

CDCB changes to evaluation system (December 2021)

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Changes to CDCB Evaluation System (December 2021)

Feed intake variance adjustments and parameters

By *Paul VanRaden, Sajjad Toghiani and Kristen Gaddis*

Genetic evaluations for Residual Feed Intake (RFI) were improved using variance adjustments and a higher estimated heritability. The RFI records are now adjusted to have equal variance across herds and across first versus later parities. New estimates of 19% heritability and 38% repeatability across parities from 7,708 records from U.S. feed intake trials will replace previous estimates of 14% heritability and 26% repeatability from 4,823 lactations. The higher estimates indicate better properties of recent data and improved heritability after adjusting for herd variance. The higher heritability increased the reliability of pedigree evaluations for RFI from 26.8% to 30.6% for sires that had at least 10% reliability. A further increase to 32.0% reliability resulted from including 998 new RFI records. The combined effects of higher heritability and more records increased the PTA Standard Deviation by 9%. The correlation of RFI PTAs before and after

the new adjustments and parameters was 0.96. The correlation before and after adding records was 0.95 and was 0.90 with all changes combined. Changes in Feed Saved will be much less apparent than for RFI because the Body Weight Composite PTAs are very stable. Thousands of records from several additional countries may be added in April 2022 that could benefit even more from these adjustments.

Exclusion of 3k animals without genotyped progeny

By George Wiggans, Lillian Bacheller, Jay Megonigal Jr., Ezequiel L. Nicolazzi and Jose Carrillo

A total of 59,917 animals are genotyped exclusively with the Illumina Bovine3K BeadChip. Since the beginning of its implementation, this chip was known for its mapping and genotyping quality issues (reference). In recent years, this chip has shown much larger imputation variability with every SNP list or SNP QC event, resulting in variability of evaluation results (reference). Over 22,000 of such animals have genotyped progeny, which provides a better imputation accuracy and stability. In July 2021, the CDCB Board of Directors approved a motion, effective with the December 2021 evaluation, to discontinue evaluations for the subset of over 37,000 animals that do not have genotyped progeny. Duplicate 3k genotypes for animals with progeny will also be withdrawn. Nearly all withdrawn animals were born prior to 2011. No impact is expected on the overall genomic evaluation estimates, as only a marginal percentage (maximum < 0.02%) of the reference populations on any breed/trait group will be affected.

Exclusion of animals with conflicting pedigree vs. genomic breed composition

By George Wiggans, Lillian Bacheller, Ezequiel Nicolazzi and Jose Carrillo

Beginning with the November 2021 genomic evaluation, animals with Breed Base Representation (BBR) high enough to be included in the reference population (BBR \geq 94) are excluded if the breeds of the parents do not match the animal's breed. This exclusion was imposed because differing breeds generated high estimates of heterosis that are inappropriate for animals in the purebred reference population. These animals will not receive an evaluation until the breed conflicts are resolved. Animals with unknown or "XX" as breed code are not among those considered as conflicts. CDCB staff communicated with the responsible nominators about the >3,000 animals with such conflicts, to resolve as many as possible prior to the November implementation of this exclusion protocol. Nominators will continue to receive communications should new cases arise. Investigation continues on ways to better align heterosis with BBR.

Haplotype calls for Ayrshire Curly Calf syndrome – publication plans and format changes

By Daniel Null, Jay Megonigal Jr., Ezequiel Nicolazzi and Paul VanRaden

In August, the CDCB Board of Directors, upon recommendation from the Ayrshire Breeders Association and the NAAB Inherited Biochemical Defects Committee, approved the publication of the haplotype calls for the genetic recessive Arthrogyrosis Multiplex (AM), commonly known as Curly Calf Syndrome (AHC). In September, CDCB released a full list of carriers, and since October has included AHC in its genomic evaluation format. The December 2021 evaluation will be the first triannual evaluation including AHC. This condition has been linked back to the elite progeny-proven Swedish Red sire Peterslund (SRSWE000120911098, among other 16 cross-referenced IDs). AGIL researchers, in collaboration with the Ayrshire breed association and Canadian scientists, recently developed a methodology to call carriers for this condition using haplotype information. For more information related to the affected genomic evaluation format please visit our [online format documentation](#).

New processing of verified Interbull pedigrees

By Gerald Jansen, Jay Megonigal Jr and Ezequiel Nicolazzi

After the December 2021 evaluation, a new set of rules will be implemented to process verified pedigrees coming from Interbull. In a test run based on the August 2021 evaluation, nearly 45,000 animals had at least one change in ID, sire, dam, date of birth or name. The new rules are set to improve the acceptance of such verified pedigrees in the CDCB database. Since these rules may affect genotyped animals, which means re-processing of genotypes, this first implementation of the new rules will not be made during the evaluation. Implementation will occur in steps of about 5,000 animals at a time, right after the triannual evaluation is completed. In April 2022, the processing will occur as usual during the evaluation, likely affecting a much lower number of animals. Most of the existing rules to include only internationally-verified pedigrees and exclude animals with ID country codes of USA/840/CAN will be maintained. The main addition to the processing is the inclusion only of animals where animal, sire and dam has international source code (avoiding modifications to pedigrees managed by CDCB nominators or breed associations). Other changes to make acceptance of the incoming pedigrees more likely have also been implemented.

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