

# Changes to evaluation system (August 2009)

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## Brown Swiss genomic evaluations

*By George Wiggans, Paul VanRaden, Tad Sonstegard, and Curt Van Tassell*

Official genomic evaluations were computed for 906 Brown Swiss animals. Reliability was improved over initial tests by genotyping additional bulls not previously available in the Cooperative Dairy DNA Repository and by trading genotypes for 115 bulls with the Swiss Brown Cattle Breeders' Federation in Switzerland in a trade arranged by Dan Gilbert and Jürg Moll. For young animals, genomic reliabilities average about 12% above parent average reliability, as compared to 20% for Jerseys and 30% for Holsteins. The U.S. Brown Swiss Association will distribute evaluations for both males and females. They offer testing of females and young bulls because testing of bulls is not restricted to NAAB members in this breed.

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## Revised marker set used in genomic predictions

*By Paul VanRaden, George Wiggans, Mel Tooker, Jana Hutchison, and Lillian Bacheller*

An expanded set of 43,385 markers was used to compute genomic evaluations for all three breeds. Previously, markers were required to have minor allele frequency > 0.05 for Holsteins and > 0.03 for other breeds (Wiggans et al, 2009), and numbers used were 38,416 for Holsteins, 31,628 for Jerseys, and 34,593 in preliminary tests of Brown Swiss. Single-nucleotide polymorphisms (SNPs) with low minor allele frequency or even monomorphic SNP were included after edits to remove SNP that had many missing genotypes or parent-progeny conflicts. Observed gains in reliability from using the new SNP set were mostly positive but < 1%. Research on evaluations and relationships across breeds has begun using the common SNP set. While reprocessing previously called genotypes, missing parentage markers from the set recommended by Heaton et al (2007) were recovered for use in verifying parentage of genotyped animals worldwide.

All laboratories now report called genotypes rather than only intensity files. AIPL has discontinued calling genotypes after verifying consistent genotyping among the laboratories. Genotypes are edited and stored in AIPL's database as received, allowing pedigree conflicts or quality problems to be resolved sooner and simplifying recovery of genotypes after conflicts have been resolved. Marker quality remains excellent. Less than 0.4% of genotypes have missing values, and 75% of the 43,385 markers have no parent-progeny conflicts among the 32,234 genotyped animals in the database.

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## Blending of genomic and current Interbull evaluations

*By Paul VanRaden and Jay Megonigal*

**Aug 14 UPDATE:** The previously announced blending of genomic and current Interbull data in the final selection index will not be implemented in August, partially because of time constraints caused by receiving corrected Interbull files later than anticipated. August 2009 evaluations will use the same methods as in April of comparing reliabilities to determine if the current Interbull evaluation is official or the genomic evaluation estimated from current domestic evaluations and previous Interbull evaluations. An exception is that the blending procedure was used for Holstein type traits, as in April. The second proposed change, that genomic evaluations replace traditional evaluations for genotyped animals even if the reliability did not increase by >1%, was implemented for August evaluations. Previously, traditional evaluations were official if genomic reliability was not at least 1% higher, for example if traditional reliability was 99%. AIPL regrets any inconvenience this may cause.