Changes to evaluation system (January 2009)

Genomic evaluations become official

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> **UPDATE (January 12, 2009)** – The previously announced plans for December 2008 and January 2009 calculations were modified as follows. On December 18, lactation records were updated and new evaluations computed using an additional 3 weeks of data for cows and more data for bulls than at the November 30 cutoff used to prepare files for the December 9 Interbull deadline. However, genomic evaluations that were released on December 1 were not recomputed in mid-December as anticipated. The genomic evaluations from December 1, 2008, are official unless 1) the bull's reliability for net merit was higher in the traditional evaluation from December 18, 2008, or 2) the bull had foreign daughters, in which case the Interbull multitrait, across-country evaluation is official. Counts of daughters and herds are from December 18, 2008, for domestic bulls and from November 30, 2008, for bulls with foreign daughters even though only daughter data from July 26 (August 2008 evaluation data) were included in genomic evaluations. Among previously active AI bulls, only 20% gained a sufficient number of daughters for their December 18 traditional evaluation to replace the December 1 genomic evaluation. For future evaluations, AIPL plans to include all new phenotypic information in genomic calculations.

> **UPDATE (January 22, 2009)** – Tables summarizing differences between December 2008 genomic and traditional evaluations are available for active AI bulls and for young bulls.

Genomic predictions of genetic merit become official in January 2009. Predicted transmitting abilities (PTAs) use genomic data derived from DNA in addition to traditional phenotypic and pedigree data. Genotypes for 38,416 single-nucleotide polymorphisms evenly distributed across all 30 chromosomes document which genes each animal inherited and provide a new source of information for genetic evaluations. Formats 38 and 105 indicate genotyped status in bytes 547 and 190, respectively. Codes are 0 for traditional evaluations, 1 for genotyped animals, and 2 for descendants of genotyped animals with reliabilities that increased by at least 1% because of inclusion of genomic information in the parent average (PA). Descendants of genotyped animals have updated PAs and PTAs using the same methods developed previously to include information from foreign parents. Ancestors are not updated because programs are not yet available to transfer genomic information from a genotyped calf to its nongenotyped dam, for example.

Genotyped heifers are eligible for elite status and have records in the format-105 files. Genotyped young bulls are not eligible for active artificial-insemination (AI) status. However, genomically tested bulls that will be marketed are identified as G status. Format-38 files include a record for each bull with a National Association of Animal Breeders (NAAB; Columbia, MO) code, and the genomic PTA is listed as official for genotyped bull calves only after they receive an NAAB code because of NAAB's 5-year exclusive license or after they reach 24 months of age. Domestic test files for cows in format 105 and for bulls in format 38 are available for inspection. Evaluations contained in these files are not from the latest December calculations but rather from an earlier test in October. A U.S.-only version of format 38 without genomic information added is provided so that genomic adjustments can be better understood. Genomic equations are solved using data from the previous multitrait, across-country evaluation from the Interbull Centre (Uppsala, Sweden). The official PTA for each proven bull includes the extra information from genomics or from new daughters added since the last evaluation, but not both, because recalculating genomic predictions after the arrival of Interbull data on the Thursday prior to Tuesday release is not feasible.

Calving-trait and type files also include genomic evaluations as official, and programming to include those records has begun. Breed associations and NAAB continue to distribute calving-trait and type files. Genomic predictions are available for 16 linear traits but not feet/legs score, rear-teat placement, or rear-udder width. Currently, genomic net merit is obtained by directly analyzing net merit as a trait, because genomic results were not available for all individual traits. Genomic evaluations for stillbirth began in October 2008. In the future, genomic net merit could be obtained as a sum of individual genomic PTAs as is done for breed association composites and indexes.

Genomic predictions for Holsteins have been computed about every 2 months since April 1, 2008. Initially, letters to owners and computer files labeled as unofficial were distributed directly from the Animal Improvement Programs Laboratory (AIPL), but breed associations and NAAB now provide those services. Jersey genomic PTAs were tested in June, found to be significantly better than PAs, and distributed unofficially to owners in October 2008. Because of limited numbers of genotyped bulls, Brown Swiss predictions were not much better than PAs and were not distributed. Negotiations have begun on obtaining more Brown Swiss genotypes from Europe. As of October 2008, the USDA database includes 368 Brown Swiss, 1,558 Jersey, and 14,720 Holstein genotypes.

Genomic inbreeding coefficients and genomic estimates of future inbreeding (GFI) analogous to expected future inbreeding (EFI) are now included in computer files for genotyped animals. Genotypes allow measuring actual homozygosity and percentages of genes in common instead of the expected fractions computed from pedigrees by Wright's 1922 formulas. For GFI, the reference population is all genotyped animals born in the last 10 years. For EFI, the reference population is a sample of females born in the last 5 years. Thus, GFI and EFI should have nearly the same interpretation and, in fact, are similar numerically. Genomic inbreeding is about 2% higher for males than for females because the X chromosome is coded as homozygous in males.

Reliability of PA for young Holstein bulls and heifers averaged 36% for net merit but increased to 66% when genomic information was included. Theoretical reliabilities were reported initially but now have been reduced by multiplying the theoretical gain in daughter equivalents by 0.6. For young bulls, genomic PTAs for some traits average a little lower than PAs because upward biases in PA are being corrected. For example, genomic net merit averaged $388 compared with $420 for traditional PA; genomic PTA protein averaged 34 pounds compared with 39 pounds for traditional

PA. For active AI bulls, genomic evaluations had significantly higher reliabilities than traditional evaluations for nearly all traits and were distributed unofficially on the AIPL web site beginning in August 2008.

Further explanation of the methods for calculating genomic evaluations are available.

Multitrait best prediction

By John Cole, Dan Null, and Paul VanRaden

Milk, fat, and protein lactation records were computed jointly by multitrait best prediction instead of separately by single-trait best prediction. Somatic cell score evaluations continue to be on a single-trait basis. Best prediction recently has been enhanced by the addition of improved lactation curve functions, new estimates of correlations among test days, and the ability to accommodate lactations longer than 305 days.

Gains in reliability for milk and components yields were expected because of the change to multitrait best prediction, particularly for bulls with many daughters in alternative test plans, because estimates of missing test-day yields can be calculated through correlations with other traits. Reliabilities for PTA protein of active AI sires increased as expected for all breeds, with gains ranging from 4.2% (Brown Swiss) to 7.5% (Jersey). Reliabilities for PTA milk increased slightly (~1%) for Guernseys, Jerseys, Holsteins, and Milking Shorthorns but were unchanged for Ayrshires and Brown Swiss. Records from milk-only herds were examined, and quality of data was found to be poor; those records continue to be excluded from routine evaluations.

Further explanation of the methods for calculating best predictions of lactation yield are available.

Cow and heifer conception rates

By Jana Hutchison and Paul VanRaden

Genetic evaluations of bulls for cow conception rate (CCR) and heifer conception rate (HCR) are being released for the first time in January 2009. The CCR is based on data and a model similar to those introduced for sire conception rate (SCR) in August 2008; HCR is based on previous research reported by Kuhn et al. For CCR, PTA ranged from −8% to +8%; HCR PTA ranged from −5% to +5%. Models and edits for CCR and HCR are described in form GE along with daughter pregnancy rate. For Holsteins, genetic correlations with traits similar to CCR from 10 other countries ranged from 0.50 to 0.90 and averaged 0.73. Correlations of HCR ranged from 0.76 to 0.91 with 5 other countries and averaged 0.83. Interbull correlations for CCR averaged 0.62 for Jerseys, 0.69 for Brown Swiss, and 0.78 for Guernseys; correlations for HCR averaged 0.88 for Jerseys, but other breeds had insufficient data for analysis because conception records were stored only after 2003. Evaluations for CCR and HCR are not yet included in net merit or in format-38 files. Instead, the 2 new traits are available in a separate, downloadable file that includes both domestic and foreign bulls.