# EPDs 401

*Redefining the Angus pedigree with genomics.*

Story & photos by Shelby Mettlen, former assistant editor

The pedigree file.

"That's what I think of as the magic behind EPDs (expected progeny differences)," said Angus Genetics Inc. (AGI) Director of Genetic Research Stephen Miller at the Fort Worth Convention Center Nov. 5. Miller gave an advanced follow-up to AGI President Dan Moser's "EPDs 101" session, as part of Angus University at the 2017 Angus Convention in Fort Worth, Texas.

The American Angus Association's database contains more than 22 million animals, he pointed out. Those pedigrees determine how animals compare across herds, how the Association accounts for genetic trends, what bull is bred to what cow — the list goes on.

Plus, those pedigrees are closely related. One bull, QAS Traveler 23-4, accounts for 10% of the genetics of calves born in the last decade.

"The pedigree file is really dense," Miller said. "There are a lot of relationships across herds. That gives us more powerful EPDs."

Today, the Association's relationship matrix is a staggering 10 million animals by 10 million animals. It's vast, and it's dense, but it's based on averages, Miller explained.

It's assumed that a sire passes half his genetics to his calf, and another half is passed on to the next



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generation. Thus, a calf is assumed to acquire one-fourth of its genetics from its maternal grandsire, for example. However, genomics may prove that the one-fourth rule isn't exact.

"It's true on average," Miller said, "but there's variation there."

Genomics allows for identification of that variation, and creates a more accurate relationship matrix and a more accurate pedigree.

"Including that information into that matrix was kind of the magic behind EPDs," he added. "It's what makes genomic selection work."

An animal's genotype is influencing the relationship matrix, and that different relationship matrix is influencing EPDs, Miller said. Launched in July of this year, single-step methodology accounts for that variation and what's

inherited from all grandparents.

"That's the power behind genomics," Miller said.

## Additional changes

Recently, AGI added weaning weight (WW) and fat traits into the carcass model, Miller said. Why is this important? It accounts for preselection bias.

"You don't typically take your light calves at weaning and keep those for bulls, then cull your heaviest ones. You might do it the other way around," he said. "If you don't fit weaning weight into the same model, you don't account for that."

Including this accounts for a better relationship between growth rate and carcass weight, Miller said. "The Angus data says the correlation between carcass weight and yearling weight is 0.75," he said. "It's not from some university study or what we think it should be. When we analyze all the records, that's the relationship." **AJ**

During his EPD 401 presentation at the 2017 Angus Convention, Stephen Miller, director of genetic research for the American Angus Association, entertained a few frequently asked questions from the switch to single-step methodology.

**How much range should you see in full siblings?**

Due to genomics and the resulting increased accuracy, breeders can expect to see more range between full sibs than they did before.

**Where does this variation come from?**

One-quarter of it is just variation in the sires used, Miller said. One-quarter is due to variation in the cow herd. Half is due to Mendelian sampling — random sampling of chromosomes between the sire and dam.

"That amount of variation is big," he said.

**Why is it called single step?**

The technology, developed at the University of Georgia, combines all the genotyped animals and all the other non-genotyped animals. That equates to a grand total of more than 400,000 genotyped animals currently within the Angus evaluation.

"But we realize that matrix [includes] 10 million animals. Percentage-wise, we don't have a lot of genotyped animals, but we have to fit all those into the same model at the same time," Miller explained. "Single step allows the equations to put those things together."

The Association has been utilizing genomic selection since 2010, but genetic trends are moving more quickly as more animals are genotyped. It has increased the rate of genetic progress within the breed, he said.

"EPDs were powerful because that pedigree tied all those animals together," Miller said, "Genomics is basically just an enhanced pedigree."