

# Changes to evaluation system (April 2013)

## Distribution and access to genomic evaluations

By George Wiggans, Paul VanRaden, and Duane Norman

Genomic evaluations were developed and have been conducted by the Animal Improvement Programs Laboratory (AIPL) for the past 5 years. A cooperative research and development agreement with the National Association of Animal Breeders (NAAB) limited genomic evaluations of males to participants in the Cooperative Dairy DNA Repository and NAAB. With the March 1 expiration of that limitation, AIPL will compute and release evaluations for males and females as directed by the [Council on Dairy Cattle Breeding](#) (CDCB). A [nonfunded cooperative agreement](#) was signed by USDA's Agricultural Research Service and the CDCB on March 27 to transfer control of the evaluation service from government to industry. The CDCB has established a [fee schedule](#), which recognizes the importance of the contribution of phenotypic data by having lower fees for herds that provide more complete data. Artificial-insemination (AI) service fees are required for multiple-herd AI bulls or multiple-owner/syndicate bulls with genomic evaluations and first released after March 1, 2013. The CDCB will use those fees in employing people to assist in receiving data, delivering evaluations, performing related service work, and establishing the capability for CDCB to maintain the database and calculate the evaluations directly when the nonfunded cooperative agreement becomes effective. [AIPL Research Report NFCA-CDCB1 \(06-12\)](#) and a [CDCB press release \(October 11, 2012\)](#) provide background on the development of the nonfunded cooperative agreement. Industry control of service functions is needed to manage the rapidly expanding database of genotypes, to invest in further collection of phenotypes, and to interact with the many suppliers and recipients of genetic information. Researchers at the Animal Improvement Programs Laboratory (AIPL) will continue to develop improved methods of analysis using the shared database and will work closely with CDCB to enhance evaluation accuracy. The CDCB has been responsible for certifying input data quality since 1999 and guiding AIPL evaluation policies since 1988. Except for the changes below, the evaluation schedule, input data provided by the industry, editing system, and evaluation programs developed by AIPL, the University of Georgia, and Gembloux Agricultural University (Belgium) remain the same.

Bulls owned by individuals and organizations with U.S. addresses will have their genomic evaluations provided in [format 38](#) and in XML files for public download. Removal of the previous age limitation added 20,861 bulls younger than 24 months to the bull evaluation file. Foreign-owned bulls younger than 24 months will have their genomic evaluations computed on the U.S. scale and provided to the foreign owners through the nominators, a continuation of previous policy. Many of the youngest bulls from foreign partners are not made public by the home country and, therefore, are also not made public in the United States. Cows with usable U.S. lactation records and all genotyped females will continue to have their evaluations provided in [format 105](#) to breed associations, dairy records processing centers, and the public if qualifying for elite or high-ranking grade lists (no change in policy). Web queries will continue to display all official evaluations. In the near future, all evaluations will be computed and delivered by CDCB. Beginning in April and during this transition period, the source of evaluations should be labeled as USDA-CDCB instead of USDA-AIPL along with the year and month of calculation (e.g., 13-04).

## Use of a new chip with 76,867 markers

By George Wiggans, Dan Null, and Paul VanRaden

Since the January 2013 monthly update, genomic evaluations have included genotypes from a new genotyping chip called the GeneSeek Genomic Profiler HD (GHD) BeadChip, which was introduced in December 2012 with 76,867 markers. Animals genotyped with this chip have GHD in the chip field in XML files. The GHD chip includes 28,376 (63%) of the usable markers from the Illumina BovineSNP50 v2 BeadChip plus 48,491 (6.2%) of the 777,962 markers from the Illumina BovineHD BeadChip that were selected as having the greatest effects for Holstein net merit. Currently, only the 28,376 markers in common with the BovineSNP50 chip are used to impute the 45,188 markers included in genomic evaluation.

Tests indicate that using a total of about 90,000 markers (45,188 current markers plus 44,925 added markers) could increase evaluation reliability as compared with evaluations based on 45,188 markers by about 0.5 percentage points on average across traits and give almost the same evaluation reliability as using high-density genotypes. Accuracy of imputing the additional 44,925 markers is high for Holsteins because BovineHD genotypes are available for 2,254 Holsteins through cooperation with Canada, Italy, and the United Kingdom. Imputation accuracy is still too low for other breeds because only 167 Jerseys and 146 Brown Swiss animals have BovineHD genotypes. Therefore, evaluations for those 2 breeds must continue to use 45,188 markers until more animals are genotyped with either BovineHD or GHD chips. The additional markers could be used for Holsteins in the near future and for other breeds as additional animals are genotyped.

Imputation was tested using simulated genotypes. In the test, markers on each chip were evenly spaced with no selection for high minor allele frequency or estimated allele effects as on the actual GHD chip. Imputation accuracy to 45,188 markers was tested using the current population structure for comparison. Imputation to 90,000 markers was tested using either the 3,000 BovineHD and GHD genotypes available soon or the 8,000 that could be available after a few months:

Genotyping chip	Markers usable for evaluation (no.)	Accuracy (%) of imputation to:		
		45,188 markers	90,113 markers	
			3,000 animals	8,000 animals
GHD	76,867	99.1	99.9	99.9
BovineSNP50	45,188	99.9	99.4	99.5
GeneSeek Genomic Profiler	8,762	98.8	98.2	98.4
BovineLD	6,909	97.1	96.2	96.5
Bovine3K	2,683	94.5	92.9	93.9
Imputed dams	0	94.8	95.4	95.8

Some imputation loss will occur initially with the GHD chip because 16,812 markers from the BovineSNP50 chip are missing and the new markers are not yet used. When the new markers are used, evaluations based on 90,113 markers should be slightly more accurate than evaluations based on 45,188 markers. With imputation from lower densities, the gain in evaluation accuracy of 0.5 percentage points from including more markers may be exactly offset by an imputation loss of 0.5 percentage points from using low-density genotyping chips. [Further research](#) quantifying these gains with actual instead of simulated genotypes will be reported by Dr. George Wiggins at the 2013 annual meeting of the American Dairy Science Association.

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## Ayrshire genomic evaluations

*By George Wiggins and Tabatha Cooper*

Evaluations were computed for >1,100 genotyped Ayrshires with records in the North American database, of which 646 were bulls with either U.S. daughter records or Interbull multitrait across-country evaluations. Gains in reliability because of the inclusion of genomic information were determined by comparing traditional parent averages and genomic evaluations from August 2008 with daughter performance for bulls born on January 1, 2000, or later and that had no daughter records before August 2008 and received a traditional evaluation in December 2012. The number of bulls tested ranged between 147 and 180 by trait. The average gain in reliability over parent average for all traits was 8.2 percentage points. The highest gains were found for milk yield (16.6 percentage points), protein yield (16.9 percentage points) and stature (16.2 percentage points). The evaluations were calculated based on the North American population and may not be suitable for all red dairy cattle (for example, from Scandinavia) because linkage disequilibrium differs by population. Breed determination uses 12 markers that are nearly monomorphic (>90%) in Ayrshires and have <30% of animals homozygous for that allele in Holsteins, Jerseys, and Brown Swiss. Fewer markers are available for determining breed for Ayrshires than for the other breeds, mostly because of the similarity of Ayrshires and Holsteins. The new Ayrshire evaluations will be provided in the same formats and on the same schedule as for the other breeds.

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## Weights used in genomic evaluations

*By Paul VanRaden, Mel Tooker, and Gary Fok*

Weights to combine direct genomic values (DGV) with traditional parent averages (PA) or predicted transmitting abilities (PTA) were revised for Holsteins based on updated genomic validation results. The maximum weight on DGV was reduced to 0.85 from 0.90 for yield traits and reduced to 0.80 from 0.90 for type traits using the methods implemented in April 2011. Estimated regressions of future daughter performance on genomic predictions of transmitting ability (GPTA) are closer to the expected regressions after these adjustments, and young animals with the highest GPTA for yield and type traits are reduced slightly. For example, the highest young animals for GPTA protein decreased by about 2 pounds, and the highest for GPTA final score type decreased by 0.15. Also, the revised genetic correlations implemented in multi-trait productive life (PL) in December 2012 now also affect the foreign bull evaluations used in computing marker effects because their August evaluations were used in December. The combined effects of these individual trait changes were small for most animals but reduced net merit by about \$25 for young Holsteins with the highest net merit. Correlations of GPTA before and after the weight adjustments were > 0.998.

For sires with many genotyped and phenotyped daughters or progeny-tested sons, traditional and genomic evaluations are now more consistent. The sire's traditional evaluation now gets a maximum weight of 99.9% in the genomic evaluation; previously, the maximum weight was 99% because published reliabilities do not exceed 99%. As a result, evaluation differences are now smaller for sires with many thousands of daughters for yield and health traits, for which the change was implemented. Type and calving traits continue to receive a maximum weight of 99% reliability.

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## Calving-ease format change

*By Jay Megonigal, Paul VanRaden, and Jan Wright*

Service-sire calving ease (SCE) and daughter calving ease (DCE) are now expressed to 1 decimal instead of as whole numbers. A test file with the [new CT format](#) was distributed by NAAB on March 4. The added precision should improve accuracy of selection and reduce rounding error in genomic evaluations, which are computed on the published scale [percentage of difficult births in heifers (%DBH)] instead of the underlying scale. Underlying solutions have a more normal distribution and are exchanged with Interbull, but genomic evaluations had very similar accuracy and properties when computed on either scale. Service-sire stillbirth (SSB) and daughter stillbirth (DSB) evaluations will continue to be published with 1 decimal as done previously. Due to the short notice, cooperators may continue to display SCE and DCE rounded to the nearest integer (values ending in .5 round up) in April and implement the decimal change in August. Holstein TPI will be calculated using rounded SCE and DCE in April.

A further change is that the traditional SCE and SSB of young bulls are included in estimating marker effects, because young bulls now obtain many calving records early in life. Previously, only older bulls that had daughters with milk records were used to estimate marker effects. Correlations between previous and new genomic evaluations for all 4 calving traits were >0.98, and the combined effects of less rounding and including younger bulls in the marker effect estimation were small.