

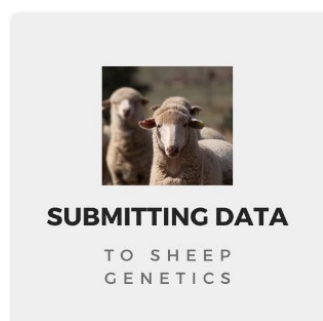
The Breeder's Guide

to Quality Assurance

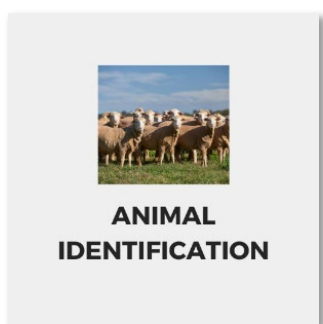


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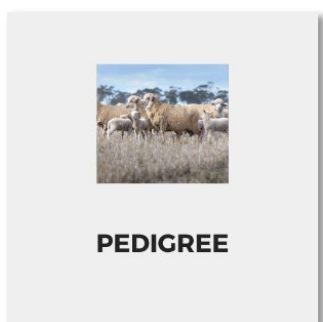
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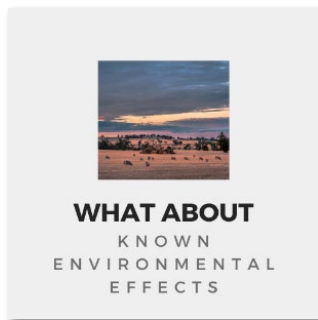
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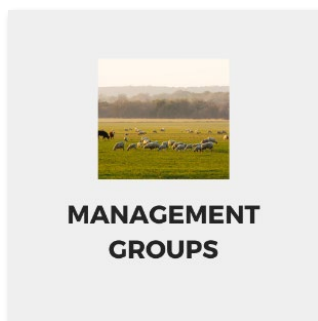


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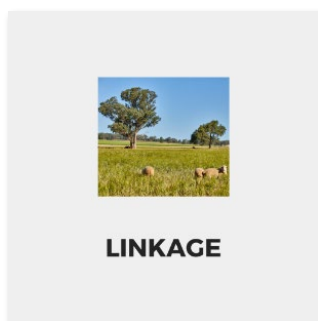
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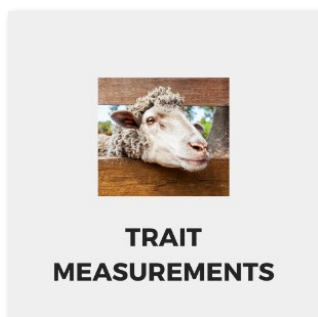
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Submitting data to Sheep Genetics

To generate breeding values you need to collect, record, and submit data to Sheep Genetics.

Recording pedigree, how animals are managed and how they perform takes effort.

To make sure you get the best return for this investment, it is important to record all data as accurately as possible.

This section explains what data you need to collect to generate an ASBV. This includes what data to submit, how to capture this data and how to submit it.

For details about how to subscribe to Sheep Genetics see the 'Getting Started' section on our website.

<https://www.sheepgenetics.org.au/getting-started/key-steps/>

How do I get my data into Sheep Genetics?

Data is supplied electronically through a software program that is compatible with Sheep Genetics evaluations. There are several commercial and free software packages available to ensure your data is provided in the correct format for Sheep Genetics.

For information about this software visit the Sheep Genetics website, click on the 'Getting Started' tab and go to 'Software for Managing Data' or contact the Sheep Genetics team.

<http://www.sheepgenetics.org.au/Getting-started/Software-for-managing-data>

Want help getting data prepared?

Sheep Genetics works with independent data managers who can help you collect and submit data.

These data managers understand how to use the software and submit good quality data. Some also help with on-farm measurement of traits and breeding program design.

A list of providers can be found on the Sheep Genetics website under the 'Service Providers' tab and by clicking 'Data Managers'.

<https://www.sheepgenetics.org.au/service-providers/>

What data do I need to submit?

The required data for each animal includes:

- [identification \(ID\)](#) – each animal has a unique 16-digit ID
- [pedigree](#) – the parents of the animal. This is the 16-digit ID of the sire and dam.
- [how the animals were born and raised](#)
- [traits](#):
 - trait measurements/records
 - the group the animal was managed in prior to the traits being recorded.
 - the date each trait was measured/recorded.

Refer to the relevant section of the guide for more information on how to capture each of these pieces of information.

When should I submit data to Sheep Genetics?

Data should be submitted as soon as possible after you have measured the whole cohort. A cohort is all the animals you are going to measure for the trait. (Note: animals are only charged once in their life, you may submit as many traits as often as you would like at no additional cost.)

Sheep Genetics update each analysis twice a month. A list of analysis cut-off dates (the final date for your data to be included in the next analysis run) are available on the Sheep Genetics website – go to the ‘Getting Started’ tab, click on ‘Data Submission Process’, and find the ‘Analysis Dates’ tab on the right.

<https://www.sheepgenetics.org.au/updates/news/Analysis-dates/>

You need to submit your data to Sheep Genetics before 5pm on the cut-off date. The earlier you submit data, the more time there is to correct any errors.

The cut off dates for inclusion in the MERINOSELECT and DOHNE evaluation are the 7th and 21st of each month, and 1st and 15th for the LAMBPLAN Maternal and Terminal evaluations, except where these dates fall on a weekend or NSW public holiday the cut off is brought forward to the business day before.

Sheep Genetics will provide your results within 10 working days of the cut-off date.

More information on the data submission process can be found on the Sheep Genetics website.

<https://www.sheepgenetics.org.au/getting-started/data-submission-process/>

Animal identification

Each animal submitted to Sheep Genetics has its own 16-digit identification number. This number is unique to that animal. If you use animals from other flocks, it is important to keep the animal's original 16-digit code.

	Breed Code	Flock ID	Birth year	Tag number
Example 16-digit ID	19	9999	2020	200001

- We assign 2-digit **breed codes** according to the table below.
- If you are a member of a breed society, we use your four-digit society **flock ID**. If not a member of a breed society, Sheep Genetics will assign you a flock code.
- The last six digits are determined by the breeder and tend to reflect the animal's **tag number**. The last 6 digits should aim to only include numbers (having no letters is preferred).

Important note: If entering these 16-digit IDs into Excel, be aware that the default formatting of the program tends to convert these IDs into incorrect scientific notation. You can overcome this by entering an ' at the beginning of the number i.e. '1999992020200001 and excel will then treat it as text and not convert.

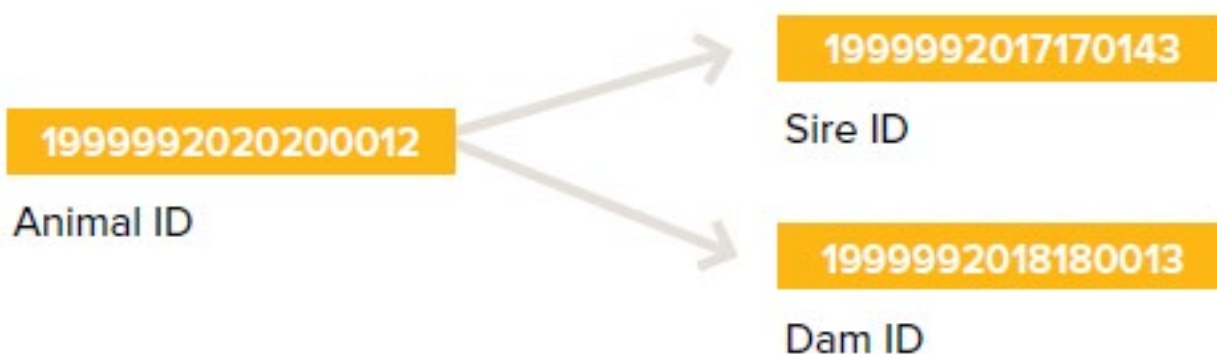
Breed code & name		Breed code & name		Breed code & name		Breed code & name	
1	Standard	25	Australian White	48	Prime SAMM	89	NZ Suffolk
2	Border Leicester	26	Research	49	Damara	90	NZ Polwarth
3	Corriedale	27	Shropshire	50	Merino	91	NZ Hampshire
4	Dorset Horn	28	Cheviot	51	Dohne Merino	92	NZ Finnsheep
5	Coolalee	29	South Dorset Down	60	Poll Merino	93	NZ Dorset Down
6	Bond	30	Carpet Wool	71	NZ Merino Composite	94	NZ Ryeland
7	Gromark	31	English Leicester	72	South American Merino	95	NZ English Leicester
8	Hyfer	32	Perendale	73	South African Merino	96	NZ Halfbred
9	Wiltshire Horn	33	Dorset Down	74	NZ Merino	97	NZ Shropshire
10	Polwarth	34	Ryeland	75	NZ Coopworth	98	NZ Gotland Pelt
11	Hampshire Down	35	South Hampshire	76	NZ Lincoln	99	NZ Southdown
12	Wiltipoll	36	Goats	77	NZ Borderdale	AF	Afrino
14	Southdown	37	Texel Downs	78	NZ Oxford Down	AG	Angora Goat
15	Coopworth	38	East Friesian	79	NZ White Head Marsh	CF	Clun Forest
16	Poll Dorset	39	Booroola	80	NZ Drysdale	CH	Charolais
17	Texel	40	Dorper	81	NZ Lincworth	CM	Composite Maternal
18	Romney	41	NZ Romney	82	NZ Border Leicester	CS	Composite Shedder
19	Suffolk	42	Suffolk Canada	83	NZ Corriedale	CT	Composite Terminal
20	Tukidale	43	Finn Leicester	84	NZ Dorset Horn	IN	Information Nucleus
21	South Suffolk	44	Elliotdales	85	NZ Poll Merino	SI	Sheep Improvement Ltd
22	Finnsheep	45	Red Deer	86	NZ Poll Dorset	SX	St Croix
23	White Suffolk	46	Elk Deer	87	NZ Texel	VR	Van Rooy
24	Ultra White	47	White Dorper	88	NZ South Suffolk	XB	Crossbred

Pedigree

Once you create a unique 16-digit ID for each animal, you can describe relationships between animals. Accurate pedigree is important because Sheep Genetics uses relationships between animals to estimate breeding values.

Pedigree is determined by entering the ID of the animal and their parents (sire and dam). Where sire or dam is not known, these fields are left blank. Full pedigree is where we have a known sire and dam for an animal.

Example of full pedigree



Sire pedigree

Sire pedigree is obtained by recording:

- Which individual rams were mated to which group of ewes (single-sire mating)
- Which ewes were artificially inseminated using semen from a ram?
- Use of DNA parentage if syndicate mating



Syndicate pedigree

Syndicate pedigree refers to when you use a team of rams for joining and do not know which individual ram sired which progeny.

Providing individual sire pedigree estimates the breeding values more accurately than when you submit syndicate pedigree.

To submit syndicate pedigree, you need to create a new ID for the syndicate. Sheep Genetics refers to these as named syndicates. For example:

199999 2019 **NAM001**

Use your breed and flock code when naming the syndicate.

The year of birth in the ID will be one year less than the progeny from the syndicate (e.g. for a 2020 drop lamb, its syndicate will contain 2019 in its ID).

NAM refers to a named syndicate.

Important

- There can be no more than 10 rams in each syndicate.
- Members of a syndicate can be from outside flocks; however, all syndicate members must exist in Sheep Genetics with ASBVs.
- All members must be listed as male in the evaluation.
- No more than 30% of the lambs within a drop can have syndicate pedigree (or no pedigree)
- The flock code in the syndicate ID must be your own (the same as the flock code of the progeny)
- The year in the syndicate ID needs to be earlier than the year in the progeny ID.
- You will need to include a list of the members of each syndicate (their 16-digit IDs) in your software.
- Syndicate pedigree is not published by Sheep Genetics in the pedigree of progeny.



How does Sheep Genetics use syndicate information?

Because which sire was mated to which dam is unknown, the breeding values of the syndicate ram team are averaged to produce the sire breeding value that contributes to the progeny. Therefore, if a syndicate must be used it is best if to use rams with similar breeding values for the traits you are interested in. By using rams with similar breeding values, the average breeding value is closer to all the sires' actual breeding values. One strategy is to use related rams in the syndicate, such as half-siblings.

The performance of progeny does not contribute information back to the sire's breeding value.

Syndicates also do not provide any linkage to the progeny.

The impact of syndicate mating on these calculations would be rectified by getting individual sire pedigree.

Why individual sire pedigree is preferable to syndicate pedigree?

Syndicate mating's are challenging because you cannot control which rams join which ewes. Additionally, twin lambs with the same dam can have different sires.

In the evaluation:

- Syndicate pedigree does not provide linkage.
- The performance of syndicate progeny does not contribute back to the ram's ASBVs (as the evaluation cannot attribute the performance to an individual sire).

Sheep Genetics strongly encourages establishing individual sire pedigree rather than using named syndicates.

If you are using DNA at a later date to determine single sire pedigree, update to the correct pedigree sire in your software and resubmit the file to Sheep Genetics. Do not update the ram joined ID in the mating module, keep that as the syndicate for the mating analysis.



Dam pedigree

Collecting dam pedigree involves recording the 16-digit ID of the mother of an animal.

Why is dam pedigree important?

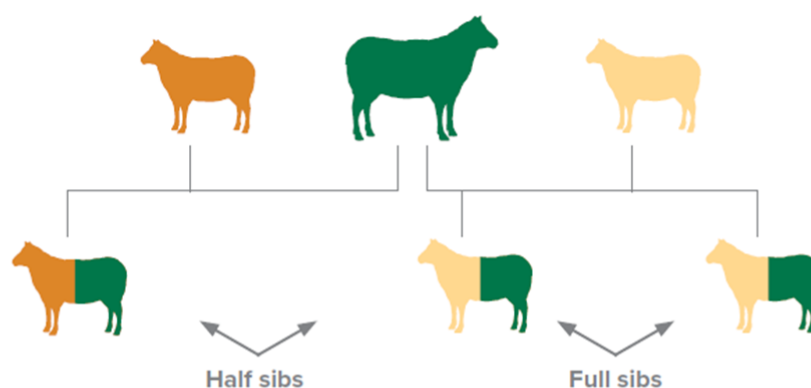
Dam pedigree is important as it allows Sheep Genetics to more completely estimate relationships between animals.

When you submit dam pedigree:

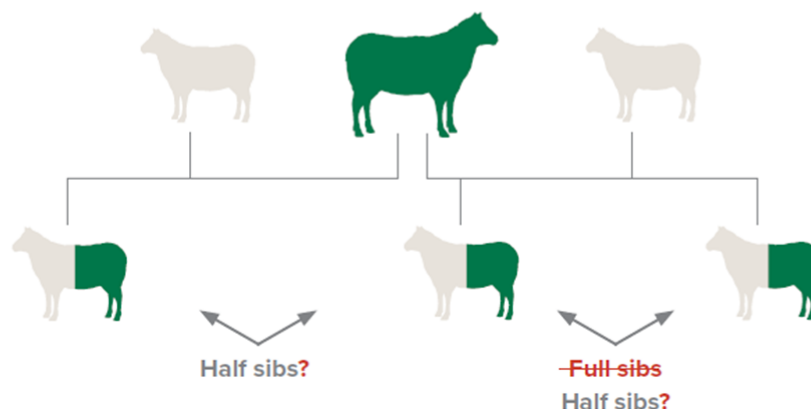
- breeding values are more accurate.
- maternal effects can be estimated.
- reproductive traits can be recorded.
- full sibling relationships can be identified.
- linkage between years is better.
- you can collect more information about how the animals are born and raised (particularly if tagging at birth)
- having full pedigree allows the calculation of inbreeding.

The impact of understanding relationships

If you know the sire and dam, you know the full relationships between the animals



If you only know who the sire is, you know these three offspring are related but not how closely. You cannot determine which are half sibs or full sibs, so have to treat them as half sibs in the analysis.



What happens if I do not know the sire or dam?

When you have missing pedigree, Sheep Genetics fills the gap with your genetic group. You can think of the genetic group as one parent which adopts all the lambs for which you do not have a sire or a dam. This genetic group gets a breeding value like all the other animals you submit.

This means if you if you do not submit a sire or dam for an animal, the breeding value of that animal is estimated assuming all the missing parents in the pedigree are the same. The breeding values of all the animals with missing pedigrees (the genetic group) are estimated based on the same breeding values. This reduces the accuracy of the estimation and may mean some animals have breeding values lower than what they really are, or do not meet the accuracy and linkage thresholds required to be reported. It is important to submit pedigrees for all animals you can.

Important

- No more than 30% of the lambs within a drop can have no pedigree (missing sire and dam) or syndicate pedigree.

Discussing pedigree recording methods

<i>Technique</i>	<i>Advantages</i>	<i>Disadvantages</i>
Tag at birth Lambing round at least once a day, recording any lambs that have been born in the last 24 hours.	Best data quality You can record: <ul style="list-style-type: none">○ accurate birth type (litter size)○ birth weight.○ accurate birth date○ deaths It's an opportunity to collect additional traits (maternal behaviour score/lambing ease)	High labour cost/input Disturbing the mother and lamb could cause mismothering. Requires single sire mating or AI (or DNA parentage) to inform sire pedigree
Lambing rounds from a distance During lambing, you check lambing ewes at least once a day to record who gave birth from a distance.	Collects accurate birth date and birth type. Minimal disruption to birth site Low labour inputs	Does not capture additional birth traits such as birth weight or maternal behaviour. You need to mother up later using another technique to actually match ewes to lambs. Requires single sire mating or AI to inform sire pedigree

DNA parentage

Lambs and all potential parents are sampled using tissue sample units (TSUs) and DNA is processed, and parentage then allocated.

You can identify individuals from a syndicate mating.

Convenient

Less labour intensive

Assigns both sire and dam (if both potential parents are also tested)

Limited control over allocation of rams to ewes if syndicate mating

Extra expense

First year particularly expensive as you need to DNA test all possible sires and dams.

No information on birth (including birth date)

Takes time to get results processed and returned

Proximity collars

You attach a collar with proximity sensor pods to both the ewes and lambs. It allocates the ewe to the lamb based on how much time they spend near each other.

Generally, a less expensive method

Quick and easy

No information collected at birth.

Single sire mating or AI required to inform sire pedigree.

Labour intensive (in short bursts) when attaching and removing collars.

Risk that the maternal mother is identified rather than the genetic mothering (where pirating has occurred)

Pedigree MatchMaker

An electronic tagging system which identifies which lamb belongs to which ewe based on how often they walk through a draft together.

Relatively cheap

Don't have to be at the birth site

Not always a viable option for some flocks, as environment may not be suitable (e.g. too many watering points)

Single sire mating or AI required to inform sire pedigree.

Requires training of animals to walk through the device.

Mothering up away from birth site

Relatively cheap

Variable accuracy depending on the age of the lambs.

You match the mother and her lamb/s in the yards by observing how lambs and ewes interact.

Mismothering

Labour intensive for short periods

Single sire mating or AI required to inform sire pedigree.



Nominating Pedigree Type

Pedigree type provides the method through which pedigree was derived for the animal. It is an important piece of information to include in your data as it is used in the check and confirm the pedigree you supply.

Pedigree type is allocated for both the sire pedigree and the dam pedigree, and can include:

- Mothering at birth, or later at marking or weaning,
- DNA parentage
- Pedigree Matchmaker,
- Single Sire lambing,
- Inferred from Dam,
- Inferred from lambing date,
- Other

This field is particularly important where DNA parentage is used, as in many cases ewes are joined to syndicate ram teams, and individual sire pedigree is gained from DNA. Where this occurs, there can be multiple lambs with the same dam, however different sires. This pedigree data is excluded from the evaluation due to “twins by different sires” unless the pedigree type for the sire is nominated as DNA.

Conception method

Conception method indicates how a lamb was conceived, and is an important validation of pedigree supplied, reproduction and can impact the grouping of animals.

Conception methods can include:

- Natural (1)
- Embryo Transfer (2)
- Artificial Insemination (3)
- Juvenile In Vitro Embryo Transfer (4)
- Multiple Ovulation Embryo Transfer (5)
- Pen or yard mated (6)

Where there is no conception method supplied, animals are assumed to have been conceived naturally. This can cause issues particularly if you are running an ET program, with common exclusions appearing:

- Too many lambs from the same dam for natural (or AI) conception
- Lambs from the same dam are born on different days.

Where these exclusions occur, the dam pedigree of the lambs is excluded from the evaluation.

What should I do if using embryo transfer (ET)?

- Enter the donor of the embryo as the dam pedigree of the lamb.
- Record the conception method of the ewe and lamb in your software (ET is 2)
- It is recommended that you use a ewe that exists in Sheep Genetics as the recipient, as we can better account for the maternal environment. Record a Sheep Genetics ID for the recipient dam.
- Have at least two sires represented among each ET drop. ET lambs are grouped separately to natural/AI born lambs.
- Use at least one of the sires used in your ET program in an AI or natural mating program to ensure good genetic linkage between ET and non-ET progeny.
- Record any naturally conceived progeny from donor dams to enable evaluation of their maternal traits.

Important

- Ewes joined in an ET program are not included in the reproduction evaluation as their performance is pharmaceutically manipulated.
- ET-born lambs are grouped separately from their naturally and AI conceived contemporaries due to the potential influence of pharmaceutical intervention on their performance (refer to Management Group section)



Known environmental effects

Differences in performance reflect both the genetic merit of the animal (the genes it carries and passes on to progeny) and environmental factors. Some of these environmental factors are known and highly repeatable, meaning the evaluation can account for them. These known environmental, or fixed, effects include information such as date of birth, birth and rear type, and dam age, as well as management groups.

The more you record about how animals were born, raised and managed, the better the evaluation can account of these differences between animals and the more reliable their breeding values will be, particularly for early in life traits.

Birth date

When you tag lambs at birth, the birth date is most accurate because you are recording the exact date of birth of each lamb.

If you do not tag at birth, there are alternative ways to record date of birth which include:

- Record lambing date from a distance. You will see (and record) which ewe lambed on which date. If you then mother up later, you already have the birth date for that lamb.
- Drift lambing – separate ewes which have lambed from pregnant ewes throughout the lambing period to get a better estimate of lambing date.
- Early, mid and late-foetal ageing – lambing dates estimated from pregnancy scanning.
- Use the middle date of your lambing period (all lambs are given the same date). If you do this, Sheep Genetics recommends a short lambing period of five weeks to minimise the bias due to age.
- Use Artificial Insemination and provide a single date of birth for the AI program. Ewes tend to lamb over 10 days. Make sure you leave at least 10 days between AI and using backup sires if using lambing date to determine sire pedigree.

Sex of animal

The sex of an animal should be recorded as male (1) or female (2).

Note: Both rams and wethers are recorded as male (1), however if wethers continue to be recorded following castration, they must be management grouped separately to their ram contemporaries for these measurements (see Management Group section).

Birth type and rear type

Birth type refers to the size of the litter the ewe gave birth to (lamb was born into). Rear type refers to the number of lambs the ewe reared.

Birth type is recorded at birth or informed through pregnancy scanning, however, must be recorded for each lamb. Rear type is recorded at weaning. Each of these should be submitted as numbers in the birth type and rear type fields, 1 = single; 2 = twin, 3 = triplet, 4 = quadruplet etc.

Lambs which are tagged but die before weaning will have a rear type of 0. It is important to adjust any sibling's rear types to reflect how the litter was raised.



Management groups

Sheep Genetics needs to know how animals are managed to account for performance differences that not related to their genetics. The information should include if groups within the flock are managed differently or if you do something to them which will impact their performance.

The management group submitted with a measurement refers to **how an animal was managed prior to the measurement being recorded.**

Animals should be placed in a different management group in your submission if their performance between measurements has been impacted by a difference in the environment or management, such as:

- Differences between paddocks
- Preferential feeding
- Illness/injury.

How do I record groups?

Step 1 – birth groups

Record animals based on how their mothers were managed during pregnancy. For example, if ewes were lambed down in different paddocks, with different feed availability or shelter, then the birth group of lambs should reflect the paddock they were born in.

Step 2 – sub management group at each age stage

At each age stage, include any subgroup (based on management) changes since the previous measurement.

For example, feeding lambs differently between weaning and post-weaning.

If you manage animals in different paddocks but the paddocks have similar history and feed available, you do not have to create subgroups based on paddocks.

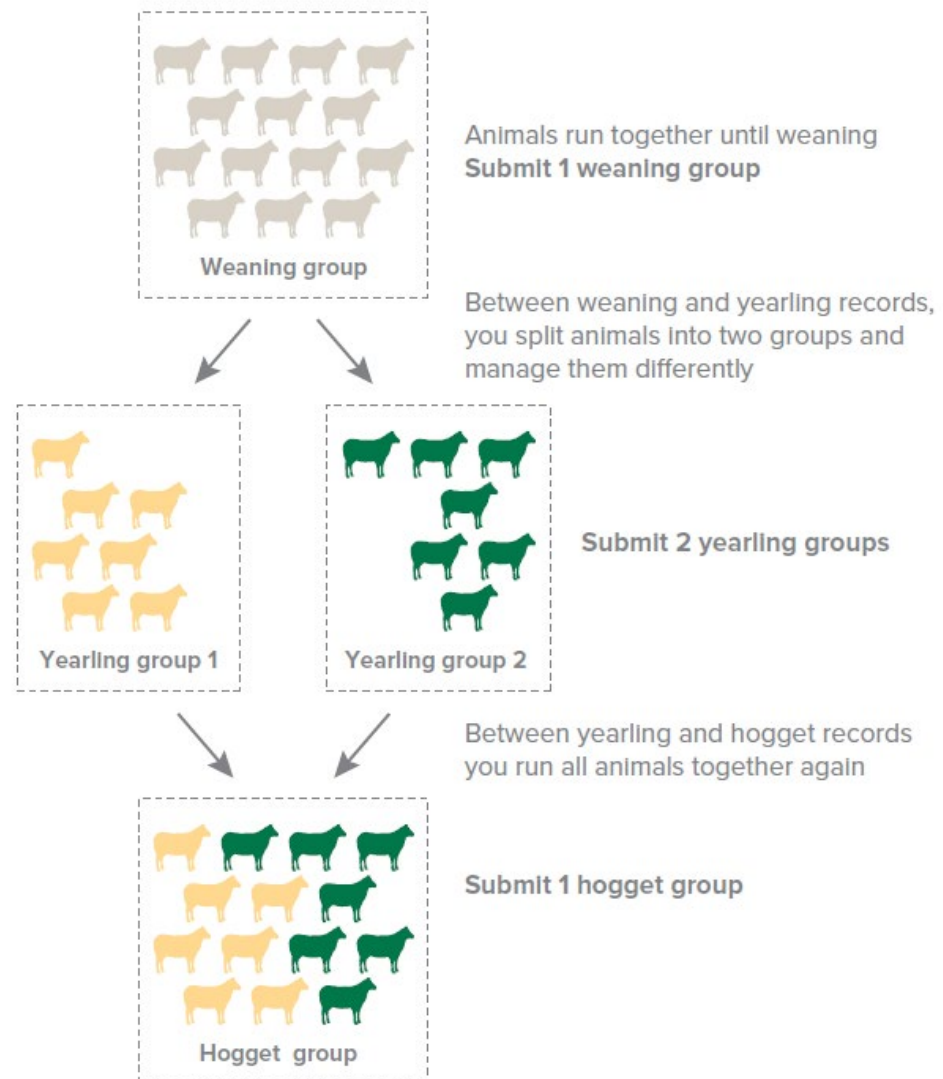
Wethers and grouping

If you retain and measure wether lambs, these wethers must be sub-grouped separately to their ram contemporaries, as castration is a management activity that will impact performance.

Do you need to keep groups separated for life when you submit?

No, the evaluation keeps track of this for you.

Understanding subgroups

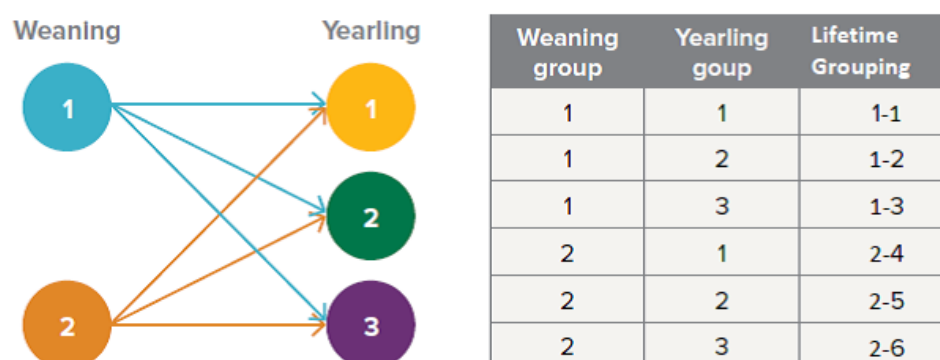


How does Sheep Genetics make lifetime groups?

The information you send Sheep Genetics about groups is combined to make sure they are properly represented across an animal's life.

The figure below shows an example where the number of groups increase at yearling stage. In this example, there were two weaning groups that were split into three yearling groups. While there were three groups at the yearling age stage, Sheep Genetics split the data into six lifetime groups to reflect any performance differences based on their past.

An example of how groups increase at yearling stage based on management



Embryo transfer impacts grouping

If you are using ET, it is important to note that these lambs are grouped separately in the evaluation to any natural or AI conceived lambs. This is due to the influence of the pharmaceutical intervention on the performance of these lambs.

Best practice ET for the genetic evaluation:

- Ensure there are multiple sires included in the ET program.
- Ensure that there is a common sire between the ET program and the natural/AI joining (refer to Linkage section)
- Ensure there are multiple progeny of each sex from each sire in the ET program (refer to Effective Progeny section)



Missed measurements

Where an animal is not present for a recording event that the rest of its group is measured at, this animal grouped separately from the cohort from that point in its life onwards.

For example, you are body weighing a group of ram lambs, however one ram was missed and left in the paddock and therefore did not have a weight recorded on the same day as his contemporaries. This one ram will then be grouped out for the remainder of its life, even if it is put back in with the original group of rams and is present for the following measurement.

This occurs because the evaluation does not know why an animal wasn't present at recording, which may be due to accidental reasons (such as mis-mustering or mis-read of a tag) or deliberate (such as the animal getting through a fence and therefore being under different management conditions or treating an unwell animal).

Complete cohort recording is important to limit the impact and prevalence of missed measurements.

Sheep Genetics QA protocol

- Management groups should reflect differences in on-farm management and environment.
- Make sure there is progeny from more than one sire in the management group.
- Once an animal is grouped out, it is grouped out for life.
- Draw out your management groups to track them over time.

Management group checklist:

- Are there progeny from more than one sire in the group?
- Are there multiple progeny of the same sex from each sire in the group?
- Is there a common sire between this group and other management groups for the drop? (Refer to Linkage section)

How are these groups analysed?

Groups and subgroups form the foundation of contemporary groups, which are the groups used in the evaluation. These contemporary groups are built based on:

- Management group supplied (and prior management grouping, or lifetime grouping)
- Date of measurement
- Flock code
- Sex
- Year drop

The evaluation further splits based on range in age to limit any bias caused by spread in age. For early-in-life traits, this split is in increments of 35 days, and from postweaning, where birth date has comparatively less impact on performance, splits based on 70-day increments.

Important

- Submit management groups that reflect how the animals are running and managed on-farm.
- The further grouping in the evaluation into contemporary groups is to further account for any known environmental effects to ensure the resulting information describes the genetic merit of the animal.
- The key components of contemporary groups to keep in mind when recording is the management group and the date of measurement you supply.

Effective progeny numbers

It is important there are enough animals in each contemporary group to provide useful data for genetic evaluation. Each sire must also have enough progeny in a group to have effective progeny numbers.

It is also important to have adequate sire representation within each contemporary group. It is recommended that you aim for a minimum of 10 progeny from each sire of the same sex within each contemporary group to maintain effectiveness of data.

Having more sires in a contemporary group also increases the effectiveness of the records because more genetics are being compared under the same environmental conditions.

If you are interested in traits which are recorded later in life, such as adult or reproduction traits, it is important to ensure that these older groups have effective progeny numbers.

Linkage

Linkage is where genes are represented across multiple environments, generally through the use of common sires between flocks, years and groups. Linkage provides a genetic benchmark so that genetic merit can be compared across flocks and environments, allowing the delivery of across-flock ASBVs.

Sheep Genetics recommends routinely using genetics that have been in other Sheep Genetics flocks, that are recording traits relevant to your recording program. Linkage is calculated at a trait level, using the last five years of pedigree, so it is important to regularly introduce link sires that have been recorded for the traits you are recording.

Where do I need linkage?

Linkage is required:

- between flocks – genetics measured in your flocks and in other Sheep Genetics flocks.
- between years – common sires across years
- between groups – common sires across management groups.

Do I need to be linked for all traits?

To be linked for a trait, the link sire needs to provide a genetic link for the trait. This sire needs to have progeny recorded for the traits you're recording in another Sheep Genetics flock.

Strong linkage with other flocks and between years is important. Strong linkage with other flocks and between years is important in providing an across-flock evaluation.

Ways to ensure across-year and across-group linkage

- Rule of thumb: For every 10 sires used, use at least one sire from the previous year in your current drop.
- Have multiple sires represented in each management group and ensure there are common sires between groups.

Ways to ensure across-flock linkage

- For every 10 sires make sure one has been used in other Sheep Genetics flocks. Artificial insemination (AI) is a good way for many breeders to use the same sires.
- Buy new sires (or semen) from other flocks which have data in Sheep Genetics and are linked for the traits you are interested in.
- Sell rams to other Sheep Genetics flocks for use and record as sires.
- Participate in a Young Sire Program which shares young sires across flocks.
- Enter a sire into a sire evaluation, Resource Flock or progeny test
- Enter a sire into a sire evaluation program or Resource Flock
- Rule of thumb: have at least 30 progeny from each link sire

Sheep Genetics QA protocols

- Ensure any link sire is recorded for the traits you are recording.
- Ensure any link sire has effective progeny numbers in your drop.



Trait measurement

Traits evaluated by Sheep Genetics

The list of traits is growing over time, as more industry data is collected, and new traits are developed.

You do not have to record every trait. Consider your breeding objective and record those traits that are important to you as directly as possible.

When to measure traits

When you submit a record, you provide the relevant age stage that reflects the age of the animals when they are recorded.

<i>Age name</i>	<i>Abbreviations</i>	<i>Average age of the management group</i>	<i>Age range</i>
Birth	B	0	0
Weaning *	W	100	40-149 days
Post weaning *	P	225	150-299 days
Yearling	Y	365	300-449 days
Hogget	H	540	450-659 days
Adult	A	700	660 days or older

** Additional weight measurement can be recorded at weaning or post weaning age stages and recorded in your software, within the early-post weaning age stage.*

Where the age of animals within a group falls across the cutoff between age stages, choose the age stage based on the average age of the group.

The evaluation does not split groups where the age range overlaps two age stages, given the whole group is allocated the same age stage for the measurement.

For example, you are recording a body weight on animals that have been managed together, and whose age at the time of recording ranges between 250 and 310 days. Based on the age stage table above, these animals could fit in either the post weaning or yearling age stage. However, the average age of the group is 270 days, therefore the body weights on these animals is allocated as postweaning (PWT).

When submitting trait data, include

- The trait code and age stage
- Trait measurement
- Management group
- Measurement date - making sure that, where possible, animals that are in the same management group are measured on the same day.

Live weight (WT)

How to collect? Using on-farm scales, or scales provided by a carcass scanner.

Recorded at:

- Birth (B)
- Weaning (W)
- Post-weaning (P)
- Yearling (Y)
- Hogget (H)
- Adult (pre-joining)

Units:

Birth weight is measured to nearest 0.1kg
Other weights are measured to nearest 0.5 kg.

Sheep Genetics QA protocols

- Before weighing, check scales are accurate using a known weight.
- Ensure animals are empty by taking them off feed and water at least four hours before weighing, so that gut fill is not a significant component.
- Measure the whole management group on the same day (because contemporary groups are split on the date they are measured)
- Birth weight must be recorded within 24 hours of birth on live and dead lambs (where whole body is available)
- Record adult ewe weights in the 30 days prior to joining. Recording pre-joining means that body weight is not affected by reproductive status. It is also easier to submit this pre-joining data in the mating module of the software so that it is exported with the relevant lamb drop (rather than exporting multiple year drops after weighing mixed age ewes)

Eye muscle depth (EMD) & fat depth (FAT)

How to collect? An accredited scanner.

<https://www.sheepgenetics.org.au/service-providers/>

Recorded at:

- Weaning (W)
- Post-weaning (P)
- Yearling (Y)
- Hogget (H)

Animals should not be recorded for EMD and FAT after being joined (or beyond the hogget age stage) as the physiological processes associated with reproduction impact the expression of this trait.

Units: EMD and FAT are measured to at least the nearest 0.5mm

Sheep Genetics QA protocols

- Must be measured by a Sheep Genetics accredited scanner.
- Animals must be over 30kg liveweight.
- Group must have an average of at least 1.5mm of fat over the C-site. The fatter the animals are, the more expression of the trait and, therefore, more variation.
- Liveweight must be recorded on the same day.
- Scan animals at a similar age to when your commercial client's market lambs.



Greasy fleece weight (GFW)

How to collect? On-farm

Recorded a:

- Post-weaning (P)
- Yearling (Y)
- Hogget (H)
- Adult (A)

Animals must be between 7 months and 6 years of age.

Units: Fleece weight is measured to nearest 0.1kg

Sheep Genetics QA protocols

- Animals must have at least 6 months wool growth
- Before weighing, check scales are accurate using a known weight.
- Fleece weighing is usually done in the shed during shearing and before skirting.
- Try and include the belly wool. If you do not include the bellies, be consistent and ensure you do not include them for all animals.
- If shearing a management group over multiple days, submit this data with **a single date of measurement**. This is to avoid the group being split based on different dates of measurement, as fleece weight data is not impacted by being overnight in the yards.
- If an accurate birth date or birth type is not known, you can shear animals early in life (tip shearing to even up all the animals) to help account for any impact of age, birth type and maternal effects.

Clean fleece weight (CFW) and yield (YLD)

How to collect? Clean fleece weight (CFW) measurements are derived from a greasy fleece weight (GFW) measurement and a yield (YLD) measurement: $CFW = GFW \times YLD$

You can either:

- Calculate the CFW yourself and submit all three trait measurements (CFW, GFW and YLD) to the evaluation.
- Submit GFW and YLD to the evaluation, which will then calculate CFW for you.

Sheep Genetics QA protocols

- Refer to the GFW protocols above.
- When measuring yield to inform clean fleece weight, ensure the yield measurement relates to the same shearing event that the greasy fleece weight was recorded.



Wool quality traits

Traits include:

- Fibre diameter (FD) – measured in microns.
- Coefficient of variation of FD (FDCV) – measured in %
- Staple length (SL) – measured in mm.
- Curvature (CUR) – measured in degrees.
- Staple strength (SS) – measured in newtons per kiloton.

Recorded at:

- Post-weaning (P)
- Yearling (Y)
- Hogget (H)
- Adult (A)

Animals must be between 7 months and 6 years of age.

Sheep Genetics QA protocols

- Animals must have at least 5 months wool growth
- Sample the fleece from either:
 - The mid-side: over third last rib, halfway between mid-line of the back and mid-line of the belly
 - The pinbone – over the pinbone
- Must use the same methodology (sample site) for all animals in the group.
- If testing a management group over multiple days, submit this data with **a single date of measurement**. This is to avoid the group being split based on different dates of measurement, as fleece data is not impacted by being overnight in the yards.

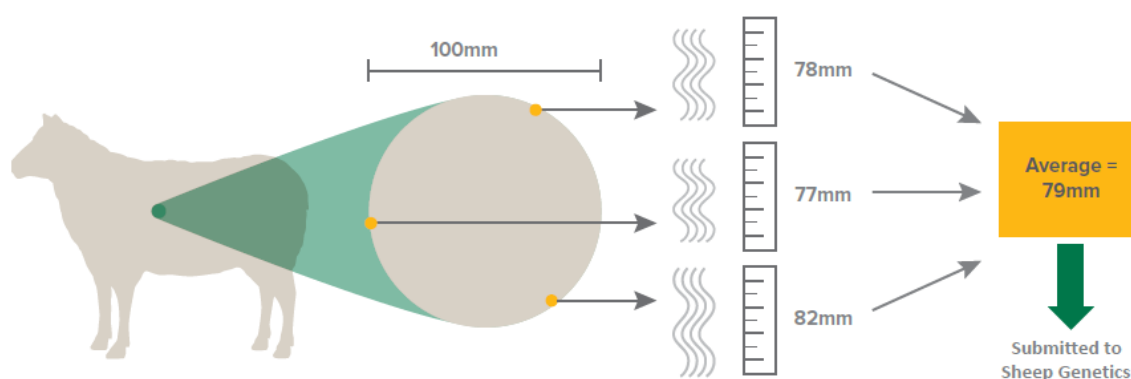
Further recommendations

- The fleece sample area should be about 100mm x 100mm.
- If you sample at shearing, find and mark the sampling site on the standing sheep before shearing (e.g. mark a spot on the animals so sampling is consistent between animals).
- If sampling at shearing, remove the sample on the board during or after shearing, or during skirting on the wool table.
- If sampling prior to shearing, shear the wool off the sample area as close and consistently to the skin as possible. If you want to measure staple length, staple strength or crimp frequency do not make second cuts.

Measuring staple length (SL) on-farm:

- Use a straight but relaxed staple from the mid-side. Measure SL in mm using a ruler (a 15cm steel ruler is recommended), and
- Measure three staples selected at random but equally distant from each other on the outer edge of an imaginary 100mm diameter circle around the mid-side. Submit the average of the three measurements to Sheep Genetics
- Mt is best to evaluate SL on sheep that have already been shorn at least once.

An example of how groups increase at yearling stage based on management



Worm Egg Count (WEC)

If you need help or advice around WEC testing, the ParaBoss website provides a consolidated list of testing laboratories and their contact details.

<https://paraboss.com.au/find-an-advisor/>

Recorded at:

- Weaning
- Post-weaning
- Yearling
- Hogget

Sheep Genetics QA protocols

- The average count for the group (when individual samples are collected) must be over 300 eggs per gram (EPG)
- Submit the total count of strongyle eggs (this includes *Trichostrongylus*, *Ostertagia*, *Haemonchus* and other minor species), unadjusted for faecal consistency.
- Management groups for WEC must reflect previous drenching protocols, particularly if selective drenching of a portion of the group has occurred.

Recommendations

- Take bulk samples of the mob to see if the worm burden is high enough prior to individual sampling.
- If you have *Haemonchus* (Barber's Pole) then the average count should be 500–1000 epg.
- If you measure WEC during weaning age, try and sample lambs at least six weeks after weaning, to reduce any influence of the dam's immunity.
- You can also submit an individual species count for *Nematodirus* separately if available. Sheep Genetics do not use this yet but could include it in the future.
- Some labs adjust WEC for faecal consistency (FC). WEC must be submitted unadjusted however faecal consistency may be submitted separately (as FC).
- Do not submit WEC samples animals that have been treated with internal parasite vaccinations (such as BarberVax) for genetic evaluation, as the influence of these treatments changes the trait definition of Worm Egg Count

Reproduction

Traits

Component reproduction is comprised of three different traits (or components) that cover the entire reproduction cycle these are:

- *Conception (CON)*

Did the ewe conceive?

Sires with higher CON will produce daughters which have a higher conception rate. This trait is reported as adult and yearling. Yearling age is for ewe joined as ewe lambs.

- *Litter Size (LS)*

How many lambs were born?

Sires with higher LS will produce daughters that give birth to more lambs., This trait is reported as adult and yearling.

- *Ewe Rearing Ability (ERA)*

How successfully did the ewe rear her litter?

Sires with higher ERA will produce daughter which rear more of their litter. This trait is reported as adult and yearling.

The three component traits are then combined into a trait called *Weaning Rate (WR)*.

WR describes the genetic difference between animals for the number of lambs weaned per ewe joined. It is expressed as number of lambs and a useful way for commercial producers to use reproduction in their selection decisions.

Additional traits that can be recorded relating to reproduction include:

- *Maternal Behaviour Score (MBS)*

How far the ewe moves from the birth site when her lambs are being tagged.

- *Pre-joining weight (AWT) and condition score (CS)*

Both the pre-join weight and the pre-join condition score need to be taken at the same time and submitted in the mating module within 30 days prior to joining (within 30 days of the rams going in with the ewes). The weight will contribute to adult weight ASBV for the ewe.

- *Lambing Ease*

Ease of which lambs are born, where a more positive ASBV indicated a better lambing ease. It is a trait scored against the lamb, therefore multiple receive separate scores. A Lambing Ease scoring guide is available.

Recording Reproduction data

Overall requirements (flock level)

- At least 70% of the lambs in a drop must have dam pedigree.

Reproduction is a trait of the dam, so complete pedigree recording ensures we are capturing the full variation of the joining cohort.

- Consistency between birth types (BT) of lambs supplied and the count of lambs in the drop.

Compare the BT of each lamb, and the total number of lambs in the drop. This validates the consistency of recording through the lambing. For example, does the total number of lambs and DAB animals match the birth types included in the drop?



Event recording (at a contemporary group level)

Joining

Data to be recorded	Why we need it	How to record it
ID of the ram the ewe is joined to	To identify if a sire fails (and there for avoid penalising the ewes he was joined to).	<p>List the 16-digit ID of the ram joined to in your software.</p> <p>NOTE: If joining as syndicate (and using DNA parentage) leave the ram in the mating module as the syndicate but update the pedigree of the progeny to the individual sire.</p>
Ram in and out date	Check dates for relevance, ensuring that it is the joining event you are recording listed and there are not future dates within the submission.	<p>List the date rams are put in and pulled out in your software.</p> <p>NOTE: Try and be as accurate as possible (to the day) and record any back up joining as well under the appropriate sections in your software.</p>
Ewe Joining weight and Ewe joining condition score	Contributes to the AWT and CS ASBVs.	Measure within the 30 days before the rams goes in. Ensure to include a date of measurement.
Management group of the ewes	Groups are checked for relevance and usefulness to the reproduction analysis e.g. are there dry ewes in the joining group showing variation	List the management group of the ewes prior to joining in your software.
Conception method of the ewe	Ensure fair comparison of the ewe's reproductive performance.	Need to include against each ewe and also notify the use of chemical intervention (such as oestrus inducing products). ET ewes are not used in the reproduction evaluation.

Pregnancy

Data to be recorded	Why we need it	How to record it
Pregnancy scan result	Informs the CON and (if not doing lambing rounds) LS ASBV	Record against each ewe and submit in your software, this allows us to identify dry ewes (either as a preg scan 0 or a DRY tag) for analysis. NOTE: Ensure that you are scanning for multiple, wet/dry results are only used for conception and will not contribute to the other reproduction traits.
Pregnancy scan date	Checks the accuracy of the scan	Record against each ewe and submit in your software. NOTE: Scan results a minimum 70 days and maximum of 110 days from ram in date are used within the analysis.
Foetal age (optional)	Can provide more accurate lamb DOB when not tagging at birth (e.g. early, mid and late)	Submit within your software
Scanner name (optional)	Looking to use this information in the future to help inform work around accuracy of pregnancy scanning.	Submit within your software

Lambing (if tagging at birth and doing daily lambing rounds)

Data to be recorded	Why we need it	How to record it
Environmental effects (fixed effects)	Helps inform the analysis of environmental differences between animals that may impact on performance	Include data such as Accurate date of birth, birth type, sex and sire or dam ID in your software. Additionally include any dead at birth (DAB) animals at this time.
Birth Weight	Contributes to the BWT ASBV.	A trait measured against the lamb (if there are multiples, they each get a measurement) within 24hrs of its birth. Measured in kg and submitted in your software.
Lambing Ease	Contributes to the LE_DIR and LE_DTR ASBVs.	Scored from 1 to 5 based on the scoring guide. NOTE: this is a trait measured against the lamb (is there are multiples they each get a measurement) when a lambing event is witnessed or in obvious events (swollen heads, yellowy colour) soon thereafter.
Maternal Behaviour Score	Contribute to the MBS ASBV	Scored from 1 to 5 based on the scoring guide. NOTE: this is a trait measured against the ewe (if there are multiples only once score the for dam) when recording other information (i.e. BWT) at how attentive and close by the ewe stays to her progeny.

Weaning

Data to be recorded	Why we need it	How to record it
Rear type	Helps with adjustments made for fixed effect, contributes to calculation of ASBVs including early in life traits and reproduction.	Adjust RT to reflect the survival of lambs, i.e. 2 were born but only 1 made it to weaning.

Using DAB tags and pedigree to estimate rear type

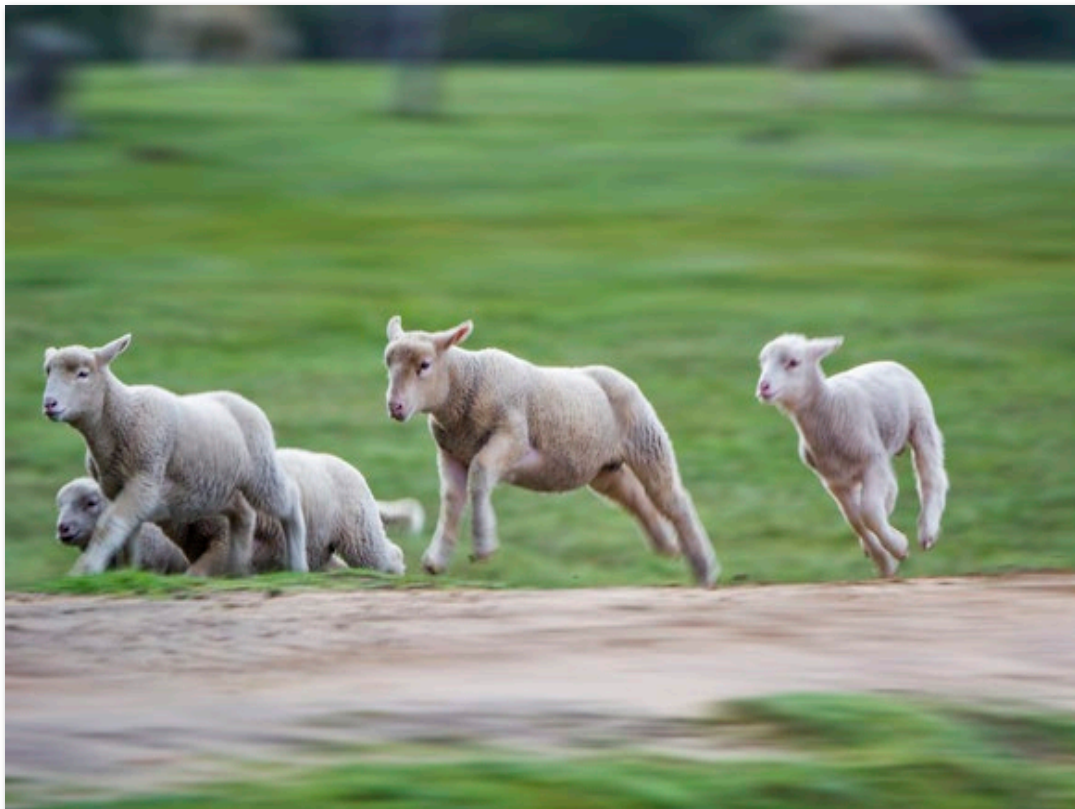
You can infer ewes which lambed and lost lambs by matching pregnancy scan to pedigree (e.g. DNA parentage). For ewes in which the pregnancy scan does not match the number of alive lambs through pedigree, the gaps need to be filled with Dead at Birth (DAB) Lambs.

results). To use this method, you must:

- have full pedigree on the whole drop cohort (not getting pedigree selectively)
- pregnancy scan for multiples
- get pedigree as early as possible (marking is preferred over weaning)
- be confident in the reliability of pregnancy scan data.

When submitting a DAB lamb to Sheep Genetics making sure that the information of the DAB lamb links up with the correct dam and alive lamb is important. Below is an example of how to submit a set of twins (pregnancy scan of 2) where one is an alive lamb and the other a DAB.

Animal ID	Sex	BT	RT	DOB	Sire	Dam
609999-2024-240001	2	2	1	01/01/2024	609999-2021-210001	609999-2022-220001
609999-2024-DAB001	1	2	0	01/01/2024	609999-2021-210001	609999-2022-220001



Visual traits

There are a number of visual traits which can be scored and submitted to Sheep Genetics.

Visual Sheep Score Guide

The Visual Sheep Scores Guide provides scoring protocol for a suite of visual traits, including conformation, wool quality characteristics, pigmentation, breech and body wrinkle and cover. The guide provides a set of illustrative standards and simple instructions on how and when to visually score animals.

Most traits in this guide can be scored to the nearest 0.5 and scores range from 1 to 5.

https://www.sheepgenetics.org.au/globalassets/sheep-genetics/resources/brochures-and-fact-sheets/Visual_sheep_scores.pdf

Shedding Score Guidelines

Work is underway to develop shedding ASBVs in the future. Breeders may collect and submit shedding score data to contribute to the evaluation.

<https://www.sheepgenetics.org.au/globalassets/sheep-genetics/news/visual-shedding-score-guideline.pdf>

Sheep Genetics QA protocols

- If measuring a management group over multiple days, submit this data with **a single date of measurement**. This is to avoid the group being split based on different dates of measurement, where this visual data is not impacted by being overnight in the yards.

Helpful hints:

- Several visual traits are recorded at marking and are therefore submitted with an M to indicate the age stage. For example, breech cover measurements captured at marking are submitted as marking breech cover (MBCOV).
- Pay careful attention to the trait code included in the scoring protocol, and ensure you use the same code when entering the data into your software.

Reporting visual traits

Although visual traits are recorded with the relevant age stage, the resulting ASBVs tend to be reported as either early (E) which encompasses the early in life age stages or late (L). Early (E) reflects early in life expression of the trait (birth through to postweaning), and late (L) reflects later in life expression of the trait (yearling through to adult).

Not all traits which are recorded on-farm have a reported ASBV, however this list is regularly growing as more data is recorded.

Submit visual traits that are in your breeding objective, so when there is enough data, they can be included in the evaluation and reported as ASBVs.

The traits which currently have MERINOSELECT ASBVs include:

- early breech wrinkle (EBWR)
- early breech cover (EBCOV)
- late dag (LDAG)
- late wool colour (LCOL)
- late fleece rot (LFROT)
- late fleece character (LCHAR)

The traits which currently have DOHNE ASBVs include:

- early breech wrinkle (EBWR)
- early breech cover (EBCOV)
- late dag (LDAG)

The traits which currently have Maternal ASBVs include:

- late dag (LDAG)

Footrot (FR)

How to collect? By an accredited scorer

Recorded: When animals are between 6 months and 2 years of age

Units:

All four feet are scored on a six-point scale (from 0 to 5)

Sheep Genetics QA protocol

- Only data collected in New Zealand currently informs the FR ASBV
- Challenge thresholds must be met where:
 - 10% of animals have at least one foot that is score 3 (underrun) or greater.
 - 50% of animals have at least one foot that is score 2 (affected) or greater.
- Must be at least 40 animals of the same sex and age in the challenge group.



Carcase and eating quality data collected in plant

*** please note, this data can NOT be supplied in your xml currently – it must be emailed directly to Sheep Genetics***

*** please contact Sheep Genetics directly in advance of consigning animals to ensure all pre-slaughter measurements are met ***

How to collect? Consign excess/cull stud animals to a processor that has objective carcase (DEXA) and eating quality (IMF-MEQ or IMF-SOMA) devices. Sheep consigned must be in the Sheep Genetics analysis with pedigree information. Pre-slaughter weight must be taken (4 hours fasted) as close to slaughter as possible – ideally the day of trucking but at least within 7 days of slaughter.

Recorded:

- Weaning (W)
- Post-weaning (P)
- Yearling (Y)
- Hogget (H)
- Adult (A)

Animals must adhere to the requirements of the processor you are consigning to.

Units :

Intramuscular fat (IMF) is measured as a % of fat in the loin muscle to the nearest 0.01%.

Lean meat yield (LMY) is measured as a % of the carcase in Kg to the nearest 0.01%.

Sheep Genetics QA protocol

- Animals must have a Sheep Genetics ID and are in the Sheep Genetics evaluation (either excess animals from the stud or have pedigree information)
- A pre-slaughter weight (4 hours fasted) on-farm prior to slaughter. Ideally pre-slaughter weight is to be recorded as close as possible to the animals going onto the truck to slaughter, however, pre-slaughter measurements can be taken up to 7 days prior to slaughter
- Please supply, date of pre-slaughter measurements, on-farm management group of animals
- Supply the abattoir that you consigned to, the kill date, and consignment number
- Where possible, we recommend taking the following on farm pre-slaughter measurements also
 - Condition score
 - Fat and muscle scan data
- Please contact Sheep Genetics before the animals are consigned to ensure that all the necessary information is collected
- Contact the processor to inform them that the consignment will involve the

collection of data for the genetic analysis and to keep an eye on hook tracking

- Given hook tracking accuracy is still an issue, kill data must be manually reviewed by Sheep Genetics/AGBU prior to submission to the analysis. This review may take some time so please consider this when supplying the data
- Following the kill, please provide Sheep Genetics with the unedited kill sheet direct from the processor, as well as the required pre-slaughter data in the appropriate template (can be downloaded off the Sheep Genetics website)

Example template layout:

ID	EID	SEX	MEASUREMENT_DATE	WT	CS	GROUP	EMD	FAT
Sheep Genetics 16 digit ID	EID or RFID that refers to the identification on the feedback sheet from the processor	1 or 2 for male or female, respectively	Date of pre-slaughter measurement	Pre-slaughter live weight	Pre-slaughter condition score	Management group for pre-slaughter measurements	Ultrasound eye muscle scan *where possible*	Ultrasound fat scan *where possible*





Contact

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