

# Genomic-Enhanced Estimated Breeding Values (GEBV) for the American Sheep Industry

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Beginning in 2021, the sheep industry will have a new tool in the genetic toolbox that will allow for more accurate selection of breeding stock. This tool is Genomic-enhanced Estimated Breeding Values or GEBVs. Simply put, genomics uses an animal's unique DNA sequence to more accurately predict their true genetic merit. Estimated Breeding Values (EBVs) have been available to sheep producers since the late 1980s. Now, thanks to work by Dr. Joan Burke and Dr. Ron Lewis, GEBVs will be available to U.S. sheep producers. This technology has been widely adopted in the cattle industry with significant improvements to breeding stock selection. Now, genomic technology combined with individual, pedigree, and progeny data will create an even more accurate selection tool for sheep producers.

Genetic traits are often categorized as qualitative or quantitative. Qualitative traits are those controlled by one gene such as Scrapie resistance, Spider Lamb Syndrome or Myostatin. Many of us are familiar with these traits and already use genomics to test for them. For example, testing for Scrapie resistance (Codon 171) returns a genotype of RR, QR, or QQ. These letters denote alleles (differing forms of a gene). This single genotype can determine the phenotypic outcome, that is resistance to Scrapie or susceptibility to Scrapie. Quantitative traits, however, are controlled by many genes! Many of our performance traits, for example weaning weight, number of lambs born or weaned, milk production, and parasite resistance, are considered quantitative traits. So, if many genes control these traits, how do we use genomics to measure them?

Within a DNA sequence, there are "markers" which make that sequence unique for that animal. These markers are called single nucleotide polymorphisms or SNPs for short. A visual representation of these markers is depicted in Figure 1. The quantitative genomic test proposed for our industry examines 50,000 of these markers (SNPs) located across an animal's entire DNA sequence. Patterns among these SNPs in the DNA sequence correlate with individual performance (phenotypic data such as weaning weight, number of lambs born, fecal egg counts, etc.). So, genomic testing, together with pedigree performance information and progeny records, generate a GEBV which more accurately predicts an animal's performance (Figure 2).

The primary benefit of genomic information is the improvement in EBV accuracy. With every EBV, there is an associated accuracy value. This accuracy is reported as a percentage

and ranges from 0 to 100%. An accuracy of 0% means we know nothing about that trait and there is no confidence in the value. An accuracy of 100% means that the “estimated” breeding value is the same as the “true” breeding value and can be used with complete confidence. Remember, the breeding values we use are simply **estimates** of an animal’s genetic potential. The accuracy represents how close the estimated breeding value is to the true breeding value for a specific trait. Accuracy depends on the amount of information (i.e., its performance and that of its close relatives) we know about a trait. The more we know about something, the better we can predict it. For example, if we knew every play in a team’s playbook, the status of every player, the weather conditions during the game, and the historical records of the team’s performance, we would be able to predict the outcome of the game more accurately than we would if we were missing any of those components. The more we know about an animal’s performance and genetic makeup, the more accurately we can predict its genetic merit. If you think about EBVs as the seat of a stool, three legs support that EBV: individual performance data, pedigree performance data, and progeny performance data. However, on the GEBV stool, there’s a fourth leg: genomic data. The GEBV has more support. It is more reliable, and therefore, more accurate.

In the past, we achieved improvements in accuracy through a greater number of progeny records in the database. This takes many years of data collection and highly accurate EBVs are typically only available on heavily used rams and older ewes that have been in production for some time. Additionally, achieving accurate estimates for maternal traits on rams requires daughters in production. Genomic data expedites this process. Improvements in accuracy will vary by trait and will be better understood as more genomic data are entered into the database. Current estimates suggest accuracy improvements in the range of 2-24% depending on the trait. This improvement in accuracy is expected to be equivalent to 5-10 progeny in the database.

Genomic data will be most beneficial in selection of young ram lambs and ewes. For example, it could take 5-6 years of production for a ewe to generate 10 progeny. A single genomic test may provide the equivalent accuracy when the ewe lamb is just a few months old. This information allows for selection of ewe lambs more accurately and with greater genetic potential for lifetime productivity. Potential stud ram lambs can be selected at a much younger age and used with more confidence in their first year. Breeders will no longer have to “try out” a young ram on a handful of ewes to confirm his worthiness as a sire. Additionally, genomic testing will boost the accuracy of a ram lamb’s maternal EBVs before his daughters ever enter production.

When used effectively, GEBVs can rapidly improve genetic progress due to the improved accuracy of selection. This technology has the potential to improve U.S. sheep genetics, productivity, and producer revenue. More information on GEBVs can be found on the National Sheep Improvement Program website at <http://nsip.org/genomic-enhanced-ebvs/>.

