

CDCB changes to evaluation system (December 2020)

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Feed Saved in Holstein

By Kristen Gaddis and Paul VanRaden

The December 2020 evaluations will include Feed Saved as an individual trait for Holsteins.

The genetic evaluation for new trait Feed Saved is based on a current database of approximately 6,300 Holstein cows with individual feed intake records. This database was collected through a 2010 National Institute of Food and Agriculture (NIFA) grant and continues today through a collaborative effort with multiple institutions throughout the U.S. with the support of CDCB and the Foundation for Food and Agriculture Research (FFAR).

Feed Saved will represent a combination of Predicted Transmitting Abilities (PTAs) for body weight composite (BWC) and residual feed intake (RFI). Body weight composite combines stature, strength, body depth, dairy form, and rump width. It is presently included in the Net Merit index with a negative relative weight, selecting for more efficient cows. Residual feed intake is the difference between a cow's actual feed intake and her expected feed intake, after accounting for factors such as production, size, and change in body weight.

The Feed Saved trait simplifies selection into a single value indicating an animal's expected feed efficiency. Feed Saved will be expressed as the expected pounds of feed saved per lactation, with larger positive values representing more pounds of feed saved and indicating a more feed-efficient animal.

Genomic PTAs for Feed Saved evaluations in bulls born since 2000 with Net Merit reliability >90% range from -605 to +409 pounds of feed saved and have an average reliability of 43%.

It is expected that Feed Saved will be included in the Net Merit index when it is next revised in April 2021.

Heifer Livability in Holstein and Jersey

By Mahesh Neupane, Paul VanRaden, and Duane Norman

Heifer Livability will be a new, individual trait for Holstein and Jersey animals in December 2020.

The genetic evaluation for heifer livability uses disposal codes for 3.9 million heifer calves of all breeds from the National Cooperators Database maintained by CDCB with birth dates between 2009 and 2017. Records are not included until three years after the birthdate so that the live status of contemporaries could be confirmed by a calving date. Herds with death losses between 1 and 25% are included, and the number of reported deaths was 155,000 (4.0%). That means that 96% remained in the file during the period studied. The evaluation is based on deaths between 2 days of age and when the heifer left the herd, or until the maximum imposed of 18 months. Stillbirths and deaths observed in the first 2 days of age are excluded as they are accounted for in the stillbirth evaluations.

Heifer livability measures the genetic ability, or probability, of a heifer to stay alive until 18 months. Heifer livability PTAs express mortality differences as percentage points, with a positive number being favorable. With an average livability of 96%, for a sire at +1.0 PTA, one would expect 97% of daughters to remain alive. For a sire at -1.0 PTA, 95% of daughters could be expected to remain alive.

Differences in breeds and sires confirmed the presence of a small genetic component (0.4% heritability) for heifer livability. Genomic predicted transmitting abilities (GPTA) for heifer livability in Holsteins ranged from -0.6% to +1.6% and had a standard deviation (SD) of 0.5%. GPTAs for Jersey ranged from -0.5% to +0.5% and had a SD of 0.2%. The reliabilities for young animals with genomic tests averaged 46% for Holsteins and 30% for Jerseys whereas reliabilities for traditional parent average averaged 16% and 12%, respectively. This illustrates once again the tremendous value of genomic testing. Even when the heritability of a trait is low, the genomic accuracy obtained is usually moderate and will continue to improve as more calf records arrive.

Heifer Livability is expected to be included in the Net Merit index when next revised in April 2021.

Genomic evaluations on 6 conformation traits

By Jana Hutchinson, Jay Megonigal, and Paul VanRaden

Several type traits that previously had only traditional PTAs will receive a genomic PTA effective in December 2020. The breed-trait combinations and reasons are:

- Rear Udder Width (**RUW**) – Now published for all breeds using data available since 1976.
- Body Depth (**BDE**) – Traditionally only reported in Holstein, now published on Ayrshire, Guernsey and Brown Swiss, using data available since 1985.
- Feet / Leg Score (**FLS**) – Traditionally only reported in Holstein. The Brown Swiss definition of this trait (**Mobility**) will be reported under this naming convention in the genomic files, using data available since 2012.
- Milking Speed (**MSP**) -New trait, reported only for Brown Swiss using data collected since 2006.
- Rear Teat Placement (**RTP**) – Traditionally only reported in Holstein. The Jersey definition of this trait (Rear Teat Placement Rear View) will be reported under this naming convention in the genomic files, using data collected since 2008.
- Rear Teat Placement Side View (**RTS**) – New trait, reported only for Jersey using data since 2008.

In conjunction to the new publication of these genomic traits, the genomic processing was reorganized to share a common list of 21 type traits for all breeds, which has simplified management of type evaluations.

Reports posting on release day timing update

By Jay Megonigal and Ezequiel Nicolazzi

Traditionally, summary and result reports such as top bulls and elite females have been published at noon of release day. Effective with the December 2020 evaluation, these results will be published on release day **with the data files as early as possible** after all checks have been completed. CDCB has made this change to provide the fastest feedback possible to the dairy industry.

Updates in the inbreeding calculation procedure

By Gerald Jansen

Following industry feedback on the inbreeding procedure (applied in August), a few changes are implemented for December 2020 to improve stability of expected future inbreeding (EFI) over time. The reference sample used to obtain inbreeding estimates has been increased from 1000 to 2000 females. Furthermore, the reference sample, traditionally updated once a year in April, is now updated using a “rolling base” of 48 months from the month of calculation. This means there will no longer be larger changes in April, and the update of the population will be gradual. In order to increase stability of estimates, the same animals are retained in the reference sample from one run to the next, except for those born in oldest month which will be replaced. Special care has been taken to randomly sample replacements while maintaining a uniform distribution across the four years in the reference population.

The introduction of this “stability package” will result in an initial variation of the estimated EFI and PTA when introduced, similar to that present in the recent full releases. Thereafter, stability across breeds and across time will improve markedly and is expected to be over 99.9%.

Breed code update for EFI and heterosis purposes in monthly genomic runs

By Ezequiel Nicolazzi

In the past year, CDCB observed a large number of cases of animals changing breed code from run to run. Since expected future inbreeding (EFI) and heterosis are used to correct the PTA, inaccurate values for these two parameters can significantly impact the final PTA of an animal. In general, a change in breed causes the animal receiving a very low EFI and an incorrect heterosis, which in turn results in highly inflated PTAs.

With the introduction of the new inbreeding procedure in August, and subsequent possibility to include the more precise inbreeding calculations in weeklies and monthlies, it became possible to increase the frequency of updates of pedigree information for these calculations.

This system was designed to be stable in the four months in between full runs, so a change to such rule required substantial development and checking.

This change was implemented in in the November monthly evaluation and will be performed on a monthly basis.

Update to blend weights in multi-breed evaluations for animals with phenotypic information

By Ezequiel Nicolazzi and Paul VanRaden

The genomic PTA is a blending of three components: the traditional PTA, a component provided by non-genotyped animals in the pedigree of the animal, and the genomic DGV. The weights used to blend these three components depend on a number of factors; the primary factor is the reliability of each of the three sources of data, with adjustments by breed and trait.

It recently came to our attention that a change in an unrelated part of the crossbred procedure caused an unexpected behavior in such animals. The intended policy for multi-breed animals was to give more weight to the traditional PTA for animals with available phenotypic information. On the contrary, crossbred bulls with high reliability (excluded from the reference population) were receiving too much weight on the DGV component. We have now restored the intended policy for all animals, resolving the incorrect weighting assignment on DGVs.

Since change is introduced to resolve an unintended behavior of an established policy, its implementation will be in the upcoming November evaluation.

In a test run using August 2020 data, nearly 5% of the animals receiving multi-breed genomic evaluations were affected (~5000 of the over 111,000) animals. The amount of the change for these animals depends on several factors (BBR, reliability of traditional PTA, difference between traditional PTA and DGV), so it's not possible to provide generalized statistics. We observed a wide range of cases, from nearly 0 variation to large variations (both positive and negative). For example, the change on the animal that triggered this investigation was a large (positive) variation on all traits, which are now – as originally intended – much more similar to its traditional PTAs.

BBR stability update

By George Wiggans and Ezequiel Nicolazzi

During our routine checks of the August evaluation, we identified four Ayrshire animals that had a genomic evaluation in both the purebred and the crossbred folders. This situation was caused by these animals receiving a Breed Base Representation (BBR) <90 when in the purebred folder and >90 when in the crossbred

folder. Since the difference was higher than 4%, their BBR got alternatively updated every month. After investigating this in all breeds in the last five evaluations, we identified only other two animals (one Holstein and one Jersey) with a similar situation. In those two cases, there was not enough change to allow the recursive “switch” between purebred and crossbred classification.

To avoid this situation, CDCB implemented in September a slight modification in the procedure for BBR. Other than a minor change in the timing in which BBR is calculated, a lower threshold (85%) is needed to allow an animal to switch between the purebred to the multi-breed group.

Updates in the genetic correlations used in evaluations

By Sajjad Toghiani and Paul VanRaden

For the December 2020 run, correlations have been recalculated and updated with a more recent population which included Holstein bulls born since 2010 with at least 85% reliabilities for yield and productive life. Genomic correlations are used to compute reliability of NM\$ and to indirectly estimate all-breed EBVs and reliabilities for fertility, productive life and gestation length, when not available for certain animals. The update of the genetic correlations on traits affects NM\$ for these animals, since all the above traits are included in the merit formulas.

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