

**2016 Annual Report on Cooperation on the Genetic Evaluation System (GES)
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the Agricultural Research Service (ARS), U.S. Department of Agriculture (USDA)
and the Council on Dairy Cattle Breeding (CDCB)**

*Prepared by Dr. João Dürr, Chief Executive Officer (CEO), CDCB, and Dr. Paul M. VanRaden (ARS liaison),
Research Geneticist, Animal Genomics and Improvement Laboratory (AGIL), ARS, USDA; April 10, 2017*

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, 2015, through December 30, 2016. 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.

Data collection and evaluation activities

- Upon completion of the transition of services from USDA to CDCB in December 2015, CDCB is now solely responsible for the cooperator database and estimates of genetic merit released in the United States. All predictions of genetic and genomic evaluations calculated and made available by CDCB must now be labeled as CDCB estimates rather than USDA/CDCB estimates.
- The release schedule continues to deliver preliminary genomic evaluations weekly, official genomic evaluations of new animals monthly, and official genetic evaluations of all animals three times per year. The CDCB and AGIL computers are synchronized daily for evaluation programs and weekly for pedigrees, phenotypes, and genotypes, which allows both groups easy access to the same data. A new working group structure for advisory support was established in May 2016. In addition to the two existing standing committees (Executive and Finance), four working groups (research advice, genetic evaluation methods, dairy data development, and evaluation review) and three task forces will be created. In December 2016, Dr. Duane Norman was designated to coordinate the working groups, and the Dairy Evaluation Review Team, Pursuing Data Quality Team, and Genomic Laboratory Guidelines Task Force will start their activities in 2017.
- The data-acquisition service fee schedule proposed by the Data Flow Working Group was adopted by the CDCB Board of Directors in February 2016. The aim is remunerate phenotypic data suppliers for additional services associated with preparation of data for the cooperator database.
- A full-day training session on rules and procedures for CDCB genomic nomination was offered in April 2016. Representatives from the American Guernsey Association, American Milking Shorthorn Association, Brown Swiss Cattle Breeders' Association, and U.S. Ayrshire Breeders' Association, and the Idaho Dairy Herd Information Association (DHIA) participated.

- The Board of Directors submitted a list of suggested research priorities to ARS in May 2016 that were incorporated into a 5-year ARS research plan submitted by AGIL for review of the Animal Improvement Program (AIP) project in November 2016. Research suggestions were proposed in 4 general areas: health and functional traits, bovine sequencing data, management of profitability of herds, and genetic evaluation methods. The 5-year plan objectives are: 1) expand genomic data used in prediction by selecting new variants that more precisely track the true gene mutations that cause phenotypic differences, 2) evaluate several new traits that can all be predicted at birth from the same inexpensive DNA sample, and 3) improve efficiency of genomic prediction and computation by developing faster algorithms, testing new adjustments and models, and accounting for genomic pre-selection in evaluation.
- A summer internship program was initiated in 2016. Ms. Amber Gabel, a BS/MS candidate at Pennsylvania State University and advised by Dr. Chad Dechow, was selected as the first CDCB intern. She was supervised by Dr. Duane Norman and collaborated with CDCB and AGIL staff on improved evaluation of fertility traits.
- An industry meeting with almost 130 participants was held in October 2016 in Middleton, WI, in association with World Dairy Expo activities. The program covered three main sections, including progress reports from CDCB, AGIL, and the Interbull Steering Committee as well as two panels (“A Taste of the Future” and “How CDCB Benefits Dairy Producers”).
- National benchmarks on behalf of the National Dairy Herd Information (DHI) Association continued by publishing annual statistics on DHI participation, State and national standardized lactation averages by breed for cows on official test, herd averages, dairy records processing center activity, somatic cell counts for DHI herds, reasons that DHI cows exit the herd, and reproductive status of DHI cows.
- Scientists in the AIP project within AGIL authored or coauthored 17 peer-reviewed journal articles during 2016 as well as 4 papers in conference proceedings papers and 22 abstracts of presentations. Most of these publications included an analysis of CDCB data and were reviewed by CDCB prior to submission, or new sources of data and methods that could contribute to CDCB evaluations in the future were investigated. Several reports were coauthored by both AGIL and CDCB staff.

Interbull interactions

- Genetic evaluations and pedigrees from the United States as well as Brown Swiss genotypes continue to be sent three times per year to the Interbull Centre (Uppsala, Sweden), and the resulting merged international data sets are then incorporated into U.S. official evaluations. Members of the CDCB and AGIL staff attended the annual meetings of Interbull and the International Committee on Animal Recording, which were held jointly in October 2016 in Chile; three papers were presented. Dr. Paul VanRaden also participated in meetings of the Interbull Technical Committee and the Genomic Reliability Working Group.
- The U.S. Brown Swiss genomic evaluations passed validation for all traits in October 2016.

GES changes

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

- Genomic reliability, genomic inbreeding, and genomic future inbreeding were provided for weekly evaluations beginning in January 2016.
- Genotype exchanges with Switzerland (February 2016) and Japan (May 2016) resulted in the addition of 1,537 Swiss Holstein and Red Holstein and 3,000 Japanese Holstein bulls to the North American reference population. After the exchanges, the Holstein reference population has increased to 34,016 bulls plus 232,919 cows.
- Genomic evaluations were implemented for Guernseys in April 2016. Genotypes from 2,376 Guernsey bulls and cows from collaboration between the United States, Canada, the United Kingdom, and the Isle of Guernsey were the basis for launching the U.S. genomic evaluation of Guernsey cattle.
- Breed base representation (BBR) was implemented in April 2016 for crossbreds based on the percentage of DNA contributed to the animal by each of 5 evaluated breeds (Holstein, Jersey, Brown Swiss, Ayrshire, and Guernsey). The BBRs provide information about breed composition that is more accurate than breed-check marker. Their use will provide a means for making genetic predictions for crossbreds possible.
- Haplotype tests were improved by using the exact location of the mutations for Holstein cholesterol deficiency (April 2016), Brown Swiss BH2 (April 2016), and Holstein HH5 (August 2016). Direct test results for these mutations could be included in the future to further improve accuracy as is done with several other recessive haplotypes.
- Age limits and age groups were updated in April 2016 to include heifer conception rate (HCR) records for younger animals. New edit limits include heifers inseminated at 8 months of age and older, and another age group was added in HCR for records from the youngest animals. About 297,231 records were added for HCR, which is about 3% of total records. Use of records from these younger animals should improve timeliness and reliability of HCR evaluations.
- New factors to adjust for reduced fertility of sexed semen were implemented in April 2016 for heifer and cow conception rates. Differences were smaller for cows than for heifers because conception rates are lower and affect fewer records because of less use of sexed semen for cows.
- Genomic edits for HCR were revised in June 2016 to improve genomic predictions for breeds with small reference populations (such as Ayrshires and Guernseys).
- Cow livability evaluations were implemented in August 2016 for all breeds. Livability measures a cow's ability to stay alive while on the farm, in contrast to productive life, which measures a cow's ability to avoid either dying on the farm or being culled. Incorporation of cow livability into the net merit indexes was scheduled for 2017.

- The size of genomic mating files was reduced in August 2016 by revising the format and excluding cows that were likely to be dead. This edit removed only about 20% of U.S. cows from the file, but will limit file sizes much more in the future as more genotyped females become older and leave their herds.
- Routine monthly exchange of genotypes of all new young genomic artificial-insemination bulls was implemented between North American and Germany in August 2016. The initial exchange included bulls 2,054 bulls from Cooperative Dairy DNA Repository members and 484 bulls from the German associations.
- Revised evaluation software was implemented in December 2016 for linear type traits and final score of Jerseys, Brown Swiss, Ayrshires, Guernseys, and Milking Shorthorns as well as Brown Swiss milking speed and mobility. All traits are solved together instead of performing separate analyses for traits introduced more recently.
- Rear and side views of rear teat placement were added as new conformation traits for Jerseys in December 2016. Heritabilities were estimated to be 21% for rear view and 13% for side view.
- Variance adjustments for cow livability evaluations were revised to include different heritabilities by parity. The new lower estimates of lactation-specific heritability were introduced in December 2016.

Current projects

- Develop a new DNA biobank to support discovery of new recessive genetic disorders in U.S. dairy cattle.
- Develop and implement sire conception rate evaluations for beef service sires bred to dairy cattle.
- Develop and implement genetic evaluations for gestation length as a trait of the service sire.
- Develop and implement genetic evaluations for feed efficiency as measured by residual feed intake.
- Develop and implement genomic predictions for crossbreds from all-breed data.
- Develop and implement genomic evaluations for direct measures of health events.
- Discover causative genetic variants using a growing collection of full-sequence data.
- Implement genomic evaluations based on approximately 77,000 markers (an increase from 61,013).
- Improve the accuracy of locations of SNPs in the genome by updating the chromosome map.

Priority issues for investigation (incorporated into the AIP 5-year research plan)

- Expand genomic data used in prediction by selecting new variants that more precisely track true gene mutations that cause phenotypic differences:
 - Use of sequence data to identify major genes affecting fertility, health, and production efficiency.
 - Identification of haplotypes and causative mutations associated with deleterious phenotypes.
 - Identification of variation that may lead to novel selection strategies or products.
 - Continued work on SNP identification, copy number variants and other types of structural variation.
 - Cooperation in international research efforts in bovine sequencing.
 - Solutions for read-depth variation associated with sequencing, which has the potential to reduce genotyping costs.
 - Determination of how CRISPR gene-editing technology could influence dairy production and human nutrition.
- Develop genetic evaluations for additional traits, especially those that can be predicted at birth from the same inexpensive DNA sample:
 - Key and novel health traits, especially those related to metabolic, transition, and mobility disorders (e.g., ketosis, metritis, displaced abomasums, hypocalcemia, retained placenta, directly measured mastitis, hairy foot wart, lameness, laminitis, digital dermatitis, calf scours, pneumonia).
 - Management traits (e.g., temperament, milking speed, locomotion score, body condition score).
 - Longevity traits (e.g., cow and calf livability) and incorporation into genetic-economic indexes).
 - Fertility traits (e.g., embryo producing ability).
 - Feed efficiency traits (e.g., energy balance, body fat mobilization, carbon emissions) and interaction with milk composition and body condition score.
- Improve efficiency of genomic prediction and computation by developing faster algorithms, testing new adjustments and models, and accounting for genomic pre-selection in evaluation.
 - Evaluation of methodology used by cooperating and competing countries and organizations to assure validation of U.S. and North American evaluations as well as those from other countries.
 - Imputation of higher density genotypes from less dense genotypes or a broader range of commercial SNP chips.
 - Implementation of one-step methodology or other approaches that are resistant to selection bias.
 - Optimized processing to provide timely genomic predictions without massive time and computing requirements.
 - Development of crossbred genomic evaluations.

- Document regional and management system characteristics that influence indexes and management decisions (e.g., geographic location, housing, milking system, feeding, milking time, calf health).
- Determine disease incidence and economic costs of key traits for genetic and management systems.
- Improve prediction of 24-hour production from single measurements; address interrelationships of milking speed with prediction of 24-hour production, somatic cell count, and milk composition.
- Assess potential and impacts of output from new laboratory technology [e.g., β -hydroxybutyrate (BHB), bovine viral diarrhea (BVD) tests, fatty acid profiles, spectral data].

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