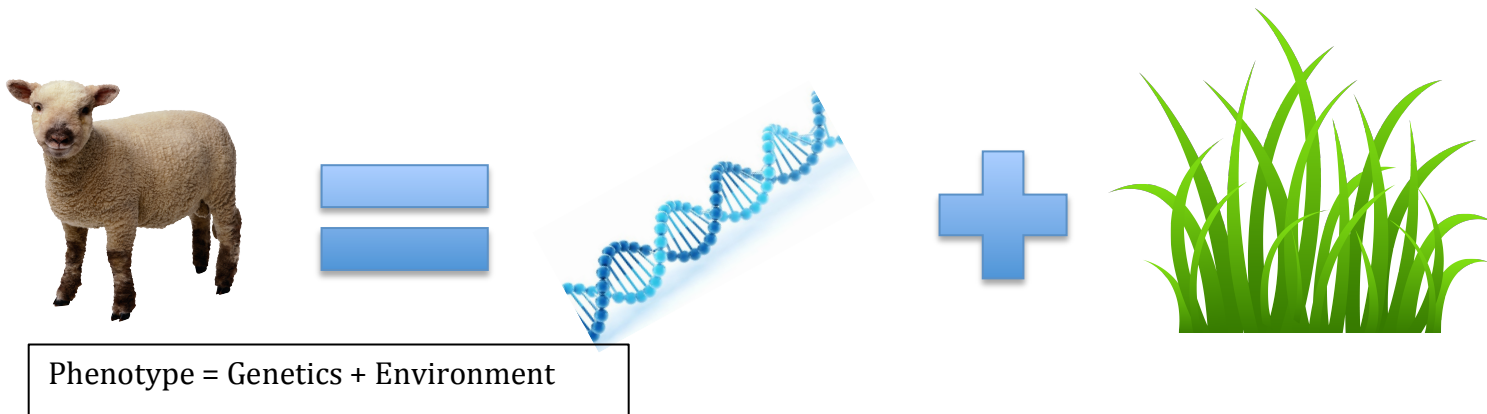


Estimated Breeding Values (EBVs): How they are calculated and what it means to producers

In today's modern agriculture with limited feed supplies, drought, regulations and tight margins, livestock producers must utilize all the information at hand to make the best possible decisions on the farm or ranch. The same can be said for selection of breeding animals within the sheep flock. But what information is needed to make that decision?

All sheep have a certain set of characteristics that describe their value to the producer, what we refer to as a **phenotype**. The characteristics include measures like number of lambs born, birth weight, weaning weight, number of lambs weaned, fleece weight, fiber diameter, mature weight, loin muscle depth or area...the list goes on. That phenotype is a product of that individual's **genetics** and the **environment** in which it is raised.



When looking at the differences in phenotype between 2 sheep in the same group, for example 1 ram has a weaning weight of 60 pounds and another has a weaning weight of 85 pounds, we do not know if that difference is due to genetics, a different environment or both.

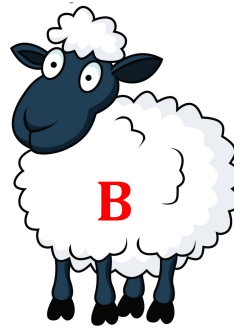
When selecting breeding animals, a producer is selecting which **genetics** they want passed on to the next generation of sheep in the flock. Herein lies the problem of selecting animals based on phenotypic traits such as weaning weight or appearance: we cannot differentiate what is caused by genetics and what the environment causes. Therefore, when that individual animal is placed in a different environment, those traits may change because they are based on genetics AND environment. When buying a ram, we want to know what its genetic merit is and how those genetics will be passed into our flocks. This is where **Estimated Breeding Values** come in!

Estimated breeding values (EBVs) are a very useful tool for sheep producers because they accurately **quantify** the **genetic merit** of a breeding sheep. The EBVs are calculated by accounting for known sources of variation for each phenotypic trait.

Let's look at the weaning weight of 2 ram lambs as an example; ram A and ram B were both born on the same day to 2 different ewes but the same sire. At 60 days of age both ram lambs were weaned and ram A weighed 60 pounds and ram B weighed 85 pounds.



Weaning Weight: 60 lbs

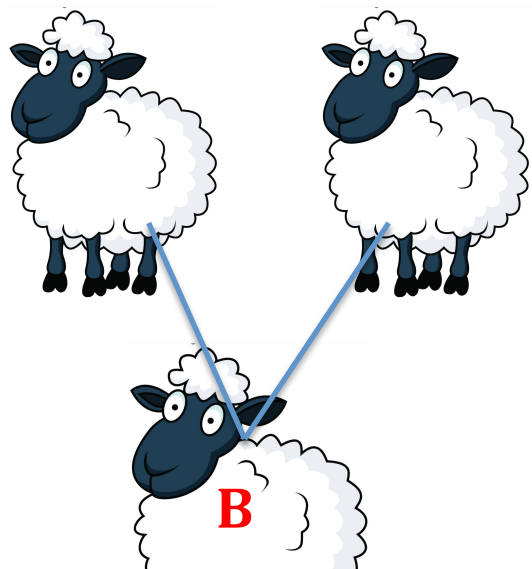
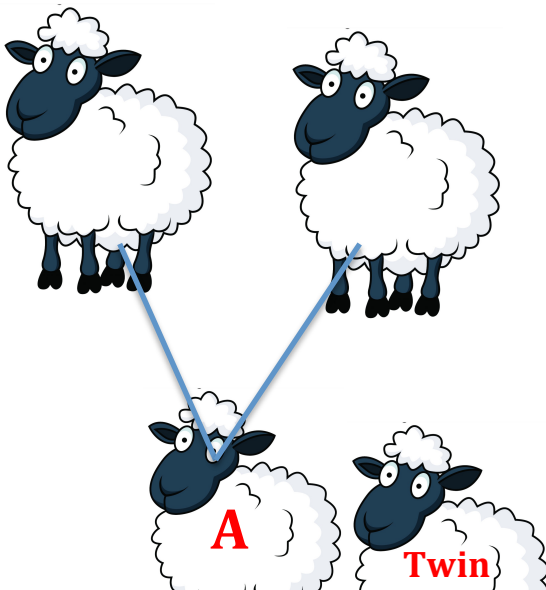


Weaning Weight: 85 lbs

We already stated that the environment that an animal is raised in is a large source of variation. Knowing this, we can raise animals in a common environment (similar pen, same diet, same bedding...) and we have already eliminated one source of variation! In our example, both ram A and B were born at the same time in the same pen so that aspect of the environment was the same.

However, it turns out ram A was reared as a twin and ram B was reared as a single. How might that impact their weaning weight, and thereby our calculation of their

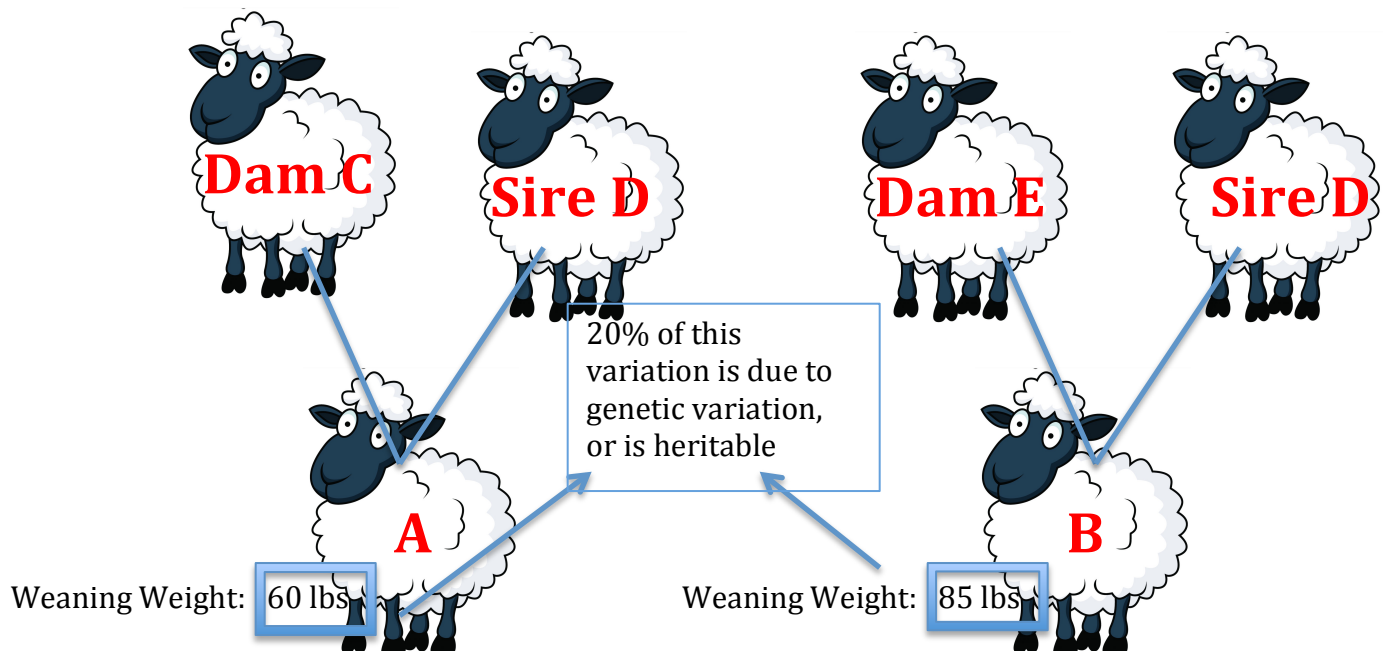
EBV?



We now will include an adjustment factor for rearing type because we know that single lambs have an advantage for growth traits over twins because they don't have to compete for milk. This adjustment factor corrects for **fixed effects** of differences in environment, in this case rearing type, and **standardizes** weights to a common rearing type. We may also wish to adjust these weights for other fixed effects such as day of age, age of dam and so on.

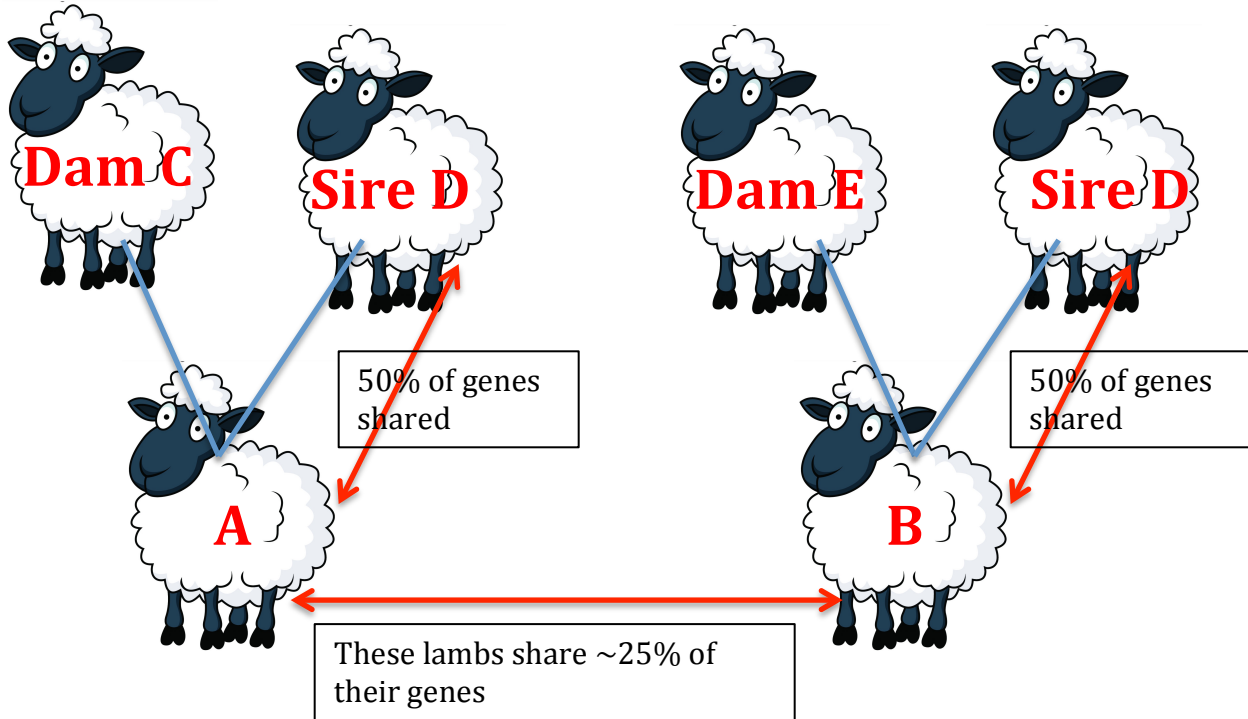
Adjustment factors eliminate other sources of environmental variation

Next, we know that certain traits are more influenced by genetics than they are by the environment and vice versa. This variation in the effects of genetics on a certain trait is called **heritability**. In humans for example, mature height is influenced 80% by genetics and 20% by the environment (nutrition, stress, injury...). Expressed another way, 80% of the **variation** in height can be explained by genetics and 20% is explained by environment and thus the heritability of height is 0.80 or 80%. Some examples of heritability in sheep are 0.3 for birth weight, 0.2 for weaning weight, 0.4 for mature weight, 0.38 for grease fleece weight, and 0.15 for number of lambs born; the higher the number, the more heritable the trait and the faster genetic progress can be made. This heritability is accounted for as a source of variation in our equation.



Next, because genes are passed from parents to offspring, we have to account for **relationships** between the animals. A lamb inherits roughly 50% of its genes from its sire and 50% from its dam. Therefore, a dam and her offspring share 50% of

their genes. A set of first cousins shares roughly 12.5% of their genes. In our example, since ram A and B are half-siblings, we would expect them to share about 25% of their genes. Even the most distantly related animals share some percentage of their genes. The percentage of genes in common is important in calculating EBVs because this accounts for the probability the lamb will inherit certain genes. With this known probability of common genes, we can account for this relationship within the analysis.



The more that animals are genetically linked (share some percentage of genetics) the stronger the genetic analysis will be within a flock. In order to compare genetic values between 2 or more flocks, the flocks must have genetic linkages or have shared genes between them.

Lastly, we must account for genetic correlations among traits. Most performance traits, like weaning weight, are not controlled by one single gene passed down from the parents but rather have multiple genes that control the genetic portion of trait expression. Furthermore, the same gene may have an effect on multiple traits, like a gene that affects both weaning weight and birth weight. A positive correlation between two traits means that if we see an increase in one trait, we will see an increase in the other. For our weaning weight example, weaning weight and birth weight have a correlation of 0.3 so we need to include account for this into our EBV calculation for an accurate result.

To put all of this together, in order to get an EBV for weaning weight on Ram A, we start with the weaning weight of Ram A's sire and dam (if they are known) then combine that with the actual weaning weight of Ram A along with all the other lambs that were raised at the same time and in the same manner of Ram A. We then

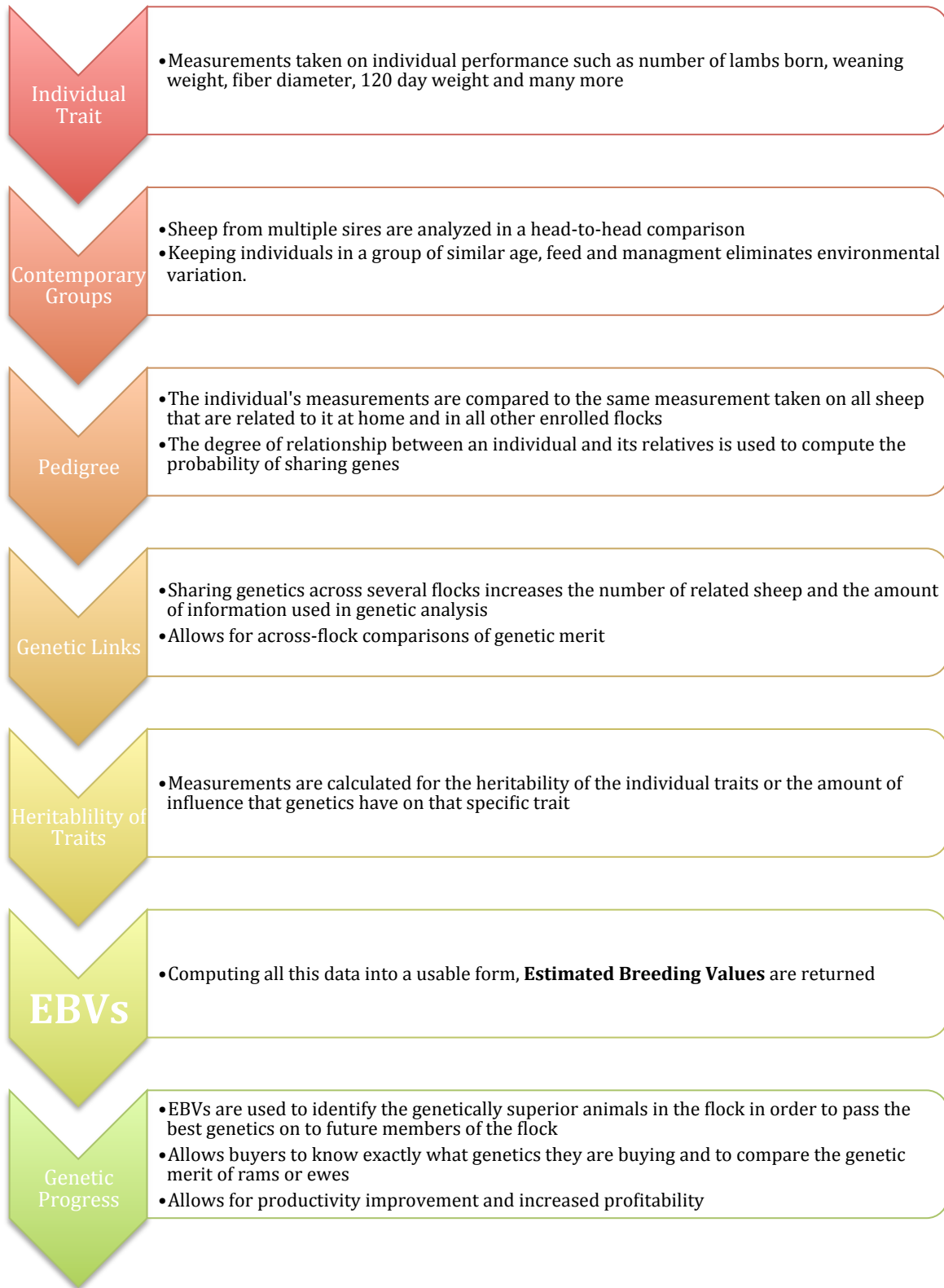
take that data, standardize it against all known fixed effects of environmental variation, take all of the data from all other sheep related to Ram A (even sheep that are in other flocks or sheep that have died), account for relationships and genetic correlations and we are able to get a value of the estimated genetic merit for Ram A for weaning weight. When all of this variation is accounted for, we can see that Ram A might actually have a greater potential to pass on the genetics for larger weaning weights than Ram B. If we just took the raw measurements of weaning weight, we would have made the wrong choice on which ram to keep and which one to cull.

The good news for producers is that **NSIP** takes care of calculating all this information for you! All producers need to do is submit the measurements taken at the set time points and submit it via Pedigree Master. Then NSIP and LambPlan in Australia work together to return data to producers. With data being processed twice each month, EBVs are never more than a couple weeks away!

There are a few key points that can be drawn from knowing how EBVs are calculated. First, because environment is such an important factor in the expression of the inherited genes, the group in which an animal is raised (contemporary group) is very important. Constructing sound contemporary groups is critical to receiving accurate EBVs and starts when planning breeding groups. A contemporary group is simply a group of animals with a similar age, raised in a similar manner that standardizes the environmental aspect of the equation and allows for accurate genetic comparisons. A contemporary group should include multiple offspring from multiple sires. A good rule of thumb is that a contemporary group should have lambs from at least 2 sires and 15 lambs from each sire. This is important because the genetic differences can only be isolated if different genetic lines are present in the same production setting and tested head-to-head. Lambs within a contemporary group must have no more than 42 days difference in age. This assures lambs are raised in a similar manner with the same environmental conditions i.e. weather, feed, pen, etc.

The importance of genetic linkages should also be evident after viewing these calculations. The true test of genetics is to compare head-to-head genetic lines in different production settings or environments. Linking flocks genetically is the only way to make across flock or whole-breed comparisons of EBVs. Truly superior genetics will rise to the top regardless of location. Also, by linking flocks, it widens the genetic pool available for comparison. Comparing one sire to another sire is beneficial but comparing 1 sire to 8 sires from across many flocks really improves your opportunity to identify the best ram to use in your breeding program.

As you can see, using the technology of EBVs provides the sheep producer with vast amounts of knowledge that couldn't have been seen without the help of NSIP. Utilization of this program gives producers a firm advantage over selecting on phenotype alone and allows them to make the most informed decision based on economically important traits. It is an investment into genetic progress and a means to minimize the risk associated with selection of breeding sheep.



For more information on the individual EBVs available and the benefits of NSIP, please www.nsip.org or send an email to info@nsip.org.