Council on Dairy Cattle Breeding

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# CDCB changes to evaluation system (April 2019)



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## Genomic evaluations including crossbred animals

*By George Wiggans, Mel Tooker, Leigh Walton, Ezequiel Nicolazzi and Paul VanRaden*

Effective April 2019, CDCB genomic evaluations will include crossbred animals. A full description of the policy applied to these evaluations is provided in the "CDCB Policy" document. In short, changes in the evaluation procedure will be:

- CDCB will update the procedures for Breed Base Representation (BBR). Updated BBRs will be obtained by setting to 0 any breed proportion ≤2% (considered statistical noise) coming from the BBR calculation. The remaining percentages will be proportionally rescaled.

- All animals will receive a new BBR in April, based on the revised methodology (see Policy). BBR will not be fixed anymore, and changes to the genotype/pedigree of the animal may cause new BBR estimates for affected animals.
- Animals with BBR≥90 will receive evaluations based solely on the (single) breed they belong to (SINGLE-group). Animals with BBR<90 (MULTI-group) will receive an evaluation based on a multi-breed population in which blended SNP effects (based on the BBR) will be used to calculate their Direct Genomic Values (DGV).
- During monthly evaluations, animals with a phenotypic-based evaluation and a BBR ≥94% for that breed will be included in the PTA reference population (population used to estimate SNP effects). Animals in the MULTI-group (BBR<90) will not contribute to any PTA reference population.
- Animals in both SINGLE- and MULTI-groups will be published in their respective breed of evaluation file, since they all share the same breed base. CDCB will label single-breed based evaluations as “S” and multi-breed blended evaluations as “M” in the genomic files.
- Animals in the MULTI-group will not receive any fertility haplotype information. Research is ongoing to validate the accuracy of the calls in a multi-breed scenario.
- Current genomic evaluations for animals in SINGLE-group are not expected to vary substantially, as they will only be affected by a slight decrease in the number of animals in the reference population (due to the more restrictive criteria used).
- Animals currently receiving genomic evaluations that will now be included in the MULTI-group, will likely be more affected as their DGV will be blended and their PTAs will be obtained based on parameters coming from a multi-breed population.

## Early first calving as a new trait

*By Jana Hutchison, Paul VanRaden, Dan Null, John Cole and Derek Bickhart*

Accurate records for age at first calving have been recorded in DHI for decades for nearly all cows. Early first calving (EFC) is defined in days and reverses the age scale so that positive PTAs are favorable.

- The EFC genetic evaluation includes 31 million records for heifers born since 1957 and combines all breeds and crossbreds. Initial research used 14 million records for heifers calving since 1997 to compute single-breed evaluations (Hutchison et al., 2017).
- The heritability of EFC was estimated to be 2.7%. The estimated inbreeding depression for EFC is -.62 days per 1% inbreeding and base heterosis is +3.3 days.
- The within-breed PTA standard deviation is only about 3 days, but some recent bulls have PTAs above 10 or below -10 days.
- In both Holsteins and Jerseys, genetic trends toward earlier calving already have resulted in about 10-day gains in EFC breeding value over 60 years due to selection on other traits favorably correlated to EFC. In each breed, an additional 1- or 2-day gains in EFC occurred in the last 5 years.
- Breed differences are large compared to within-breed differences. Jerseys have a 4-day average genetic advantage for EFC breeding value compared to Holsteins, whereas Brown Swiss calve 28 days later, Ayrshires 41 days later, Guernseys 18 days later, and Milking Shorthorn 15 days later based on heifers born together in the same herds.

- Reliabilities of EFC genomic predictions for young animals averaged 66% for Holsteins and 51% for Jerseys.
- Net Merit (NM$) is expected to include EFC in a later revision, and then EFC could get 3% of the total emphasis in NM$. The relative emphasis on heifer conception rate (HCR) would then be reduced because HCR currently accounts indirectly for some of the EFC benefits. Traits EFC and HCR have a genetic correlation of about 0.5. In the future, EFC could be incorporated into a fertility index such as that published by Holstein Association USA. The next base change in April 2020 may be a chance to review how to group traits into sub-indexes or options for changing the presentation.

## Variance adjustments for health trait evaluations.

*By Kristen Gaddis, Jay Megonigal and Paul VanRaden.*

A pre-adjustment for variance across lactation in health traits will be applied in April 2019. The current PTAs were compared to variance-adjusted values.

- The largest changes from previous were for Milk Fever. All other traits had PTA correlations .92 to .98 for bulls with >70% REL born since 2000.
- The Standard Deviation (SD) of Health$ should change little, although slight increases in SD were observed for Mastitis and Displaced Abomasum. Slight decreases were observed for the other traits. The SD of all lactation evaluations are expected to be about 5% more than first lactations due to higher reliability, and all traits except Displaced Abomasum were closer to this expectation.
- The first lactation evaluations were also more correlated to new than to previous evaluations for all traits except Metritis. Genetic trends were compared using correlations of PTA with birth year to automatically adjust for the differences in SD. For all traits, the first lactation trends agreed with the new trends more closely than with the old trends.
- The variance-adjusted PTAs for Mastitis (the only trait evaluated at Interbull) passed both Interbull trend validation methods. CDCB will submit these records as official in April. In August, CDCB will include MACE information in the evaluation of Mastitis.

## Correction of AY heterosis calculation for MACE from Scandinavian breeds

*By Paul VanRaden*

Since August 2018, Scandinavian Red breeds are treated as being the same as Ayrshire (AY) when computing pedigree heterosis to be consistent with Breed Base Representation (BBR) genomic methods. The AY PTAs submitted to Interbull used the new heterosis definition, but the MACE files received from Interbull continued to be adjusted using the previous heterosis formula that treated each breed (SR, NR, and RE) as unique. This mismatch of definitions reduced the MACE PTAs for bulls that had more inheritance from these breeds. The heterosis adjustment will be applied consistently in April. We thank Gary Rogers for discovering this error from differences between published daughter yield deviations and PTAs for bulls with U.S. daughters.

## Genomic parent averages in monthly and weekly files

*By Gary Fok, Jay Megonigal and Paul VanRaden*

Traditional parent averages (PAs) were provided since 2009 in monthly and weekly update files, whereas genomic PAs (average of parents' official evaluations) have been provided since 2013 in the triannual full releases. For consistency, genomic rather than traditional PA will be provided in the monthly and weekly files.

Traditional PAs originally allowed breeders to see the differences caused by adding genomic information but are less relevant today because most calves are now two generations removed from their proven grandsires, and the traditional PA does not reflect the genomic selection already done in the parent's generation. Monthly and weekly file formats will supply genomic PAs for most traits but still report traditional PAs for type and calving traits. For those traits, no PAs are supplied in the triannual formats because calving traits are evaluated using a sire–maternal grandsire model where dams are not evaluated. For type traits, PAs are computed by breed associations or they show both the sire and dam PTAs separately.

## New genomic evaluation file formats (CSV)

*By Ezequiel Nicolazzi and Jay Megonigal*

In February, CDCB released the first test run of the new genomic evaluation. Among many other changes, the new genomic evaluation files contain the aforementioned genomic parent averages instead of Traditional PTA and reliabilities. The first official release of the new format was on March 2019. In April 2019, these new file formats will be released publicly. A transition period of 6 months, in which CDCB will release both old and new formats, will follow after the first official release. On September 2019 monthly and weekly evaluations release day, CDCB will only distribute the new file formats. All XML and old CSV formats will be discontinued after that date. Although CDCB will be distributing both formats during the transition period, the old formats will not be maintained after April 2019. Therefore, further development of the formats will only affect the new formats.



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