

**2014 Annual Report on Cooperation on the Genetic Evaluation System (GES)
Under the 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, 2013, through December 30, 2014. Information on use and validation of CDCB data by the International Bull Evaluation Center (Interbull, Uppsala, Sweden), explanations of significant GES changes, current research projects, and priority issues for investigation are included.

Effective April 8, 2014, the Animal Improvement Programs Laboratory was merged with the Bovine Functional Genomics Laboratory forming the Animal Genomics and Improvement Laboratory. Dr. George Wiggans continued as the liaison between ARS and CDCB.

CDCB activities

- Dr. João Dürr began as the CDCB's permanent CEO in October 2014 and began recruitment of a technical director and a systems administrator; two independent contractors (Dr. Duane Norman and Mr. Leigh Walton) continued to serve during 2014.
- A Research Advisory Working Group was established to provide technical review on issues related to the GES and promote research in priority areas.
- An open meeting was held in August 2014 in Linthicum Heights, MD; speakers included Drs. Ole Meland, João Dürr, and Erin Connor followed by research reports from Drs. John Cole, Derek Bickhart, Paul VanRaden, George Wiggans, Chuanyu Sun, Tad Sonstegard, and Robert Fourdraine and Ms. Tabatha Cooper and an open question-and-answer session with the CDCB Executive Committee.
- A change in the fee schedule for genotyped animals was implemented so that partners do not have to pay an initial fee for foreign bulls; this enabled them to resume receiving U.S. genomic evaluations for their young bulls.
- A new file with predicted genomic inbreeding values for each female with each marketed male has been made available for use by CDCB members and approved genomic nominators after the August, December, and April full genomic evaluation releases. Monthly updates are provided for females not previously genotyped, and each breed has a separate file. Mating programs that use genomic instead of pedigree inbreeding are expected to improve economic merit by \$30 per calf.

- To facilitate identification of the Dairy Herd Information (DHI) herd for fee determination, a query was developed to provide herd information for the animal and its dam; to allow breed associations to use information that they have on animal location, they are allowed to specify why the herd information they provide differs from DHI herd information.
- To assist in tracking nominator performance, a summary table of quality metric information now is generated.
- A conference call was held with nominators to discuss how the management of information related to genomics could be improved; improvements in the way that the herd code is chosen for fee determination were discussed.
- The CDCB sponsored the seminar “Why We Are Genomic Testing” during World Dairy Expo in Madison, WI, and also held a press conference to announce changes for the December 2014 evaluation as well as weekly genomic preliminary predictions.
- Payment for data flow (records in progress, calving ease and stillbirth records, and breeding records) that was previously done by the National Association of Animal Breeders was assumed by CDCB in December 2014; a database table was created to capture counts as data are loaded.
- Educational materials on the genetic base change and merit index updates were prepared.
- A proposal from the American Dairy Goat Association (ADGA) to transfer the service portion of genetic evaluations and distribution of results from ARS to ADGA was approved; data will continue to be stored on the CDCB server, and CDCB staff will offer limited technical support.

Interbull interactions

- Interbull distributed genotypes of more than 5,000 young Brown Swiss bulls in addition to those exchanged since August 2012 for older bulls with daughter evaluations; the nominator for the resulting genomic evaluations for the young bulls is Interbull, and the Brown Swiss evaluations should be labeled as a product of Inter-genomics, which provides the exchange service.
- An Interbull test run that included evaluations from new U.S. multitrait software showed little change in genetic correlations between U.S. and other country’s evaluations, which indicated little change in international rankings from implementation of the new software.
- The CDCB board proposed contributing U.S. genomic evaluations for young bulls to the January 2014 Interbull genomic evaluation test under the condition that two comparison tests (one with U.S. data and one without) were performed in an effort to ensure that Interbull results are accurate regardless of whether a major country’s data (such as the United States) are included or excluded; the proposal was not accepted by Interbull because of lack of resources, and U.S. evaluations were not submitted for genomic multitrait across-country evaluation (GMACE).

- Following a CDCB board request, Interbull developed a system of reporting country of control so that a GMACE evaluation is now distributed only if the controller chooses to participate; therefore, evaluations for U.S. bulls submitted by foreign CDCB genotype collaborators (Canada, the United Kingdom, and Italy) can provide information without the release of U.S. GMACE evaluations. If the owner wishes to have a GMACE evaluation released, another country can be reported as the controller.
- A system for managing and reporting bulls under U.S. control was developed because GMACE results for all participating foreign bulls are made available on each country's scale as required by Interbull beginning in August 2014.

GES changes

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

- Evaluation of daughter pregnancy rate (DPR) was changed from a single-trait evaluation based on a linear approximation from days open to a multitrait evaluation with a heritability of 1.4% per 21 days; evaluations and definitions of DPR and conception rate are now more similar, which adds stability to multitrait evaluations.
- Genetic bases for all traits were updated by 5 years.
- Economic values in the net merit, cheese merit, and fluid merit indexes were updated, and a grazing merit index was introduced to rank animals on economic merit in grazing herds.
- Flexible software was introduced to allow more efficient model changes and multitrait processing of genetic evaluations.
- The discovery of maternal grandsires (MGSs) was improved by increasing the threshold for conflicts by 3 percentage points and reducing the minimum age of an MGS at the animal's birth to 1,150 days; accuracy of MGS discovery increased by 5.5 percentage points in a test set.
- A web application was developed to make 116 parentage single-nucleotide polymorphisms (SNPs) available to approved nominators and genotyping laboratories for verification of calf identity.
- Recently received or pedigree-corrected genotypes now are processed each week to generate approximate genomic evaluations for new animals, and to minimize processing time, reliabilities are not provided; the increased frequency of the evaluations provides an incentive for smoothing genotype submission workloads as well as allows earlier sale or culling of animals (or embryos) not needed for breeding purposes.
- Genotypes for progeny-tested Danish Jersey bulls were added to the predictor population for monthly genomic evaluations to increase accuracy of estimated SNP effects.

- Genotypes from the slightly revised Illumina low-density genotyping chip (LD2), from version 3 of the GeneSeek Genomic Profiler, and from version 2 of the Zoetis low-density genotyping chip are included in evaluations.
- Genomic future inbreeding (GFI) for Holsteins is now calculated as the average genomic relationship of each animal to proven bulls born in the last 10 years (and no longer includes cows with records) to reduce computation time, which had become excessive.
- Files with genomic relationships of each genotyped female with each marketed male now are provided to industry cooperators for use in genomic mating programs.
- Several tests for simply inherited genetic conditions that are on GeneSeek chips (but were not previously provided) now are provided to CDCB.
- A second haplotype that affects fertility in Jerseys (JH2) was discovered from CDCB data; embryos are lost by 60 days after insemination.
- Two new haplotype tests that track dominant red (HDR) and black/red (HBR) are now reported along with the recessive red haplotype test (HHR) reported since August 2013.

Current projects

- Investigate the benefit of extending genomic evaluation to Guernseys.
- Discover causative genetic variants using a growing collection of full-sequence data.
- Improve the accuracy of locations of SNPs in the genome by updating the chromosome map.

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 so that the most accurate rankings of foreign young bulls on the U.S. scale can be determined.
- Work with genotyping laboratories to improve the utility of genotyping chips primarily by adding informative markers for genetic defects and causative genetic variants that affect traits of interest.
- Define a CDCB data-accessibility policy for university researchers.
- Monitor the effects of genomic preselection as a source of bias in genetic evaluations.