

Sheep GEMS News Brief 4 – mid-August 2024
Building the foundations for genomic selection in U.S. sheep

The Sheep GEMS project, together with NSIP members and other sheep industry organizations, have been working to create the building blocks for the implementation of genomic selection in the U.S. sheep industry. In this second article of the Sheep GEMS update related to genomic predictions, we describe the practical aspects for application of genomic selection in our industry.

Genomic selection is the process by which genomically-enhanced estimated breeding values (GEBV) are used for selection of individuals to become the parents of the next generation. The first question one may ask is “How are GEBV different from EBV routinely provided by NSIP?” The short answer is “their accuracy – GEBV tend to be more accurate than EBV, especially for younger animals”. This is because GEBV are based on genomic relationships among animals instead of only pedigree-based relationships that tend to be less accurate, more incomplete, and contain more errors. However, the interpretation of (G)EBV is the same. Both estimate the genetic merit of an animal for a given trait. Still, obtaining and using more accurate GEBV allows for quicker genetic improvement because our selection decisions become more accurate. One of the key goals of Sheep GEMS, therefore, has been to develop strategies for incorporating genomic information in our estimating breeding values.

Many factors influence the accuracy of GEBV. First and foremost is the size of the reference population, which is the number of individuals with both genomic data and phenotypic records for the traits of interest. Basically, the larger the reference population, the more accurate the GEBV. As a starting point, our target is at least 3,000 animals per breed before GEBV can be reliably provided. So far, only the Katahdin breed (12,500 animals) has met this target, while Polypay (1,270 animals), Rambouillet (1,250 animals), and Suffolk (520 animals) are still working to get to that goal in their respective reference populations. Second, we build a stronger reference population if it represents more flocks. There are 100, 30, 17, and seven NSIP-member Katahdin, Polypay, Rambouillet, and Suffolk flocks that have contributed until now to their respective reference populations.

Collecting phenotypic records for the various traits of interest is as important as genotyping animals. By linking genotypes to the performance of animals, we improve our ability to predict their genetic merit. This is particularly the case for traits measured later in life, expressed in only one sex, or that are difficult to assess. Many such traits reflect the robustness and resilience of our flocks, including ewe longevity, lamb survival, and udder health, and are the focus of Sheep GEMS.

Genomic selection has already been implemented in the Katahdin breed with Katahdin producers benefiting from using more accurate GEBV in their selection decisions. We are now in the process of performing genomic analyses for various novel indicators of robustness and resilience. These traits are heritable, influenced by many important genes, and can be predicted with greater accuracy when large enough reference populations are available. The opportunities from incorporating genomic information in genetic predictions are tremendous. However, to be realized, we need to continue building robust reference populations in more U.S. sheep breeds.

For further information contact Dr. Luiz Brito (britol@purdue.edu) or Dr. Ron Lewis (ron.lewis@unl.edu).

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