

GE-EPD Best Measure

Combining all the information that's known on an animal for a particular trait, the genomically enhanced expected progeny difference provides most comprehensive look at an animal's genetic merit.

by Shauna Rose Hermel, editor

The best criterion for genetic selection is the genomically enhanced expected progeny difference (GE-EPD), Dan Moser told a standing-room-only crowd in Kansas City, Mo., Nov. 4. The president of Angus Genetics Inc. (AGI) and director of performance programs for the American Angus Association addressed the group during the breed improvement breakout session at the Angus Means Business National Convention & Trade Show hosted Nov. 4-6 at the KCI Expo Center in Kansas City.

DNA testing provides opportunity to characterize animals at a younger age, which reduces the risk involved in using a young animal if you are seeking to make directional change in a trait, Moser said. "It doesn't totally take away the risk, but it lessens the risk, because of what we know about an animal that's too young to be progeny tested."

Even though it might be tempting to focus on the DNA information only, Moser encouraged cattlemen to focus on the GE-EPD, which includes all the information.

While DNA is the new, exciting technology, birth-weight scales are good technology, too, he noted. "That tells us some things that the DNA by itself doesn't tell us."

Moser explained how GE-EPDs are calculated and why they are recalibrated.

Calculating traditional EPDs, he explained, involves combining (1) pedigree information, (2) performance information on the individual of interest and (3) progeny performance (see Fig. 1). Each of the three inputs is weighted in the equation according to how much information it contributes. As more performance information is available on the animal, it plays a greater role in the calculation than pedigree, and as progeny data accumulate, they are weighted more heavily than pedigree or individual performance.

"It gets the most weight because it's the most reflective of the animal's merit," Moser explained, "and the rest of these things stay in the background on the most proven sires."

The only difference between traditional EPDs and GE-EPDs is the addition of genomic testing as a fourth source of information, he noted, emphasizing that pedigree, performance and progeny



► "The database that the American Angus Association has, combined with genomic samples, is unrivaled throughout the industry. The rate at which this technology is being adopted is really making a difference in our population and gives us even more powerful tools to move forward," said Dan Moser.

performance are still important (see Fig. 2).

While addition of information from pedigree, individual performance and progeny information happens in a sequence, information from genomic testing can happen at any time, Moser pointed out. "It could happen on a baby calf."

When the genomic information is added doesn't matter, he added. Weighting of the factors is determined by how much information it provides to that particular evaluation so "we have the optimal number that does the best job of describing the animal."

Fig. 1: Traditional EPDs



Fig. 2: GE-EPDs

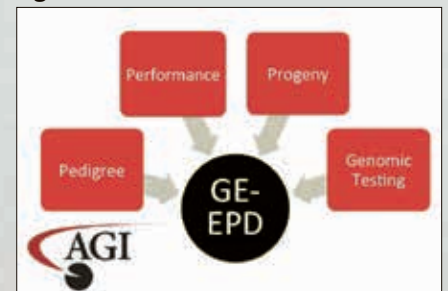


PHOTO BY SHAUNA ROSE HERMEL

Calculating a GE-EPD

“There’s a two-step process whereby the equations are built for genomically enhanced EPDs,” Moser said. The first is the process of building molecular breeding values (MBVs) using archived test results and Association data. The second is incorporating those MBVs into the EPD calculations.

“Along all 30 pair of chromosomes in cattle, there are some places where they are exactly the same. Every living, breathing beef animal — or dairy animal — has an ‘A’ in this spot. There’s no variation there,” Moser said, referring to a nucleotide, one of the building blocks of an animal’s genetic code. “There are a lot of spots — many, many spots — where there is variation.”

DNA testing using today’s high-density genomic tests look for those places in the chromosome where one animal has an “A” and one animal has a “T,” Moser explained. “That’s a SNP (pronounced snip); that’s a single-nucleotide polymorphism, and they exist all over the chromosome. The chips (used in DNA typing) that we work with test for 50,000 or more different SNPs, or points of variation.”

For cattle that have been tested, we have information on what they have at each of those spots, said Moser. “We also have the data that you folks have submitted — generations of weights and measures, carcass characteristics, docility scores.”

Actual measurements are more important than they’ve ever been, noted Moser, “because not only are they being used directly in the EPD equation, but they are also driving the genomic part. We build the genomic equations based on your good data.”

The SNPs are evaluated for whether they affect traits. When looking at a particular trait, many of the SNPs won’t seem to matter, Moser admitted, “but many of them do. They have a significant, statistical association with the higher or lower level of that trait. Those are the SNPs that are identified and tracked.”

So, for any given trait, whether calving ease or docility, SNPs are selected that are associated with that trait, he said. SNPs selected are not the same for every trait. Some of them don’t matter for any trait. Some may influence several traits. Each one has more or less its own EPD for having an “A” vs. a “T” at that spot. What does that mean to weaning weight? What does that mean to docility?

An animal’s MBV, the DNA only, is just

adding all those up for every trait.

In the second step of calculating a GE-EPD, the MBVs are incorporated into the EPD equation like a correlated trait. The molecular value is correlated to actual measurements, such as weaning weights. How well they correlate is an indication of how well the DNA is

describing genetic merit. The higher the correlation, the better the DNA test is at describing variation among animals, Moser explained. So, as the correlation gets higher, its impact in the EPD calculation increases.

Fig. 3 reflects how far the Association has come since unveiling the first GE-EPDs in 2010.

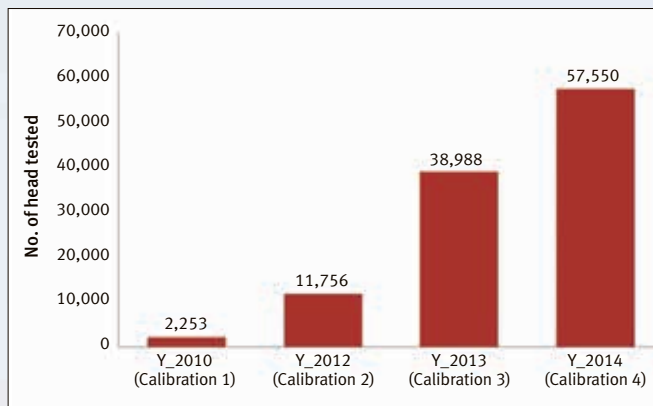
Moser explained that in each recalibration, such as the one released in September, the Association trains the DNA analysis to the current population by recalculating the MBVs using animals in the data set that have both DNA samples and actual data.

The original GE-EPDs released in 2010 were built upon a training population of only 2,200 animals, said Moser. The recalibration in September was based on 57,550 animals, increasing almost 20,000 animals in one year.

Other breeds are back where Angus started, he added. “There’s certainly a healthy advantage due to the effort you folks have made submitting that data.”

The larger test population provides stronger correlations, explaining a greater

Fig. 3: Increase in data over the four calibrations



share of the genetic variation (see Fig. 4).

“Even for a trait like marbling that worked really well in the beginning, you can see the increase each time the recalibrations have occurred; the relationships got stronger,” Moser said. “With more data and more samples, we’re able to do a better and better job of characterizing the cattle with DNA tests.”

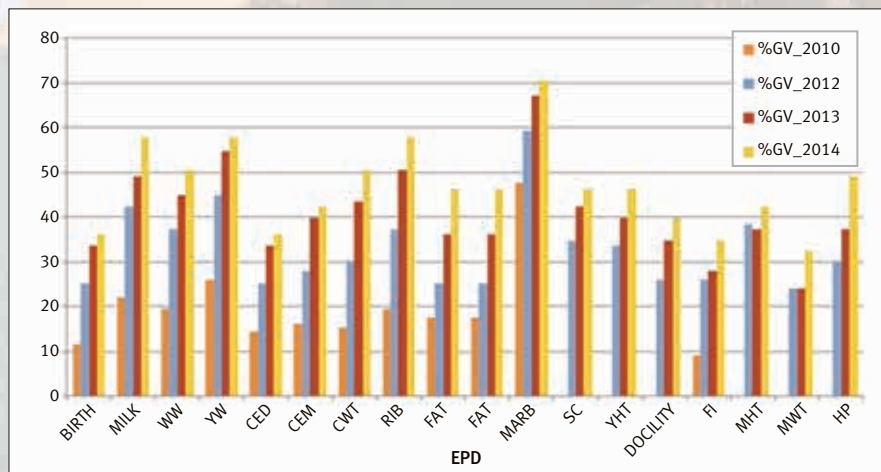
Moser pointed out that none of the lines in Fig. 4 reach 100%.

“That’s a message I want you all to take home,” he emphasized. “This is a useful tool, just like having the actual measurement on the animal is useful, having the pedigree is useful, but no one item by itself gives us the whole story. We really gain from combining those various sources of information together to get the best picture of the animal.”



Editor’s Note: Moser spoke at the breed improvement workshop at the Angus Means Business National Convention & Trade Show. To listen to his presentation, access his PowerPoint or read summaries of other presentations at the convention, visit the newsroom at www.angusconvention.com.

Fig. 4: Percent genetic variation explained with a common data set with marker effects from different calibrations



Source: Prashanth Boddhireddy, Zoetis.