

Phenotypic Data in a Genomic World

How DNA and data points work together to give the full picture of an animal.

by Miranda Reiman, senior associate editor

There was a time when cattlemen and geneticists alike hoped they'd be able to genotype their way out of recording phenotypes.

But if you're employing that strategy today, chances are it's not working as well as you think it is.

Esther McCabe, director of performance programs for the American Angus Association, says they commonly get the question: "If I can just use a genomic test to get back information on my animal, pay a one-time fee and then have all of my boxes filled, why do I need phenotypes?"

In general, the further an animal is from actual phenotypic measures, the harder it is to characterize it correctly, she says.

"If those phenotypes go away, genomics lose what they're tied to," McCabe notes. "Genomics are only as good as the database behind it."

Historical hope turned to new knowledge

In fairness, the idea of genotyping instead of taking multiple measurements seems like a logical conclusion at first blush, says Kelli Retallick-Riley, president of Angus Genetics Inc. (AGI). Why not just take a blood, hair or tissue sample and get all the data on the whole animal all at once?

"When we first started digging into these individual DNA markers on individual animals in the early 2000s, the thought was that we were going to collect a bunch of genotypes and we're going to overlay them with phenotypes and we're going to find every single causative," she says. "Since that time, we've been humbled as animal breeders."

Almost every trait is polygenic, or controlled by multiple genes and locations within that genome.

Some of the early genomic work may have given false hope of a world without so many records.

"I think a lot of people thought, well, we're just going to find these particular markers. It's going to be a finite number that we find, and they work across every breed and every type," says Larry Kuehn, research geneticist with the U.S. Meat Animal Research Center (USMARC) at Clay Center, Neb., part of the USDA Agricultural Research Service (ARS).

When dealing with complex living beings, it's not that simple, he says.

"We still have markers that are spread across the genome that we need to account for all at the same time, and almost none of them are really proven by themselves yet. They're proven as a group," Kuehn explains.

Yet, the technology provides an important chance to know data about an animal sooner, and more objectively.

Spot on data

Due to the size of the Angus database, the original pedigree-based expected progeny differences (EPDs) were already doing a good job of predicting animal performance on many traits when Angus genomically enhanced expected progeny differences (GE-EPDs) were introduced in late 2009.

Increased data can help get at traits that aren't so easy to measure, such as fertility, feed intake or even immunity in the future.

"Genomics has increased that power, but we really need data recorded to do that well," Kuehn says.

Genomic predictions were first trained on phenotypes, and are still calculated in tandem with them today.

"We need a whole lot of data to get the accuracy up there into the ranges our producers expect to select on to make good decisions."

Genomic data does not improve the heritability of a trait, Kuehn notes, but they do increase the accuracy of the EPDs for those traits. That's even more apparent after GE-EPDs moved to a more advanced method of calculation.

"Single step is much more accurate and doing a better job, but it also shows you can't just throw phenotypes out," Kuehn says.

Single step refines traditional pedigree relationships to make them more accurate.

"Relationships to animals with phenotypes remain important, and can't just be proxied through a set of equations based on marker predictions," he says.

The lower the heritability, the more data that's needed. Today's most routinely collected measures, like birthweight, weaning weight, yearling weight and ultrasound, are also rather heritable. That leaves a lot of opportunity for collection of phenotypes to back up newer traits, Retallick-Riley says.

Some of the more recent Angus EPDs that fit into the category of "management EPDs," include things like foot conformation (claw set and foot angle) and pulmonary arterial pressure (PAP). The relatively low number of data points in those traits allows for bigger movement as records are added, even if those animals have been individually tested. Sometimes producers are surprised when the phenotypes have such a big influence.

"That's exactly what should happen, but they get a little thrown off because they're so used to looking at those core EPDs — birth weight, weaning weight,

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yearling weight, and marbling — that have millions and millions of data points already in the database. When they send in their heifer pregnancy or PAP measurement scores from our high-altitude breeders, they'll see those EPDs shift and change," Retallick-Riley says. "That's because the genotype does not increase the accuracy of that early EPD prediction as much because the amount of information, or phenotypes, it has to leverage to make those early predictions is far less."

One example of a novel trait would be foot score measurements. First recorded in 2015, they have climbed to 30,000 individual data points recorded this last fiscal year, up to 149,000 total in the entire database.

"As long as the phenotypes are showing variation in groups, as we collect more and more phenotypes, we'll start to see the initial accuracy increase when we genotype young, unproven animals, because the evaluation has more data to utilize for early predictions," she says.

"The more data, the better" is the mantra when trying to build up a new trait; but it is also the mantra when trying to get solid numbers on a new animal.

Young and accurate

When producers test a young sire, and then add progeny data in later, they might not see as much movement as they expect, Retallick-Riley says. Breeders often wonder: How much weight does that genotype vs. that individual phenotype have?

"On a young animal, who doesn't have a lot of data in the evaluation, that genotype is going to play a larger role in EPD prediction," she says. "Then as we add progeny, that value of the genotype for that individual animal starts to diminish, because now we have all these progeny phenotypes that are leading us to the a more complete answer."

Which one is more valuable? It's not either/or, it's both, she answers.

"Those phenotypes really work hand-in-hand with the genomics to make sure that early prediction — when we can't collect a whole bunch of data on a young calf — is as accurate as it can be because we already have all of these other millions of weights and records in the system," Retallick-Riley explains.

It might be tempting to let other breeders take individual animal measures and rely on those numbers



to back your genotype, Retallick-Riley says, but that will land many animals closer to breed average, especially in newer traits like hair shed.

The early adopters were capturing that variation in their herd and making decisions based off their knowledge.

“By collecting that data, they were actually able to make better selection practices. Now we’re starting to see more members play a little bit of catch up, get some more mature weights in, get some more foot scores, more docility scores in and they’re starting to deviate their cattle, too. You can’t necessarily find the winners if you don’t send in the data,” she says. “Don’t get me wrong, you’re going to find some losers, too. That’s the way this works.”

Kuehn grants that it is more work and more cost to collect both genotypes and phenotypes, but as an outside observer, he sees it paying off.

“I would argue the increased cost has been driving sales and profit pretty well. It’s not just genotype and you pay me more. It’s that the cattle are getting better as a result, and people are proving bulls faster on some of the traits that are tougher to measure,” he says.

A world without phenotype

“If everybody would’ve said ‘We’re going to stop collecting that ultrasound scan data, and only genotype our animals to predict those carcass EPDs,’ what would have happened?” Retallick-Riley asks.

They modeled the answer, and the research suggests lower EPD accuracies on young animals, along with a slowed genetic improvement. Basically, it increased the chances of picking the wrong bull, she says.

Last year, 71,000 ultrasound scans were turned in to the Association, down from its one-time peak of 112,000. An increasing amount of data would be ideal. Although with the trend going in the opposite direction, there could be a day when the research uncovers the lowest acceptable limit, McCabe says.

“At what point do you lose prediction power? Are we there yet? No, but we don’t want to get there,” she says.

Records that work for you

Esther McCabe says data that’s not helping you make decisions is like a check waiting to be cashed.

She encourages breeders to participate in whole-herd inventory reporting with the **Angus Herd Improvement Records (AHIR®)** program to “help turn some of that information into something that’s more informative than just weight on a paper.”

Most cattlemen already know why a cow is leaving their herd, for example, but reports help see the bigger picture trends.

For anyone looking to take a new measure, the American Angus Association has scoring guides for everything from body condition to feet to udders.

The biggest tip she offers is to record the data objectively.

“Reporting the data for what it is, not what you want it to be,” McCabe says. “Take them for what they are, and as you move forward, you can make adjustments based off of true and actual fact.”

Visit www.angus.org to access those how-tos or get more information on AHIR.

Data isn’t just nice, it’s essential


What’s that mean for Angus breeders?

Data collection isn’t just something that’s nice to have, it’s essential to long-term improvement, both in individual herds and for the breed as whole.

In fiscal year 2021, members submitted more than 774,000 weights (birth, weaning and yearling) to the Association, indicating a strong commitment to individual animal records, says Retallick-Riley. In total, there are more than 10 million weaning weights, dating back to the 1960s.

“That allows us to not only use the data from a standpoint of running your National Cattle Evaluation (NCE) and generating EPDs, but also doing further research on those phenotypes once they get sent in to the office,” she says. “That helps us keep Angus breeders on the cutting edge of technology, because we can continue to mine that data for future tools.”

Data collection can be time-consuming and costly, but if you’re doing genotypes without phenotypes or vice versa, you’re only getting part of the gain for your time and dollars invested, Retallick-Riley says.

Yes, data collection can be time-consuming and costly, but it is cheap insurance against making the wrong breeding decision. 

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