How Genomics Can Break the Tie

While phenotypes are an important aspect of cattle selection, genomics take care of what's underneath the hide.

*by **Jamie T. Courter***

We have all heard the saying, "You can't judge a book by its cover." However, the cover often draws a person to pick up the book in the first place. The same is true with selecting and breeding cattle. What the animal looks like matters. However, what the saying really means is it's what is inside the book — or underneath an animal's hide — that adds the most value.

In the last issue, we discussed the importance of phenotypic selection. But, once someone has made the initial gate cut, there are two ways genomics can help add value to sale bulls and heifers.

Table 1: Expected progeny differences for calving ease direct, birth weight and ribeye area for a sire and dam, along with six full sibling progeny resulting from said mating[1].

Animal	CED	BW	REA	AHA GE-EPDs
Sire	+2.3	+2.9	+0.67	Yes
Dam	-4.7	+5.5	+0.35	Yes
Heifer 1	-3.9	+5.8	+0.46	Yes
Heifer 2	-9.2	+8.1	+0.55	Yes
Heifer 3	-5.7	+7.4	+0.60	Yes
Bull 1	-1.3	+4.2	+0.51	No
Bull 2	-1.3	+4.2	+0.51	No
Bull 3	-1.3	+4.2	+0.51	No

[1]Data reported are real EPDs and GE-EPDs from AHA, pulled July 9, 2021.

Genomics for differentiation

Cattlemen and women do their best to select elite bulls to pair with their cows. Unfortunately, basic biology reminds us that variability exists even within the best mating plans. Exactly how much variability? Cattle inherit 30 pairs of chromosomes (60 total), one set of 30 from their sire and the other set of 30 from their dam.

Math aside, this means that in a single sperm cell, there are one billion possible combinations of chromosomes to be passed down to offspring. The same is true in the egg of a female. In a single full-sibling mating, there are more than one quintillion possible combinations of chromosomal inheritance. Therefore, producers could be standing in a pen looking at two prospective, full-sibling, sale bulls that phenotypically look the same, but whose genetic merit could be different. But differentiating those cattle on sale day goes one step beyond looks and expected progeny differences (EPDs).

Using Table 1 as an example, data has been captured on six embryo transfer (ET) calves (three bulls and three heifers) born from the same sire and dam mating. Phenotype-based EPDs are estimated using the pedigree, phenotype and progeny information on an animal. Yet, when full siblings are born, they share the same pedigree, and therefore the same phenotypic information stored within the genetic evaluation. This means that until their own phenotype or progeny information is reported, their EPDs for all traits are simply the average of their parents.

This is illustrated in Table 1 when looking at the bull progeny who all appear to have the same genetic merit for calving ease direct (CED), birth

weight (BW) and ribeye area (REA). However, unless identical twins, no two siblings share the exact same genetic potential. Seldom do siblings look, act or perform the same.

On the other hand, collecting DNA from an animal early in its life and reporting that to the evaluation will immediately reflect the genetic differences inherited from the sire and dam and more quickly differentiate cattle, as can be seen in the heifer progeny listed in Table 1 that have a genomic profile on file.

Figure 1: Probability of a given expected progeny difference (EPD) for birth weight, based on whether an animal has been genotyped (black line) or not (brown line).
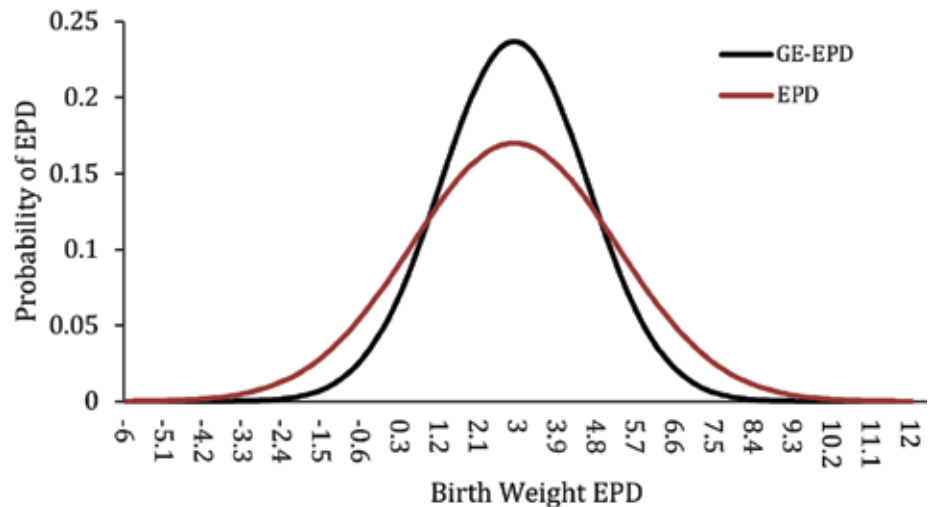
Genomics for risk management

In addition to differentiating genetic merit, genomics also help increase the accuracy of EPDs, which increases a bull buyer's confidence and their ability to manage risk. EPDs are defined as "expected" because they are the best understanding of an animal's genetic potential based on the information available. However, there is not a single cattleman or woman reading this article who has not bought a bull whose EPDs did not slightly shift up or down over time.

This shifting is a result of additional phenotype or progeny information being reported to the evaluation, leading to an increased understanding of the overall genetic merit of an animal. Instead of waiting for those values to change, running a genomic profile on an animal can add the equivalent of anywhere from 2 to 17 progeny records to the evaluation, immediately increasing the accuracy of the prediction.

This phenomenon is illustrated in Figure 1, where the horizontal axis represents a range of EPDs for BW, and the vertical axis represents the given probability that the EPD is, in fact, the true value for the animal. The same sire listed in the table above has a BW EPD of +2.8 lbs, with a corresponding accuracy of 0.65. Although the bull was born in 2017, this increased accuracy is most likely due to BW records being reported on progeny along with the fact he is genomically tested. In comparison, without genomics the accuracy of his BW EPD would be around 0.23.

Notice that while both lines are centered at the +2.8 EPD, the black line is both higher and narrower than the brown, while the brown line is shorter and wider in distribution. This reflects the increased confidence and probability in the estimate of an EPD when genomic information has been added, and it also shows the increased variability and uncertainty without genomic-enhanced expected progeny differences (GE-EPDs). The lines do, however, intersect at +0.9 and +4.9 lbs. To translate, there is a 60.5% probability that the sire's true BW EPD is between those values without genomic information. This probability jumps to 76.5% when the sire has a genomic profile.

Selection decisions impact our operations and our customers for years, if not decades. By incorporating genomics into our management criteria, we're able to mitigate risk and add additional assurance that the best possible genetic investment is being made. While phenotypic selection offers a great first sort on animals for sale day, genomics offers breeders additional protection to help understand what cannot be seen. Not only could this lead to a better understanding of the cattle, but it helps to better establish the value an animal brings to the potential buyer. **H**W

Editor's Note: Jamie T. Courter, Ph.D., is a beef products manager for Neogen Genomics.

Genomic-enhanced expected progeny differences (GE-EPDs) allow commercial and seedstock producers to make more reliable selections and breeding decisions on younger animals. Each animal tested is recognized with the American Hereford Association GE-EPD logo when searching EPDs at *Hereford.org*.