# 2015 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, 2014, through December 30, 2015. 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.

## CDCB activities

- Five permanent CDCB staff members were hired: a systems administrator (Mr. Dave Ashley, March 2015), a data scientist (Mr. Jay Megonigal, July 2015), a genomic data analyst (Kaori Tokuhisa, July 2015), an administrative assistant (Ms. Kendra Randall, July 2015), and a database administrator (Mr. Marius Temzem, September 2015). Two independent contractors (Dr. Duane Norman, technical advisor and industry liaison, and Mr. Leigh Walton, technical applications manager) continued to serve during 2015.

- A consulting service (Mr. Raymon Bacchus) was engaged in April 2015 to facilitate the initial implementation of the CDCB administrative and human resources infrastructure. The Otsuki Group was hired to facilitate the development process of a strategic business model, which was started in August 2015.

- An office space was established in Bowie, MD, in April 2015. Strategically located between Washington, DC, and Annapolis, MD, the new offices are convenient to the Beltsville Agricultural Research Center, ARS, USDA, and Baltimore/Washington International Thurgood Marshall Airport.

- Investments in internet connectivity, hardware, and software were completed, and the database and genetic evaluation programs were transferred and operational by December 11, 2015. In July 2015, the CDCB database surpassed genotypes for 1 million animals. Predictions of genetic merit are made available to the industry 55 times per year.

- Material license agreements were finalized with all data providers in June 2015 and signed by December 2015.

- A Working Group was established to develop the request for proposals for the administration of a quality certification program for genomic nominators and genotyping laboratories. Quality certification for genomic nominators and laboratories is under review.

- The Data Flow Working Group presented a data-acquisition service fee proposal to remunerate phenotypic data suppliers for additional services associated with editing, storage, and delivery of data to CDCB.

- A joint meeting between representatives of both Boards of Directors was held with the Canadian Dairy Network in Toronto, ON, Canada, in April 2015 to discuss a common agenda and develop further cooperation between countries.

- An industry meeting was held in September 2015 in Middleton, WI, in association with World Dairy Expo activities; more than 130 guests attended, and the program covered 3 main sections, including progress reports from CDCB, AGIL, and the Interbull Steering Committee as well as 2 panels ("Status of Dairy Cattle Breeding Research in the U.S." and "One Million Genotypes: How Genomics Re-Shaped the Dairy Industry").

## Interbull interactions

- The CDCB was the exclusive sponsor of the Interbull/ADSA-ASAS Joint Annual Meeting afternoon symposium (Use of Genomics To Improve Limited and Novel Phenotypes in Animal Breeding) held in July 2015 in Orlando, FL.

- Bulls with breed codes for Montbeliard, Normande, Simmental, and Fleckvieh had evaluations on the Simmental scale in the Interbull multitrait across-county evaluation instead of the Holstein scale in December 2015. As a result, about 7,000 of those foreign bulls were converted onto the U.S. Holstein base.

- Milking Shorthorn evaluations from Interbull for heifer and cow conception rates were adjusted to the correct genetic base.

## GES changes
*(details available at https://www.cdcb.us/News/News.htm)*

- Bulls from organizations not previously participating in sire conception rate phenotypic evaluations began to have their evaluations released in April 2015. Some bulls from organizations not previously participating in calving ease genetic evaluations started to have evaluations released in April 2015 and more in August 2015.

- A Brown Swiss haplotype for polledness was developed for April 2015 evaluations.

- Adjustment of genetic standard deviations for productive life to match Holstein standard deviations was removed for other breeds in April 2015. The precision of adjustments for heterosis and inbreeding of productive life was improved in April 2015.

- Over 50,000 carriers of a lethal Holstein haplotype for cholesterol deficiency were identified in August 2015 evaluations. This newly described defect when homozygous causes calf death at few months of age.

- Genetic standard deviations were reduced for several Jersey conformation traits in December 2015 to correct a problem with herd variance adjustments.

- The automated system to assign unknown-parent groups was revised in December 2015 to improve stability and convergence with data updates. The new group definitions were applied to yield traits, productive life, somatic cell score, daughter pregnancy rate, and heifer and cow conception rates.

- Several edits for variables used in calculating sire conception rate were changed. The edit for difference between expected and actual subsequent calving date was modified to be consistent with the industry definition for estrous cycle. The edit for gestation period was made breed specific. The range for acceptable herd conception rate was reduced. The number of age categories was reduced for Jerseys to make them more closely resemble a smooth biological curve.

## Current projects

- Implement genomic reliability, inbreeding, and future inbreeding for weekly genomic evaluations in January 2016.

- Develop and implement cow livability (survivability) evaluations.

- Implement genomic evaluations for Guernseys in April 2016.

- Implement genomic evaluations based on approximately 77,000 markers (an increase from 61,013).

- Develop and implement a breed base representation (breed composition) for crossbred animals.

- Update age limit and age group edits for heifer conception rate.

- Document effects of changes in the use of sexed semen on fertility evaluations.

- 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 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.

- Monitor the effects of genomic preselection as a source of bias in genetic evaluations.