

BY THE NUMBERS

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Weighting of Genomics Inside of EPDs

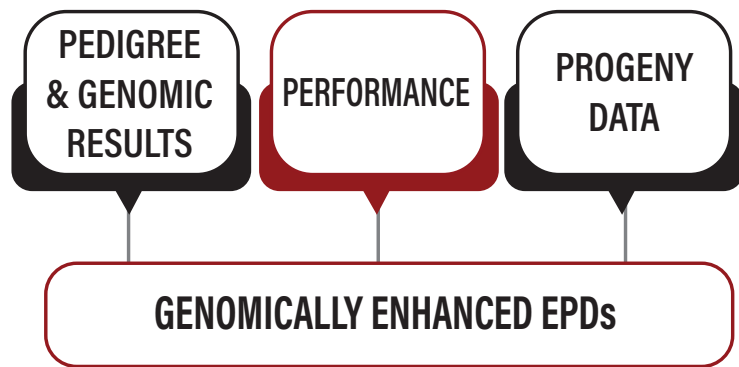
EPDs are predicted with the use of several different sources of information including the pedigree, individual performance, progeny data and genomics.

Many times, when submitting information on individual animals, the question arises: how much weight does each piece of information have inside of the expected progeny difference (EPD) calculation?

While each of the four parts play a critical role in predicting the genetic value of an individual animal, the quantity and quality of the phenotypic information surrounding that animal determines how accurate the prediction of the EPD is and how far the potential of that EPD can deviate from the average of its parents. In the case of genomic technology, the number of phenotypes included in the database determines how much weight the genomic information will have in that initial EPD prediction.

One way to dissect the weight genomic information has within

Figure 1: Information contributing to the GE-EPD



the prediction is by examining the average accuracy boost a genotype gives to a young, unproven animal upon inclusion.

To demonstrate, let's look at approximately 55,000 embryo transfer (ET) calves out of unregistered recipient dams, born from 2019-2021, right after their genotype is added to the national cattle evaluation (NCE) and before any of their progeny data is included. Keep in mind this group of animals without a genotype will have a published accuracy of 0.05.

Accuracy with genomics

With genomics, accuracy increased, on average, from 0.05 to 0.34 for all reported EPDs. Even more interesting is the way the average EPD accuracy differentiates itself based on the reference phenotypes of each trait. For example, with a trait like weaning weight, the average accuracy for an ET calf with no individual performance or progeny data in the evaluation is 0.42, whereas for a trait like claw set, the average accuracy is 0.27.

Why?

This is because the amount of information that can be harnessed by including the genotypes in each

WEANING WEIGHT

10 million phenotypes
0.42 average accuracy

CLAW SET

110,000 phenotypes
0.27 average accuracy

of these evaluations is based on the number of phenotypes reported for each trait. Weaning weight has nearly a 100-fold advantage in recorded phenotypes compared to claw set. As a result, the average accuracy boost for weaning weight is far greater.

Not only does the amount of information play a dynamic role in average accuracy between traits, but it also plays a dynamic role on individual animals within traits.

For example, the minimum accuracy value of the 55,000 animals predicted for birth weight EPD was 0.25 with a maximum of 0.62. Compare that with claw set, where the minimum accuracy predicted was 0.05 and the maximum accuracy was 0.36. Animals with higher accuracies for each trait are more

closely related to animals with actual phenotypes in the evaluation. For that reason, genomics are leveraged to a higher degree.

Accuracy is a good proxy to understand how much weight a genotype has on the initial EPD prediction on young, genotyped animals. But there is not a simple pie chart that can be devised and published for all traits to depict what piece of the pie each of the four different sources have inside the EPD. Each trait is different based on the number of phenotypic records in the database, and each individual animal is different due to how closely related the newly genotyped animal is to the actual phenotypic population.

In a population like American Angus, breeders have committed to

large-scale phenotyping. As a result, genomic evaluations are able to leverage this large data set to make powerful predictions on young animals. If the database lacked the phenotypic information, the increase in accuracy and hence the value experienced by breeders with the addition of genomics would not be as great. ^{AJ}

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