Changes to evaluation system (April 2011)

Adjustment of yield evaluations for all cows

By George Wiggans, Tabatha Cooper, and Paul VanRaden

Yield trait evaluations for all cows are now adjusted to match properties of bulls, whereas previously only genotyped animals were affected by that adjustment. For cows with domestic evaluations, the standard deviation of the difference between the cow's evaluations and parent average (**PA**) is reduced by a factor that ranges from 0.32 to 1 depending on reliability. Within each birth year, 40% of the difference between a cow's PA and average cow PA for that year is subtracted from the Mendelian sampling portion (adjustment is reduced to zero with increasing reliability for cows with yield reliability above 75), which brings the average for cows in line with that of bulls across the range of PAs. The adjustments have little effect on the average. Further adjustments are applied to the evaluations of genotyped cows, which are used to estimate the SNP effects, to bring their evaluations in line with their direct genomic values based only on bulls. The adjustments for genotyped cows with domestic evaluations and yield reliability over 0.55 is (169.7 pounds for milk, 8.3 pounds for fat, and 4.2 pounds for protein for Holsteins and 165.9 pounds for milk, 6.4 pounds for fat, and 5.8 pounds for protein for Jerseys and Brown Swiss) which is smaller than previous adjustments; thus, genotyped and nongenotyped animals can now be compared more easily. Foreign evaluations are not used in the calculation of SNP effect estimations. However, they are adjusted for genotyped animals to be used in the calculation of PAs and genomic predicted transmitting abilities (**PTAs**). Foreign adjustments for genotyped Holstein cows is (420.1 pounds for milk, 15.2 pounds for fat, and 12.6 pounds for protein for cows with reliability <0.55 and 700.7 pounds for milk, 25.9 pounds for fat, and 21.4 pounds for protein for cows with reliability > 0.55). No adjustment is needed for Jersey or Brown Swiss where there are few foreign cow evaluations included. Expected changes are closer to 0 when nongenotyped animals become genotyped. Table 1 shows changes in genomic **PTA**s (April 2011 - December 2010) of yield traits. Methods are described more fully by Wiggans *et al.* (2011, *Journal of Dairy Science* 94(Suppl. 1):in press). Further information is available in "Adjustments Make All Cow PTAs Similar to Those on Genomically Tested Cows."

Table 1. Changes in yield PTAs for genomically tested Holsteins, Jerseys and Brown Swiss (April 2011 - December 2010).

Holstein					
Males		**Mean (lbs)**	**Standard deviation**	**Minimum**	**Maximum**
Predictor	Milk	22	106	-686	771
	Fat	1	4	-34	31
	Protein	1	3	-21	23
Young	Milk	85	153	-1504	1191
	Fat	4	6	-53	42
	Protein	3	5	-41	24
Females		**Mean (lbs)**	**Standard deviation**	**Minimum**	**Maximum**
Predictor	Milk	104	194	-1627	1202
	Fat	4	7	-59	62
	Protein	4	6	-54	40
Young	Milk	82	216	-1871	1068
	Fat	4	8	-62	46
	Protein	3	6	-57	28

Jersey					
Males		**Mean (lbs)**	**Standard deviation**	**Minimum**	**Maximum**
Predictor	Milk	34	91	-641	720
	Fat	2	4	-21	32
	Protein	1	3	-17	22
Young	Milk	158	138	-582	609
	Fat	8	6	-23	35
	Protein	6	5	-21	26
Females		**Mean (lbs)**	**Standard deviation**	**Minimum**	**Maximum**
Predictor	Milk	236	164	-481	801

	Fat	12	7	-20	52
	Protein	9	5	-13	35
Young	Milk	153	194	-528	826
	Fat	9	8	-23	36
	Protein	6	6	-15	27

Brown Swiss					
Males		**Mean (lbs)**	**Standard deviation**	**Minimum**	**Maximum**
Predictor	Milk	-27	67	-717	442
	Fat	-1	3	-24	18
	Protein	-1	2	-24	11
Young	Milk	-80	103	-367	367
	Fat	-3	4	-21	21
	Protein	-3	3	-20	20
Females		**Mean (lbs)**	**Standard deviation**	**Minimum**	**Maximum**
Predictor	Milk	-187	151	-548	205
	Fat	-8	6	-19	11
	Protein	-6	5	-16	5
Young	Milk	-113	138	-542	199
	Fat	-4	6	-21	14
	Protein	-3	5	-17	12

Improved imputation

By Paul VanRaden and Dan Null

Beginning with March 2011 evaluations, haplotyping and imputation used a new version of the program findhap.f90. Several changes increased the proportion of correctly imputed genotypes. Instead of choosing one optimal segment length, haplotyping begins with long segments to detect matches for close relatives and then uses shorter segments to detect matches from more distant relatives. Version 2 also searches for great-grandparent haplotypes (not just those for genotyped parents and grandparents) and does population and pedigree haplotyping in one loop versus two separate loops. Those changes improved reliability by about 2 percentage points for animals with full pedigrees and by larger amounts for animals with limited pedigree or few genotyped ancestors. Further improvements may also be possible in the future by using the program FImpute from the University of Guelph. Additional details are provided on marker selection and imputation properties by VanRaden *et al.* (2011, *Journal of Dairy Science* 94(Suppl. 1):in press) and on new edits for 2,900-marker (3K) genotypes by Wiggans *et al.* (2011, *Journal of Dairy Science* 94(Suppl. 1):in press).

Chip type and genomic inbreeding in formats 38 and 105

By Paul VanRaden and Leigh Walton

Three fields containing genomic information previously provided only in XML format will be added to format 38 and format 105 because those are more widely used for updating databases. A numeric chip type field in bytes 616–617 of format 38 and 398–399 of format 105 will contain a value of 1 (50K), 2 (50K, version 2), or 3 (3K). Values of 4 (Illumina 777K (HD)) and 5 (Affymetrix 648K) are also assigned but will not yet appear in files because genotyping for those chips is still in the research stage. If an animal is genotyped with more than one chip, the highest density actually used in the evaluation will be reported. Nongenotyped imputed dams are reported in a separate genomic indicator field as done previously.

An animal's genomic inbreeding is now reported in bytes 618–621 of format 38 or bytes 400–403 of format 105, and its genomic future inbreeding (half of the animal's average relationship to other genotyped animals) is in bytes 622–625 of format 38 or bytes 404–407 of format 105. These inbreeding fields indicate the actual proportion of DNA shared instead of the proportion expected from the pedigree.

Multitrait heifer and cow conception rates

By Paul VanRaden, Mel Tooker, and Gary Fok

Heifer conception rate (**HCR**) and cow conception rate (**CCR**) have many missing records but moderate to high genetic correlations with existing traits. Approximate multitrait methods have been used to compute productive life (**PL**) since July 1994 and were revised in August 2000. For daughter pregnancy rate (**DPR**), multitrait methods have been used since February 2006 only to fill missing DPR PTAs for foreign bulls and for domestic cows that lacked fertility records, but those methods are not used to replace single-trait DPRs. The same approach is now used to fill missing HCR and CCR PTAs instead of using PA. Records for PL and DPR are available for cows that have calved since 1960, but records are available only for calvings after 1995 for CCR and after 2003 for HCR. Genetic correlations are high for CCR with DPR (0.86) and PL (0.59) but moderate for HCR with DPR (0.36), PL (0.24), and CCR (0.45). Filling the missing PTAs is helpful, but use of approximate or exact multitrait methods for all animals and genomic evaluations may be needed to make HCR and CCR more accurate for potential inclusion in net merit and other indexes in the future.

Genomic Reliability Discount

By Paul VanRaden, Katie Olson, Mel Tooker, and Jeff O'Connell

Holstein and Jersey genomic reliabilities were discounted further below theoretical reliabilities to match observed reliabilities from the most recent genomic validation. Comparing December to April, published reliabilities of proven bulls decreased by about 2% for net merit and 1-4% across traits for Holstein and 1% for net merit and 0-2% across traits for Jersey, with larger adjustments for less heritable traits. Young bull reliabilities decreased 6% for net merit and 3-9% across traits for Holstein and 3% for net merit and 2-6% across traits for Jersey. Brown Swiss were not discounted further because published and observed reliabilities from the validation study were similar on average. Theoretical reliabilities were reported initially in 2008, but discounts from theoretical have become larger as the predictor population grew. Discounts were last adjusted in April 2010 using validation data truncated in 2006 and were updated again now using data truncated in 2007. Precise genomic reliabilities are not easy to extrapolate because the truncated Holstein evaluations included 6,499 proven bulls and 3,375 cows with phenotypes whereas April 2011 evaluations include 12,152 proven bulls and 11,776 cows. Genomic evaluations were also computed from cows only and bulls only to verify that the two sexes provide consistent information for most traits.