

Changes to evaluation system (January 2010)

Base change

By Paul VanRaden, George Wiggans, John Cole, and Tabatha Cooper

Genetic bases for all traits were updated by 5 years. For most traits, average predicted transmitting abilities (**PTAs**) decreased. For traits affected by herd-variance adjustments, standard deviations were revised to reflect genetic standard deviation for cows born in 2005 instead of cows born in 2000. Changes for each breed are reported in "[Genetic Base Changes for January 2010](#)." The next base change is scheduled for 2015.

Net merit revision

By John Cole, Paul VanRaden, and S-1040 research project

Economic values of all traits were updated for the net merit, cheese merit, and fluid merit indexes. Assumed prices, formula derivations, and comparison with previous versions are provided in "[Net Merit as a Measure of Lifetime Profit: 2010 Revision](#)." The main changes were more emphasis on longevity, fertility, and smaller body size with less emphasis on yield as a result of higher feed, breeding, and replacement costs and lower interest rates and profit margins per lactation.

Heifer and cow conception rates

By Gary Fok, Jana Hutchison, and Paul VanRaden

Heifer and cow conception rates are now provided in columns 568-603 of [format 38](#). Previously these were provided in a separate file. Usability codes report whether the PTAs are from multitrait, across-country evaluation or from domestic data. Heifer and cow conception rates are not yet reported for cows or used in selection indexes for lifetime profit but could be added in the near future.

Revised genomic evaluation methods

By Paul VanRaden and Mel Tooker

Genomic and current Interbull data are blended in the final selection index for all traits. Previously that update was implemented only for Holstein type traits. Thus, bulls with foreign daughters now receive credit for the latest genomic and phenotypic information from all sources. However, because Interbull files are received on Thursday and results must be available to Holstein Association USA on Friday, genetic marker effects are not updated for the new phenotypes from foreign daughters of genotyped bulls until the next evaluation release. The selection index step also is applied to animals with domestic data only if the reliability increases by at least 1%. Thus, the released PTA will exactly equal the direct genomic value for more domestic animals, such as those with both sire and dam genotyped.

Polygenic effects were included in the October genomic update, and January is the first release for which the change affects evaluations of all animals. The evaluation model assigns 90% of genetic variation to markers effects and 10% to residual effects inherited with a pedigree relationship matrix. The change had little effect on progeny tested bulls but decreased standard deviations and improved regressions of later on earlier evaluations for younger animals.

Approximate reliabilities were updated to equal observed reliabilities from a [preliminary study based on August 2006 input data](#). Observed reliabilities averaged 3% lower when only U.S. Holstein bulls were predicted compared with previous tests that predicted both U.S. and Canadian bulls. The reliability approximation now differs by breed. Daughter equivalents from genomics are computed by adding traditional reliabilities and subtracting parent-average reliabilities of all genotyped animals, then multiplying by the ratio of error to sire variance, and finally dividing by a constant of 150,000 for Holsteins, 70,000 for Jerseys, and 120,000 for Brown Swiss. Populations with lower average inbreeding (such as Holstein) require more genotypes to achieve the same genomic reliability.

Genomic inbreeding and genomic future inbreeding (**GFI**) previously were computed using estimates of allele frequencies in the base population but now are computed without considering allele frequencies. In the new method, counts of homozygous loci are adjusted by regression of genomic on pedigree relationships within each breed. Averages of genomic and pedigree inbreeding coefficients were more similar, and correlations within each breed improved by 0.05 to 0.12. For bulls born since 1990, inbreeding estimated from the new method, old method, and pedigree averaged 11.0, 20.8, and 5.5% for Holsteins; 4.6, 16.1, and 6.5% for Jerseys; and 5.4, 9.2, and 5.1% for Brown Swiss, respectively. Averages of GFI changed only slightly, but correlations between GFI and expected future inbreeding computed from pedigree decreased by about 0.07 to about 0.80 within each breed.

Web query to track genotypes

By George Wiggans, Jay Megonigal, Frank Ross, and Lillian Bacheller

Participants in the genomic evaluation program now can access the genotype database table to see if an animal has a genotype stored and if that genotype was usable or why it was not. The descriptive information identifies the requester, laboratory where the genotyping was done, and genotyping date. Counts of parents and progeny with genotypes that do not conflict are displayed. This access should enable participants to answer most questions about the status of individual animals during the genotyping process.

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