

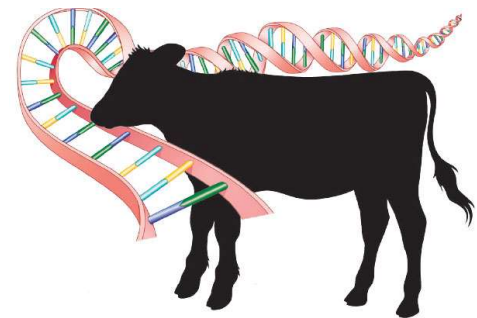
Key Research Projects Nearing Completion

Three large research projects are nearing finalization, as part of the close collaboration between CDCB and USDA-AGIL* for continuous assessment and improvement of U.S. dairy genetic evaluations. Although implementation plans have yet to be determined, this article provides a “sneak peek” into future developments. CDCB will provide updates and implementation plans when final, allowing preparation time for all partners.

- **Update of the reference genome assembly:** USDA-AGIL and USDA-ARS researchers, in cooperation with the University of California-Davis, released a new version of the cattle DNA reference genome assembly named ARS-UCD1. The updated assembly is expected to improve imputation accuracy and recessive haplotype calculation, and lead to a new SNP list for genomic evaluations.
- **New trait: Age at first calf (AFC):** Research conducted at AGIL, originally prompted by the NAAB Dairy Sire Evaluation Committee, led to the development of the first AFC evaluation on a research level.
- **Evaluations for crossbred animals:** Following robust research at AGIL, CDCB is quantifying all potential impacts of the proposed methodology. CDCB’s Genetic Evaluation Methods committee (including academia and industry), breed associations and other stakeholders are engaged in the research review and validation. CDCB’s goal is to publish genomic evaluations on crossbred animals in 2019.

Update of the reference genome assembly

An updated genome sequencing reference map – called the genome assembly – can now be utilized by all cattle researchers worldwide, with the ultimate goal to continually improve accuracy of genomic predictions. In 2018, USDA-AGIL and USDA-ARS* researchers, in cooperation with the University of California-Davis, released a new version of the cattle DNA reference genome assembly named ARS-UCD1. The new assembly replaces the University of Maryland version used since 2009 (UMD3). International researchers in the 1000 Bull Genomes Project, the largest sequencing effort in cattle, have decided to use the new ARS-UCD1 reference genome instead of UMD3 as the common language for tracking variation in cattle. Review the genome assembly modernization [here](#).



Both old and new maps sequenced DNA from a highly inbred Hereford cow named “Dominette.” The ARS-UCD1 map used a new sequencing technology able to yield longer “reads,” or pieces of DNA sequence, which provides higher accuracy. In CDCB calculations, the reference assembly provides the position of the SNPs used in the evaluation, so precision is important. The breed of the reference is not relevant to performance, because in “DNA years,” dairy and beef breeds were differentially selected too recently to have substantial structural differences.

As SNP positioning is improved, the new reference map will improve the imputation accuracy of genotypes. Thanks to the supporting research performed at AGIL, recessive haplotypes will likely be more accurate and include more precise information in their calculation. Finally, the new reference assembly will update the SNP list used in CDCB evaluations, including SNPs selected to have larger effects on traits. CDCB and AGIL research over the past year shows this update will be beneficial toward greater accuracies of traits currently evaluated.

New trait: Age at first calf (AFC)

Research completed by AGIL shows benefit to developing the new trait, Age at First Calf (AFC). Research results will soon be transferred to CDCB, and an implementation plan will be provided in future CDCB communications.

Accurate reports of age at first calving are available from nearly all cows on Dairy Herd Information (DHI) since 1960, for a national database of approximately 15 million records. Using this data, AGIL staff conducted research originally prompted by the NAAB Dairy Sire Evaluation Committee, which led to



the development of the first AFC evaluation on a research level. [Click here](#) for the 2017 research publication in *Journal of Dairy Science*. AFC heritability is 2.7%, and the trait is negatively correlated to Heifer Conception Rate (HCR; correlation of about -0.5). Reliabilities of AFC genomic predictions for young animals averaged 66% for Holsteins and 51% for Jerseys.

Evaluations for crossbred animals

Producing accurate genomic evaluations of crossbred animals has been an objective for more than a year, involving a robust, two-phase process coordinated between AGIL and CDCB. The first phase was driven by research at AGIL and concluded in April 2018, when the genomic evaluation process was changed to an “all-breed” system, similar to that used in traditional evaluations since 2007.

The second phase is the implementation plan. Prior to final decisions, the potential impact on every aspect of the evaluations must be assessed and quantified, including a series of hypothetical long-term scenarios. The CDCB staff is collaborating with breed associations and CDCB’s Genetic Evaluation Methods committee to ensure a smooth implementation. Preliminary results and action plan have been drafted, and the impact assessment is underway.

**USDA AGIL = United States Department of Agriculture, Animal Genomics and Improvement Laboratory
USDA-ARS = United States Department of Agriculture, Agricultural Research Service*

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