

# Changes to evaluation system (April 2012)

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## Adjustments to genomic evaluations and reliabilities

By Paul VanRaden, George Wiggans, Jan Wright, and Tabatha Cooper

Genotypes from a new chip named the Geneseek Genomic Profiler (GGP) were included beginning with March evaluations. It was built from the Illumina BovineLD (LD) chip using the add-on capability. The chip code is GGP in XML files, and the chip number is 7 in formats 38 and 105. Markers on the chip include the 6,909 from the LD chip plus 45 new markers and selected additional markers from previous chips: 518 from the Bovine3K (3K), 702 from the BovineSNP50 (50K), and 479 from the BovineHD (HD). The use of additional GGP markers from the 3K and 50K chips improves the percentage of correctly imputed 50K genotypes to 99.2% for GGP versus 98.9% for LD in Holsteins and 98.9% versus 98.3% in Jerseys. Published reliabilities also increase by about 0.3% for young animals. Genomic evaluations use 8,031 of the GGP markers; the additional markers from HD and the new markers are used only in research. The GGP also provides genetic tests for several known recessive conditions, but those are not yet provided to the Animal Improvement Programs Laboratory.

Revised weights were used to combine information for genotyped animals. Genomic evaluations estimate marker effects and sum those into direct genomic values (DGVs). Information from nongenotyped ancestors is then included by a selection index that combines 3 terms according to their reliabilities: the DGV including polygenic effects, the traditional evaluation (PTA), and a subset evaluation (SPTA) estimated from pedigree relationships among the genotyped animals. For young Holstein bulls, those weights have averaged 0.99 for DGV, 0.12 for PTA, and -0.11 for SPTA. Alternative weights can increase reliabilities and regressions of predicting future data from past. Most regressions were close to expected values and increased when some weight was removed from the DGV and added to either the PTA or SPTA. For each 0.1 decrease in DGV weight, regressions increased by about 0.02 and standard deviations of young animal predictions decreased by about 4%. This reduces evaluations of top young animals as compared with older animals. For example, genomic PTAs for the highest young Holsteins decreased by about 100 pounds for milk, 4 pounds for fat, 3 pounds for protein, 0.2 months for productive life, 0.15 for final score type, and \$20 for net merit. Correlations of new with previous GPTAs were above 0.998. Instead of the theoretical value of 1.0, the DGV weight was limited to 0.95 for health traits, 0.90 for type traits, and 0.75 for calving traits. Limits for yield traits were 0.90 for Holsteins and 0.80 for Jerseys and Brown Swiss. Reliabilities changed only slightly with those adjustments but would decrease if DGV weights were reduced any further. Regressions for a few traits had been lower than expected, and the revised weights helped bring those into compliance with validation tests. (For further information, see VanRaden et al., [JDS 95\(Suppl. 1\):accepted.](#))

Published reliabilities were revised to agree more precisely with observed reliabilities from truncated data. Reliability formulas were adjusted to match observed reliabilities from August 2008 predictions, and published reliabilities for current data are extrapolated to include the added information since 2008. Previously, the extrapolation would reach 99% reliability with an infinitely large reference population but was revised to have a 90% asymptote calculated as 100% minus the estimated percentage of polygenic (unexplained) genetic variance. As a result of those adjustments and the revised selection index weights, published reliabilities for young Holstein animals were adjusted downward by about 3 percentage points for yield traits, upward by 3 to 6 percentage points for fitness traits, downward by 7 to 10 percentage points for calving traits, and upward by 1 percentage point for type traits.

An edit previously introduced in April 2010 to not use traditional productive life evaluations for females less than 36 months of age in the genomic evaluation is now extended to 48 months of age. Use of multitrait productive life improves accuracy; however, for a few bulls, the early correlated trait information from many genotyped daughters caused large differences between genomic and traditional productive life. For daughter pregnancy rate, multitrait evaluations are calculated for cows that do not yet have fertility records, but use of those also caused large differences between genomic and traditional daughter pregnancy rate evaluations for a few bulls. An edit analogous to the previous productive life edit was introduced to exclude traditional daughter pregnancy rate evaluations for genotyped cows less than 36 months of age. An analogous edit was also introduced for cow conception rate but does not yet affect official evaluations because traditional evaluations are still reported for cow conception rate. When tested using data from August 2008, these edits removed some of the previous upward bias in productive life and greatly improved reliability of young animal predictions for productive life and daughter pregnancy rate.

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## Data cutoff date for sire conception rate

By Jana Hutchison and Duane Norman

Edits for sire conception rate (SCR) were modified to use the latest test date for each herd rather than a constant cutoff date for all SCR data. This edit more precisely measures the days of opportunity for a cow to be diagnosed as pregnant or not pregnant following insemination. The SCR correlations before and after the edit change were 0.96 for Holsteins and slightly lower for other breeds, with little change in mean or standard deviation. The female fertility traits (cow conception rate and heifer conception rate) use a constant cutoff date but might also benefit from introducing herd test-date edits in the future.

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## Productive life field format

By Jay Megonigal

Months of PL has exceeded the +9.9 limit that the field was designed to store. Instead of moving to a new field, the plus sign is not included for values of 10.0 or higher. Values lower than -9.9 continue to have a floor of -9.9, but this affects only a few animals no longer of interest. This same coding change was made for daughter pregnancy rate, but no animals have exceeded +9.9 for that trait yet.

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## Sire-dam multitrait across-country evaluation (MACE)

From "[Interbull introduces Sire-Dam pedigree in MACE](#)" by the Interbull Centre Team

The Interbull Community has decided to introduce a new MACE model including relationships on bull dams in the April 2012 run. The background for the change is to move genetic groups further away from animals with data in order for them to have less impact on the proofs. The consequence is changes in proofs especially for bulls with no progeny test in own country and an average increase in reliabilities. The main reason for changes in proofs for this group of bulls is that the parent average of the bull is computed differently for sire-dam (SD)-MACE compared to the sire-maternal-grandsire(S-

MGS)-MACE model due to the change in pedigree structure. This due to the fact that the bull dam in the SD-MACE model gets a breeding value based on the relatives she has in the system. A national breeding value of the bull dam is not included in the MACE model. The breeding value of the dam is therefore only influenced by the performance of her relatives in the MACE system. A very positive performance of a dam, solely based on her relatives, will give a boost to a parent average of a bull compared to the parent average he had in the S-MGS system. A change in the parent average of a bull will therefore impact his converted proofs to other country scales and is the main cause of changes between systems. The usage of the sire-dam pedigree gives the MACE system more information on the genetic background of a bull. In case a dam has several sons tested in several countries, better links between countries are created.

[Download the whole fact sheet about SD-MACE.](#)