Changes to evaluation system (August 2011)

Inclusion of British and Italian Holstein genotypes

By Katie Olson, Paul VanRaden, George Wiggans, and Mel Tooker

Exchange of genotypes with the Italian Holstein Association (ANAFI) and the Agriculture and Horticulture Development Board (DairyCo division) of the United Kingdom resulted in about 3% higher reliability for most traits of young animals as compared with previous genomic predictions from North American data. The Bovine SNP50 BeadChip (**50K**) genotypes for 3,038 proven bulls provided by ANAFI were used in monthly updates beginning in June. The DairyCo data included high-density (**HD**; >750K) genotypes for 566 bulls and 50K genotypes for 316 bulls, of which 781 were progeny tested. The DairyCo genotypes were used in August, but only a 50K marker subset was included from HD genotypes because the use of HD genotypes in evaluations still is being researched and has not yet shown large improvements in reliability. Correlations between young animal evaluations with and without the Italian genotypes ranged from 0.991 for protein yield to 0.980 for rear legs (rear view). Stillbirth evaluations from Italian bulls were excluded to avoid a slight loss of genomic reliability that would result from very low genetic correlations with the United States. The bull genotypes contributed by Italy and the United Kingdom were used in estimating marker effects for other animals, but traditional multitrait across-country evaluations are still reported for the bulls themselves because genomic information is not yet official within Italy and the United Kingdom. Further research and individual trait statistics on including Italian bull genotypes are available.

Reporting of haplotypes that affect fertility

By Paul VanRaden, Katie Olson, Dan Null, and Jana Hutchison

Five haplotypes were recently discovered that appear to cause embryo loss when homozygous as indicated by fertility records from thousands of matings where daughters of heterozygous sires were bred to heterozygous sires. The XML files now provide information about the status of these haplotypes for all genotyped animals. Because the conditions are not directly observable and exact genetic or biological cause is not known, simple labels of Holstein Haplotype 1 (HH1), Holstein Haplotype 2 (HH2), Holstein Haplotype 3 (HH3), Jersey Haplotype 1 (JH1) and Brown Swiss Haplotype 1 (BH1) are used for these haplotypes that impact fertility. Test files containing the July data plus the 5 new fields were made available in July. The new fields contain a “1” for animals that have one copy of this haplotype, a “0” for animals that have no copies of the haplotype and blank for haplotypes that do not occur in the animal’s breed (e.g., HO animals have only HH1, HH2 and HH3 reported). Another new field JH1_PC, reports pedigree confirmation of the JH1 haplotype. Animals with one copy of a haplotype impacting fertility that traces back to a genotyped ancestor that also has the same haplotype within the first four generations of pedigree are coded as “C” for confirmed, whereas others with this haplotype are coded as “N” for not confirmed. An N code may result from missing pedigree, non-genotyped ancestors or being the source animal. The haplotype test does not require confirmation by pedigree, but that field provides supporting information. All genotyped animals in the XML file have their status reported. Genotypes based on the low-density Bovine 3K BeadChip and those for imputed dams are less accurate, and at each evaluation a few of those animals may change status. Haplotypes of animals tested at 50K are usually stable from month to month, but changes will occur between July test files and August official files because the new marker edits (explained below) cause shifts in the positions of haplotype segments.

These haplotypes affecting fertility have small economic effects and their expected losses are already included to some degree in released rankings for sire conception rate (**SCR**), cow conception rate (**CCR**), heifer conception rate (**HCR**), and daughter pregnancy rate (**DPR**). Of those, net merit includes only DPR and thus does not fully account for economic effects of the haplotypes. Current frequencies of heterozygotes range from 4.5 to 23.4% for these five haplotypes. A heterozygous sire mated at random to females in the breed would reduce average conception rate by conception rate multiplied by the frequency of heterozygotes divided by 4. For example, if average conception rate is 31% and the frequency of heterozygotes is 5%, the average loss from using a heterozygous sire is 31%(0.05)/4 = 0.39%, which is fairly small compared with normal variation among animals for conception rate. Standard deviations of total sire effects or transmitting abilities are 2.3% for SCR, 2.9% for CCR and 2.4% for HCR, and many heterozygous bulls have positive fertility evaluations due to other favorable genes. Population conception rates would increase by less than 1% by eliminating any of the haplotypes below from the population. Therefore continued selection for net merit with some attention to SCR, CCR and HCR is recommended instead of direct selection against these haplotypes. Because inheritance appears to be recessive and an animal’s status is reported for genotyped bulls and cows, avoidance of mating heterozygous cows to heterozygous bulls using computerized mating programs will be an effective and economical method to improve fertility. A more complete report is being reviewed by *Journal of Dairy Science*, and the abstract is available.

Table 1. Frequency of heterozygotes, impact on conception rate if heterozygous bulls are mated randomly within breed, and earliest genotyped heterozygous ancestors for the five haplotypes.

Haplotype name	Earliest genotyped heterozygous ancestors	Frequency of heterozygotes (%)	Impact on conception rate (%)
HH1	Pawnee Farm Arlinda Chief	4.5	-0.35
HH2	Willowholme Mark Anthony	4.6	-0.36
HH3	Glendell Arlinda Chief, Gray View Skyliner	4.7	-0.36
JH1	Observer Chocolate Soldier	23.4	-2.22
BH1	West Lawn Stretch Improver	14.0	-0.98

Changes in marker edits

By Mel Tooker, Paul VanRaden, and George Wiggans

New marker edits have added 3K SNPs whose quality has improved recently and removed some 50K SNPs because of Hardy-Weinberg edits. These edits also changed some SNPs from usable to unusable or vice versa because of added data. Many more 50K version 2 SNPs were added that were not on version 1. Previously, 42,503 50K SNPs were available for use in genomics, but after edits removed 670 SNPs and added 3,351 SNPs, there are 45,184 SNPs currently available. Similarly on the 3K version, edits removed 25 SNPs and added 91 additional SNPs resulting in 2,680 SNPs currently being used. The usability of many HD SNPs was changed because 1100 HD genotypes are now available rather than the initial 300 HD genotypes. From the HD genotypes, only the 50K subset is used officially and another 600,000 SNPs are used in research. The new edits caused some changes to the haplotypes affecting fertility for individual animals. Additional information on marker edits is available in this 2011 *Journal of Dairy Science* abstract 330 and a presentation.