

**2017 Annual and Final 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, 2016, through December 30, 2017 (the agreement termination date). Information on use and validation of CDCB data by the International Bull Evaluation Center (Interbull, Uppsala, Sweden), and explanations of significant GES changes are included as well as highlights of accomplishments for the entire 5-year agreement. A new 5-year material transfer research agreement was established on November 1, 2017, and replaces this NFCA.

Data collection and evaluation activities

- The 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 are labeled as 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 3 times per year. The CDCB and AGIL computers continue to be synchronized daily for evaluation programs and weekly for pedigrees, phenotypes, and genotypes, which allows both groups easy access to the same data.
- Four working groups were established in early 2017 to provide independent, objective, and impartial feedback on CDCB services and AGIL research. The Dairy Evaluation Review Team reviews CDCB triannual dairy genetic evaluation results prior to public (official) release in April, August, and December. The Pursuing Data Quality Team provides advice and strategic guidance on dairy data quality. The Genetic Evaluation Methods Group provides advice and strategic guidance on development of dairy genetic evaluations. The Genomic Laboratory Guidelines Task Force (GENLAB) developed guidelines for quality certification of laboratories that generate genomic data on behalf of genomic nominators.
- Look East PR was selected to support CDCB public relations and promotional activities in May 2017; Amy te Plate-Church is CDCB's key contact. The CDCB Connection was launched in June 2017 to provide timely updates on U.S. dairy genetic evaluations and activities; the newsletter is e-mailed after each monthly genomic evaluation to enhance communications among CDCB members, industry stakeholders, and dairy producers.

- The first annual CDCB Genomic Nominators Workshop was held in May 2017 in Linthicum Heights, MD, to review the genomic nomination process, exchange experiences among genomic nominators, and present new quality certification evaluation procedures. About 25 participants represented artificial-insemination companies, breed associations, genomic laboratories, and the National Dairy Herd Information (DHI) Association.
- Educational presentations on the U.S. dairy genetic evaluation system were given to the GeneSeek Genetic Advancement Committee (Lincoln, NE; May 2017), representatives of the Turkish Ministry of Food, Agriculture, and Livestock (June 2017; Bowie, MD), veterinarians at the University of Liverpool (September 2017; Liverpool, UK), the Breeding for Efficiency – 2017 EDGP Symposium (October 2017, Guelph, ON, Canada), a National Institute of Food and Agriculture’s listening session (November 2017, Greenbelt, MD), and the BAIF International Workshop (November 2017; Pune, India).
- The summer internship program to benefit CDCB, support AGIL research, and expose students to national genetic and management programs continued in 2017. Mr. Isaac Haagen, a Ph.D. candidate in Animal Science at Pennsylvania State University under the guidance of Dr. Chad Dechow, and Ms. Maci Lienemann-Mueller, an M.S. candidate in Animal Science at the University of California–Davis under Dr. Alison Van Eenennaam were selected. Haagen worked on determining the accuracy and effectiveness of multibreed genetic evaluations, and Lienemann-Mueller investigated innovative strategies for managing traits controlled by recessive or dominant genes in dairy cattle.
- New quality certification requirements for genotyping laboratories went into effect in September 2017. The new standards include a proficiency test, ISO certification (or equivalent), a certification fee, and new performance metrics for submitted genotypes.
- An industry meeting with 175 participants was held in October 2017 in Middleton, WI, in association with World Dairy Expo activities. The program focused on the potential to improve cow health further through genetic selection and was headlined by a producer panel on dairy health data and genetic evaluations.
- The CDCB web site infrastructure was completely renewed in October 2017 to improve collaborator’s data security while improving user experience. All users are now required to register to access CDCB queries (including public queries); access is free, and all queries maintain the same functionality. A new system to document and ticket customer service had already been implemented in August 2017.
- National annual benchmarks for Dairy Herd Information (DHI) information continued for participation, standardized lactation averages, herd averages, dairy records processing center activity, somatic cell counts, culling, and reproductive status.
- Scientists in the Animal Improvement Program project within AGIL authored or coauthored 15 peer-reviewed journal articles during 2017 as well as 16 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 were sent to the Interbull Centre (Uppsala, Sweden); resulting merged international data sets were incorporated into U.S. official evaluations.
- Interbull evaluations for rear udder width began to be used for Brown Swiss, which is the only breed with rear udder width evaluations from Interbull, in April 2017.
- All traits passed required genomic and traditional Interbull validation.

GES changes

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

- Cow livability was included in net merit indexes beginning in April 2017 along with a body weight composite (a revision of the body size composite).
- Heterosis adjustments were revised for Montbeliarde and Simmental bulls and crossbred cows in April 2017.
- Computer programs for contribution of cow unknown-parent groups to traditional evaluations for somatic cell score were corrected in April 2017. Unknown-parent group definitions were changed in August 2017 so that groups are merged separately by breed with the next most recent group instead of merged across breeds. New unknown-parent grouping was established in November 2017 for polygenic effects in the genomic model to represent genetic trend more accurately for animals with partially unknown pedigrees.
- Genetic evaluations of males and genomic predictions of both sexes were provided for gestation length as a new trait expressed in days in August 2017; gestation length evaluations show the influence each service sire is expected to have on the number of days his mates carry their calves during their pregnancies.
- The feet/leg composite used in Holstein net merit indexes was modified to include direct evaluations of feet and legs score in August 2017. Definitions of Holstein udder and feet/leg composites and Jersey and Brown Swiss body weight composite were updated in December 2017 to match those introduced by breed associations.
- A new set of edits was introduced in August 2017 for calving ease and stillbirth data to increase accuracy and robustness of phenotypic data entering the evaluation system.
- Computation time for monthly genomic evaluations of Holsteins was reduced in August 2017 based on techniques used for weekly evaluations so that errors could be corrected and distribution deadlines met.

- Animals determined to have an unlikely grandsire began to be excluded from receiving weekly or monthly genomic evaluations if their genotypes were received after October 2017 to improve evaluation accuracy.
- Age groupings for Holstein sire conception rate (SCR) was modified in December 2017 to reflect the increased use of young genomic bulls; this change produces a relationship between age and SCR that resembles more closely a smooth biological curve and produces SCR evaluations that are slightly more accurate.
- Preliminary genetic evaluations for health traits (hypocalcemia, displaced abomasum, ketosis, mastitis, metritis, and retained placenta) were released to nominators, breed associations, and dairy records processing centers for review in December 2017; official health trait evaluations will be released in April 2018.

Accomplishment Highlights

- The CDCB assumed service responsibility for management of the national dairy database and calculation, inspection, and distribution of genetic evaluations for U.S. dairy cattle.
- An annual educational industry meeting was established and is held in conjunction with World Dairy Expo activities; a summer internship program was initiated in 2016.
- National benchmarks on behalf of the National 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.
- Genetic evaluations and pedigrees from the United States as well as Brown Swiss genotypes continue to be sent 3 times per year to the Interbull Centre, and the resulting merged international data sets are then incorporated into U.S. official evaluations.
- The number of genetic markers used in computing genomic predictions was increased to 61,013 in 2013 from the 45,195 used previously.
- Genetic bases for all traits were updated by 5 years in 2014.
- Economic values in the net merit, cheese merit, and fluid merit indexes were updated, and a grazing merit index was introduced in 2014 to rank animals on economic merit in grazing herds
- Weekly genomic evaluations for new animals were begun in 2014 to allow earlier management decisions on sale or culling of animals (or embryos) not needed for breeding purposes. Genomic reliability, genomic inbreeding, and genomic future inbreeding were provided for weekly evaluations beginning in 2016.
- Genomic relationships of each genotyped female with each marketed male began to be provided to industry cooperators in 2014 for use in genomic mating programs.

- The first genomic evaluations for Ayrshires (2014) and Guernseys (2016) were computed and released.
- Breed base representation (BBR) was implemented in 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); BBRs provide more accurate information about breed composition as well as a means for making genetic predictions for crossbreds possible.
- Cow livability evaluations were implemented in 2016 for all breeds to measure a cow's ability to stay alive while on the farm; cow livability was incorporated into net merit indexes in 2017.
- Gestation length evaluations were implemented in 2017 to show the influence of each service sire on how long his mates carry calves.
- Two million genotypes were recorded in the U.S. dairy database in 2017.
- Six new haplotypes that affect fertility (HH4, HH5, JH2, BH2, AH1, and AH2) were discovered for the Holstein, Jersey, Brown Swiss, and Ayrshire breeds; 3 new haplotype tests that track dominant red (HDR) and black/red (HBR) coat color and a lethal recessive for cholesterol deficiency (HCD) also are provided for Holsteins, and a Brown Swiss haplotype for polledness was developed.
- Genetic evaluations for health traits (hypocalcemia, displaced abomasum, ketosis, mastitis, metritis, and retained placenta) were developed for official release in 2018.

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