Questions & Answers: Ultrasound and DNA

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***The USDA**, Agricultural Research Service, U.S. Meat Animal Research Center (USMARC) at Clay Center, Nebraska, is a hub of beef genetic research. Dr. Larry A. Kuehn, PhD, research geneticist for USMARC answers a few basic questions about DNA, ultrasound, and carcass trait improvement.*

Q: What are the differences in accuracy of EPDs for marbling, rib eye area, and back fat between DNA tests only, ultra-sound only, or both DNA test and ultra-sound?

A: The American Angus Association (AAA) has, to my understanding, been incorporating marker data into their genetic evaluations using genetic correlations estimated from the mid 50s to 60 percent for marbling, fat thickness, and ribeye area. Relative to BIF accuracy, these correlations equate to somewhere between 0.13 and 0.2. That's not very high BIF accuracy necessarily, but we don't generally see high BIF accuracies for carcass characteristics until bulls have steer progeny tests anyway.

The genetic correlation of ultrasound predictions to actual carcass data is around 0.5-0.7. On the higher end of this range, ultrasound could explain more of the variation in carcass traits and have as high accuracy as some DNA tests. But, in order to achieve that accuracy with ultrasound, the producer has to do a fair amount of progeny testing. Part of the strength of ultrasound is that you can collect it cheaply on a bunch of progeny in order to increase its accuracy in genetic evaluation.

If ~40% of the genetic variance is explained by either DNA tests or ultrasound, we could achieve a BIF accuracy ~.23. I think that's pretty important. When used together, both tools can increase the initial BIF accuracy before actual carcass information is collected on the animals. Although I don't have a great estimate, I'd speculate that together they likely explain 45 to 55 percent of the variation (for a BIF accuracy of 0.26 to 0.33).

These conclusions are all relative to the amount of progeny phenotypic data available. If the animal has no other information, the impact of DNA tests/ultrasound is very large (the full 0.23 BIF accuracy). The return gradually diminishes as more information raises the EPD (Expected Progeny Difference) accuracy.

Q: Does a large set of progeny phenotypes ever triumph over initial DNA tests?

A: Basically, the more progeny data (actual carcass records) you have, the less influence the DNA testing has on EPDs. Eventually the actual progeny data becomes a test of the true breeding value of an animal; the DNA test result is no longer important.

The relationship between ultrasound data and actual carcass data is similar; ultrasound has a limit just like the DNA on how much it can help the actual carcass data accuracy. At some point both DNA and ultrasound get trumped by actual data if there are enough progeny with actual carcass data.

Q: How is DNA information incorporated into EPD predictions?

A: Right now the beef industry has been using DNA information to develop a prediction of genomic merit based on the animal's genotypes. DNA companies provide a number, or score, that the animals can be ranked on, based on genomics. The DNA score then becomes another trait in the genetic evaluation analysis just as ultrasound is another trait in the analysis of actual carcass data.

That's basically what Angus is doing to run their genetic evaluation with a DNA score (molecular breeding value) as a second trait that adds accuracy to the trait of interest – the actual carcass measure.

Multiple trait methodologies have long been used in genetic evaluation programs. It has been the principal methodology used to incorporate ultrasound data into carcass EPD predictions. For instance, we can add progeny phenotypes for ultrasound marbling and they add to the accuracy of actual marbling EPDs. It works the same way when DNA molecular breeding values are incorporated. They just become another trait in a multiple trait model.

Q: Why do DNA results vary across different breeds in marbling, rib eye area and back fat?

A: So far, when we've implemented DNA marker tests using large marker arrays (>50,000 markers genotyped on each animal), they have seemed to work best (accounted for the most variation) if they're developed on the same breed they're applied on. The breed with the most capacity to do that so far has been Angus. I mentioned earlier that they have 50-60 percent genetic correlations between DNA score and actual carcass measures - they achieve that correlation because they have data that was trained on other Angus. Their tests are very accurate for Angus, but if you would apply the same test to Simmental, Hereford, or some other breed, it would be much less accurate. They would not account for the differences we observe in carcass characteristics in Hereford or Simmental nearly as well as they do for Angus.

Basically, that's a function of how distantly related the breeds are genomically. Marker predictions are more accurate when animals are more closely related. Since several generations have passed since the breeds diverged, the relationships the markers might have with actual genes that are causing variation in economically relevant traits probably aren't the same from breed to breed.

Part of our own impetus here (at USMARC) is we want to be able to eventually develop tests that are more robust across breeds. I do think it's important to try to get down to that level if we're going to make this truly a usable project for the commercial producer as well as the seedstock industry. It's not just about purebreds; composite breeders need to know where their animals rank. Having some idea of what's going on in a crossbred is relevant to a large segment of the industry.

Q: Why is reporting phenotypes on a sire's progeny absolutely essential to finding outliers and improving breeding animals?

A: Phenotypes of all types will continue to be very important for many reasons. One is that DNA tests do not explain all of the genetic variation we see in our economically relevant traits; phenotypic data is still needed to improve EPD accuracy. In order to provide accurate DNA tests, we need phenotypes to train and validate prediction equations that are being developed.

Also, we need many more phenotypes than we once expected to achieve a robust set of prediction equations. This is particularly true if we want DNA tests that have the potential to be effective for multiple breeds.

As one final point, the efficacy of DNA tests may decrease over time as the animals being evaluated become more distantly related to those used in training. We need strong phenotypic databases to retrain our predictions in future generations.

Gathering data on phenotypes is essential and will continue to be in the future.