APRIL CHANGES

Genomic evaluation of Guernseys

By Tabatha Cooper, George Wiggans, Sophie Eaglen, Janez Jenko, William Luff, John Woolliams, and Brian Schnebly

Genotypes from 2,376 Guernsey bulls and cows from collaboration between the United States, Canada, the United Kingdom, and the Isle of Guernsey are the basis for launching the U.S. genomic evaluation of Guernsey cattle. A study in which data from August 2011 were used to predict April 2015 performance showed a gain in reliability over parent averages of 16.8 percentage points averaged across traits. Breed determination uses 21 markers that are nearly monomorphic (over 90%) in Guernseys and have less than 30% of animals homozygous for that allele in Holsteins, Jerseys, Brown Swiss, and Ayrshires. The number of markers is small because finding ones that meet the requirements becomes more difficult as more breeds are added. A major genetic effect was discovered on chromosome 19 near 27,000,000 base pairs. Its effect is as large as that of the gene for diacylglycerol O-acyltransferase 1 (*DGAT1*) and affects many more traits (milk, productive life, somatic cell score, daughter pregnancy rate, cow conception rate, size, rump, udder, and teat length). However, it does not affect NM$; therefore, the trait effects must be almost canceling. The new Guernsey evaluations will be provided in the same formats and on the same schedule as for the other breeds.

The research leading to these results has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no 289592 -Gene2Farm. Select Sires (Plain City, OH) and the American Guernsey Association (Columbus, OH) contributed to project development and provided genotypes; CDCB (Bowie, MD) supplied pedigree, performance, and genotypic data.

Breed base representation for crossbreds

By Paul VanRaden, Tabatha Cooper, Jay Megonigal, Duane Norman, and Jo�o D�rr

Most crossbreds have not been included in genomic evaluations because marker effects are computed separately within breeds. Edits that determine which animals are evaluated use a small set of breed-check markers. Using all markers allows each animal's ancestry to be estimated more precisely. Breed base representation (BBR) will now estimate the percentage of DNA contributed to the animal by each of 5 evaluated breeds: Holstein, Jersey, Brown Swiss, Ayrshire, and Guernsey. These 5 new fields sum to 100 (with a minimum of 0 and a maximum of 100). BBR values of 94 to 99% are set to 100% such values occur often even for animals with 100% purebred ancestry. The initial BBR estimates have a standard error of about 2% caused by normal variation within a breed as well as additional error caused by imputation from lower density chips. BBR values will be distributed only once for each animal, and update files will then include only the new animals.

The genotyped, progeny-tested bulls within each breed of evaluation serve as the reference population for that breed. Scandinavian Red bulls are included in the Ayrshire population and are all treated as if purebred Ayrshire. The BBR values can provide (1) information about breed composition that is more accurate and much easier to interpret than breed-check markers and (2) a method for combining the marker effects from different breeds into accurate genomic predicted transmitting abilities (GPTAs) for crossbreds. Such GPTAs must be computed on the all-breed instead of within-breed bases, and crossbred GPTAs for conformation traits are difficult for that reason. About 12,000 crossbred animals were not

evaluated previously. It is believed that the use of BBR can provide the means for making genetic predictions for crossbreds possible in the future. For further information, see:

- VanRaden, P.M., and T.A. Cooper. 2015. Genomic evaluations and breed composition for crossbred U.S. dairy cattle. Interbull Bull. 49:19–23. | PowerPoint presentation

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Edits and adjustments for heifer conception rate

By Jana Hutchison, Paul VanRaden, and Leigh Walton

Age limits and age groups were updated to include heifer conception rate (HCR) records for younger animals. Previously, records had been excluded for heifers inseminated before 1 year of age. New edit limits include heifers inseminated at 8 months of age and older, and another age group was added in HCR for records from the youngest animals. About 297,231 records were added for HCR, which is about 3% of total records. Use of records from these younger animals should improve timeliness and reliability of HCR evaluations. Earlier fertility is desired in recent years because of greater use of sexed semen and sires with improved calving ease as well as earlier maturity either from improved management or genetic differences.

The HCR model previously used a constant across all years to adjust for reduced fertility of sexed semen. The new model estimates within-year differences between conception rates (CRs) based on conventional or sexed-semen breedings, and those estimates are:

Year	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
CR difference (%)	25.8	14.1	18.1	16.4	15.1	15.1	17.0	15.0	12.4	9.5

Conception rates for sexed semen have greatly improved in the last 2 years (from more than 15 percentage points lower than conventional semen in past years to less than 10 percentage points lower in 2015). This better fertility is likely the result of improved sorting methods and products with reduced sort ratios. The new adjustment factors will be implemented along with the age edit change for HCR. Sexed-semen adjustments will also be revised for cow conception rate, but differences are smaller than for heifers because conception rates are lower and affect fewer records because of less use of sexed semen for cows.

Mutations in HCD and in BH2

By Dan Null and Paul VanRaden

The Holstein haplotype test for cholesterol deficiency (HCD) was improved by using the exact location of the mutation. Two research groups (Charlier, 2016; Menzi et al., 2016) reported that the mutation is a mobile element insertion of DNA from another chromosome into an exon of gene APOB at location 77,958,994 on chromosome 11 (UMD3). Previously animals were labeled as carriers only if they received the full haplotype of length 3.5 Mbase from bull Storm, but now only the portion of the haplotype containing the mutation is required. Previously 32,712 animals were code 1 carriers with pedigree verification, and 5,643 additional animals became code 1 using the known location of the mutation. Similarly, 27,658 were code 3 possible carriers without pedigree versification, and 5,704 code 3 animals were added. Soon, direct test results could also be included within the haplotype to further improve accuracy, as is done with several other recessive haplotypes.

Brown Swiss haplotype 2 (BH2) test results were also improved using the exact location of the mutation at 11,063,520 on chromosome 19 (Schwarzenbacher et al., 2016). A 1.1 Mbase

region containing the mutation had previously been used to examine crossover haplotypes, and 49 additional carriers were identified using the exact location. Direct laboratory tests for the BH2 mutation in gene TUBD1 may be available in the near future. Nearly all calves homozygous for BH2 or for HCD die at young ages. Genomic testing, selection, and mating programs are all useful to reduce the occurrence of these and other recessive defects.

Reliability and inbreeding in weekly evaluations

By Paul VanRaden, Jay Megonigal, and Gary Fok

Genomic reliability (GREL), genomic inbreeding, and genomic future inbreeding (GFI) have been provided in the weekly automated processing since January 2016, whereas previously those fields were computed only during the monthly reprocessing of all data. Weekly evaluations include only animals with new genotypes or pedigrees that changed (Wiggans et al., 2015), and an approximate 2-part instead of 3-part selection index is used to compute GPTA. A similar 2-part instead of 3-part selection index approximation was developed to compute GREL. To compute GFI, the relationship of each animal to an average genotype for reference bulls born in the last 10 years was computed instead of computing all individual relationships and then averaging. To compute expected future inbreeding (EFI), the reference bulls and their ancestors were included in the pedigree file; for each new animal, an average pedigree relationship to the reference bulls was computed using the method of Colleau (2002) and software provided by Ignacio Aguilar and Ignacy Misztal (University of Georgia, Athens, GA).

Results for a test of weekly data were consistent with the following official monthly evaluation for 11,426 animals that were in both. For Holstein net merit, GREL of the new animals averaged 72.2% with a standard deviation (SD) of 2.2 percentage points for the weekly evaluation compared with 72.4% (SD of 2.2) for the monthly full evaluation; GREL correlation for the weekly and monthly evaluations was >0.99. New animal GFI averaged 6.9% (SD of 0.9) for the weekly data compared with 6.7% (SD of 0.8) for the monthly data; correlation of weekly and monthly GFIs was 0.98. The average EFI was 4.9% (SD of 1.5) for weekly data compared with 5.5% (SD of 1.7) for monthly data. The animals' own genomic inbreeding averaged 5.9% (SD of 3.5) for both weekly and monthly data (correlation of 1.0), whereas own pedigree inbreeding averaged 4.7% for weekly compared with 4.5% for monthly data (correlation of 0.96). Pedigree corrections during the week after genotypes arrived caused some of those differences.

Good approximations for GREL and inbreeding fields were obtained by outputting summary data for the reference bulls during monthly processing and inputting that summary data during weekly processing. Full monthly processing now takes more than 4 days; if sufficiently accurate, the weekly system could replace some of the monthly evaluations as computing times continue to increase.

References

- Colleau, J.J. 2002. An indirect approach to the extensive calculation of relationship coefficients. Genet. Sel. Evol. 34:409–421.
- Wiggans, G.R., P.M. VanRaden, and T.A. Cooper. 2015. *Technical note:* Rapid calculation of genomic evaluations for new animals. J. Dairy Sci. 98:2039–2042.
