

Changes to evaluation system (April 2009)

Revisions to genomic calculations

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The order of calculations for genomic evaluations was changed so that new lactation records received between January and April could be included in April genomic evaluations. Thus, traditional April evaluations for domestic bulls and January multitrait across-country evaluations (MACE) for foreign bulls were the input data for estimating the effects of single-nucleotide polymorphisms (SNPs). Current MACE evaluations still are official for bulls with foreign daughters rather than using the previous MACE evaluation plus genomic information. Although new programs to combine genomic information with current MACE evaluations are ready, they were not introduced because the April genotype file was received by the Animal Improvement Programs Laboratory 1 week later than expected, which did not allow adequate time to check results of the new blending procedure.

Approximate genomic reliabilities replaced exact reliabilities because of insufficient time for matrix inversion and multiplication due to the delay in receipt of genotype data. The total number of animals genotyped now exceeds 25,000, and the time required for exact reliability calculations increases with the cube of that number. Computation of exact reliabilities would have required about 2 days, whereas approximate reliabilities require only about 2 minutes. With the matrix inversion used previously, the number of daughter equivalents from genomic information differed for each animal depending on how many close relatives were genotyped. The new approximate formula adds the same number of daughter equivalents for each genotyped animal. The sum of traditional reliabilities minus parent-average reliabilities for all genotyped animals in a breed is divided by a constant chosen to make exact and approximate daughter equivalents equal on average. Both the exact and approximate methods are multiplied by 0.6 to match reliabilities observed in data cutoff studies. As a result of switching to the approximation, genomic reliabilities for individual animals with many or few genotyped relatives decreased or increased slightly in April as compared with January. The approximate reliabilities could be improved, or exact reliabilities could be calculated in the future if adequate time is available. Use of the approximate procedure for Holsteins is expected to continue as the number of genotyped animals increases.