

Changes to evaluation system (December 2012)

Correction and adjustment of health trait evaluations and reliabilities

By Paul VanRaden, Gary Fok, and Mel Tooker

In August 2012, bulls that were progeny tested in at least 10 herds for yield but fewer herds for some other traits had their genomic PTAs (GPTAs) mistakenly used instead of PTAs or parent averages (PAs) as input data when solving for marker effects for those traits. That problem was corrected in the September 2012 XML file for new animals and in December 2012 for previously evaluated animals. It affected only a few newly proven domestic bulls but many more foreign bulls because some traits are not evaluated by all countries. Traits most affected were heifer conception rate (HCR) and cow conception rate (CCR), with smaller effects on DPR and productive life and no effect on other traits. Changes in GPTAs generally were small, but reliabilities (RELs) for the affected traits were lower in December than in August 2012 for the affected bulls, their progeny, and for young animals because REL was recalibrated using the corrected data. Evaluations of the young animals were also reduced toward PA because less emphasis was placed on the direct genomic value (DGV).

Trait correlations used in computing multitrait productive life were updated in December 2012 to reflect more recent data. As compared with previous estimates, genetic correlations with productive life changed from 0.51 to 0.60 for DPR, from -0.38 to -0.45 for somatic cell score, from -0.16 to -0.26 for size composite, from 0.30 to 0.15 for udder composite, and from 0.19 to 0.08 for feet-and-leg composite. Similar changes occurred for phenotypic correlations. Those changes may simply reflect differences in recent culling emphasis by dairy producers rather than biological effects of selection. Productive life evaluations and computed RELs of the top animals decreased, with small changes in rank tending to favor animals with those traits most strongly correlated with productive life.

For the top 100 young bulls ranked on August 2012 net merit, their December evaluations decreased by 0.9 months of productive life and \$53 of net merit because of the combined effect of these changes. For the top 100 daughter-proven bulls, averages also decreased by 0.4 months of productive life and \$25 of net merit because many of their daughters also have predicted rather than observed productive life. For fertility traits and productive life, young animal REL decreased by about 6 to 8 percentage points (for example, from 70 to 63% for productive life). These corrections and adjustments reduce biases and make evaluations of young and old animals more comparable.

PTA for days from calving to first insemination

By Paul VanRaden and Jana Hutchison

Predicted transmitting abilities (PTAs) for days from calving to first insemination (CFI) were estimated from PTA for daughter pregnancy rate (DPR) and CCR. The CFI PTAs were sent for the Interbull fertility evaluation instead of sending DPR PTAs as a substitute trait. With this change, U.S. evaluations include 4 of the 5 fertility traits evaluated by Interbull. Several other countries evaluate CFI and CCR (or cow nonreturn rate) and add the 2 together to obtain a trait that corresponds to DPR (or calving interval). The reverse procedure can subtract the effect of CCR from DPR to estimate CFI. Correlation of estimated and actual CFI was maximized using research data (VanRaden *et al.*, 2004, *Journal of Dairy Science* 87:2285–2292) to obtain the following regressions for PTA and REL:

$$PTA_{CFI} = 1.2(PTA_{CCR}) - 3.6(PTA_{DPR});$$

$$REL_{CFI} = 0.37(REL_{CCR}) + 0.63(REL_{DPR}).$$

The REL weights indicate the relative contributions of CCR and DPR to the prediction. For CFI, more days are unfavorable, and predicted CFI was correlated by -0.54 with CCR and -0.88 with DPR because the ability to conceive contributes less to DPR than does the ability to begin cycling. The estimated heritability of CFI was 0.066, and the genetic standard deviation (SD) was 9.1 days; therefore, the PTAs had an SD of about 4 days. The trait is not easy to measure with U.S. data because many herds use timed artificial-insemination (AI) breeding rather than waiting for natural estrus. For the net merit index, CFI was not included because DPR already includes variation from CFI. However, CFI has more value in herds that do not use timed AI than in those that do.

When the United States included CFI in the September 2012 Interbull test run instead of sending DPR as a substitute trait, genetic correlations increased by 0.06 to 0.08 with the other 8 countries that measure CFI. Genetic correlations averaged 0.79 using CFI as compared with 0.73 using DPR for Holsteins, 0.79 compared with 0.72 for Jerseys (3 other countries), and 0.80 compared with 0.74 for Brown Swiss (5 other countries). The trait CFI is not distributed nationally but provides a better substitute trait internationally. Direct evaluation of CFI instead of calculating CFI from DPR and CCR could provide further improvement in genetic correlations and REL in the future.

Changes in HH1, HH3, and JH1 status

By Paul VanRaden and Dan Null

Exact locations of the loss-of-function (LOF) mutations in Holstein haplotype 1 (HH1) and Jersey haplotype 1 (JH1) are now used instead of fine-mapped regions to determine heterozygous (carrier) status for genotyped animals. Causative mutations were discovered for HH1 in the gene for apoptotic peptidase activating factor 1 (*APAF1*) by Adams *et al.* (2012, *Proceedings of the Plant & Animal Genome XX Conference*, abstract P0555) at the University of Illinois and for JH1 in the *CWC15* spliceosome-associated protein homolog gene by Sonstegard *et al.* (2012, *PLoS ONE*, submitted) at the Bovine Functional Genomics Laboratory, ARS, USDA, Beltsville, MD. For animals genotyped with the Illumina BovineSNP50, BovineLD, and Bovine3K BeadChips, detection of heterozygotes improved slightly because the fine-mapped regions previously contained 27 markers and 2.2 million base pairs (Mbp) of DNA for HH1 and 15 markers and 0.8 Mbp for JH1, whereas crossovers now are tested using the exact locations. For more than 25,000 animals genotyped with the GeneSeek Genomic Profiler (GGP), HH1 status further improved slightly by directly testing the mutation in the gene instead of using haplotypes. Concordance of haplotype tests with LOF mutation tests was 99.3% for JH1 and 99.7% for HH1, but 837 of the 235,525 Holsteins (0.3%) previously listed as noncarriers are now detected as heterozygous for HH1 by the LOF mutation test. The JH1 mutation test has been added to the GGP chip more recently and will be used directly when available. Further information on combining LOF mutation tests with haplotype tests is available (VanRaden *et al.*, 2012, poster presentation, annual meeting of the American Dairy Science Association).

Status for HH3 changed from normal to heterozygous for 501 of the 211,918 Holsteins (0.2%) in the October 2012 genomic evaluation because a new crossover haplotype narrowed the location of the causative mutation. The HH3 haplotype was discovered initially as a 74-marker haplotype and then fine-mapped to a 56-marker region. This month a new calf homozygous for most of the HH3 haplotype ruled out all except 8 markers in the fine-mapped region. The search area had been 2.9 Mbp of DNA but now is only 0.4 Mbp. An HH3 heterozygous bull (O Man) has been sequenced, but the exact mutation has not yet been detected. Monthly XML files report haplotype status for newly genotyped animals using the latest information, whereas status codes for bulls with public evaluations are updated only in full releases.

New reproductive status and culling annual reports

By Jan Wright and Suzanne Hubbard

Annual reports are now available for reproductive traits and termination codes of cows. Both provide more detailed phenotypic summaries of Dairy Herd Information data by breed and across years than were available previously. The [reproductive status report](#) includes numbers of breedings per conception, days from calving to first breeding, days from calving to last breeding, conception rates (first and all breedings), and calving intervals. The [culling report](#) includes percentages of cows completing lactations and percentages of cows leaving the herd except for dairy purposes by reason for termination.

Automated processing of genotypes

By George Wiggans, Tabatha Cooper, and Jay Megonigal

The processing of incoming genotype files was automated, and provision was made to include the animal identification (ID) along with the sample ID in the file identifying the genotypes. A report card is generated reporting how many single-nucleotide polymorphisms (SNPs) had excessive missed calls, parent-progeny conflicts, or unusual frequency of heterozygotes compared with homozygotes (Hardy-Weinberg test). The thresholds vary by sample size. Submissions that pass all tests in the report card are automatically added to the database. Others require an explanation of the steps taken to improve the genotypes and then are considered for manual initiation of loading. Reports have been added to assist in discovering switched sample ID. After loading, genotype conflict files and parentage validation records are placed on the ftp site for requesters to access.