

Enhancements to U.S. genetic and genomic evaluations in 2018 and 2019

E.L. Nicolazzi¹, L.R. Bacheller^{1,2}, G.C. Fok², K.L. Parker Gaddis¹, L. Jensen¹, J.H. Megonigal Jr.¹, H.D. Norman¹, D.J. Null², L.M. Walton¹, G.R. Wiggans¹, J.B. Cole², J.W. Dürr¹, P.M. VanRaden²

¹ Council on Dairy Cattle Breeding (CDCB), 4201 Northview Dr., Bowie, MD, 20716, USA

² Animal Genomics and Improvement Laboratory, Agricultural Research Service, U.S. Department of Agriculture, Beltsville, MD 20705-2350, USA

Abstract

In 2013, the Council on Dairy Cattle Breeding (CDCB) started calculating and releasing U.S. genetic and genomic evaluations, which historically had been totally managed by USDA. The role of USDA in the U.S. dairy genetics industry is still extremely important because USDA's Animal Genomic and Improvement Laboratory conducts most of the research for developing the cutting-edge methodologies applied by CDCB. This presentation reviews the latest enhancements to U.S. evaluations during 2018 and 2019, all of them result of the interaction between public service and private U.S. industry. In April 2018, CDCB introduced six new health traits for Holsteins; these traits were included in lifetime net merit in August 2018. Early first calving, another new trait, was introduced in April 2019. In April 2018, CDCB also extended genomic evaluation to an all-breed system, which had been used for traditional evaluations since 2007. This, together with further methodology developments to determine an animal's breed composition (breed base representation, or BBR), resulted in the first release of a multi-breed genomic evaluation for crossbred animals in April 2019. In December 2018, the reference genome assembly was updated from the UMD3 version to the latest ARS-UCD1 version. At the same time, the number of markers used in genomic evaluations was increased from 60k to 80k. The new set of markers included more exact gene tests, removed poorer performers, added new variants with larger effects on traits, and changed the marker order based on the new assembly. The latest discovered recessive haplotype in Holsteins (HH6, BTAU-16) also was released in December 2018, and haplotypes BH1 (Brown Swiss) and JH2 (Jersey) were discontinued. Further enhancements were applied to productive life and fertility traits in 2018. Future projects include the release of evaluations for Jersey health traits, further improvements to the marker set, and enhancements of crossbred evaluation.

Key words: dairy cattle, genetic evaluation, genomic selection, crossbred evaluations, genome assembly, genomics

Introduction

In the last year alone, CDCB and AGIL staff have introduced a large number of new developments into the U.S. dairy genetic and genomic evaluations. The most noticeable change in the U.S. dairy evaluation is the inclusion of crossbred animals in the genomic evaluation in April 2019. This novel methodology, unique in the world, has allowed CDCB to publish genomic evaluations for over 30,000 genotyped animals that were not receiving evaluations before because of their mixed breed genetic make-up.

Another improvement to the genomic evaluation setup was the update of the SNP set used for genomic evaluations, which resulted in nearly 20,000 more SNPs being included, and the update of the SNP positioning to the latest ARS-UCD1 reference genome assembly. In this genomic update, a number of changes were introduced in the identification and accuracy of the recessive haplotype information, provided by default to all animals receiving an evaluation.

Finally, 7 new traits – 6 disease resistance and one fertility trait – were introduced between April 2018 and 2019.

In this paper we will review the main changes introduced in the evaluation, and briefly discuss future developments.

Materials and Methods

Except for the “Future developments” section, all the results presented in this paper are addressed in papers presented in the 2019 Interbull and A.D.S.A. (joint) meetings held in Cincinnati (OH), in June 2019.

Results & Discussion

Including crossbred animals in the genomic evaluation in U.S.

This enhancement to the U.S. dairy evaluation system is an over 10-year development that started with the introduction of the all-breed animal model for traditional evaluations in 2007 (VanRaden *et al.*, 2007). In short, within the all-breed system, all animals are included in a single evaluation, expressed on a common breed base using an all-breed pedigree. This means that all animals, including crossbreds, contribute to the PTA calculations. However, the all-breed system was not extended to genomic evaluations until April 2018 (VanRaden and Cooper, 2015). Having a common breed base was the first important step towards the publication, one year later, of the first genomic evaluation in the U.S. including crossbred animals. Briefly, the percentage of DNA contributed to an animal by each of the five breeds in evaluation (Holstein, Jersey, Brown Swiss, Guernsey and Ayrshire), named Breed Base Representation (BBR; Norman *et al.*, 2016) is used to separate animals receiving single-breed evaluation ($BBR \geq 90$) or a blended multi-breed evaluation ($BBR < 90$) with SNP effect weights based on their BBR. The new evaluation affected over 69,000 animals. A total of 31,894 animals received a genomic evaluation for the first time, whereas 36,790 animals that were receiving an evaluation as purebreds started receiving multi-breed evaluations. Further details of the methodology are explained in Wiggans *et al.*, 2019(a).

New SNP set for genomic evaluations

Since 2014, the number of SNPs used for genomic evaluations has been 60,671. In December 2018, the CDCB increased that number to 79,294. According to Wiggans *et al.* (2016), the expected reliability increase was 1.4% points across all traits for Holsteins. In terms of PTAs, correlations for yield traits across breeds were 99%. Single animals were affected, especially: i) foreign animals loosely connected to the U.S. population; ii) animals with a large proportion of missing pedigree, and; iii) animals genotyped at lower (e.g., 3k) SNP densities.

Further details on this enhancement can be found in Wiggans *et al.*, 2019(b) and Null *et al.*, 2019.

ARS-UCD1 reference genome update

Another update introduced in December 2018 was the transition to the latest ARS-UCD1 (Rosen *et al.*, 2018) reference genome assembly from UMD3.1. The new assembly, that combined Illumina and Pacific Biosciences sequencing technology, has not only better annotation properties but also gave much better imputation performance (lower non-inheritance and fewer haplotypes identified per segment). Further details on this update can be found in Null *et al.*, 2019.

Recessive haplotypes enhancement

A direct consequence of the use of a larger SNP set in the genomic evaluation procedure and the new reference genome assembly was the complete review of the recessive haplotype procedure. CDCB publishes recessive haplotype information on most animals receiving evaluations. In fact, as of now, the only subset of animals excluded from this publication is all crossbred animals, as the determination for them is currently being developed.

In December 2018, CDCB introduced the following changes to this procedure:

- i) Inclusion of HH6 determination in Holstein animals, which has a 0.5% frequency in the U.S. population.
- ii) Discontinuation of BH1 in Brown Swiss (effect no longer significant) and JH1 in Jersey (difficult to track in new ARS-UCD1 reference genome).

- iii) Inclusion of nine gene tests to improve haplotype calling in nine haplotypes. The gene-test for HH5 in Holstein was the only available gene test excluded because of inconsistent and dubious results.

More details provided in Wiggans *et al.*, 2019 and Null *et al.*, 2019.

New traits

In April 2018, CDCB introduced the evaluation of six health traits, expressed as resistance to the disease: hypocalcemia, displaced abomasum, ketosis, mastitis, metritis, retained placenta. In only a year of evaluations, the amount of DHIA records used for the evaluations increased 32% (adding 1.1 million records between April 2018 and 2019). Health dollars index (HTH\$), a combination of all six health traits, was included in NM\$ formula in August 2018 with a total weighting of 2.3%. Furthermore, (direct) mastitis evaluation was validated in March 2019 and started being submitted to Interbull in April 2019. In August 2019, international mastitis evaluations began being used in U.S. PTA calculation. A full review on health evaluations is provided in Parker Gaddis *et al.* (2019).

A new fertility trait Early First Calving was introduced in April 2019. Over 30 million DHIA calving records recorded for decades were used to provide this new fertility trait to all U.S. farmers. The trait is expressed in a reverse scale from age at first calving to make positive values desirable.

Future developments

The developments described in this paper are only the most noticeable of a large series of improvements to the U.S. dairy genetic and genomic evaluations. A number of further developments are ongoing and briefly described below:

- i) Extending health trait genetic evaluations to Jersey. See Jensen *et al.* (2019).
- ii) Publication of a feed efficiency (or feed saved) trait. CDCB is co-sponsoring with FFAR a project that includes a large phenotyping effort, and is collaborating internationally to increase the phenotypes used in its evaluation.

- iii) Extending pedigree information based on genomic information. The introduction of a “virtual dam” will allow linking animals with missing pedigree to all the known ancestors using genomics.

- iv) Improvement to crossbred evaluations:
 - a. New methods to calculate reliabilities on crossbred animals. Currently under review, reliabilities for crossbred animals will be linked to the breed of evaluation of the animal instead of a multi-breed reference population.
 - b. Publication of recessive haplotype calling for crossbred animals.
- v) Further update of SNPs set used in evaluations (inclusion of SNPs associated with traits of interest for non-Holstein breeds). For more information see VanRaden *et al.*, 2019.

Conclusions

The CDCB has been providing services to the U.S. dairy industry since 2013. A large number of improvements and new services have been introduced in the last year alone. Enhancement to already published methods are necessary to maintain the highest standard possible in terms of quality of genetic and genomic evaluations.

Acknowledgements

Authors wish to recognize the contribution of participating dairy producers to all the research and services provided by CDCB. Dairy herd improvement organizations, dairy records processing centers, genomic nominators and genotyping laboratories are acknowledged for processing and relaying the information to the CDCB. Purebred breed associations provided their pedigree data.

References

- Norman, H.D., VanRaden, P.M., Megonigal, J.H., Durr, J.W., and Cooper, T.A. 2016. Breed base representation in dairy animals of five breeds. *J. Dairy Sci.* 99, 1:151–152
- Rosen, B.D., Bickhart, D.M., Schnabel, R.D., Koren, S., Elsik, C.G., Zimin, A., Dreischer, C., Schultheiss, S., Hall, R., Schroeder, S.G., Van Tassell, C.P., Smith, T.P.L. and Medrano J.P. 2018. Modernizing the bovine

- reference genome assembly. *Proceedings of the 11th World Congress of Genetics Applied to Livestock Production. Auckland, New Zealand*, 6-11
- Jensen, L., Parker Gaddis, K.L. and Norman, H.D. 2019. Extending genomic evaluations to direct health traits in Jerseys. *J. Dairy Sci.* 102(Suppl. 1): 257 (abstr. 281).
- Parker Gaddis, K.L., VanRaden, P.M., Cole, J.B., Nicolazzi, E.L. and Durr, J.W. 2019. Development, implementation and future perspectives of health evaluations in the United States. *J. Dairy Sci.* 102(Suppl. 1): 141 (abstr. 175).
- Null, D.J., VanRaden, P.M., Rosen, B.D., O'Connell, J.R. and Bickhart D.M. 2019. Using the ARS-UCD1.2 reference genome in U.S. evaluations. *Presented at the 2019 Interbull Meeting, Cincinnati, OH, USA.*
- VanRaden, P.M., Tooker, M.E., Cole J.B., Wiggans, G.R. and Megonigal J.H. 2007. Genetic evaluations for mixed-breed populations. *J. Dairy Sci.* 90:2434–2441
- VanRaden, P.M. and Cooper, T.A. 2015. Genomic evaluations and breed compositions for crossbred U.S. dairy cattle. *Interbull bulletin.* 49,19-23
- VanRaden, P.M., Null, D.J., O'Connell, J.R., Cole, J.B., and Li, B. 2019. Genomic prediction and marker selection using high-density genotypes from 5 dairy breeds. *J. Dairy Sci.* 102(Suppl. 1): 400 (abstr. 471).
- Wiggans, G.R., Cooper, T.A., VanRaden, P.M., Van Tassell, C.P., Bickhart, D.M., Sonstegard, T.S. 2016. Increasing the number of single nucleotide polymorphisms used in genomic evaluation of dairy cattle. *J Dairy Sci.* 99, 4504–11.
- Wiggans, G.R., VanRaden, P.M., Nicolazzi E.L., Tooker, M.E., Megonigal J.H. and Walton, L.M. 2019. Extending genomic evaluation to crossbred cattle – U.S. implementation. *Presented at the 2019 Interbull Meeting, Cincinnati, OH, USA.*
- Wiggans, G.R., VanRaden, P.M., Null, D.J., and Cole, J.B. 2019. Genomic predictions using more markers and gene tests. *J. Dairy Sci.* 102(Suppl. 1): 397 (abstr. 462).