We have been selecting breeding livestock for over 10,000 years through visual appraisal; however, this method of selection has several downsides. It is because each animal is the combination of the genetics it inherits from its parents and the environment in which it is raised, as well as the management it is exposed to. About eighty percent of what we observe is due to environment factors that do not pass down to the next generation. The remaining twenty percent is controlled by genetics (depending on trait; some more, some less) and will pass onto the next generation.

We cannot tell the true genetic potential of an animal simply by looking at it. We need additional information. An animal's type of birth and rearing (single, twin or triplet), birth weight, weaning weight, level of parasite infection (measured by fecal egg count, FAMACHA© score, or deworming need) and other phenotypic observations provide some information about the genetic potential of an animal. There are

ways to predict the genetic potential of an individual animal. We have tools to predict what genes from the sire and dam are going to pass to the next generation.

WHAT ARE EBVs?

An animal's breeding value is defined as its genetic merit for each trait (e.g., prolificacy, birth weight, eye muscle area, carcass weight, etc.). It is not possible to determine an animal's true breeding value, but it is possible to estimate it. Thus, an estimation of an animal's true breeding value is called estimated breeding value or EBV. EBVs depend on the heritability of the trait and the difference between the individual's performance and the average performance of its contemporaries. A contemporary group is a group of animals (usually lambs/kids) that are approximately the same age and are managed together in the same group.

To determine EBVs, performance data collected on each lamb or kid is entered into a computerized database program. Its data is compared to its dam and sire, to all the animals in the same contemporary group, with known relatives within the same flock, and across other genetically-connected flocks. All this information adds statistical power to determine the estimated genetic potential of the animal. In short, EBVs are computer-generated predictions of the genetic merit of animals for economically important traits such as growth rate, prolificacy, mothering ability, and parasite resistance. EBVs help in selection decisions to improve economically important traits in a flock/herd.

An estimation of an animal's true breeding value is called estimated breeding value (EBV).

Quantitative genetic evaluation of sheep (and goats) in the US is conducted through the National Sheep Improvement Program (NSIP), which began in 1987 at Iowa State University and was led by Dr. Dan Morrical. Later (in 2000) it shifted to Virginia Tech under the mentorship of Dr. Dave Notter. In 2010, NSIP established a partnership with LAMBPLAN (Animal Genetics and Breeding Unit) in Australia. Since then, LAMBPLAN has done the data processing for NSIP to determine estimated breeding values on select traits specific to each breed. The main role of NSIP is to provide EBVs based on flock data and pedigrees to the producers for animals that are enrolled in NSIP and help them understand how to use them for selection purposes.

Use of estimated breeding values for internal parasite control

Animals with greater parasite resistance shed fewer parasite eggs. Identification of superior sires, dams, and offspring for parasite resistance is made possible by using fecal egg count (FEC) estimated breeding values. FEC EBVs can greatly reduce the need for deworming. In the US, FEC EBVs are available for Katahdin, Polypay, Dorper, and any other breed willing to submit fecal egg count data, including goats. Fecal egg counts can be recorded at 1) weaning between 42 and 90 days of age if lambs/kids are provided access to pasture prior to weaning; 2) at early post weaning between 91 to 150 days of age; and 3) at post weaning after 150 days of age.

GENOMIC ENHANCED EBVs

Estimated breeding values are calculated using performance records of the individual, its ancestors, collateral relatives, and any progeny it has. Genomic enhanced estimated breeding values (GEBVs) include genomic data together with the individual's performance, pedigree information, and progeny records for a more accurate prediction of animal's genetic potential. This new modern molecular technology (new to sheep, but not other livestock species) became available to US sheep producers enrolled in NSIP in late 2021. Dr. Joan Burke, Dr. Ron Lewis, and a team of scientists and producers (funded by a USDA, NIFA, Organic Research and Extension Initiative grant) played a vital role in the development and implementation of genomic enhanced estimated breeding values, including collection of DNA samples, analyzing the data, and validating the models to commercialize this technology.

Sample collection and data submission process for genomic enhanced EBVs

To determine genomic enhanced estimated breeding values, we combine genomic information with data we currently collect based on pedigree and performance.
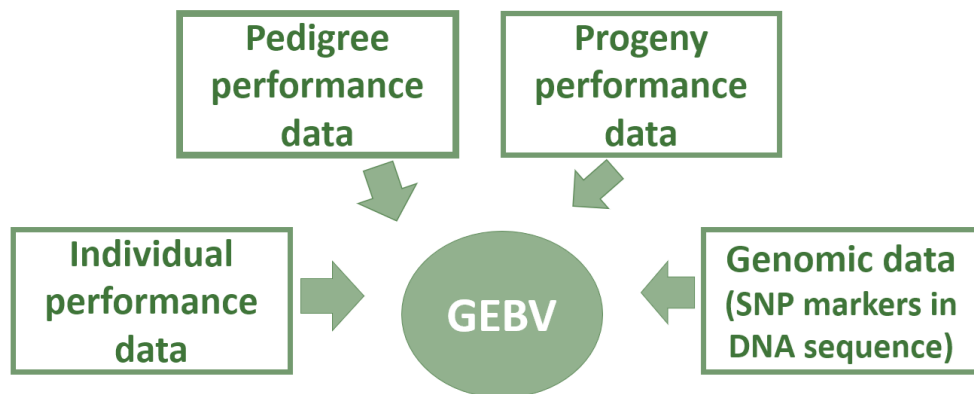
To obtain genomic enhanced EBVs:

1. Producers need to submit: a) tissue samples (collected from ear of the animal in a AllFlex® Tissue Sampling Unit) of an animal enrolled in NSIP; b) NSIP Genomic Sheep Submission Form; and c) $30 per sample payment to NSIP prior to genotyping.

2. NSIP forwards the forms and samples to a genomic lab (Neogen) for DNA testing.

3. Neogen genotypes all samples and forwards the results to the Animal Genetics Breeding Unit (AGBU) in Australia for the parentage analysis and genetic conditions. AGBU sends the results to NSIP.

4. NSIP forwards the reports to producers for their final review and validation of parentage and genetic condition. Producers review the results and make any necessary corrections to the flock data in Pedigree Master (the NSIP software).

5. Producers submit phenotypic data (birth weight, weaning weight, fecal egg count, etc.) and corrected genomic-based parentage (if any) to the database administrator of LAMBPLAN from Sheep Genetics in Australia for further evaluation.

6. Sheep Genetics sends the final results directly to the producer via email with a link to download the updated database.

More details regarding the process are available on the NSIP web site: nsip.org.

Genomic analysis along with performance records serves as a point of reference for the selection of breeding animals.

> *Genomic information in combination with EBVs improves the accuracy of selection.*

Tissue sampling units

Performance records are required for genomic enhanced EBVs.

Genomic information in combination with EBVs will improve the accuracy for the identification of the best animals for breeding. However, we will always need to collect performance data on animals that have genomic information. Performance data from thousands of animals are needed to calibrate genomic enhanced breeding values in order for the genomic tool to be useful. As of January 2024, the Katahdin breed had more than 10,000 genotyped animals in NSIP. We need to relate positive markers with animal's performance to have an association between markers and performance data. How accurate the estimated breeding value is depends on the performance records available on the individual and its relatives.

Genomic enhanced estimated breeding values can theoretically be used at an early age once the animal is genotyped and in LAMBPLAN. Therefore, the genomic test will be an addition to what we previously had, but not a replacement for performance data. Not every animal in a flock needs to be genotyped. Research is ongoing to determine the best strategy for genotyping within a flock since the technology is more costly than collecting phenotypic data alone. In an ideal world, an individual receives one-half of

their breeding value from sire and the remaining half from dam. The true proportion of genes that pairs of full-sibs share is not known. It is hard to determine which alleles a lamb will inherit from its sire and which alleles from dam. Genomics helps us to track which one it inherited from whom. Genomics allows for more accurate selection. We may be able to estimate breeding values even before animals start a performance record. It can thereby shorten the time to realize genetic progress. Thus, we will be able to improve the rate of genetic progress quicker. Genomics is a very accurate additional source of information that we can combine as we estimate breeding values.

Breeding stock with GEBVs

Breeding stocks with genomic enhanced estimated breeding values for Katahdin hair sheep are available on the NSIP website (http://nsip.org/katahdin-breeders/). NSIP breed coordinators can assist producers to find such breeding stock. Additionally, The Eastern Alliance for Production of Katahdins (EAPK) organizes online sales of breeding stock that includes sheep with genomic enhanced estimated breeding values (https://easternalliancekatahdins. com/).

Advantages of Genomic EBVs

- By using genomics, we can get better genetic evaluation at an earlier age, thus keeping economically sound animals and culling non-elite animals.

- GBVs can save time and cost of raising animals. Genomic evaluation at an early age will also decrease the generation interval and eliminate animals that need to fed to maturity.

- Genomic EBVs will not benefit traits that we already have a lot of performance records on, such those of an old stud ram with hundreds of progeny from multiple flocks.

AUTHOR:

Mohan Acharya, PhD
Lincoln University
Jefferson City, Missouri

Edited by Susan Schoenian

REVIEWERS:

Joan Burke PhD
USDA ARS Dale Bumpers Small Farm
Research Center, Booneville, Arkansas

Scott Bowdridge, PhD
West Virginia University
Morgantown, West Virginia