

Predictable and Accurate

See how data from the Whole Cow Herd DNA project will improve the American Hereford Association's genetic evaluation.



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Another day brings beef to another table and this success is possible because of all you hardworking and passionate Hereford breeders. Beef month is here, and there is no time like the present to put your core values in life into perspective. Those core values for me are God, family, country and Hereford genetics, and I'm proud to say all are woven tightly in my daily life.

As we work through these trying times, it has been refreshing to see the resounding appreciation and demand for beef. Consumers have prioritized beef as an essential part of their diets, and this demand is evident in every retail outlet across America. Although this shift is largely due to the shift away from foodservice, it proves consumers need and want *real* beef — not media-hyped fake meat. This is a great success story we must share, while also promoting beef production as one of the most sustainable technologies we have.

I also want to give a shout out to the breeders of the 2019 Certified Hereford Beef Sires of Distinction. These bulls are a very impressive group that continue to have a lasting influence on the breed and the beef industry overall.

Genetic evaluation improvements

The breed improvement shop has been busy working on improvements to the genetic evaluation. Many of you participated in the Whole Cow Herd DNA project, which netted over 10,000 genotypes. This project allowed our science team to better understand the genomic contributions and relationships of the markers impacting maternal traits like Sustained Cow Fertility (SCF), Calving Ease Maternal (CEM) and Milk (M). Currently, when an animal is genotyped, there is no genomic contribution to the aforementioned traits and, thus, no improvement in accuracy. With the submission of female genotypes, the Association now has the

data to be able to take this needed step.

These improvements will be implemented into the genetic evaluation in early July, and genotyped animals will receive increased accuracies not only for SCF, CEM and M but will also receive improved predictions for each of these traits. Some changes for these specific expected progeny difference (EPDs) will be noted, particularly for nonparent animals without production data in regard to maternal traits. Adding the genomic component to SCF, CEM and M is great step forward in determining a sire's maternal ability earlier in life as opposed to waiting until he has daughters in production for results.

Beyond adding the genomic component to the SCF model, the way contemporary groups are handled in that model will be restructured, as well. In the current model, all daughters of a sire are compared across the breed to one another. In the new SCF model, the herd will be fit for comparison and, consequently, the new analysis will factor in environment more suitably.

Because of this improvement, you may see changes in SCF values for some proven sires, although the correlation to the current and new SCF models is 0.70. Given SCF is a significant driver for the Baldy Maternal Index and the Brahman Influence Index, some animals will move ranks in their respective indices. Stay tuned for more detailed articles and webinars that explain the improvements to the genetic evaluation as we approach the rollout of these changes this summer.

Experience BIF at home

This year's Beef Improvement Federation Research Symposium and Convention will be a virtual event, scheduled for the week of June 8. I encourage you all to take advantage of having access to this event from your home. More details and a complete schedule are available at BeefImprovement.org. **HW**