



Genetic Evaluation Updates

The American Hereford Association outlines major revisions to its genetic evaluation.

by *Shane Bedwell*

The American Hereford Association (AHA) will continue to offer the most robust and progressive genetic evaluation, helping to identify Hereford genetics that are the most profitable for the commercial industry.

Over the last two years, the American Hereford Association (AHA) Board of Directors and staff have researched and thoroughly evaluated the

necessary steps to implement a single step genomic evaluation using the Biometric Open Language Tools (BOLT) software.

Along with this, AHA is introducing two new economically relevant traits included in an updated set of economic indexes. The following outlines the major revisions implemented into the AHA genetic evaluation planned to be released late in 2017.



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1 The Genomic Component

Today's evaluation utilizes Molecular Breeding Values (MBVs) to predict the genomic contribution. This post-evaluation blending exercise correlates the genetic relationship between the MBVs and the traits of interest.

The updated genetic evaluation can more precisely evaluate the genomic differences between animals. This single-step analysis evaluates Single Nucleotide Polymorphisms (SNPs) markers on cattle DNA using an analytical approach called the Marker Effects Model. The set of markers used has been selected to be the most informative for the traits in the genetic evaluation. Like phenotypes, the marker effects of a genotype directly impact an animal's expected progeny difference (EPD).

2 Model Changes

The AHA has long conducted a full multitrait genetic evaluation, meaning all traits are correlated to one another either through a favorable or unfavorable relationship. With the implementation of the new evaluation, traits have been grouped together into meaningful subsets

that are optimal for inclusion in the Marker Effects Model analysis.

The AHA implemented the decoupling of models to more efficiently perform more frequent evaluations. Plus, moving away from a full multitrait evaluation will better allow for estimating traits of interest rather than building these traits through correlation, as was done in the older analysis. The models are listed below.

2a. Birth weight, weaning weight, yearling weight and maternal milk

The main growth model will stay the same with little effect to traits in the model. However, because of the new analysis' use of the single-step Marker Effects Model, some animals' EPDs will change. These changes will primarily be the result of increased accuracy, using the new methods and reduced bias.

2b. Scrotal circumference and weaning weight

Scrotal circumference is correlated with weaning weight, but only scrotal circumference EPDs will be reported out of this model. There is a decrease of correlated data impacting scrotal EPDs, but this impact will be very small. Again, because of the change in the way the updated genetic evaluation is handling the genomic component, there are changes in some animals' scrotal circumference EPDs.

2c. Birth weight, ultrasound back fat, ultrasound intramuscular fat, carcass weight, carcass back fat and carcass marbling score

Birth weight is used as the correlated trait with the carcass traits to account for selection that may occur. Weaning and yearling weight are no longer included as correlated traits with carcass fat and carcass marbling. Instead scan fat and intramuscular fat, along with birth and carcass weight, are used to resolve traits of interest when real carcass data are not collected.

This method could create some changes in carcass fat and marbling EPDs, the two traits reported out of this model. Also, the variance components used as part of the analysis procedure were reestimated for all carcass traits and the correlation between scan intramuscular fat and carcass marbling decreased from 0.70 to 0.54.

Finally, because of the change in the way the updated genetic evaluation is handling the genomic component, there can be changes to some animals' EPDs.

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2d. Weaning weight, ultrasound ribeye area, carcass ribeye area and carcass weight

Weaning weight will be used as the correlated trait as birth weight is not adequate to solve for weight traits. However, yearling weight will no longer be included as a correlated trait with carcass weight and carcass ribeye area. Instead, scan ribeye area and birth weight are included with any available carcass data to resolve the traits of interest. Carcass ribeye area and carcass weight will be the only two traits reported out of this model.

Analyses comparing the previous carcass trait EPDs to those coming from the new analyses are very high but can be different for some animals, especially because of the change in the way the updated genetic evaluation is handling the genomic component.

2e. Calving ease, calving ease total maternal and birth weight

The updated genetic evaluation uses a random regression statistical procedure to calculate calving ease and maternal calving ease (total maternal calving ease). Birth weight is used as the correlated trait in this model, but is not reported.

The birth weight EPD that is reported comes from the Growth Traits analysis (2a.) discussed previously. This evaluation moves away from the threshold model previously used, in part because it required that observations that are the same within a contemporary group (e.g., herd) could not be used.

This means that the new analysis can use all observations regardless of score as well as use the corresponding birth weight phenotype. Even though this evaluation uses only data from two-year-old heifers, more observations will be used, resulting in a more comprehensive calving ease evaluation than what is being performed today. Also, because of the change in the way

the updated genetic evaluation is handling the genomic component, there can be changes to some animals' EPDs.

2f. Mature cow weight and weaning weight

Mature cow weight is analyzed with weaning weight, but only mature cow weight will be reported out of this model. The published weaning weight EPD comes from the previously discussed Growth Traits analysis (2a.). Even though the new mature cow weight EPDs are highly correlated to the old analysis, small changes may be seen in part because yearling weight is no longer used as a correlated trait.

Finally, because of the change in the way the updated genetic evaluation is handling the genomic component, there could be changes in some animals' EPDs.

2g. Sustained cow fertility

Sustained cow fertility is analyzed by itself, without a correlated trait, using the random regression statistical model to predict female fertility/longevity. This trait predicts a female's ability to stay in the herd through the age of 12 (10 calvings after calving as a two-year-old heifer).

The EPD is reported on a probability scale, meaning a higher EPD for a sire means his daughters are more likely to remain fertile and to produce more calves throughout their lifetimes. Because of the limited number of phenotypes collected that have a corresponding genotype, the genomic component is not included in this model.

2h. Udder and teat

The udder and teat evaluation remains the same basic model as it is today with the exception that it includes the genomic information to increase the accuracy of prediction.

2i. Dry matter intake, weaning weight and yearling weight

Dry matter intake includes weaning and yearling weight as correlated traits, but dry matter intake will be the only trait reported out of this model. This EPD predicts the daily consumption of feed. Because of the limited number of phenotypes collected that have a corresponding genotype, the genomic component is not included in this model.

3 Data Pruning Strategy

In the updated genetic evaluation, phenotypes only from progeny born after 2001, the advent of Whole Herd Total Performance Records (TPR™), are used. The pedigree data include at least three generations of pedigrees from the observations

(i.e., through great-grandparents). This data cutoff was implemented to reduce the biases from the incomplete reporting of data that were submitted prior to Whole Herd TPR. The Whole Herd TPR program is based on a cow inventory system. The older data were collected only when a breeder chose to register a calf.

Sires or dams that have had progeny born on both sides of Whole Herd TPR may see EPD and accuracy values change due to not including progeny born before 2001 in the genetic evaluation.

Being able to have a genetic evaluation backed solely by Whole Herd TPR leverages the AHA's commitment to its performance program and increases its reputation as a leader among breed organizations.

4 Accuracy Calculation

Because of the computing power of BOLT, the updated genetic evaluation will be able to more precisely calculate accuracy. Accuracy is quite possibly the hardest piece of a genetic evaluation to correctly compute, and because of this complexity, an approximation technique has been used to calculate accuracy by all breed organizations, including the AHA.

Because of the vastly improved computing methods, a technique known as "sampling" allows the direct calculation of key variables used in calculating accuracy rather than approximating these variables. The previously used approximations overestimated the accuracy of EPDs, especially for young animals. Accuracy of animals can change with the updated evaluation because the direct method does not contain the bias from the approximations.

5 Updated Profit (\$) Indexes

Both Dry Matter Intake (DMI) and Sustained Cow Fertility (SCF) will now be included in the AHA \$Indexes along with other key Economically Relevant Traits (ERT's) including Carcass Weight (CW) and Mature Cow Weight (MCW).

Adding these ERTs into the \$Indexes will provide a more robust and comprehensive selection tool for commercial producers to select Hereford bulls to be used on British-based cows and heifers. DMI and CW will be included in all three AHA \$Indexes to help predict the cost associated with feed inputs and to measure the end-product pounds that are critical for profit.

SCF will replace scrotal circumference as the predictor of fertility and will be a large contributor to both maternal indexes. Because of the inclusion



of these key ERTs, animal index values may change. Watch for future *Hereford World* articles breaking down the key differences of the new index calculations.

The AHA would not have been able to complete this genetic evaluation overhaul without the guidance of several key scientists. Bruce Golden, co-founder, CEO and president of Theta Solutions LLC, and Dorian Garrick, co-founder, CSO and CFO of Theta Solutions LLC, have developed the BOLT software and engineered the script writing and provided the genomic expertise for the updated genetic evaluation.

Brad Crook and Shalane Weerasinghe of Agriculture Business Research Institute (ABRI) orchestrated the genetic evaluation to run with Canadian Hereford and provided the technical support to ensure the evaluation is performing accurately.

Mike MacNeil, Delta G; Matt Spangler, University of Nebraska; and Larry Kuehn, Meat Animal Research Center, provided expertise and technical backing in the update of the new economic indexes.

Finally, an advisory committee was assembled to review the revisions made to the updated genetic evaluation. This committee was charged with providing feedback to the proposed changes and ultimately giving the recommendation of approval to the AHA Board of Directors. Advisory committee members include Joe Ellis of Ellis Farms, Chrisman, Ill.; Jack Holden of Holden Herefords, Valier, Mont.; Paul Bennett of Knoll Crest Farm, Red House, Va.; Lee Haygood of Indian Mound Ranch, Canadian, Texas; and Mitch Abrahamsen, Recombinetics Inc. chief commercial and scientific office. **HW**