



## Genetic Improvement of Reproductive Traits in Sheep

The rate of genetic gain that you can achieve in most traits is related to the heritability of that trait. Most traits we wish to improve in sheep breeding have high heritability estimates and therefore the reasonable rates of gain can be expected. Unfortunately, reproduction is lowly heritable although there are some methods available to increase reproduction over time.

If you collect full dam pedigrees for your sheep flock, the collection of additional data such as dry ewes and dead lambs can assist you to begin to collect estimates of the genetic merit of your sheep.

Choosing to collect this information can be incorporated into datafiles submitted to Sheep Genetics Australia (SGA). SGA has developed systems to handle this data which are described below.

If you do not collect full dam pedigrees for your sheep flock, then there are slower methods available that can assist. We call these methods "indirect selection criteria".

### 1. Direct selection criteria

To calculate NLW and NLB, producers need to identify dry ewes and ewes with dead lambs

**Dry** ewes can be added to the SGA dataset by creating a "dummy" ID for the lamb that was not born that has the code DRY in the animal tag part of the 16 digit ID.

For example,  
if ewe 5012342002123456 is DRY, this can be included to estimate her EBVs for reproductive rate by giving her a "dummy" ID of the form:  
5012342006DRY001

with a sire & dam, therefore the pedigree file becomes:

id	sire	dam
5012342006DRY001	5012342002SIRE01	5012342002123456

**Dead lambs** can also be recorded in the database by creating a "dummy" ID for the dead lamb, with the code DAB in the animal tag part of the 16 digit ID.

For example, if the ewe has a lamb that is dead at birth, we create a dummy ID for the dead lamb following the format:

id	sire	dam
5012342006DAB001	5012342002SIRE01	5012342002123456

### 2. Indirect selection criteria

Measure scrotal circumference - this is correlated with ovulation rate in ewes. Column heading: SC

Measure body weight, this is genetically correlated with increases in reproductive performance. Column heading: BW

Count number of ram's testicles and record this and send to SGA database. Column heading: Testicles