

# Changes to evaluation system (August 2012)

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## Revisions to heifer and cow conception rates

*By Jana Hutchison, Paul VanRaden, Mel Tooker, Jay Megonigal, and Gary Fok*

Predicted transmitting abilities for heifer conception rate (HCR) and cow conception rate (CCR) were improved both by edit changes and by using genomic instead of pedigree relationships. Edits for HCR and CCR were modified to use the latest test date for each herd rather than a constant cutoff date for all HCR and CCR data. This edit more precisely measures the days of opportunity for a cow to be diagnosed as pregnant or not pregnant following insemination. The HCR and CCR correlations before and after the edit change were 0.99 or higher for all breeds, with little change in mean or standard deviation. An edit for breed purity was decreased from 97% to 75% for the Milking Shorthorn breed to allow more records to be included. A very similar edit for herd test date was introduced for sire conception rate (SCR) in April 2012.

Genomic evaluations replaced traditional evaluations for both HCR and CCR. Estimated reliabilities for HCR of young Holsteins average 61% if genotyped with the BovineSNP50 (50K) BeadChip and a few percentage points less with lower density chips. Reliabilities for CCR average 69% with 50K genotypes. Corresponding reliabilities for young Jerseys and Brown Swiss average 39 and 32% for HCR and 49 and 38% for CCR, respectively. These estimated genomic reliabilities are lower than for other traits, but parent average reliabilities are also lower so that gains are reasonably good. The HCR and CCR traits have not yet been validated because no official traditional evaluations were computed prior to 2010 and because the historical database includes many fewer years than for other traits. Genomic fields were added to XML files in the July monthly release to allow inspection of these evaluations.

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## Specific cow adjustments by country of evaluation for Holsteins

*By George Wiggans and Tabatha Cooper*

Cow evaluations are obtained from 10 countries to improve parent averages and genomic evaluations of cows. Conversion equations from Interbull are used to put these foreign evaluations on a U.S. base. The sire-dam model implemented by Interbull in April affected the conversion equations, generally lowering evaluations converted from other countries and reducing the magnitude of adjustments needed. When the cow adjustment was implemented, converted cow evaluations were excluded from estimation of the marker effects but still contributed to parent averages and the cow's own genomic evaluation. An overall adjustment to force these evaluations to average the same as their direct genomic values (which do not include the polygenic effect) was implemented. Recently, variation by country in the appropriateness of the conversion equations was discovered, and individual country adjustments were developed. Foreign cow evaluations were classified by country of evaluation, and the average difference between the evaluation and direct genomic values was calculated. For Italy and Canada, separate adjustments were calculated for evaluations with reliability (excluding contribution from parent average) above and below 55% to continue the classification practice that had been used previously. For other countries, too few cows were available to estimate differences adequately for the high-reliability group. The adjustment difference between countries with the largest and smallest adjustments was over 890 pounds of milk. This refinement of the cow adjustment procedure improves the comparability between cows with domestic evaluations and those with foreign evaluations as well as among cows with foreign evaluations. These adjustments will be updated with the triannual traditional evaluations when new foreign evaluations are received. Few Jersey and Brown Swiss cows have foreign evaluations; therefore, no country-specific adjustments were calculated for them.

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## Genomic and pedigree inbreeding match better

*By Paul VanRaden*

A new adjustment method equates average genomic inbreeding with average pedigree inbreeding and average genomic relationship with average pedigree relationship by solving 2 equations for 2 unknowns. Genomic relationships were previously adjusted by regression to approximate pedigree relationships. The previous method put more emphasis on relationships than inbreeding because matrices have many more off-diagonal than diagonal elements. The shift resulting from the new adjustment makes genomic inbreeding closer to pedigree inbreeding on average and acts like a base change by changing the scale but not the animal's rank for genomic inbreeding. Thus, genomic relationships, inbreeding, and future inbreeding from August are not directly comparable to those from previous evaluations. Breeders are encouraged to use genomic rather than pedigree measures of similarity in their selection and mating decisions.

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## Mobility for Brown Swiss and additional traits for Milking Shorthorns

*By Jan Wright and George Wiggans*

Mobility was added as an official trait for the Brown Swiss breed. Milking speed and rear legs rear view (RLRV) were also added for Milking Shorthorns. The format 40 has been increased in length (327 bytes) to allow for the inclusion of mobility for those cooperators affected. Further details regarding mobility were provided in a presentation at the 2012 joint annual meeting of the Federation of Animal Science Societies ([abstract T43](#) and [poster](#)).

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## Additional Brown Swiss genotypes from Interbull

*By George Wiggans, Paul VanRaden, and Jana Hutchison*

Genotypes for 4,212 Brown Swiss bulls were received from the InterGenomics project at Interbull. Of those, 140 did not meet standard edits and were not used. Also, 99 bulls born before 1980 whose national evaluations are not included in multitrait across-country evaluations (MACE) were not used. U.S. data already had included genotypes from 773 foreign bulls obtained in trades with Switzerland, Germany, and Austria. The increased sharing of genotypes among 7 major Swiss populations improves accuracy for national services such as monthly processing, low density imputation, and female evaluation that are not offered by Interbull. Most gains in published reliability for young animals were from 5 to 10%, and correlations between U.S.

evaluations before and after adding the foreign genotypes ranged from 0.91 to 0.95. Exceptions were almost no change for rear legs / rear view because this trait is not included in MACE for Brown Swiss. Also, reliability gains for calving ease averaged only 3% because some countries do not participate or have low genetic correlations with the United States. The added genotypes included 3,467 bulls with daughter yield records; young bull genotypes are not exchanged yet. The genomic evaluations of foreign young bulls computed by Interbull continue to be provided in a separate file rather than in format 38.

Reliability gains were estimated using phenotypes available before August 2008 to predict degressed evaluations for 25 traits of 129 U.S. bulls proven after August 2008. Observed reliability with the additional foreign genotypes averaged 8% higher than with the previously available genotypes and 18.5% higher than parent average. Reliability increased for nearly all traits, and the observed increase was highest for fat percentage and lowest for daughter calving ease. Predictions were also examined for 1,058 bulls from all countries that were proven after August 2008. Probably because the majority of information used to estimate marker effects is now from Europe and because reliability of parent average is lower for foreign than for domestic animals, gains above reliability of parent average were even higher for foreign bulls than for U.S. bulls. Gains are less than forecast by simulation ([VanRaden and Sullivan, 2010](#)) but indicate large benefits from cooperation across countries.

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## Updated Chromosomal PTA Query

*By John Cole and Dan Null*

The [public query to display chromosomal predicted transmitting abilities for all genotyped animals](#) has been modified to display haplotype information. The query searches the AIPL database and returns genetic evaluation information for genotyped Brown Swiss, Holstein, and Jersey bulls and cows. Other changes include new options for controlling the range of values used in setting plot axes, the addition of heifer and cow conception rate evaluations to the results, code speed-ups that substantially reduce the amount of time for queries to run, and correction of a programming error that prevented animal ID information from linking to animal records correctly. A [user's manual for the query](#) describing the query controls and output in detail also is available.