

Educational Forum Focuses on Breed Improvement

Recently we completed another very exciting American Hereford Association (AHA) Annual Meeting. On Friday afternoon, the educational forum focused on genomics, the new udder trait and how Hereford genetics affect the commercial cow herd.



Jack Ward

Genomics update

Jerry Taylor, University of Missouri Curators' distinguished professor of animal sciences and Wurdack chair in animal genomics, focused his presentation on the U.S. Department of Agriculture (USDA) feed efficiency and fertility grants and how Hereford has helped with this research.

In addition, Taylor updated attendees on the progress of the fertility work, which has allowed him to whole genome sequence highly used artificial insemination (AI) sires of various breeds. AHA identified 18 bulls to be sequenced. This sequencing could also aid in the development of Hereford panels that may find causative genes for various traits of interest or, at least, genes with a large impact on various traits.

Dorian Garrick, Iowa State University Lush chair in animal breeding and genetics and National Beef Cattle Consortium executive director, gave an update on the strength and power of AHA's genomic-enhanced expected progeny differences (GE-EPDs). He commended the membership for getting more than 2,000 new high accuracy sires high density (HD) genotyped in order to redo training and validation of the Hereford-specific panel.

With the addition of these sires, the panel more than doubled the average correlation, which accounts for nearly 27% of the genetic variation on average for the various traits. In addition, Garrick challenged the AHA to look at adopting a more frequent run of the analysis, which may make inclusion a bit easier. He also stated that even though we are getting more genotypes done, we need to continue to build our HD tests at this point and to look to move toward a lower density (LD) panel when imputation seems possible from the LD to the HD.

The take-home message was genomics is a great tool. Phenotypes must still be collected, and we need breeders to adopt the technology in order to build our training and validation population and to provide the strongest and most predictable information. Remember, when you test non-parent animals, EPDs will not always move in a favorable direction for the traits of interest.

Udder EPD

Heather Bradford, an AHA member who did her master's work at Kansas State University on the development of the udder trait, gave a presentation on how she developed the Udder EPD. You can find a list of high accuracy bulls for this trait and more detail on its development at Hereford.org. This trait will become part of the national cattle evaluation (NCE) next summer.

Cow herd efficiency

David Lalman, Oklahoma State University beef

cattle specialist, shared his findings from looking at the commercial industry throughout the Great Plains and how increases in size, milk and muscle can be antagonistic to efficiency.

In most cases, the plan in the past was to breed for extremes. This mentality has worked well to produce more pounds of product for end merit but has issues in the cow herd. Weaning weights have not kept up with size, milk and muscle. So, the challenge was to look at ways to increase efficiency and to breed for optimization while maintaining performance in the feedlot and on the rail.

This issue brings to light the importance of \$ indexes and the importance of the AHA building the current \$ indexes as strong as possible with the proper relative weightings for traits and accurately measuring the economic component.

There have been four new traits developed since the introduction of the \$ indexes, which are mature cow weight (MCW), heifer calving rate (HCR), sustained cow fertility (SCR) and udder trait. These traits will add strength to the indexes. We need to continue to look at feed efficiency, disposition and tenderness.

Congratulations to the honorees recognized Friday, especially Hall of Merit Inductee Dorian Garrick. Through his leadership, the AHA has been able to properly build its genomic tools that have allowed breeders to identify and rank animals for genetic improvement. His work in this area is truly exemplary. **HW**