Data + DNA =
Selection Tools That Work

Retallick discusses evolution of Angus genetic evaluations at Angus Convention.

by Kindra Gordon, field editor

Performance

Genomic Testing

Pedigree

Progeny Data

Measuring livestock performance has evolved greatly over the decades. That was the message Kelli Retallick shared with Angus producers attending the 2017 National Angus Tour near Fort Worth, Texas, Nov. 3. Retallick, who is genetic service director with the American Angus Association's Angus Genetics Inc. (AGI), talked through the decades of progression, noting, "Weaning weights and yearling weights are where things started. That was the first step in selecting and measuring livestock."

Within-herd ratios followed, and then expected progeny differences (EPDs) were developed. Retallick shared that the American Angus Association printed its first EPD report on 23 bulls in 1974.

"EPDs were useful because, for the first time, you could compare animals in one herd to another herd," she added.

Modern values

In more recent years, $Values, which are bioeconomic indexes, were developed, and finally genomic-enhanced EPDs (GE-EPDs) and indexes, which incorporate genomic data, have been created.

Retallick explained that today's EPDs have four parts:

1. the pedigree, with dam, sire, grandparents, siblings, etc.;
2. performance;
3. genomic test results; and
4. progeny data.

"Progeny data is always king," she emphasized. "We need the actual performance to make GE-EPDs work." She used the analogy of a credit card, and said, "You need the cash — the actual data — to pay the bill."

In the framework of that historical progression, Retallick noted that the American Angus Association evolved again in July 2017 when the Association moved its genetic evaluation from a multi-step to a single-step method.

Of this, she said, "On July 7, we had a big change."

The reason for the change was that the genetic prediction models were getting too big and harder to estimate, she explained. "The two-step methodology calibration was challenging with all the molecular breeding values (MBVs) as separate traits."

The move to single step makes the process more efficient.

To help people understand the change, Retallick showed a picture of a binder and a thrasher — two different pieces of equipment previously used to harvest grain. They were then combined into one piece of equipment that had the capability to do both jobs.

"That's why it's called the combine," Retallick said as she flashed a picture of a combine over the top of the binder and thrasher. Similarly, Retallick said, the single-step genetic evaluation combines the previous two-step process into one single step.

Specifically, she explained, "The single-step approach redefines the pedigree relationship among animals based on genetic markers. So it is basically tracking inheritance, but it's a more direct model because we are not dealing with so many traits."

This means for proven animals that have already been tested with progeny data, their EPDs changed minimally with the move to the single-step evaluation, according to Retallick.

However, for younger animals, she explained, "We had some pretty big changes because they didn't have the progeny data."

Additionally, Retallick said the single-step evaluation is revealing more variation in half- and full-siblings. That's because progeny get a random draw of alleles from parents — as was discovered by Gregor Mendel and is termed Mendelian Sampling, Retallick explained, pointing to human family members. "This is why not all siblings look alike."

She continued, "We know that DNA gets passed down in chunks from ancestors. If I get a bigger chunk of DNA from my great grandsire (i.e., for higher marbling), I'm more related to that sire. ... Single step is showing us and uncovering that variation, because it is picking

Like a "combine" combines the binding and threshing tasks into a single process, the single-step genetic evaluation combines the previous two-step process into one single step.

up on the random assortment of genes being passed down."

Other changes

With that said, Retallick explained that single-step genomic evaluation is not the only change that was made to the Angus evaluation July 7. The evaluation was also modified to include:

- improved models for carcass traits;
- additional genotypes and data; and
- updated heritability and genetic correlation estimates.

Ultimately, Retallick said, these enhancements allow for a more complete model and a more accurate prediction of progeny genetics. Evaluations are being updated weekly, which allows for nearly immediate use of data collected, putting the producer ahead.

"The reason these genomics work well and are the envy [of other breeds] is we have a lot of data to work with," she added.

Retallick shared a slide titled, "Data

PHOTO BY SHELBY METTLEN

Single-step evaluation is revealing more variation in half- and full-siblings, said Kelli Retallick, AGI director of genetic service. That's because progeny get a random draw of alleles from parents — as was discovered by Gregor Mendel and is termed Mendelian Sampling.

+ DNA = Selection Tools That Work." It summarized the volume of data compiled by the American Angus Association:

- 7.8 million birth weights;
- 8.6 million weaning weights;
- 4.2 million postweaning gain records;
- 1.5 million heifer calving ease scores;
- 116,000 carcass records;
- 1.9 million ultrasound records;
- 21,000 individual intake records;
- 256,000 docility scores;

- 61,000 heifer pregnancy observations;
- 204,000 mature cow weights; and
- 398,000 genotypes.

In closing, Retallick noted that with today's technology, the ability to evaluate young stock sooner also exists. She pointed to the ability to biopsy embryos, profile the DNA and determine which embryo to select for maximized genetic improvement.

"The dairy industry has gotten very good at selecting genetics using genomic predictions on young animals, and I have no doubt this crowd [of Angus breeders] will eventually do the same," she said. **AJ**

Editor's Note: Kindra Gordon is a cattlewoman and freelance writer from Whitewood, S.D. This article is part of Angus Media's coverage of the 2017 Angus Convention available online at www.angus.org/Media/News/ AngusConvention.aspx.

PHOTO BY SHAUNA ROSE HERMEL

Adding weaning weight as an indicator trait for carcass weight helped to eliminate the selection bias that occurs when the lower-performing animals in a contemporary group are culled from the group, leaving only the higher-performing calves to be measured for yearling or scan weight, Retallick explained.