Council on Dairy Cattle Breeding

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CDCB changes to evaluation system (April 2021)

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Fertility traits editing update

By Jana Hutchinson and Paul VanRaden

Several small adjustments to fertility traits editing will be introduced with the April 2021 evaluation to better account for late-term abortions. Fertility credits for traits Heifer Conception Rate (HCR) and Cow Conception Rate (CCR) now treat the last service as a failure instead of success if the next calving is coded as an abortion. Similarly, when computing Daughter Pregnancy Rate (DPR), days open is now topped at 250 instead of the reported days open, if the next reported calving is an abortion. Similar edits had been implemented for Early First Calving (EFC) in August 2019.

Abortions, mostly accounted for in the past, are now fully accounted for in the existing fertility traits. The new edits were validated in the January international (Interbull) and in a full internal test run. **Since most of the abortions were already accounted for, the impact of this new editing is very minor**, with almost negligible changes in trait standard deviation and correlations higher than .997 for new PTAs, compared to official December PTAs (values obtained using ~20,000 HO bulls born since 2000 with >50% reliability). Trends will be also affected very slightly, with a 0.1 average decrease in bulls born in recent years for Holstein and Jersey bulls.

Feed Saved: Inclusion of Canadian data

By Kristen Gaddis, Javier Burchard and João Dürr

The reference population for Feed Saved evaluations* now includes feed intake records from >650 lactations in two Canadian herds. This phenotype exchange is part of a larger collaboration between CDCB and Lactanet. The +10% gain in records should improve genomic prediction reliabilities by 1 to 2%. The Canadian cows are born after 2012, and many of the older cows have only later lactations (like some U.S. research cows), and a few have 4-week instead of 6-week trials. The Canadian research cows already had genotypes at CDCB which simplified merger of the data into the Feed Saved evaluation.

**Feed Saved was first published by CDCB in December 2020, and a Feed Efficiency evaluation will be launched in Canada in April 2021.*

Cow Livability edits corrections

By Rodrigo Mota, Ezequiel Nicolazzi and Paul VanRaden

In a recent review of our phenotypic pipeline, we identified (and corrected) an unintended flaw in the routine that prepares the phenotypes for the traditional evaluation of Cow Livability (LIV) . Extremely old (pre-1957) and very recent (3 years prior to the evaluation date) data was unexpectedly entering the evaluation, causing some instability in the evaluation due to extra unknown parent groups with little data.

In a test run based on December 2020 evaluations, no variation in trends was observed in Ayrshire, Guernsey and Brown Swiss. In Holstein and Jersey, a positive trend of approx. +0.4 was observed in the most recent bulls with phenotypes (born 2018-2019).

New genomic inbreeding calculation method

By Gerald Jansen, Juan Pablo Nani and Paul VanRaden

In April 2021, the following improvements to the inbreeding calculations will be implemented:

- Sex differences will now be accounted for to adjust inbreeding, with the objective to make genomic and pedigree averages match for both sexes.
- Average genomic inbreeding for full brothers and sisters will now be used.
- Methods of genomic inbreeding will be now aligned to official instead of approximate pedigree inbreeding.
- A correction to the pedigree inbreeding was made for crossbred animals, to better account for multi-breed contribution.
- Highly-improved computation efficiency was implemented.

The new adjustments to the inbreeding procedures will help dairy producers manage inbreeding and relationships more precisely using genotypes versus only pedigrees.

More detail

Genomic measures of inbreeding and relationships may differ for males and females due to markers on the X chromosome. Those differences will now be adjusted to make genomic and pedigree averages match for both sexes. This will be achieved by using only males with progeny (typically having more complete pedigrees) to obtain the values used to harmonize the scale of genomic and pedigree inbreeding, which are typically on a different scale. Also, a new adjustment will equalize average genomic inbreeding for full brothers and sisters.

Genomic inbreeding calculation includes the X chromosome (about 3% of the total SNP count used) because it can contribute to inbreeding depression. However, the 3% of markers on the X chromosome caused homozygosity of females to appear 3% less than males, affecting the genomic inbreeding values. This new adjustment does not affect comparisons within sex, only of males versus females.

The new calculation will not only impact the reported genomic inbreeding values, but will also slightly affect the genomic mating calculations and the average relationship values used in the process that obtains the genomic reliability for all animals. In a test run based on the February genomic evaluation, a very small sample of animals had large changes in reliability (animals with incomplete pedigree, animals with no ties to U.S. reference population). **However, the expected average change in reliability for most of the breeds were lower than +0.2% (0%/0.08% average change for HO and JE)**. For Brown Swiss, likely due to the different “depth” of pedigrees and the reduced ties to the US reference population of genotyped animals, the reliability reduction was in the order of -1.6% and in crossbred animals of -0.8%.

Finally, a correction to the pedigree inbreeding for crossbred animals was included to better account for the unknown parent groups contributions from multiple breeds. This change is expected to have some degree of impact the Predicted Transmitting Abilities (PTAs) in the traditional evaluation for crossbred animals.

Parent average recalculation and various revisions to the evaluation workflow

By Ezequiel Nicolazzi and Paul VanRaden

In recent years, the number of pedigree changes in genotyped and ungenotyped animals has increased dramatically. On a monthly basis, the CDCB cooperator database receives approximately 5,000 animal’s ID breed changes and over 25,000 pedigree changes, mostly triggered by genomic parent (sire/dam and grandsires) and breed verification.

To update all information as soon as possible, changes to the evaluation workflow have been introduced to more frequently recompute heterosis (August 2018) and Expected Future Inbreeding (December 2020). However, animals entering the traditional evaluation had their parent averages (PA) carried over until a new traditional evaluation was calculated 4 months later, irrespective of pedigree or other changes.

Effective with the April 2021 evaluation, animals will get fresh PA based on their latest pedigree at the time of every evaluation cutoff. This change will not affect animals with phenotypes, as phenotypic evaluations are still being calculated every 4 months.

Other changes introduced in this revision:

• The policy of including foreign evaluations if the reliability is at least .5 higher for PA is now extended for PTAs also. This modification is to increase the stability of evaluations that have substantially the same reliability.

• A thorough revision of the Unknown Parent Groups (UPG) used in all 6 health traits and other minor improvements affecting all traits were implemented on the usage and extension of UPG across years. These changes will affect animals with incomplete pedigrees.

• Genomic evaluations are now carried over to the formats 105 and 38 irrespective of their reliability. The change affects mostly F1 crossbred animals. The new policy prevents a misalignment in the NM$ results in the purely genomic files (.csv) and the formats 105/38 (which combine traditional, foreign and genomic evaluations), caused by the substitution of type composites genomic evaluation by traditional values because of their higher reliability.

Results in a test run showed over .999 correlation with December 2020 genomic evaluations in most traits for all breeds. Correlations for health traits were lower because of the UPG revision. Since the change in policy can affect the traits being used in the multiple-trait calculation, Productive Life, fertility traits, Gestation Length and Livability in the test run showed (slight) differences with the official December 2020 evaluations.

CDCB haplotype determination extended to Canadian population

By Ezequiel Nicolazzi and João Dürr

As part of a bilateral collaboration, CDCB will start calculating and sharing haplotype results for all the Canadian population with Lactanet in April 2021. All publishable males and a subset of females – irrespective of their initial fee code – will now enter the evaluation only to obtain haplotypes for this exchange.

The sharing of haplotype calls to Canada and the exchange of phenotypes for Feed Saved evaluation are the first steps implemented in the framework of a much larger and fruitful collaboration between the U.S. and Canadian evaluation systems.

Clinical mastitis (CMA) introduced as independent international trait

By Rodrigo Mota and Paul VanRaden

Effective with the April 2021 evaluation, Interbull will introduce a new trait named CMA (Clinical Mastitis) to better estimate SNP effects specifically for clinical mastitis. Like fertility traits, the new edits were validated in January in a full test run. In the April evaluation, CMA results will be used for genotyped bulls with an international evaluation from the other participating countries (Canada, Switzerland, Germany, Norway/Finland/Sweden, France, Great Britain and the Netherlands). For non-genotyped animals, the previous trait combining mastitis from some countries and correlated SCS from others will be used.

Since CDCB's launch of the Mastitis (MAS) trait in Holsteins in April 2018 and Jerseys in April 2020, the bull evaluations for MAS have been exchanged with countries participating in Interbull. Until December 2020, countries were given the choice to exchange pure clinical mastitis (as the case in the U.S.), SCS (for countries without a health evaluation), or a combination of methodologies (clinical/subclinical mastitis or a multi-trait approach using multiple sources of information). For this reason, only data coming from certain countries with similar trait definitions were being used in the U.S. evaluations.

The contributions from most of the participating countries for this new trait have been already accounted for, thus **only a minor impact to the U.S. evaluations is expected.**

Heifer livability update in heritability

By Mahesh Neupane and Paul VanRaden

The estimated heritability for Heifer Livability (HLIV) increased to 0.7% from the previous 0.4% estimated in 2015, used in December 2020 evaluation. The higher estimate is likely due to some invalid records from earlier years now being excluded and many new records being added during the last 5 years. The heritability was estimated by sire model REML using records from 3,175,916 heifers sired by 9,961 Holstein bulls. The new estimate was computed as part of the review process for a scientific article describing the new evaluation.

Change in determination of breed conflicts and initial BBR

By George Wiggans, Jose Carrillo and Gerald Jansen

For April, an approximate procedure (“quick BBR”) to estimate Breed Base Representation (BBR) was implemented. This new procedure replaces the use of the breed SNP in determining breed errors and assignment to crossbred processing. The primary benefit is for the weekly evaluations, where quick BBR increases the portion of genomic evaluations that qualify for processing in the purebred evaluations to be processed there from the outset.

Quick BBR does not require genotype imputation and is fast enough to be integrated with the genotype loading process. The initial BBR is immediately available to determine if a genotype should be processed as a purebred or crossbred and provides a breed error if the BBR is high for a breed other than the breed of the animal ID. An 85% BBR threshold is used both for designation of breed errors and assignment to purebred processing. Because quick BBR is approximate, setting the threshold below the threshold of 90% from the full BBR (i.e. BBR obtained from imputed genotypes, calculated during weekly/monthly evaluations) allows most genotypes that qualify for a purebred evaluation to be processed with the correct breed. The current practice of moving animals with full BBR < 90% to the crossbred evaluations will continue.

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