

2013 Annual Report on Cooperation on the Genetic Evaluation System (GES) Under Nonfunded Cooperative Agreement (NFCA) 8042-31000-101-07 Between the Agricultural Research Service (ARS), U.S. Department of Agriculture (USDA) and the Council on Dairy Cattle Breeding (CDCB)

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Introduction

Pursuant to Section 4.6 of the ARS-CDCB NFCA, the following report summarizes cooperation between ARS and CDCB in maintaining and improving the GES for dairy cattle from December 31, 2012, through December 30, 2013. Information on use and validation of CDCB data by the International Bull Evaluation Center (Interbull, Uppsala, Sweden), explanations of significant GES changes, and priority issues for investigation are included.

During 2013, CDCB was restructured to assume the service responsibilities of managing the national dairy database and the highly visible function of calculating and distributing the genetic evaluations for U.S. dairy cattle. On March 27, 2013, an NFCA between ARS and CDCB was signed and started the transfer of those responsibilities from ARS to CDCB. The CDCB gradually assumed responsibility for calculation, inspection, and distribution of evaluations as well response to questions from the field. The CDCB declared December 17, 2013, as the effective date for the NFCA (Section 1.16); i.e., the date that CDCB was able to manage the national database and calculate genetic/genomic evaluations.

CDCB Interim Staff

Two independent contractors were hired by CDCB in February 2013. The interim administrator and interim technical applications manager have carried out the transfer of service responsibilities from ARS to CDCB.

CDCB Fee

The CDCB is financed by a fee per genotyped animal. A substantial effort was required to integrate the fee information into the GES. The nomination process was modified to accept the fee information. The program that updates the genotype table was modified to store and update the fee information. The extract program was modified to access fee information in

determining which genotypes to use. Queries were added or modified to display fee information and provide reports to assist nominators in managing the information. A system to validate fees and prepare invoices was developed so that nominators can be billed by the CDCB Treasurer.

Interbull

- U.S. genomic evaluations were sent to Interbull for April and December 2013 genomic multitrait across-country evaluations (GMACE) but not for August (following the decisions of CDCB). Files were also sent for Interbull test runs in January and September 2013. Genomic validation was applied to all traits of Holsteins in January 2013, and nearly all passed except stillbirth. Resulting GMACE files from Interbull were combined across traits to compute net merit and were distributed by CDCB to artificial-insemination organizations and breed associations but were not made public. In April and December 2013, those files included only foreign bulls without official U.S. genomic evaluations, whereas the August 2013 file also included U.S. bulls with GMACE computed using only foreign genomic evaluations but not U.S. genomic evaluations.
- Multitrait across-country evaluations (MACE) were received a week earlier in August 2013, which allowed use of current instead of 4-month old MACE to compute marker effects. Parent averages for young bulls are now calculated using genomic instead of traditional evaluations of parents. With additional processing, parent averages for young bulls and genotyped females are recalculated to include both the latest available foreign and genomic information.
- The new multitrait, multibreed evaluations of heifer and cow conception rates were sent for Interbull's September 2013 test evaluation, and both traits passed the genetic trend validation tests. Scandinavian Red bulls were accidentally excluded from the test files sent to Interbull because all of their daughters were crossbreds; Scandinavian Red cattle will be included in 2014.

GES Changes

(details available at <https://www.cdcb.us/News/News.htm>)

- Genomic evaluations included genotypes from a new genotyping chip with almost 77,000 markers. Two new genotyping chips from Zoetis and one from Europe were introduced.
- The number of markers used in computing genomic predictions was increased to 61,013 from the 45,195 used previously. For Holsteins, the average gain in reliability across all traits was 0.5 percentage points using the additional markers.

- The first genomic evaluations for Ayrshires were computed and released.
- Weights to combine direct genomic values with traditional parent averages were reduced for Holsteins so that declines over time in average predictions of young bulls with highest genomic evaluations would be eliminated.
- The weighting factors to include cow records in genomic evaluations and the deregression methods to obtain pseudo-records from traditional predicted transmitting abilities were both revised to improve the accuracy of predictions.
- Traditional service-sire calving-ease and service-sire stillbirth evaluations of young bulls were included in estimating marker effects because now they obtain many calving records early in life.
- Evaluations for heifer and cow conception rates were calculated using multitrait, multibreed procedures, which replaced the previous single-trait, single-breed method; this change benefits fertility traits because genetic correlations are high and many observations are missing.
- Four new haplotypes that affect fertility (HH4, HH5, BH2, and AH1) were discovered for the Holstein, Brown Swiss, and Ayrshire breeds. Exact tests for loss-of-function mutations within Jersey haplotype JH1 and Holstein haplotype HH3 were used to improve determination of heterozygous (carrier) status for genotyped animals and provided in place of less reliable information obtained earlier from haplotypes. Haplotype tests for bovine leukocyte adhesion deficiency (BLAD), complex vertebral malformation (CVM), deficiency of uridine monophosphate synthase (DUMPS), mulefoot, Weaver, spinal dysmyelination (SDM), spinal muscular atrophy (SMA), red hair color, and polledness were developed and reported (HHB, HHC, HHD, HHM, BHW, BHD, BHM, HHR, and HHP, respectively). A Jersey haplotype for polledness (JHP) was introduced.

Priority Issues for Investigation

- Evaluate information on additional traits when it becomes available to see if it is suitable for genetic evaluation.
- Obtain access to genotypes from other countries and assess their contributions to the U.S. predictor population and to obtain the most accurate rankings of foreign young bulls on the U.S. scale.

- Work with genotyping laboratories to improve the utility of genotyping chips primarily by adding informative markers for genetic defects or that are causative genetic variants affecting traits of interest.
- Improve access to the CDCB database for university researchers.
- Develop and implement new software to simplify model changes and facilitate multitrait analysis.
- Monitor the effects of genomic preselection as a source of bias in genetic evaluations.
- Update the net merit indexes and add a grazing index.