

National Sheep Improvement Program Technical Committee Report

Guidelines for sheep genotyping strategies: building the basis for successful implementation of genomic selection in U.S. sheep populations

Dr. Luiz Brito¹ and Dr. Ron Lewis²

¹Purdue University; ²University of Nebraska-Lincoln

Document last updated on: 02/18/21

Recommendations to implement genomic selection

- To establish a reference population within individual breeds in the National Sheep Improvement Program, collect genotypes and well-recorded pedigrees and performance information on at least 3,000 animals.
- Use a genotyping platform with many genetic markers spread across the genome (e.g., 50,000 markers).
- In order of priority, genotype rams that have or will be used as sires, ewes with multiple parities, and lambs with at least some performance data (e.g., weaning weight).
- As much as possible, include animals representing the breadth of performance levels in a flock.

Background

Currently, Estimated Breeding Values (EBV) are predicted from performance records and pedigree relationships collected through the National Sheep Improvement Program (NSIP) in collaboration with Meat and Livestock Australia Sheep Genetics. This approach has yielded the most accurate genetic improvement tool available to U.S. sheep producers to date. However, with the introduction of genomic technologies there is opportunity to increase the accuracy of EBV by incorporating DNA information into our genetic predictions, particularly in younger animals and for traits that are more difficult to measure.

The use of DNA information for breeding decisions and optimization of breeding programs is now a reality in many livestock breeding programs around the globe. There are millions of

animals currently genotyped for thousands of genomic markers distributed across the genome. The information from these genomic markers [Single Nucleotide Polymorphisms (SNP)] are combined with pedigree and phenotypic records to calculate Genomic-enhanced Estimated Breeding Values (GEBV) in a process known as genomic prediction. The outcome is that rates of genetic progress per year are being increased at an unprecedented rate in sheep and other livestock species, especially in lowly heritable and difficult to measure traits (> 60% for some traits).

Genomic prediction enables breeders to obtain more accurate breeding values in young animals that have not yet been measured for the traits of interest (e.g., number lambs born and reared), which then can be used in selection decisions. Genomics will be most advantageous for traits that are difficult or expensive to measure (e.g., disease resistance, feed efficiency, meat quality), sex limited (e.g., litter size), or measured late in life (e.g., longevity). Research into the best approaches for evaluating such traits is a necessary precursor to their incorporation into NSIP. Furthermore, justification for incorporating genomics into the NSIP genetic evaluation program will benefit from a broader consideration of breeding objectives within our sheep industry, with the anticipation that these novel and often more difficult-to-measure traits will ultimately be incorporated. In addition, genomic information enables the estimation of more accurate relationship among animals and, therefore, better estimates of inbreeding coefficients and genetic diversity in general. Such information also allows the identification of animals carrying lethal or unfavorable genetic conditions and can be used for parentage verification to correct pedigree errors.

Genomic selection is a routine practice in sheep breeding programs around the world, including Australia, New Zealand, France, Ireland, and the United Kingdom. Considering the great advantages of this technology, it is paramount to implement genomic selection in U.S. sheep breeding programs to remain competitive in national and international markets. In this context, NSIP has assembled a technical committee to establish strategies and recommendations for incorporating genomics into the NSIP genetic evaluation. Its goal is to establish guidelines to combine genotype information with pedigree and performance data collected on NSIP flocks to generate GEBV.

The successful implementation of genomic selection requires two steps: 1) research stage; and 2) practical implementation in the industry, which includes outreach to stakeholders. Both steps require the **establishment of a reference population**. A reference population is a large set of animals genotyped for many markers across the genome (e.g., 50,000 SNPs). These genotyped animals need to have accurate pedigree information and be measured for the main traits of interest. Since the reference population serves as the reference point for selection, it should also capture the genetic diversity present in a breed. Based on previous experiences with these technologies, **each breed should aim for at least 3,000 animals** in their reference population to generate accurate predictions of GEBV. In this document, we provide some suggestions and recommendations on how to choose these animals for maximizing the industry investments. As observed in sheep breeding programs in other countries, and in other livestock species in the U.S. (e.g., dairy and beef cattle), the industry (breeders, AI companies, and farmers) covers most genotyping and phenotyping costs. This has become common practice as these industries have recognized the benefits of these investments.

Establishing a reference population

The composition of the reference population will have an impact in the accuracy of GEBV. Therefore, the following factors are key. First, the reference population needs to represent the genetic diversity observed in the breed under selection. In other words, it is important to choose key ancestors and animals from multiple farms and genetic backgrounds to fully capture this genetic diversity of the breed. Second, when establishing the reference population, all the genotyped animals should also have performance records, or progeny with performance records, for the most important traits. The animals to be genotyped do not need to be measured for all traits of interest, but at least for some of them. Third, key ancestors (rams and ewes with multiple parities) should be prioritized as they have contributed more to the genetic pool. Lastly, those animals genotyped should not be chosen solely based on their performance. In other words, the reference population needs to contain animals across the continuum of performance levels. In this context, our main recommendations for establishing a reference population are:

- 1) A reference population of at least 3,000 animals per breed (with pedigree and performance records in NSIP, and with genomic data) should be established.

- 2) The first group of animals to be genotyped are the rams that have or will have progeny recorded in NSIP.
- 3) Next, ewes that have more than two parities with recorded progeny should be genotyped.
- 4) Subsequently, lambs with a performance record (at least a weaning weight) should be genotyped. We propose two options. Genotype all lambs for those litters from which you anticipate retaining replacement animals. Alternatively, choose one lamb from every litter.
- 5) We suggest choosing animals (rams or ewes) that have been recorded for the main traits of interest, or that have progeny with performance records, and are drawn from different sire families (to capture more genetic diversity of the population). The animals genotyped should not be chosen solely based on their performance but to represent the breadth of performance levels in a flock.

Genomic testing

We suggest genotyping all the animals with a medium-density SNP panel (~50,000 genomic markers). We also recommend collecting and storing samples of animals that due to cost might not be genotyped at present, as they may be useful for future genotyping activities. Therefore, we suggest collecting biological samples (ear punches collected using a Tissue Sampling Unit) on at least one lamb per litter (male and female).

Next steps

Once a reference population is established within a breed, it is key that genotyping **and** phenotyping continues. The accuracy of GEBV depends on animals currently in use being added to the initial reference population. As before those animals need to have the full set of genomic, pedigree and performance information collected, and submitted to NSIP. As more animals are genotyped, higher GEBV accuracies will be observed and, consequently, greater rates of genetic progress achieved over time. The use of genomics will also enable the refinement of the current breeding goals to incorporate novel traits, especially those that are currently difficult or expensive to measure. Developing pragmatic on-farm tools to measure these novel traits will be key to their incorporation in the NSIP genetic evaluation. Beyond the implementation of genomic selection, the datasets generated will be useful for research to optimize the genomic selection pipelines adding value to the investment made by sheep producers.