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Selecting Better Genes

Genetic selection is the process of selecting which animals become parents, how many offspring those parents produce and how long they remain in the breeding population.

The goal of effective selection in population genetics is to increase the frequency of the favorable genes that support individual breeding goals as quickly as possible.

To do so, breeders try to select animals with the best set of genes for breeding purposes and reject those with poorer sets of genes, in hopes of creating animals with better sets of genes in the next generation. As breeders continuously select the animals with better sets of genes, these genes increase in frequency across the population, and the entire population starts to move in a favorable direction.

Evolution

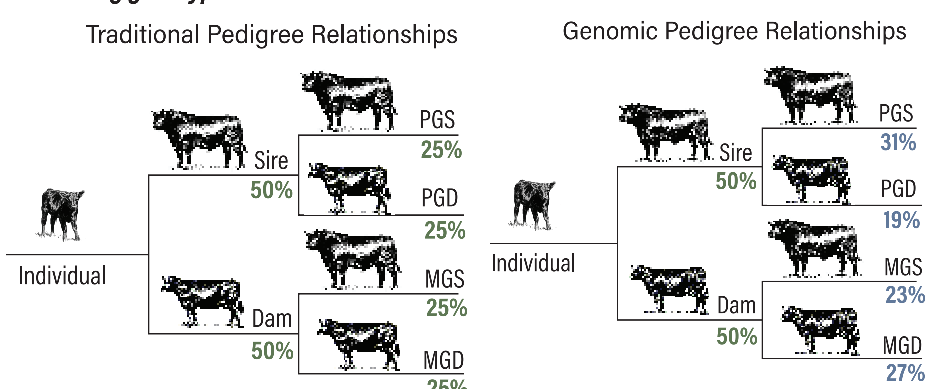
Over time, several different tools have been used in order to sort out which animals have the best sets of genes. Performance tests to record phenotypic data have become standard for seedstock producers wishing to propagate good genetics. Within-herd ratios use performance data to rank individual progeny within a contemporary group after age, sex and differences in dam age are accounted for. The advent of these ratios started to weed out some of the known factors that influenced performance traits to more accurately select progeny with better sets of genes.

From there, expected progeny differences (EPDs) made it possible to compare animals across different groups, herds and environments, which was accelerated by Angus's early adoption of allowing members to register calves resulting from artificial insemination (AI). This created links among herds across the country. Then in 2010, the American Angus Association released some of the beef industry's first EPDs to combine both phenotypic and genomic data, which have evolved over the last decade.

When genomics first came on the scene, the hopes of being able to find a few specific genes targeting each individual trait of interest were high. However, after several years of work, it has been solidified continued phenotypic data capture will remain one of the most important factors in order to continue to produce an accurate genetic evaluation. In today's evaluation, genotypes are used to create more accurate relationships among the animals located in Angus pedigrees. These relationships, termed genomic relationships, more precisely track gene overlap than is assumed by a traditional pedigree relationship.

Figure 1 assumes a traditional pedigree relationship vs. another

Figure 1: ***Depicts the differences between the expected average relationships within a traditional pedigree vs. the estimated genomic relationships within a pedigree that is utilizing genotypic information.***



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pedigree which is influenced by genomics. Whether influenced by genomic data or not, a parent-offspring relationship will always be near 50%; however, differences come into play as generations are traced back. The example in Figure 1 shows instead of the expected 25% relationship between offspring and paternal grandsire, the genomic relationship is higher. The genetic evaluation can then use the information about this relationship to better inform the EPD predictions on younger generations.

Embracing change

Even though changes to genetic evaluation tools have resulted in more accurate ways to predict which animals have better sets of genes, embracing these changes tends to take time. When EPDs were first released, within-herd ratios were the prevalent tool for genetic selection. Because ratios held little value in comparing animals across herds, EPDs were used as a complement to these early tools. In the early years of genomic testing, genomic scores were predicted to rank individual animals against the tested population, and those scores were used to create an EPD which was enhanced by genomics.

Fast forward to today, and these genomic scores have now become obsolete for genetic prediction of registered animals with known pedigrees. Instead, the value of genomic testing comes from the added accuracy gained through calculating more precise relationships among animals in the Angus pedigree, which include both direct (progeny, sires, dams, grandsires, granddams, etc.) and collateral (siblings, aunts, uncles, nieces, and nephews) relatives.

Figure 2: ***Comparison between the information sources that are included in the EPD versus the genomic score ranks and their relationship between each other.***

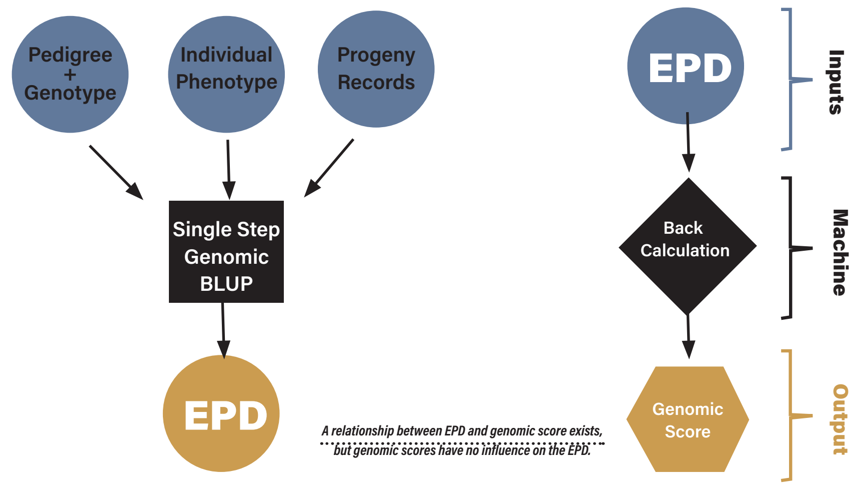

Figure 2 shows a relationship does exist between genomic score ranks and EPDs, but genomic scores have no direct influence on EPD calculations. Genomic scores are a back calculation from the genetic evaluation that allows members to look at partial genetic information before those animals are registered.

Once those animals are registered and the evaluation is able to leverage all the information available, including the pedigree influenced by the genotype (genomics), individual performance data (individual phenotypes) and progeny records, the EPD should always be the tool of choice when deciding between EPD or genomic score ranks. Because EPDs are used as inputs to back solve the genomic score component and EPDs are always changing, members will see changes in genomic scores over time.

First, the population of tested animals is always growing, so ranks will change as the population grows. Moreover, as more information is fed into the system, EPDs become more “knowledgeable,” which then influences the genomic score back calculation. This does not mean the animal’s DNA is changing; it merely supports that the information that feeds how that DNA relates to performance traits is becoming more informed as more data are submitted.

Staying the course

From individual weights to within-herd ratios to EPDs enhanced with genomics, many different tools have manifested over time to sort out which animals have the best sets of genes. Using these tools when making breeding and selection decisions supports breeders trying to move the population in favorable directions for economic traits.

Breeders should keep a sense of realism when using these tools to increase the accuracy of mating decisions with the understanding that, on average, the system does a very good job at predicting an individual animal’s genetic potential. Staying the course will allow all breeders to make steady progress over time. Feeding the system with updated phenotypic information will increase the value of these predictions and continue to make the genetic evaluation accurate.

All in all, leveraging these tools along with good cowboy logic and informed management decisions will work together for maximum returns. AJ