year groups are now redefined to instead gradually slide forward every four months. The April fertility PTAs were recomputed with this revised model, and for young animals the resulting trend returned about 60% of the way toward the December trend rather than maintaining the lower April trend. The age-parity definition change had a downward effect on the trend for older animals. The preliminary results in August indicate the trend for young animals is closer to December results in most breeds for DPR and CCR. As a general indication (since calculations are still ongoing), PTAs for recent birth years that had decreased in April are expected to be closer to the December values in August. In all cases, within-year rankings of animals were affected only a little.

Norman, H.D., Meinert, T.R., Schutz, M.M., and Wright, J.R. [Age and seasonal effects on Holstein yield for four regions of the United States over time](#). J. Dairy Sci. 78(8):1855–1861. 1995.

## EFI update and changing of heterosis procedure on genomic evaluations

*by Ezequiel Nicolazzi, Gary Fok, Leigh Walton, Jay Megonigal and Paul VanRaden*

Expected future inbreeding (EFI) is included in PTAs, but approximate adjustments were used in the all-breed weekly and monthly files after the April release until early May. Exact EFI is now used if both parents were in the pedigree file from the previous full run, and an approximate EFI is used only for new animals whose parents are also new since the last full release. Approximate methods were needed because reprocessing inbreeding for all 78 million animals takes nearly a day and is done only three times per year. **Effective with the August 2018 genomic run, calculation of heterosis – previously reprocessed for all animals three times a year – will now be run on a monthly basis.**

In light of the growing importance of heterosis and inbreeding values in the all-breed system introduced in April 2018, this critical change to the monthly processing – which required an extensive review – will better account for animals changing pedigree, especially those with changes of breed in their pedigrees (including own breed). Such enhanced procedure will also run during triannual genomic runs, so that all 78 million animals will undergo the procedure two times. The first heterosis run will be used exclusively for the traditional evaluation, and a second run will be used for the genomic evaluation and for reporting of final results. In the rare cases where progeny tested animals change pedigree, they could receive traditional and genomic PTAs with misaligned heterosis. However, the decision was to report PTAs reflecting the most current information available.

## Exclusion of IDs from Interbull pedigree

*by Jay Megonigal and Ezequiel Nicolazzi*

Interbull pedigrees include dismissed IDs and non-standard IDs for some animals. For several years AGIL and CDCB have accepted these IDs as a way to track the past animal IDs. However, recently we discovered that such practice might create a misalignment that can cause old bulls to be submitted to Interbull with incorrect IDs. For August 2018 onwards, bulls with dismissed IDs (labeled as “X”) or that contain “\_IMAG\_” in their numeric IDs in the Interbull pedigree are now immediately excluded from the CDCB system.

## Genomic mating file in HO – full implementation of rules

*by Leigh Walton and George Wiggans*

With the objective of reducing the dimension of the G-mating inbreeding file, and after discussions with National Association of Animal Breeders (NAAB) and two of its committee chairmen, an editing criteria was applied to females in the genomic mating inbreeding file in August 2017. The new criteria would include genotyped females with a usable genotype if any of the following conditions are met:

1. The last processing date received from the DRPC is within the past six months and the termination code does not indicate that they are dead.
2. If the DRPC does not indicate they are dead, they have a progeny born in the last 18 months.
3. If the DRPC does not indicate they are dead, they were born in the last five years.

These rules were intended to limit the growth of the file by eliminating cows that are not on DHI and are over five years old without progeny in the pedigree table, therefore not of interest for the industry. Applying these restrictions, the file included less than 800,000 animals from the nearly 1.3 million genotyped Holstein females.

After reviewing files distributed in April 2018, CDCB discovered the above criteria was not implemented in full as originally intended. **The August 2018 inbreeding file and those in subsequent runs will contain such definition applied in full.**

### Changes in content of Format 38

No new changes in the formats were introduced, but a number of changes were introduced in the routine programs that generate format 38. All special characters are now routinely excluded from the file; sampling status, average standardized milk (protein) and DYD milk (protein) fields are now blanked. Daughter averages are not shown for traits with less than 10 daughters. **As per the industry request, the strategy implemented in April 2018 of publishing daughter/herd information for all traits irrespective of the number of daughters available was reversed.** Starting the August 2018, daughter/herd information for all traits, except HCR and GL (as data arrives before milk data), will be blanked for bulls having less than 10 daughters on milk yield.

### Change in Jersey elite cow criteria

*by Jay Megonigal and Ezequiel Nicolazzi*

The elite cow criteria was edited to include the current registry code practices of the American Jersey Cattle Association (AJCA). The association's current practice is to use numeric registry codes (01 to 06, indicating generation count number) and HR (Herd Register; animals with such status have seven or more unbroken generations of known Jersey ancestors recorded by AJCA). Such criteria was first implemented in March 2017, but never adopted on the elite cow criteria. In collaboration with AJCA, CDCB has modified the JE elite cow criteria to include cows having a numeric registry code greater than 02, or HR. The modification is in effect starting August 2018.

### Guernsey phantom group reinstated

*by Jana Hutchison, Jay Megonigal and Paul Vanraden.*

The exception encountered in **April 2018** involving the program that created the unknown parent groups (UPG) for the breeds during the traditional evaluation was edited, in order to allow the creation of the Guernsey UPG irrespectively of their low number of unknown parents in the last 15 years. All genomic breeds will receive their own UPG as was originally intended.

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