

# NSIP Genotyping Strategies: guidelines for on-farm DNA sampling to generate Genomic-enhanced Estimated Breeding Values

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In 2020, efforts to develop and commercialize Genomic-enhanced Estimated Breeding Values (GEBVs) began in earnest within the U.S. Sheep Industry. By summer 2021, Katahdin producers became the first to obtain GEBVs for their sheep. Simultaneously, a few other breeds began internal discussions about building their genomic reference populations, a key first step in generating GEBVs. Brito and Lewis (2021) developed a set of guidelines for implementing genomic selection in U.S. sheep breeds. Their recommendations are especially useful for breeds that have yet to establish their reference population. However, more discussion of sampling strategies within individual flocks is needed once the reference population has been built.

Several documents discuss the history and importance of GEBVs to the U.S. Sheep Industry (see <http://NSIP.org/genomic-enhanced-ebvs>). None, though, fully consider the next steps for determining which individuals within a flock should be sampled to ensure the greatest benefit of genomics. There is no simple right or wrong approach. Instead, producers should consider several variables including the amount of phenotypic data collected on individuals in a flock and the genetic connectedness among flocks.

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## General Considerations

*One and Done* – An individual should only need to have its DNA sampled and be genotyped once in its lifetime. With few exceptions, such as changes in genotyping technology, an individual will not need to be re-genotyped for the purpose of obtaining GEBVs. On occasion, errors encountered in assigning parentage may result in an individual needing to be genotyped a second time. So, great care should be taken to prevent contamination of the sample or sampling materials as well as to properly record the sample ID number (TSU number) and matching it to the sampled animal's NSIP 16-digit ID number.

*Building a Better Pedigree* – The offspring of a sire and a dam inherit one-half of their genes from each parent. However, those siblings often do not inherit the same set of genes from those parents. Genomic selection is more powerful than traditional approaches because it can estimate what proportion of genes are truly shared among relatives. The result is a better, more accurate genomic pedigree. The decisions we make as producers are greatly enhanced by this more accurate pedigree with the value compounding as better selection decisions are made generation after generation. On farm sampling strategies should consider the costs and benefits of building genomic pedigrees for individual sheep in our flocks.

*Importance of Sampling Females* – Because sires have such a strong influence on our lamb crop, and because it is relatively inexpensive to sample all breeding rams, it makes sense to do so. However, we should not overlook the importance of sampling females (i.e., brood ewes and replacement ewe lambs) in our flocks. Many of the traits whose accuracies are most effected by GEBVs are those that have low heritability (such as number weaned), are exhibited later in life (such as ewe longevity) and are difficult or expensive to measure (such as feed efficiency or meat quality). Also, many traits are only directly measured in females, such as number born, maternal ability, and milk production. In addition, desirable traits that are not currently tracked by NSIP, but could have strong economic importance to our industry are also only measured in females (udder health, for example). Sampling directed disproportionately towards males overlooks the importance of these female-oriented traits and should be avoided.

*Costs* – The cost of genotyping may be an overriding factor effecting your decision making. Some long-term planning may be warranted, especially in large flocks, flocks with few genetic linkages to other NSIP flocks, or simply flocks with limited phenotypic data in NSIP. Fortunately, genomics remains beneficial even when not all individuals can be genotyped. In some cases, it may be easier to simply budget a dollar amount each year and thoroughly consider the strategies discussed below to build the genomic pedigrees for your flock over time.

*Effect of Reference Population* – Each breed that wishes to develop GEBVs must first establish a baseline genomic and phenotypic database of a few thousand individuals representing the genetic diversity within that breed. Some enrolled flocks will be closely related to their breed’s reference population, while others less so. Those flocks that are more closely related will benefit to a greater extent by having a more complete genomic pedigree. That is, there will be more individuals in a pedigree that have been genotyped lending greater confidence to the GEBVs. Flocks with close ties to their breed’s reference population should consider prioritizing their sampling from individuals (certainly sires but also dams) that have few genetic linkages to the reference population, as that will enhance genetic connectedness.

*Genetic Linkages among NSIP Flocks* – How closely related flocks are within NSIP has some bearing on deciding which individuals to sample within your own flock. In general, two flocks that are closely related (e.g., one flock purchased all their ewes from the other, a pair of flocks that share the same rams year after year, etc.) may be able to “share” the genotyping effort (and costs), or at least strategize which sire or dam lines need genotyping.

*Within Flock Genetic Diversity* – There are many new flocks added to the NSIP database every year. In some breeds, many of these are smaller flocks with less than 100 breeding ewes. Many have assembled ewe flocks from a variety of sources and not necessarily from NSIP-enrolled flocks. Flocks comprised largely of ewes with few genetic connections to either their breed’s reference population or to other NSIP flocks, frequently lack an abundance of phenotypic data (weights, fecal egg counts, carcass scans, etc.). In flocks with multiple dam lines with little phenotypic data, care should be taken to prioritize sampling among individuals within each of these genetically divergent lines.

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## **Sampling Strategies**

- Sires – Producers should collect DNA samples and genotype all rams used as sires. Also, having genotypes on all sires within a flock on file with Australia’s Animal Genetics and Breeding Unit (AGBU) will increase the likelihood of successfully establishing genomic parentage, a key first

step in generating your GEBVs. This is the most cost-effective means to obtain genomically-verified sire parentage and to build a genomic pedigree.

- Breeding Ewes - Priority should be placed on ewes that have successfully reproduced multiple times in your flock.
  - This should include any younger ewes ( $\leq 5$  yrs) with at least two lambings that were not genotyped as part of the reference population.
  - Any exceptionally influential older ( $>6$  yrs) brood ewes.
- Lambs – Lambs with at least some phenotypic data (birth weight, weaning weight, fecal egg count, etc.) on themselves or their sire or dam should be given priority over lambs without these data.
  - If your flock has little phenotypic data in NSIP overall, or few genetic connections to flocks in NSIP:
    - Select 1 lamb from all or most litters for DNA sampling
    - Include both sexes in sampling
  - If your flock has considerable phenotypic data in NSIP or well-established genetic connections to flocks in NSIP:
    - Sample all lambs within a litter from which you will:
      - Keep replacement ewe lambs or potential sires for your flock.
      - Anticipate selling ewe lambs or ram lambs to other NSIP flocks.
    - Include both sexes in sampling

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## In Practice

The following three scenarios describe 3 possible approaches to DNA sampling. Producers need to recognize that all flocks are different and what works for one producer may not work for others.

Scenario #1 – Farm flock with 80 ewes, 3 sires, and a tight budget. Flock has been submitting data to NSIP for 10 years and is well connected to 3 other NSIP flocks through both ewe and ram purchases in recent years.

- Sample all 3 sires as none have been previously genotyped.
- Sample no dams. Instead, allow genomic pedigree to build over time on dam's side by sampling all replacement ewe lambs each year.
- Sample all lambs from litters from which you will keep replacement females.

Scenario #2 – Flock with 225 ewes and 7 sires. About 10% of the younger breeding ewes were purchased from NSIP flocks as lambs. Only 1 of the sires originated from an NSIP flock and it was genotyped as a lamb. Flock is relatively new to NSIP having submitted data from 4 lamb crops.

- Sample the 6 sires that have not been genotyped.
- Sample all dams with 2 or more lambings if you will keep replacements from their litters.
- Sample all lambs from each litter from which you will keep replacements.

Scenario #3 – Flock with 30 ewes and 2 sires. Flock is new to NSIP having submitted data for only 1 lamb crop and has no sheep originating from NSIP flocks.

- Sample both sires.
- Sample 1/3 of dams each year for 3 years prioritizing those from which you will keep replacements and those with at least 2 lambings (and with phenotypic information).
- Sample 1 lamb from each litter prioritizing those that may be sold as breeding stock, retained as replacements, and some from each sex.

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### Sources

**Brito, L. and R. Lewis. 2021.** Guidelines for sheep genotyping strategies: building the basis for successful implementation of genomic selection in U.S. sheep populations. National Sheep Improvement Program Technical Committee Report. 4pp.