

Changes to evaluation system (April 2010)

Cow adjustments in genomic evaluation

By George Wiggans, Tabatha Cooper, and Paul VanRaden

Traditional predicted transmitting abilities (PTAs) are inputs for genomic evaluation, but cows with high traditional PTAs for yield traits may be overevaluated. Adjustments were developed to rescale cow PTAs for yield traits to be more comparable to bull PTAs. Resulting genomic evaluations were more accurate when the rescaled cow PTAs were included in estimation of marker effects. Genomic evaluations for the top cows, top young bulls, and top heifers decreased by about 250 pounds for milk, 8 pounds for fat, and 5 pounds for protein, whereas genomic evaluations for the top bulls with daughters decreased only by about 70 pounds for milk, 3 pounds for fat, and 2 pounds for protein. Adjustments were largest for foreign bulls with a high proportion of genotyped daughters. The population average of all bulls with daughters decreased slightly by 40 pounds for milk, 1.5 pounds for fat, and 1.5 pounds for protein; standard deviations also decreased slightly by about 1%. Correlations between genomic evaluations before and after the adjustment were 0.997 for bulls with daughters and 0.990 for cows and young animals. Net merit decreased by as much as \$40 for many of the top cows and young animals because of the yield trait adjustments. Only yield and component percentage traits were adjusted because non-yield traits had less variance in females than males and did not benefit from applying these same methods for PTA adjustment. [See [Wiggans et al. \(2010\)](#) for further documentation of methods.]

March 30 update 1: The PTAs computed from February genotypes and January yield data with the cow adjustments applied are available for preview to help in understanding differences directly caused by the change. Files containing Holstein and Jersey evaluations for both young and old bulls are available for download at http://aipl.arsusda.gov/pub/outgoing/UNOFFICIAL_1002_NEW_MODEL.zip. Evaluations in the preview files were not calculated using the new edit for productive life (PL) described in March 30 update 2.

March 30 update 2: A new edit was introduced for multitrait PL of cows. Previously, correlated traits measured during first lactation received credit when calculating genomic PTAs of genotyped cows. For a few prominent sires, this created an upward bias in PTA PL because many live, genotyped daughters received credit in marker effect estimation before information from any of the culled daughters entered the sire's traditional PL evaluation. The new edit includes only multitrait PL of genotyped daughters after they reach 36 months of age so that records from living and culled daughters enter equations at the same time.

The Document '[Imputation of Cow Genotypes and Adjustment of PTAs](#)' is available for further explanation

Haplotypes used for imputing genotypes

By Paul VanRaden, George Wiggans, and Jeff O'Connell

New methods were used for imputing missing genotypes in genomic evaluation. About 1% of marker genotypes are missing in initial data, and previously about half of those were imputed using gene content of relatives and an algorithm that did not use neighboring markers or map location on the chromosome. Program findhap.f90 was developed to determine the paternal and maternal haplotypes that sum to the animal's genotype. Simulation results indicated that the initial rate of 99.0% for correct genotypes was increased to 99.95% after imputing the missing values with haplotypes. The same methods will allow imputing the much higher proportions of missing data that will result when lower or higher density marker sets are mixed with current data containing 50,000 markers. More than 1,000 nongenotyped cows had at least 90% of their single nucleotide polymorphisms (SNPs) correctly imputed using genotypes from multiple progeny (usually 5 or more). Those imputed genotypes are included in SNP estimation, and such cows will be listed in evaluation files with the genomic indicator set to 1 and will have a sample identification of "imputed" in the XML file. [See [VanRaden \(2010\)](#) and [VanRaden et al. \(2010\)](#) for further documentation of haplotyping methods.]

Breed-specific markers

By Tabatha Cooper, George Wiggans, and Katie Olson

Genotypes are checked using breed-specific markers to verify that the reported breed matches the animal's actual breed as part of routine USDA data edits. Breed is validated using SNPs that are nearly monomorphic in 1 breed and have fewer than 30% of animals homozygous for that allele in another breed. A total of 672 SNPs were selected with approximately equal numbers of SNPs that were monomorphic for each of 3 breeds (Holstein, Jersey, and Brown Swiss). The number of SNPs for which the genotype differed from the monomorphic genotype was counted separately for each breed, and the lowest breed count identified the breed of the sample. In addition to determining an animal's breed, the number of breed-specific SNPs can indicate partial contribution of another breed to the animal. More accurate estimates of breed composition can be produced using regression coefficients for all 43,385 markers, but that test is not yet used routinely. The simple SNP test may underestimate the actual percentage of other breed genes present in the animal. For example, full siblings with a great-grandparent of another breed may have a range of 12 to 26 SNP conflicts with breed-specific SNPs (5.4 to 11.7%). The tool was developed primarily to detect breed reporting errors, and breed purity should not rely solely on the approximately 200 SNPs used in detection. Because of the variation in inheritance of the 200 breed-specific SNPs, some animals with an ancestor of another breed may not be detected, and other animals with many generations of pure breeding may have some SNPs specific to another breed. Animals with 10 conflicts or more at the breed-specific SNP locations are reported to the requester (breed association or artificial-insemination organization) of the genotype. If more investigation is needed, the requester may ask for additional data from USDA. [For more information on selection of breed-specific SNPs, see [Wiggans et al. \(2010\)](#).]

New fertility records excluded from sire conception rate

By Duane Norman and Paul VanRaden

The numbers of new records received for evaluations for sire, cow, and heifer conception rates are considerably lower than in past evaluations. As of January 2010, fertility data in format-5 (reproductive) records were provided for most herds by 3 dairy records processing centers (AgriTech Analytic, AgSource, and Dairy Records Management Systems) and for 6 herds by a fourth processing center (DHI-Provo). For April 2010 evaluations, records from AgriTech Analytics continued to be provided for most herds, but records from Dairy Records Management Systems and AgSource were provided

only for cows inseminated to Genex/CRI bulls. The reduction in additional numbers of format-5 records had a small limited effect on daughter pregnancy rate evaluations because current days open are reported in format-4 (lactation) records. However, April genetic evaluations for cow and heifer conception rates have less increase in reliability than in January for most bulls. When genetic evaluations for conception rate are released in the future (possibly August 2010) for cows, any cow without a breeding record will not receive an evaluation.

Evaluations of sire conception rate from January will remain official and will not be updated in April until the partial data can be modeled properly or the unusual results obtained from it can be explained. The input records caused distortions for individual bulls in the proportion of mates observed to be not pregnant by later inseminations versus confirmed pregnant by examination. This caused changes in rank much larger than expected from the number of new records received. Thus, the format-38 (bull evaluation) file in April will contain sire conception rates from January. Further work is needed to resolve the data submission issues and the bias created by partial record submission.

Genotypes from Switzerland

By George Wiggans

An additional 400 Brown Swiss genotypes were traded with Switzerland prior to the February genomic update. This increased the size of the reference population by about 50% and increased the genomic reliabilities.

Improved reliability for genomic evaluations

By George Wiggans and Paul VanRaden

The contribution to reliability from genomics was modified to consider the sum of genomic relationships of the animal with each animal in the predictor population weighted by the reliability of that predictor animal's evaluation. Previously, the contribution to accuracy from genomics was assumed to be the same for each animal within a breed. The standard deviation of the change in reliability was about 2 for young bulls and heifers and 1 for bulls that had daughters included in their traditional evaluations. [For more information on the genomic reliability approximation, see [Wiggans and VanRaden \(2010\)](#).]