A Series of Numbers: Genomics and Data

Welcome to the final installment of a three-part series. I hope you have been able to read August's article on our carcass EPDs and the data that drives them, as well as September's maternal EPD conversation. To wrap up the discussion, I'll examine data, genomics, and their relationship to each other.

With genomic technology becoming commonplace in the purebred industry, some producers believe that taking a DNA sample and running tests for genomically-enhanced EPDs can replace the classic method of data collection. We have talked about the role that different data points play in the calculation of some of the breed's EPDs the past months, but is that information still important in the age of genetic technology? Absolutely.

Without data alongside genomic information, it's much harder to figure out the relationships between performance for a trait and the genes that control them. When the industry started the work to build genomically-enhanced EPDs, there was already years and generations of data in place. When breeds started collecting genotypes, they were able to analyze what they already had in their arsenal (performance data) to look for the markers that have an impact on the traits measured for years. If all the heavy weaning weight sires had similar sets of markers in their genomic tests, the geneticists could start to surmise that those markers influenced heavy weaning weights. While this example oversimplifies the process, it does illustrate that without data the genomics aren't near as valuable. Genomics without supporting data are akin to a credit card bill without money in the bank to pay for it. Eventually, they both will catch up to you.

Fortunately, we've already been through the process of fine-tuning the genetic markers and determining impacts on traits to develop our genomically-enhanced EPDs. Being a part of IGS gives our breed the advantage of having a team of geneticists who are continually working on making our genomically-enhanced EPDs more accurate. Recently, the IGS team worked for months to develop a stronger set of DNA markers for making genomic predictions. We saw the fruits of their labor in the changes to our EPDs back in August. The partnership between Neogen and IGS combines forces to make genomically-enhanced EPDs better for all breeders in the IGS cooperative. Neogen's move from a 50K genomic test to a 100K test doubled the number of markers a breeder gets in its test while keeping the price the same! As more genotypic and phenotypic data continues to enter the system, the better we can get at making genetic predictions about the capabilities of our cattle.

Across the industry, there are still traits that we simply don't have enough data in the bank to develop satisfactory genomically-enhanced predictions. This is the case for pretty much all breeds in the industry, and Shorthorns are no exception. The traits we've talked about in the previous parts of this series are prime examples. If you have ever looked at an IGS progeny equivalent table for GE-EPDs, you will notice that the numbers for carcass traits are lower than for growth traits. The value of genomic testing on weaning weight (equivalent to 22-25 calves worth of data) is triple that of ribeye area and marbling (6-8 calves). Why? Because we have so much more weaning data to work with! We have over 200,000 weaning weights in our ASA records, but only about 15,000 carcass measurements (ultrasound and actual carcass combined).

Maternal traits are not immune to this concept, either. Some of the larger breed databases have recently released maternally-oriented EPDs, such as Mature Cow Weight and Udder and Teat Scores. Why did it take them this long to develop a prediction for such important traits? They just now have adequate performance data to tabulate these EPDs. The work on genomically enhancing those newest EPDs is still ongoing. Traits such as udder scores and cow weights are found at a smaller proportion in the Shorthorn database. The number of weaning weights is over 100 times greater than the number of mature cow weights! Programs like the Genomically Enhanced Female Project are designed to help the breed and the participating breeder with this challenge in a two-fold manner. While you're able to get genomic information on your females at a discounted price, it also helps us grow a weak point in our database with breeders collecting mature weights and udder scores to qualify for the pricing incentive. While we are a long time from being able to compute EPDs for these traits, we sure can't get there if we don't start making strides towards that goal now.

Even with genomic information, we still need to collect performance data. The data that is submitted to ASA is the fuel that runs the engine calculating the entire genetic evaluation. Like any engine, the better the fuel that goes into it, the more efficiently it is going to run. I hope you have learned something over the last three months of this series. There's plenty of information to digest when it comes to the statistics of cattle breeding. It's important to be able to take that information and make it easily applicable for the folks breeding cattle. Otherwise, you're just pouring your fuel on the ground instead of in the engine.