Changes to Evaluation System (August 2007)

Breed-composition file for crossbreds

By Paul VanRaden, Melvin Tooker, Leigh Walton, Joel Megonigal, Jr., and John Cole

Beginning in August 2007, breed compositions are made available for crossbred animals. Crossbreds are animals with a sire and dam of known but differing breeds. The new crossbred-fields format will include sex code, breed code, country code, identification number, heterosis percentage, sire breed stack, pedigree breed stack, and breed percentages. A crossbred-fields file is available for download at the same time as the format-105 cow evaluation file.

A breed stack is a system for designating crossbreeding over generations. The pedigree breed stack uses two-character breed codes and is a way to visualize an animal's pedigree. Unknown ancestors are indicated by "--". Reference note 158 shows the order of breed codes in the pedgree breed stack.

Breed composition of most crossbreds can be identified quickly from breed codes of the sire, maternal grandsire, dam's maternal grandsire, etc. This list of breed codes is called a sire breed stack and provides a complete picture of the mating system except for pedigrees that include crossbred sires. Reference note 157 shows the order of breed codes in the sire breed stack. For example, suppose a purebred Holstein is mated to a purebred Jersey sire. The breed code in the progeny's identification number could have been recorded by the farmer as HO, JE, XX, or even WW, but the sire breed stack of all progeny is reported as JEHO. The order reflects that a Jersey sire was used in the last generation and that the dam's sire was a Holstein. A reciprocal crossbreeding would have the reverse order of HOJE for resulting progeny. If JEHO cows are backcrossed to a Holstein sire, the sire breed stack of the next generation would be their sire's breed followed by the dam' s breed-composition code (HOJEHO). Another generation of mating to a Holstein bull would produce progeny with 12.5% Jersey genes, and the sire breed stack would be HOHOJEHO.

The breed-composition code shows the percentage of genes from any breed within a breed stack. The portion of genes from each breed equals 0.5 if the sire is of that breed plus 0.25 if the maternal grandsire is of that breed and then continue to add 0.5^n until the earliest known sire, which receives twice that credit so that the sum is 1. Both parents of the earliest known maternal ancestor are assumed to be of the same breed. If any sire along the maternal path is coded as crossbred, its breed portions must be obtained first and then multiplied by 0.5^n. Breed portions are multiplied by 100 to be included as percentages in breed-composition codes.

The reported percentage of heterosis is the 100 times the coefficient of heterosis, which equals 1 minus the sum of the sire's breed portion times the dam's breed portion for each breed.

Examples

A Holstein sire is mated to a Brown Swiss-Jersey crossbred (BSJE) dam, which results in progeny with a HOBSJE sire breed stack. The sire is 100% Holstein, and the dam is 50% Brown Swiss and 50% Jersey. The breed compositon for their progeny is listed as 50HO25BS25JE, and the percentage of heterosis is 100.

More complex calculations can be demonstrated using a rotational-cross pedigree with a sire breed stack of JEHOBSJEHOBS. This animal's breed composition is $0.5 + 0.5^4 = 0.5625$ Jersey, $0.5^2 + 0.5^5 = 0.28125$ Holstein, and $0.5^3 + 2(0.5^6) = 0.15625$ Brown Swiss, which is listed as 56JE28HO16BS. The sire is 100% Jersey, and the dam is 56.25% Holstein, 31.25% Brown Swiss, and 12.5% Jersey. Thus, the coefficient of heterosis is $1 − 0(0.5625) − 0(0.3125) − 1(0.125) = 0.875$, a heterosis percentage of 88.

Adjustments to all-breed model

By Paul VanRaden and George Wiggans

Revisions and corrections were made to the all-breed evaluation system introduced in May 2007. Methods to account simultaneously for inbreeding and heterosis were revised, and the programs that assign management groups and adjust cow predicted transmitting abilities (PTAs) for expected future inbreeding (EFI) were corrected to work as intended. The programs used in May had accidentally grouped registered and grade Holsteins together instead of separately, and incorrect EFI adjustments for cows were responsible for some of the slight shifts in genetic bases that were observed. Jersey bull PTAs increased on average by 101 pounds of milk, 3 pounds of fat, and 3 pounds of protein in August after decreases of 184 pounds of milk, 5 pounds of fat, 7 pounds of protein in May. August increases for Brown Swiss bulls are 73 pounds of milk, 2 pounds of fat, and 2 pounds of protein, with smaller changes for other breeds and almost no change for Holstein bulls. The base changes will make August evaluations more similar to evaluations from the previous within-breed system.

Previously published estimates of heterosis and inbreeding depression were included in the May 2007 all-breed model. Combined effects of the two factors resulted in larger adjustments for heterosis than intended. The inbreeding depression that has accumulated in purebreds since 1960 accounts for some of the heterosis when purebreds are mated to obtain crossbreds and should be subtracted when both effects are included in the same model. Heterosis estimates of VanRaden and Sanders (Journal of Dairy Science 86:1036, 2003) were from a model that did not include inbreeding adjustment. Records from cows born from 1990 through 1998 were used, and average inbreeding during those years was 3.4% for Holsteins, 4.5% for Jerseys, and 3.5% for Brown Swiss versus 0% for crossbred cows. For productive life, the estimate of heterosis used records of cows born from 1960 through 1991; average inbreeding during those years was only about 2%. Regressions on coefficients of heterosis and inbreeding could perhaps be estimated simultaneously in the all-breed model. However, Cassell et al. (Journal of Dairy Science 86:2967, 2003) recommended that inbreeding regressions are more accurate if obtained from only cows with complete pedigrees.

Adjusted heterosis was calculated as the published heterosis plus the inbreeding regression times the average inbreeding percentage:

	Milk (pounds)	Fat (pounds)	Protein (pounds)	Somatic cell score	Productive life (mo)	Daughter pregnancy rate (%)
Published heterosis	700	35	26	0.02	0.3	1.8

Inbreeding regression	−65.3	−2.37	−2.15	0.02	−0.22	−0.078
Inbreeding percentage	3.8	3.8	3.8	3.8	2.0	3.8
Adjusted heterosis	452	26	18	0.10	−0.1	1.5

which can be interpreted as heterosis among base animals in 1960. For productive life, published heterosis was slightly less than that expected from the inbreeding loss alone, and an adjusted heterosis of 0 will be used instead of −0.1.

Use of adjusted heterosis in the all-breed model avoids double counting of inbreeding loss. Breed effects changed little when adjusted heterosis was used in August, probably because most information comes from purebred rather than crossbred comparisons. Crossbred cows had slightly higher PTAs on the all-breed base after reducing heterosis estimates, but correlations of PTAs before and after heterosis revision were 0.99998 for recent cows and for recent bulls. Combined effects of all three changes (heterosis, management groups, and EFI) resulted in correlations of about 0.995 for cows but little reranking of bulls.

Parent averages for young bulls

By George Wiggans, Paul VanRaden, and Gary Fok

Parent averages for young bulls are now recomputed after receiving multitrait across-country evaluations (MACE) for all traits from Interbull. Previously, parent averages for young bulls used 3-month-old MACEs from Interbull for milk, fat, and protein and only domestic data for other traits. Evaluations for cows and for bulls progeny tested domestically continue to include adjustments for sire MACE from the previous evaluation and for foreign-dam evaluations of production traits, but other traits are not adjusted for foreign-parent information.

Revised definition of Interbull type-of-proof code

By George Wiggans

One of the key variables that determines whether a bull is included in Interbull evaluations is the "type of proof" code in the record sent to the Interbull Centre (format 010). Bulls that are reported as having semen distributed in the United States by the time that they are 48 months old but are over 7 years old when they first have 10 herds included in their evaluation are no longer coded as having an evaluation based on imported semen of a proven bull (second-crop daughters only; code 21) when the bull is under the control of a foreign organization. Those bulls now are coded as having an evaluation based on first-crop sampling daughters (code 11) or as having an evaluation based on first-and second-crop daughters (code 12). This change was made because some bulls that originate in Canada but are progeny tested in the United States previously had no country that reported a first-crop evaluation.