BY THE NUMBERS

by Stephen Miller, Angus Genetics Inc.

Influence of Genomics in the Angus Genetic Evaluation

Performance and genomics — how do they work together to determine non-parent expected progeny differences?

The uptake of genomics by Angus breeders is incredible. With more than three-quarters of a million genotyped animals in the weekly evaluation, that's far greater than any other breed.

Angus added genomics into the expected progeny difference (EPD) calculations as a third source of information in 2010. Until then, the "classic" EPDs combined performance and pedigree information. With only those two sources of data, a young animal would have his EPD anchored on his parental average EPD, and then deviate from this according to his own performance record.

The problem with starting with a simple parent average is that, although correct on average, there is a lot of variability in the genetics individual full sibs will inherit from the same parents. I think any of us with siblings can see that's most certainly true. The animal's own record gives some indication if that animal is above or below the average of his parents, there is a correlation between an animal's performance measure and his underlying breeding value.

Heritability is a key parameter in the calculation of EPDs, and is the square of the correlation between performance measures and breeding value. That number is the proportion of the variation, or differences, we see between animals that is due to genetics.

So, with a trait like weaning weight, about a quarter of the variation in a group of weaned bull calves is due to genetics. The rest is due to environmental factors that we cannot measure. The animal's weaning weight has some relationship with their underlying breeding value, but it is not high, so we can't attain a high-accuracy EPD on young non-parent animals with classic EPDs (see Table 1).

Adding genomics into the EPD calculation provides additional information to generate the same number that used to rely on the young bull's performance record in the era of classic EPDs. With the moderate heritability for these traits, we know there is considerable "noise" — or anomalies in the data — with an animal's own weight that is not determined by his genetics.

Table 1: ***Heritabilities of some traits in the Angus weekly genetic evaluation***

Trait	Heritability
Birth Weight	0.46
Weaning Weight	0.28
Postweaning Gain*	0.27
Bull ultrasound IMF*	0.41

*Postweaning gain and Bull ultrasound IMF are underlying traits in the genetic evaluation that contribute to EPDs for yearling weight and carcass marbling, respectively

Tracking inheritance

The genotype is powerful. Instead of starting from the average of the parents when calculating an EPD, the system can drill down to just what was transmitted from the parents to the young bull. We know each young bull does not inherit exactly a quarter from each grandparent, etc.. But without genomics the only way to determine if an animal inherited more or less was to use the animal's own performance record as an indicator. Genomics tracks this inheritance directly.

With more genotypes and data, the calculations can relate the DNA to EPDs with greater accuracy. So with more genotyping, the young bull's

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EPD will be influenced to a greater extent by his genotype and less by his own performance record. It is a bit like splitting up a pie. If one piece gets larger, another needs to get smaller.

As breeders see this phenomenon play out, they're asking if all this weight on genomics is correct. Are genomics really better than the bull's own record at predicting his underlying breeding value? I addressed this topic during my Feb. 25, webinar, available at: *www.angus.org/Education/AngusEducation.aspx.*

Phenotype vs. genotype — what's better?

We didn't just randomly assign a weighting to the genotypes. It's backed by data. The team at Angus Genetics Inc. (AGI®) recently completed a research project to determine how well performance and genomics predict an animal's underlying breeding value, since that represents his true genetic merit. The animal's EPD is not his breeding value, but the best estimate of his breeding value based on the information available. The E in EPD stands for "expected" for a reason.

Finding and evaluating benchmark sires

To compare different EPDs with and without genomics and phenotypes, we needed a good indicator of the animal's true breeding value. The best way to estimate this is through progeny. This is why we can obtain high accuracy across all EPD traits, even ones with lower heritability, on a sire with many progeny. We identified 178 genotyped sires in the Angus evaluation that were born in 2015 to 2016 and have gone on to have a minimum of 25 progeny recorded for Birth Weight (BW), Weaning Weight (WW), Yearling Weight (YW) and ultrasound IMF (IMF). These progeny records were used as an indication of the animal's true breeding value. We are referring to these 178 sires as "benchmark sires." Some sires had a large number of progeny, up to more than 8,000 progeny birth weight records for one sire. Table 2 summarizes those data.

Feeding program, weather, location, dam genetics and so on influence the progeny; so we couldn't use a simple average as an indication of their true breeding value. That's where genetic evaluation methodology comes in as a solid way to adjust for all these variables. We generated classic EPDs, without genotypes, to isolate just the impact of these sire progeny records in determining our estimate of their true breeding value. Their own records were also removed, as were any descendants beyond direct progeny, so benchmark sires were evaluated just on their parents and own progeny to create a "classic progeny EPD."

Predictive ability of four EPDs

The ability of four different EPDs to predict "classic progeny EPD" was determined. We wanted to test how an early EPD on these young bulls, back before they had progeny, would relate to future progeny performance. To make a fair comparison, we had to blank out all progeny and other descendants from these 178 sires in the Angus evaluation before estimating their EPD with these different sources of information. Table 3 compares the different EPDs, and describes the sources of information used.

In all the scenarios, an EPD generated with just a genotype is better at predicting the future of a young bull's progeny performance than an EPD that includes his performance data, but no genotype. Figure 1 shows the statistical measurement of the degree of

Table 2: ***Information content on the 178 benchmark sires used in the analyses***

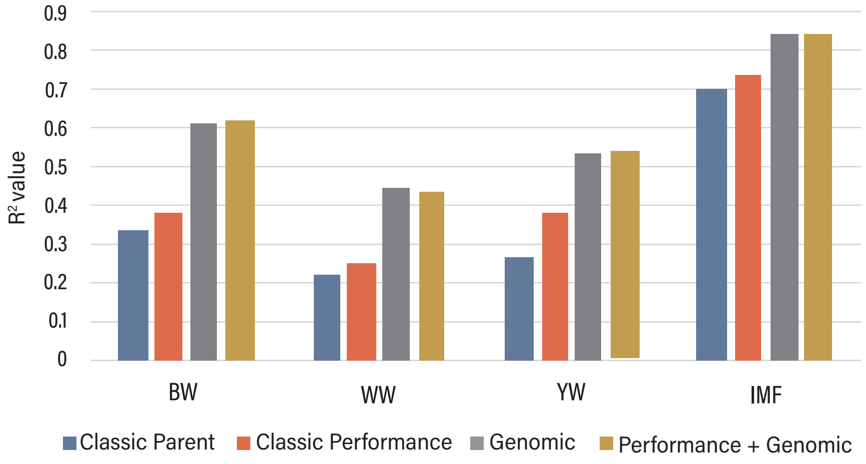
	BW	WW	YW	IMF
Number with own record used in evaluation	135	135	126	156
Median number of progeny records	179	151	72	49
Min number of progeny records	29	28	26	26
Max number of progeny records	8099	7017	3538	3037

*Note this a median, not average, to illustrate a typical number of progeny per sire.

Table 3: ***Sources of information used in different EPD comparisons for 178 benchmark sires***

EPD Scenario	Classic	Own Genotype	Own Performance	Progeny Performance
Classic Progeny	Y	N	N	Y
Classic Parent	Y	N	N	N
Classic Performance	Y	N	Y	N
Genotype	N	Y	N	N
Genotype and Performance	N	Y	Y	N

Figure 1: ***Relationship between EPDs with different sources of information early in a young bull's life and EPDs based on 25 or more progeny.***



relationship (R^2) for each trait for the four different combinations of data included. A perfect relationship would be 100% and no relationship would be 0%.

Comparing traits, the prediction was best for IMF and lowest for WW. This pattern follows the heritability of the traits since IMF and BW have a higher heritability than WW and YW. The one result not expected was a slight drop in R^2 for WW when adding the performance information to the genomic EPD for these bulls. We would not expect this across a larger group of bulls with more accuracy. As genomics continue to gain momentum over the years, more powerful analyses like these will be possible with larger data sets, over longer periods of time.

The EPD based on a genotype proves to be a more accurate prediction of future progeny performance than alternative scenarios, but the genomic prediction is still not perfect, which is why the accuracy values presented on these genotyped young bulls' EPDs are not 0.99. Improving the accuracy of the genomic prediction remains a priority for the AGI team and our academic collaborators. Over time we expect to further improve methods, which will increase R^2, and most importantly result in more accurate selection tools for breeders. Still, this research project demonstrates that Angus is on the right track with what is being delivered now.

Classic EPDs aren't perfect either, so we wouldn't expect a perfect relationship with them and the test numbers. These bulls will not have an accuracy for their progeny based EPD of 0.99. The average BW accuracy printed on these bulls for their classic progeny BW EPD was 0.78.

These results are encouraging. Breeders can use a $37 test that greatly improves the predictability of the genetic package they are selling to their customers. One benefit is that breeders will label more bulls as heifer bulls that actually end up being heifer bulls, and fewer heifer bulls that turn out not to be. Buyers of Angus genetics want the most accurate information possible, and these results demonstrate the real value of genomics in improving that predictability. Of course, genomics do not improve predictability just for bull customers. The breeder can more accurately select donor females, replacement heifers and young sires to expedite genetic progress in their own herds as well. These results demonstrate that the use of genomics in the calculation of EPDs is superior to EPD calculation based on performance information only.

The bottom line is this: genomics increase the accuracy of EPDs faster than phenotypic data alone. We need both because genomic accuracy is only as good as the performance data that support it.

In next month's By The Numbers, we'll take a deeper dive into the ways added data specifically affect BW, WW, YW and IMF. AJ

smiller@angus.org

Editor's note: If you have questions, please contact the Performance Programs department at 816-383-5100.