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Creating Variation in the Next Generation

EPDs add accuracy when making breeding decisions; but variation still exists.

Expected progeny differences (EPDs) have been available for many decades. Over the years, EPDs have gone through multiple rounds of improvements and integrated new technologies to make them more accurate. With the use of genomics, EPDs on young animals have reached new accuracy levels earlier in the animals' lives.

Members have invested large amounts of time and money collecting phenotypes and both performance and genomic data to make these predictions more accurate.

Meticulous culling and mating and selection decisions are made with these tools. Yet even with all this planning and investment with each calf crop comes an unexpected and sometimes unfavorable EPD result.

Reviewing accuracy

Why does this variation still exist? Even with all this accuracy and generations of planned breeding, why do animals still fall above or below parent average?

First, let's review accuracy. Pedigree information, an animal's own performance data, genomic data, and information on descendants for the trait of interest and the correlated traits are information points used to calculate an animal's EPD. The amount and quality of these data affect the accuracy of this prediction. Classical accuracy would be the correlation between predicted and true EPDs.

However, in the American Angus Association genetic evaluation, a slightly different approach called BIF Accuracy is used, which is a function of true accuracy. This BIF, or published, accuracy is better able to differentiate between a sire with a great deal of data (thousands of progeny records) vs. those with just a moderate amount of data making comparisons easier for each user.

Accuracy ranges from zero to one. Higher accuracy uncovers something about the reliability of the EPD as a predictor of mean, or average, performance of an individual's offspring. Still, it tells us nothing about variation in offspring.

Variation causes

So, what does?

How far animals deviate from the mean has to do with the amount of variation that trait has in the population. In many cases, this variation is represented as the standard deviation of a trait. For most quantitative traits, this variation is normally, or near-normally, distributed. Figure 1 depicts what a normal distribution looks like graphically.
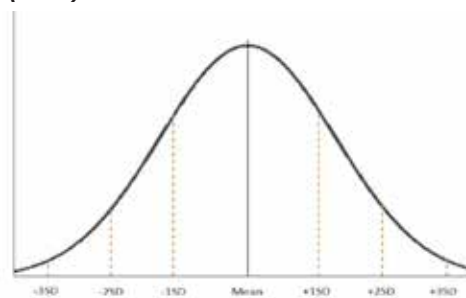
A normal distribution has a symmetrical bell-shaped curve, where the center of this curve lands at the population average. In the case of EPDs, the horizontal axis represents the EPD value, and the vertical axis represents the frequency of different levels of the EPD value in the population. The shape of the curve, or how wide or narrow the curve, is very closely related to the standard deviation of the trait. A large standard deviation will cast a wider bell-shaped curve, while a trait with less variation will be narrower.

Knowing the mean and standard deviation for each trait can help one make better generalizations about the distribution of the EPD value in that population. For normally distributed values, approximately two-thirds, or 68% of all observations are within one standard deviation from either side of the mean. Then

95% of all observations will fall within two standard deviations and 99.7% of the population will fall within three standard deviations away from the mean leaving less than one percent of animals falling further than three standard deviations away from the mean.

The American Angus Association provides the standard deviation of each trait inside the American Angus Association Sire Evaluation Summary. Table 1 depicts the EPD average, standard deviation, and minimum and maximum value for birth weight, weaning weight direct, and yearling weight EPD for the entire population. Understanding these values becomes important to understand the spread of EPDs and changes that are statistically possible when adding information to EPDs.

How is the amount of variation changed in the population?

As members continue to select toward individual breeding goals, they continue to move the entire population bell curve up or down the horizontal axis. Doing so creates a population that, on average, is better than the last. Figure 2 represents how changing the population for weaning weight by increasing the average moves the entire population up the number line, but does not eliminate the existing variation.

Mating animals that are less similar or using an outcross in the population tends to drive more variation to exist, leading to more variable EPDs in the next generation. On the contrary, if all members aimed toward a particular or singular EPD value, the variation in the population could shrink.

The shrinking of this variation would lead to less variable EPD predictions for the next generation, as very similar animals would be selected to maximize that single EPD. Doing

so would lead to less variable EPDs and more accurate selection.

Breeding animals more tightly together would decrease the amount of genetic variation for a particular trait, but also increase the amount of inbreeding in the population. Inbreeding can have severe negative effects, such as uncovering recessive phenotypes that could cause birth defects or fertility issues. Therefore, when variation exists in a population, it is a good thing, even though it can lead to gene combinations in the next generation that can equate to unfavorable EPD or progeny performance outcomes.
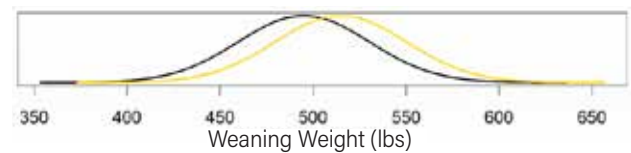
Shifting variation over time

When dealing with a population size as large as the Angus breed, the shift in genetic variation is slow. Multiple breeding goals and selection of animals to thrive in differing environments aids in keeping genetic variation alive and well. Even dollar value indexes ($Value) themselves do not eliminate the genetic variation in the next generation like complete selection for an individual EPD would.

Even though producers tend to target the maximum value of any one of the $Values, the nature of an index is that it is made up of several combinations of different EPDs all rolled into a profit calculation for the industry segments. This means achieving the highest value for any one of the $Values available for commercial cattlemen

to make selection decisions with can be arrived at with a different combination of individual EPDs. The nature of $Values tends to keep genetic variation alive.

All in all, if animals never fell above or below parent average, progress would never be made. Breeders are astute when making mating decisions for the next generation. Using all available tools from performance collection to genotyping and EPDs allows members to create profitable cattle for commercial cattlemen.

Moving the entire population up or down the number line for each given trait will protect producers on just how unfavorable EPDs may be. Yet in the end the genetic variation exists, and that is not a bad thing. **AJ**

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Editor's note: For more information, visit www.angus.org/performance *or contact the member services department at (816) 383-5100.*

Table 1: *Expected progeny difference (EPD) averages, standard deviations, and minimum/maximum value for birth weight, weaning weight, and yearling weight.*

Trait	No. Records	No. EPD	Avg.	SD	Min	Max
Birth weight, lb.	9,277,952	11,944,820	1	2.3	-12.7	16
Weaning weight direct, lb.	9,764,628	11,944,820	28	24	-80	126
Yearling weight, lb.	4,791,216	11,944,820	49	43	-138	227

Figure 2: *Population for weaning weight*

Weaning Weight (lbs)