Council on Dairy Cattle Breeding

One Town Center, 4201 Northview Drive, Suite 302, Bowie, MD 20716 | Ph: 301 712 9339

Changes to CDCB evaluation system (August 2021)

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New Lifetime Net Merit (NM$) including 3 new traits

By Paul VanRaden, John Cole, Mahesh Neupane, Sajjad Toghiani, Kristen Gaddis, and Rob Tempelman

The new Lifetime Net Merit (NM$) including Feed Saved (FSAV), Heifer Livability (HLIV) and Early First Calving (EFC), along with a number of new parameters and assumptions, will be introduced in the August 2021 evaluation. Residual Feed Intake (RFI) will be displayed directly, rather than FSAV which combines RFI and Body Weight Composite (BWC).

A large communication campaign has been in place since the CDCB Board of Directors approved its implementation. Resources include:

- Main document including all technical details (AGIL)

- Net Merit 2021 FAQ document
- Videos
  - Net Merit 2021: Tom Lawlor (HAUSA)
  - Net Merit 2021, the producer perspective: Lloyd Holterman
- Webinar recordings
  - Including more information on Feed Saved and Residual Feed Intake
- June 2021 webinar slides
- *Hoard's Dairyman* article, "More feed efficient cows are on the way," June 2021
- *Dairy Business* article, " LNM revised in August for balanced selection, profitable dairy cows," July 2021

New SNP set and SNP-by-chip quality revision

By Dan Null, Paul VanRaden, and Ezequiel Nicolazzi

In August 2021, the genomic predictions will be based on 78,964 SNPs. The previously used list of 79,060 SNPs was slightly reduced by removing poor quality or incorrectly mapped SNPs. Also, the SNP list on chromosome 6 was revised to better track the Jersey Neuropathy with Splayed Forelimbs (JNS) defect and reserve a SNP to accept gene tests for JNS if provided.

CDCB deploys a robust QC process with genomic nominators and the laboratories that provide genotypes. Genotypes from each new chip are inspected before first use, and reports are provided back to laboratories with each new batch of genotypes received. There is also a need for a routine comprehensive QC re-check on each chip and across all chips as more data accumulates. Until May 2021, SNP-by-chip quality revision was done when revising the evaluation SNP lists. Since the last SNP list revision (2018), 12 new chips and about 2 million genotypes were added to the database. Considering the large yearly increase of genotypes, moving forward, an annual re-inspection of all data is planned.

These edits will improve the imputation accuracy and therefore the genomic predictions of recent animals. The QC process checks genotype conflicts between parents and progeny separately in the 5 breeds, merges the results, and then indicates which SNPs have high error or missing rates on individual chips. Those SNPs are set to unusable on a chip basis or the entire SNP is set to unusable if the SNP is unusable on most chips. Other SNPs that were previously not used are set to usable if their properties improved above the edit limits. Several of the 12 most recent chips have >1,000 of their 25,000 to 60,000 currently used SNPs set to unusable in the QC update.

Discontinuation of long-range haplotyping

By Ezequiel Nicolazzi, Rodrigo Mota, Gerald Jansen and Paul VanRaden

In conjunction with the new SNP set, starting in August 2021, imputation processing will not be performed over long-range haplotypes. Research on imputation demonstrated that using medium- and short-range haplotypes on all breeds has only a 0.3% average maximum reduction of filling rate, whereas greatly reducing memory and processing usage. Tests performed on the combination of the new SNP set and new imputation parameters had negligible impact on most animals.

Animals genotyped with the old 3k SNP chip – especially crossbred animals – showed relatively larger variation than the rest of the population depending on availability of close relatives' genotypes, pedigree closeness with U.S. population and other factors.

Changes in genomic evaluation parameters

By Rodrigo Mota and Paul VanRaden

Four main changes to the parameters used to obtain genomic evaluations will be introduced in the upcoming August 2021 evaluation:

1. **Minimum reliability to consider non-genotyped parents' contribution to final EBV**: Variations in evaluations of animals with partial or completely missing pedigrees were observed in relation to changes in Unknown Parent Group (UPG) or pedigree of ancestors. Small changes in reliability caused large evaluation changes for these animals, especially in Guernsey. A solution was found by adding extra information – only if non-genotyped ancestors add more than 1% reliability compared to the reliability from genotyped ancestors. **Nearly negligible impact is expected in Holstein and Jersey. For Brown Swiss and Guernsey, some variation was observed on animals with low traditional reliability and disconnected pedigrees; however, these evaluations should be more stable moving forward.**
2. **Increase of weights for direct genomic values (DGV) in Holstein for yield and type traits:** A new validation method demonstrated the benefits of applying more weight on the DGV rather than the traditional parent average when blending genomic evaluations. For Holsteins, the genomic/traditional components weighting rates since 2013 were 85/15% and 80/20% for yield and type traits, respectively. Effective with the August 2021 evaluation, the ratio will be changed to 90/10% for both traits. To limit the increase in reliability values, as genomic evaluations are generally more reliable than traditional, the daughter equivalent discounts parameters included were reduced. **As a result, individual reliabilities will only increase slightly. Bulls with high traditional reliability will not be affected by this change. As traditional reliability decreases, the higher genomic component weighting will have an effect on the final PTAs. Further background on this change was presented at the ICAR/Interbull 2021 conference.**
3. **Increase in female reliability weighting:** Ten years ago, female genotyping was restricted to a small group of elite cows. To reduce the bias of that pre-selection, female contribution to prediction accuracy was reduced to 70% of their calculated reliability since 2013. In recent years, female genotyping has been more broadly adopted, so the pre-selection assumptions do not hold anymore. Therefore, effective with the August 2021 evaluations, female contribution will be considered 100%. **The impact on evaluations is expected to be fairly small, practically null for most animals in larger breeds. The biggest impact was for a few Holstein foreign females and for females without pedigree born around 2010, possibly due to parent grouping differences. Bull PTAs and reliabilities were not affected, except for some very old Ayrshire and Guernsey bulls that are now inactive and less important than current sires.**
4. **Reduction in SNP variance for RFI in Holstein:** A reduction of the parameter used to quantify the distribution of SNPs with large effects in the BayesA genomic model will be implemented in August 2021. This change was introduced because the low number of phenotypes available for RFI can result in the model artificially identifying regions in the genome associated with large RFI effects. The current value makes the model used for RFI closer to GBLUP (in which no marker is assigned a large effect). Tests with this parameter show PTAs with high correlations and constant means and standard deviations.

Faster heterosis calculation

By Gerald Jansen

The number of crossbred animals in the CDCB cooperator database is growing rapidly, and the time for computing heterosis has grown dramatically in recent years. Furthermore, considering the different timing for heterosis and inbreeding calculations during the run, there is currently minor misalignment between the pedigree info used to compute both.

In August 2021, CDCB will implement a new program to speed up the computation of heterosis and integrate heterosis and inbreeding calculations. **The new calculation will not impact the heterosis values on most animals (99.7% identical values considering all evaluated animals), but will affect ~ 4% of animals with non-0 heterosis values. Therefore, this change is expected to impact the heterosis regressions used to correct multi-breed PTAs.**

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Council on Dairy Cattle Breeding - MARYLA

One Town Center
4201 Northview Drive, Suite 302, Bowie, MD
Ph: 240 334 4164 | Fax: 614 861 8040

Council on Dairy Cattle Breeding (Accounti

6486 E Main Street, Reynoldsburg, OH 43068
Ph: 614 861 3636 | Fax: 614 861 8040

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