SGA Breeder's
Quality Assurance Manual






SHEEP GENETICS

MEAT & LIVESTOCK AUSTRALIA

Australian Wool Innovation Limited

ACKNOWLEDGEMENTS

NSW DEPARTMENT OF
PRIMARY INDUSTRIES

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As author I would like to thank sincerely the wide range of people who voluntarily contributed a large amount of their time, knowledge and understanding of sheep breeding to ensure this manual becomes a valuable industry resource for breeders participating in Sheep Genetics Australia (SGA). In particular, I would to thank the following people.

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Mrs Kerry Casey, Ms Emily Wright, Mr Richard Apps, Mr Sam Gill, Mr John Karlsson,
Ms Linda Hygate, Mr Stefan Spiker, Mr Bill Smith.

Foreword

Dear Breeder

Like all progressive businesses, Sheep Genetics Australia (SGA) is developing a quality assurance system to ensure that the breeding values calculated on behalf of Australian sheep breeders and their clients are accurate.

When followed correctly, the quality assurance procedures outlined in this manual will enable you to collect and submit accurate pedigree and performance information to SGA. By collecting accurate records and submitting these to SGA you will be playing a vital role in the SGA quality assurance system. In turn, SGA will be able to deliver you and your clients credible breeding value estimates to maximise the genetic improvement of your flocks.

We encourage you to review the areas in the manual of relevance to your breeding program. While all relevant procedures are important and need to be met, it is essential you attend to certain key areas so that you can make accurate genetic evaluations across-flocks:

- Ensure your mating program is carried out so that you create good genetic linkage to previous drops and other flocks.
- Manage evaluated progeny so they have equal opportunity to express their genetic potential. This will enable a fair and accurate comparison between sheep.
- Whichever traits you choose to evaluate, use the optimum system of measurement for that trait.
- Seek information, advice and help from suitably skilled data managers and genetic advisors to assist you to submit data, and access and understand SGA reports.

If these key areas are not carefully incorporated into your breeding program the QA system will fall short of its potential. This will almost certainly affect the accuracy and value of SGA breeding information for you and your clients.

Where appropriate, seek advice from your advisors to maximise the benefit of SGA to your breeding operation. Convey any concerns you have regarding SGA either directly to SGA staff or to your advisor so that they can follow up on your behalf.

We are extremely pleased with the huge effort and co-operation shown by all sectors of the industry that has enabled SGA to move into operation. We are confident that this industry input will continue to make the QA system a success for Sheep Genetics Australia.

We look forward to your involvement.

Mr David Palmer
Managing Director
Meat & Livestock Australia
Limited

Dr Len Stephens
Chief Executive Officer
Australian Wool Innovation
Limited

How to use this manual

The SGA breeder's quality assurance manual outlines the minimum quality assurance (QA) standards breeders need to achieve when collecting and reporting information about the genetic performance of their sheep. By submitting genetic performance data to SGA that meet these minimum standards, SGA can prepare accurate and credible genetic performance reports to enhance your breeding program and those of your clients.

There are two critical sections in the manual:

1. The minimum standard procedures located in Section 4.
2. The 'QA Check List' located in Section 5 that needs to be completed before your sheep data are submitted to SGA.

Getting started:

Breeders already involved in across-flock evaluation will find the procedures in this manual very similar to those they currently use to generate high-quality breeding information. In fact many breeders will probably already adhere to standards of higher quality than those required in this manual. The QA procedures outlined in this manual represent the minimum standards required, not best practice.

Most breeders will need to review only a portion of the procedures in the manual. Use Table 1.1 on page seven to identify the traits that can be evaluated and then browse Section 3.2 to get a feel for the QA procedures relevant to your enterprise. When you review an area of the procedures in Section 4, the underlined text can be used to identify the key points. Use the QUICK SEARCH in Section 7 to find the sections in the manual that relate to a term of interest to you.

A breeder's obligation:

For your breeding information to be accepted into the SGA database, you need to meet all areas listed under the Procedures headings in Section 4. These represent the minimum standards that every dataset is required to meet.

Before submitting a dataset to SGA you need to complete a 'QA Check List' for each dataset submitted. The QA Check List verifies that your data has been collected using all the relevant QA procedures.

Should you require clarification regarding any of the information or procedures within the manual please contact a service provider. A list of data managers and genetic advisors can be found on the SGA website or by contacting SGA.

SGA contact details:

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1.0 INTRODUCTION

Sheep Genetics Australia (SGA) reports information about the genetic performance of sheep breeds, such as Merino, maternal breeds and terminal breeds. Most flocks involved in SGA have adequate pedigree links to other flocks within their breed group to enable their genetic performance to be compared across-flock and to industry benchmarks.

Breeders involved with SGA can choose to evaluate a wide range of performance traits at appropriate ages, from birth through to adult, within their breeding flock (Table 1.1). There are no compulsory traits and it will be straight forward for you to ensure your current breeding and management practices meet the required procedures.

All breeders who provide SGA with data that meet the required quality assurance (QA) procedures will receive a private genetic evaluation report for the submitted traits. Progeny groups that can be reported across-flock will have their trait performance described as an Australian Sheep Breeding Value (ASBV). An ASBV will be accompanied by an accuracy value that is expressed as a percentage.

Progeny groups that cannot be reported across-flock will have their trait performance described as a Flock Breeding Value (FBV). FBVs are readily distinguished from ASBVs as they are not reported with an accuracy value. ASBVs and FBVs are allocated on a trait group basis.

The SGA logo accompanying all reports verifies the quality assurance of the ASBVs and FBVs. Only sheep issued with an ASBV can be reported under their relevant brand name logos. For example, MERINOSELECT or LAMBPLAN.

SGA uses sophisticated genetic evaluation software called OVIS to evaluate genetic performance. OVIS has recently been developed further to accommodate the wide diversity of genetic types within the Merino breed group and to increase the accuracy of breeding values for all breed groups. The SGA evaluation system will be constantly refined using the database records supplied by breeders.

Confidence in SGA reports will depend largely on breeders submitting data that meet the required QA procedures described in this manual. Before breeding information can be accepted into the SGA database for analysis, all areas listed under the Procedures headings in the manual need to be met. These represent the minimum standard that every dataset is required to meet.

SGA will carry out data integrity checks before data enters the analysis database. Information reported by SGA is calculated to give the best possible estimate of the genetic performance. However, since SGA does not control or audit the collection of data it cannot be responsible for the accuracy of data used in the analysis.

Breeders using muscle and fat ultra-sound scanning, fleece testing or worm egg counts to evaluate sheep in their flock need to have these evaluations carried out by operators that meet the standards required by SGA.

SGA breeders' workshops and the Ram Breeder's Guide booklet will provide additional information for breeders on how to structure their breeding program and make the most effective use of SGA genetic performance information.

There will be a period of two years from 1 November 2005 to allow breeders the time to make any adjustments to their breeding operations and to comply with the QA procedures.

TABLE 1.1 SGA traits and ages of evaluation

Ages used to describe the performance of various traits	Age of evaluation[1]	Live weight (kg)	Muscle & fat depth (mm)	Fleece traits[2]	Scrotal cricumference (cm)	Worm egg count (epg)	Type & structural traits[3]
Birth	Birth to 24 hours	✓					
Weaning	42-120 days (7-16 weeks)	✓				✓	
Early post weaning	120-210 days (4-7 months)	✓	✓		✓	✓	
Post weaning	210-300 days (7-10 months)	✓	✓	✓	✓	✓	✓
Yearling	300-400 days (10-13 months)	✓	✓	✓	✓	✓	✓
Hogget	400-540 days (13-18 months)	✓	✓	✓	✓	✓	✓
Adult	540 days or older (18 mths or older)	✓		✓			✓

1 The average age of the sheep in the Management Group.

2 Fleece traits: The minimum fleece growth at evaluation varies for different traits as follows: six months: fleece weight (kg); five months: fibre diameter (μm); coefficient of variation of fibre diameter (%); staple strength (N/ktex); staple length (mm), crimp frequency (crimps/cm), and the scored wool quality traits (fleece rot, fleece colour, fleece character and staple weathering).
Breeding values will not be reported for fleece traits at the post-weaning age until research on the value of post-weaning fleece traits and subsequent industry consultation is completed.

3 Scored type and structural traits (face cover, neck/body development and feet/leg conformation are available - 4.13).

Table 1.1 provides a summary of the traits that breeders can submit to SGA. A tick (✓) in the table indicates the trait can be evaluated at the age specified on that row. There are no compulsory traits and breeders can choose any of the trait ages marked with a tick. For example, live weight can be evaluated at any age from birth through to adult while fleece traits can be evaluated from ten months through to adult.

When you have selected the traits and ages you wish to submit to SGA, you can then use Section 3.2 to identify the QA procedures that are most relevant to your breeding program. A review of the relevant QA procedures will enable you to determine whether your current practices meet the required QA procedures or if some adjustment is required.

The traits or ages that cannot currently be reported by SGA as breeding values are highlighted in **blue** - they are expected to be able to be reported by the end of 2007. Traits highlighted in red are the Base Traits - see 4.8 (v) and 4.8 (vi) for details.

2.0 SCOPE OF THE MANUAL

2.1 The scope of this manual

The QA procedures outlined in this manual have been developed to help breeders provide accurate information to SGA.

The QA procedures outlined in this manual have been developed to help breeders provide accurate information to SGA. This, in turn, will enable SGA to deliver credible genetic performance reports to breeders and their clients.

The information contained within this manual has relevance for sheep breeders who supply pedigree or performance information to SGA and those who receive SGA reports. The manual includes details on how to identify sheep and evaluate breeding traits as well as how to manage sheep and report SGA information.

2.2 Key components of the SGA quality assurance system

The SGA quality assurance system consists of four key elements:

(i) Collecting and submitting sheep performance data;

(ii) Checking the integrity of submitted datasets;

(iii) Processing submitted data; and

(iv) Reporting of genetic performance information.

1. Data collection and supply

This manual outlines the procedures that breeders need to follow when collecting data and reporting SGA information. All breeders need to complete and submit a QA Check List with each dataset. The QA Check List verifies that the relevant QA procedures have been carried out.

The QA Check List can be completed in writing or on-line via a computer. You may be able to complete an electronic form of the QA Check List using your on-farm database software when exporting data to your data manager or the SGA database. Alternatively, you can complete the QA Check List on-line when submitting your data through the SGA website. The Check List is tailored to the needs of different breed groups. In addition, if you are submitting more than one set of data for a Management Group, you can add to the Check List completed for the first data set rather than using a new form.

Before a submitted dataset can enter the SGA master database, it will be checked for integrity in a holding database

It is advisable to keep a copy of each QA Check List you submit to help resolve any discrepancies in data reported to the database. It is also recommended that you maintain a copy of your original pedigree and performance records to enable any data errors to be highlighted or lost data to be replaced.

All scanners, fleece testers, worm egg count laboratories, data managers, genetic advisors used by breeders, as well as breeders reporting data directly to SGA need to meet the standards required by SGA.

On-farm data recording software is expected to help breeders record and manage their flock's QA reporting requirements very efficiently. This software is also expected to have a range of validation and export routines designed to help breeders meet SGA standards. Instructions on how to prepare data files in the format required by SGA can be found on the SGA website.

2. Data integrity checking

Before a submitted dataset can enter the SGA master database, it will be checked for integrity in a holding database (Figure 2.1). Data integrity checking involves checking the range of the dataset, identifying any performance outliers and cross checking sheep identification numbers (IDs). Data that require clarification after integrity checking will

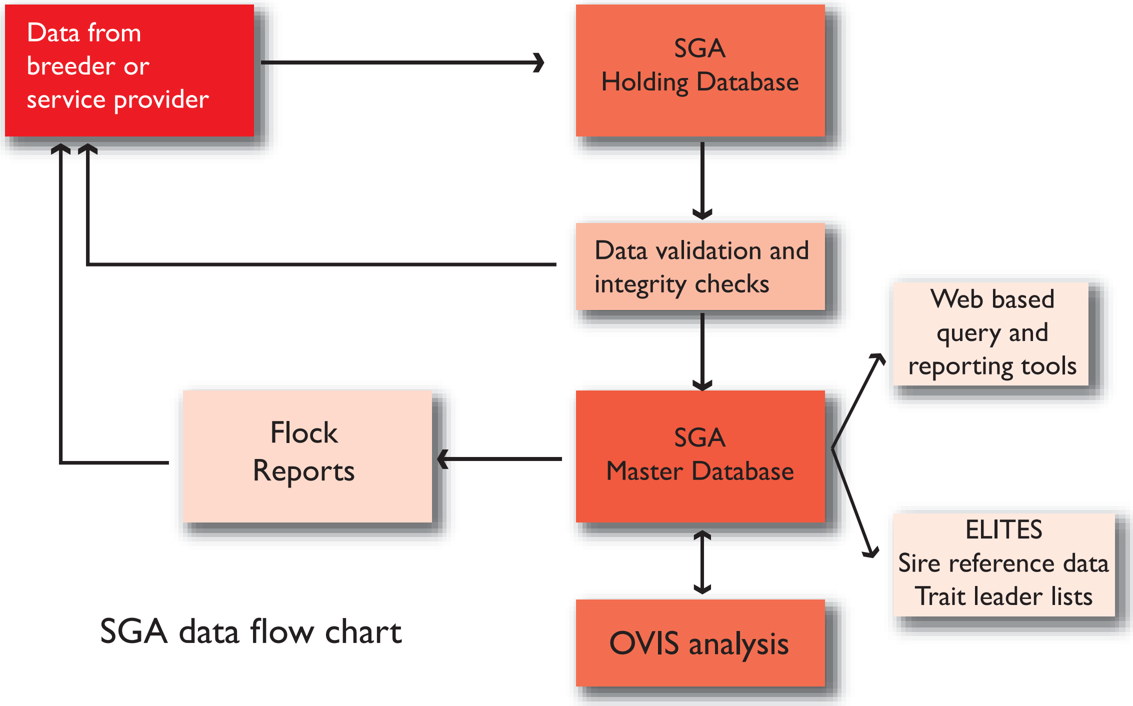


Figure 2.1 SGA data flow chart

be returned to the breeder. Any concerns about a particular dataset that cannot be resolved by the breeder need to be clarified by a data manager or genetic advisor who meets the standards required by SGA. Data cannot proceed into the master database unless all the relevant QA procedures have been adhered to and the data meet the minimum standard of integrity checking.

SGA uses database QA procedures to carry out data handling, data integrity checking, data processing and reporting.

3. Data processing

SGA uses sophisticated across-flock genetic evaluation BLUP software called OVIS to evaluate the genetic performance data submitted by breeders. OVIS has now been updated to accommodate the wide diversity of genetic types within the Merino breed group and to generate more accurate breeding value estimates for other breed groups.

The genetic parameters used in the SGA data analysis have been defined by the SGA technical committee and can be found on the SGA website. SGA breeders will be informed via the SGA website of any changes to the method of data analysis. The SGA website will identify the date the change was implemented and highlight the implications of the change for breeders.

4. Reporting

When data is submitted to SGA that meets QA standards, the breeder will receive a private genetic evaluation report for the sheep that were submitted with new data. The majority of flocks involved in SGA have adequate pedigree links to other SGA flocks within their breed group. These pedigree links enable breeders to compare their sheep against a breed group benchmark and to sheep in other flocks in the breed group.

Progeny groups that can be reported across-flock will have their trait performances described as Australian Sheep Breeding Values (ASBVs) and each ASBV will be accompanied by a trait accuracy value.

Only sheep with satisfactory genetic linkage (ASBVs) can be reported using brand name logos, such as MERINOSELECT or LAMBPLAN.

Progeny groups that cannot be reported across-flock will have their trait performance described as Flock Breeding Values (FBVs). FBVs are readily distinguishable from ASBVs as they are reported without an accuracy figure.

The SGA logo that accompanies reports verifies the quality assurance of the ASBVs and FBVs. Only sheep with satisfactory genetic linkage (ASBVs) can be reported using brand name logos, such as MERINOSELECT or LAMBPLAN.

All ASBVs will be presented relative to the base of the breed group and this base represents an industry benchmark. The base is the trait performance of all 1990-drop progeny in a breed group with the exception of WEC that is the 2000-drop.

A breeder can only report the performance data of a sheep publicly if:

(a) The breeder owned (or part owned) the sheep (or held ownership rights to the genetic material of the sheep) at the time of evaluation in the case of performance records or the time of mating in the case of sires and dams, or

(b) The breeder has obtained genetic material from the sheep (e.g., semen, embryos) that has no public reporting restrictions, or

(c) The breeder has written permission from the owner to report publicly the SGA performance of the sheep, or

(d) The SGA performance of the sheep has already been reported publicly by SGA or its owner.

Unless otherwise notified, SGA may report publicly the performance data of sheep deemed to be trait leaders from each breed group. It is the responsibility of a breeder who submits data to SGA to notify SGA if you do not want SGA to report the sheep you own. Any concerns about a particular dataset that cannot be resolved by the breeder need to be clarified by a data manager or genetic advisor who meets the standards required by SGA. Data cannot proceed into the master database unless all the relevant QA procedures have been adhered to and the data meet the minimum standard of integrity checking.

SGA uses database QA procedures to carry out data handling, data integrity checking, data processing and reporting.

All ASBVs will be presented relative to the base of the breed group and this base represents an industry benchmark.

2.3 SGA quality assurance manager

The SGA QA manager will assist the implementation of the SGA QA program. The duties of the QA manager are to:

- Provide advice to SGA service providers on all aspects of the SGA QA program.
- Ensure effective monitoring of the SGA QA procedures.
- Inform the SGA manager when problems are discovered.
- Analyse the operation of the QA procedures regularly and examine feedback on the system from SGA breeders and others in the sheep industry.
- Use analysis and feedback from all sources to recommend changes to the SGA technical and advisory committees about how the QA procedures can be improved.
- Draft any manual amendments in consultation with, and with the approval of, the SGA technical and advisory committees and communicate these changes.
- Distribute all approved QA Manual amendments to SGA breeders to ensure the manual is kept up to date.

3.0 BREEDER'S COMMITMENT

3.1 Breeders need to meet all relevant QA procedures

As an SGA client, it is critical that you are committed to submitting accurate data to SGA. The procedures (Section 4) and QA Check List (Section 5) described in this manual are the minimum standard that you need to follow when collecting and submitting data to SGA. In addition, you need to meet all QA procedures relevant to your breeding program. The aim is to ensure the accuracy of information reported by SGA and ensures that breeders and their clients have confidence in SGA reports.

Each time you submit a dataset to SGA you need to supply a QA Check List. The QA Check List verifies that you have followed the required QA procedures for the dataset being submitted (also see 2.2).

Each time you submit a dataset to SGA you need to supply a QA Check List. The QA Check List verifies that you have followed the required QA procedures for the dataset being submitted (also see 2.2).

If you wish to provide data to SGA but cannot meet a relevant procedure or need more explanation to do so, you should contact a relevant service provider for assistance.

Data managers as well as breeders reporting data directly to SGA need to meet the standards required by SGA from 1 November 2007.

Breeders will not be required to meet all QA procedures until 1 November 2007. Before November 2007, datasets that do not meet all relevant quality assurance procedures need to be reported and advice needs to be obtained from a genetics advisor or SGA staff to help the breeder overcome the areas where QA procedures have not been met.

3.2 Targeting the procedures and terms relevant to you

There is no need for you to read all the QA procedures in Section 4 as many will not be relevant to your breeding program. By reviewing the following summary you will readily locate the procedures in Section 4 of relevance to your operation. Also, within a procedures area that is broadly relevant to you there will sometimes be procedures that you can pass by. For example, terminal sire breeders will not need to consider the fleece weight procedures but muscle and fat depth will be important, even if you are experienced in evaluating these traits.

Section	Procedure
4.1	All breeders are required to follow the sheep identity system because it enables the genetic linkage between flocks to be established and therefore allows the performance of sheep in different drops and flocks to be compared.
4.2	The facilities and equipment procedures will help you make accurate evaluations.
4.3	Mating groups enable the genetic performance of sheep groups to be compared. These procedures are particularly important for breeders who do not submit full pedigree records.
4.4	All breeders submitting data to SGA need to follow the management procedures as these enable the genetic performance of sheep within a group, between groups within a flock and across-flocks to be compared. Mating management is the first of the three management sections.
4.5	Managing pregnancy is the second of the three management sections.
4.6	Ear tagging is the start of performance recording of sheep in many flocks and is also vital to obtaining good pedigree records.
4.7	Recording at lambing and weaning - all breeders are encouraged to consider these early age records as they can be a very efficient way of improving trait evaluation.
4.8	The management of progeny while they are being evaluated is the third of the management periods and defines how sheep need to be grouped during the analysis. If live weight or fleece Base Traits are submitted, all progeny with pedigree will usually need to be evaluated. Breeders are encouraged to review this area of the manual as it highlights changes to current procedures.
4.9	Trait evaluation gives a brief overview of the wide range of traits available and others under development. Breeders do not need to look over procedures for traits that are not relevant to them. None of the traits are compulsory.
4.10	Greasy fleece weight provides detail for breeders who wish to evaluate this trait.
4.11	Wool sampling provides detail for breeders evaluating fibre traits.
4.12	Worm egg count (worm resistance) is a relatively new trait that is covered in detail for those breeders who wish to evaluate this trait.
4.13	Scored traits are also new and are backed by AMSEA and SGA scoring systems for the visual evaluation of traits.
4.14	All breeders should review procedures for culling and castration as there have been some changes to conventional practices in this area.
4.15	The level of genetic linkage is a critical area for all breeders aiming to evaluate across-flock performance. The method of evaluating genetic linkage has changed for all flocks and this area needs careful consideration.
4.16	Breeder's reporting covers the use of SGA, LAMBPLAN and MERINOSELECT logos, as well as the reporting of ASBVs and FBVs. For anyone who is marketing sheep with SGA genetic information this area is a must.
4.17	Training is an integral component of any QA program. This area of the manual outlines the training required for the people involved in carrying out the QA procedures.
5.0	A QA Check List needs to be provided with each set of data submitted to SGA. The QA Check List is easy to fill out on paper or on computer, whichever is best for you. Section 5 of the manual describes the Check List and how to complete it.

4.0 QUALITY ASSURANCE PROCEDURES

If you wish to submit data to SGA but cannot meet a relevant procedure, or need more explanation on how to do so, you should contact a data manager or genetic advisor for assistance.

This section presents the QA procedures that need to be carried out when collecting and submitting data to SGA. The procedures are printed within the boxed areas and under the heading **Procedures.**

Within each section of the procedures the key areas are underlined to allow you to gain a feel for the priority issues. However, if you intend to submit data to SGA the underlined procedures cannot be considered in isolation and need to be considered in context with all the procedures.

If a procedure is not applicable to your breeding operation, you should select 'NA' for that practice when you complete the QA Check List.

Section 5 is an example of a QA Check List and describes how it should be completed. On-farm recording software that caters for reporting to SGA is likely to be upgraded over time to streamline the QA Check List routines.

If you wish to submit data to SGA but cannot meet a relevant procedure, or need more explanation on how to do so, you should contact a data manager or genetic advisor for assistance.

4.1 Sheep identity records

The sheep breeding identification system used by SGA enables sheep in all flocks to be uniquely identified. SGA analysis software can then evaluate the genetic performance of sheep within and between flocks.

At present visual or electronic ear tags are the major methods used to identify sheep. These ear tags link the sheep and all the stored records describing the sheep's performance and pedigree. Other devices, such as electronic implants and rumen capsules, can also be used to identify sheep.

Please note: in this manual electronic implants and rumen capsules are also referred to as ear tags.

Procedures

(i) All sheep performance or pedigree records submitted to SGA need to be identified using the 16-digit Australian sheep identification (ID). The ID can only contain numeric (i.e. 0 to 9) and upper case alpha (i.e. A to Z) characters. Further details on the structure of an ID are presented following the sheep identity procedures.

(ii) While there are some basic requirements when formatting an ID, the format of the last six digits of the ID is largely the breeder's choice. The sheep's ID needs however to clearly reflect the numbers and/or letters on a sheep's ear tag.

Where possible it is recommended to include the last two digits of the year of drop as the start of the last six-digits of the ID and also on the ear tag. For example, sheep born in the 2005 drop should have 05 at the start of the last six-digits of their ID and the start of their tag number.

While the last six digits of the ID need to clearly reflect the sheep ear tag number, they can be varied to suit the needs of the individual breeder. Preferably a sheep born in 2005 and a within-drop ear tag number of 12 should have 050012 as the last six digits of the ID and the tag number. Alternatively, the ear tag number can have a different format, for example, 5012 or 512. The last six digits of the 16-digit ID can also be varied, for example 005012 or 000012. A breeder can use an ear tag colour to identify the year of drop of a group of sheep and when this colour is combined with a tag number it reflects the sheep's ID. For example, a tag may read, 000012 or 12 and the ear tag colour identifies that it is 2005 drop - the resulting last six digits of the 16-digit ID could therefore be, for example, 050012, 005012 or 000012.

For within-flock use such as an on-farm ram sale it is common to provide only the last six digits of the ID. If this is the case you need to display the remainder of the ID in a prominent place, for example, the front of the sale catalogue. This allows breeders who buy a ram to record and report the correct 16-digit ID.

(iii) When you submit data to SGA that includes a sheep you did not breed (e.g. the sire or dam of the progeny) the sheep's ID needs to be described using the full 16-digit ID used by its breeder or using an ID developed in consultation with the breeder. If you are unsure about the correct ID for a sheep, ask the sheep's breeder or consult the SGA sire reference search.

(iv) If a sheep loses its ear tag and its ID cannot be determined, a new ear tag (that has not been used by any other sheep) and 16-digit ID should be compiled. When possible, the new ear tag ID and 16-digit ID should include the year of drop of the sheep.

(v) The ID of a sheep already submitted to SGA cannot be changed retrospectively unless it is clearly established that the ID was incorrect at the time of recording. For example, when a flock changes their flock prefix (such as when an unregistered flock becomes a registered flock) or when a flock changes the format of the last six digits of their ID (such as adding the last two digits of the year of drop to the last six digits of their ID) cannot retrospectively change the ID of sheep in their previous drops.

When you submit data to SGA that includes a sheep you did not breed (e.g., the sire or dam of the progeny) the sheep's ID needs to be described using the full 16-digit ID used by its breeder or using an ID developed in consultation with the breeder.

4.0 QUALITY ASSURANCE PROCEDURES

The Australian sheep identification (ID) system provides a unique 16-digit identification for all sheep and enables sheep to be linked genetically within and across flocks.

Australian sheep identification system

The Australian sheep identification (ID) system provides a unique 16-digit identification for all sheep and enables sheep to be linked genetically within and across flocks.

The identification system is used by SGA and allows each sheep breed, flock, year of drop and on-farm number to be established correctly.

An ID is constructed in the following way:

First two digits	Breed* of the flock - BB
Next four digits	Registered (or unregistered) flock - FFFF
Next four digits	Year of birth - YYYY
Last six digits	On-farm identification number - TTTTTT
The complete ID is therefore	BBFFFFYYYYTTTTTT

For example, the ID 5049672005050012 is read in the following way:

First two digits	50 - is the breed (in this case the Australian Horn Merino*).
Next four digits	4967 - is the flock (usually maintained by the breed society**).
Next four digits	2005 - is the year of drop.
Last six digits	050012 - is the on-farm sheep identification number.

* Breed code details are available on the SGA website or by contacting a service provider for assistance.

** Unregistered Merino and Poll Merino codes (e.g. CTSE sites) can be obtained from NSW Department Primary Industries Sheep Breeding Group - phone 02.6391.3812. Unregistered codes for flocks of other breeds can be obtained from SGA.

16-digit ID's need to be one continious string of digits - there should be no gaps, dots or dashes between the digits.

Example 16 digit ID:	**50**	**4967**	**2005**	**050012**
Information provided in the ID:	**Breed**	**Flock**	**Year of Drop**	**On-farm ID**

The breed and flock sections (1st six digits) of the ID are known as the 'flock code'.

The ID can only contain numeric (0 to 9) and upper case alpha (A to Z) characters.

When submitting an ID in a dataset the 16-digit IDs need to be one continuous string of digits – there should be no gaps, dots or dashes between the digits. If a section of the ID is less then its allocated number of digits, for example if a flock's registered code is one digit, say number 5, when 4 digits are allocated to flock code in an ID, the digit is padded out with zeros so that in the example above the flock code will be 0005.

4.2 Facilities and equipment

Procedures

(i) All evaluation procedures need to be carried out in a manner that safeguards the welfare of the sheep involved.

(ii) All facilities used for handling sheep during data collection need to enable:

- a. Each sheep to be identified accurately.
- b. Each sheep to be sufficiently restrained to allow accurate data collection.
- c. Sheep to be prevented from escaping or mixing with different groups of sheep.
- d. All measurement equipment to be tested for accuracy and calibrated before and regularly during data collection.

(iii) All weigh scales, including fleece and live weight scales need to be calibrated at the start of each weighing session to ensure they are accurate.

To calibrate scales weigh a known standard weight on the scales three times to ensure the recorded weight is consistently accurate. The standard weight should be of similar weight to the fleeces or sheep to be weighed. Before calibrating the scales ensure the tare adjustment is set to zero. If the scale reading differs from the standard weight by more than 0.1 kg (fleece weight) or 0.5 kg (live weight), adjust or repair the scale until the required level of accuracy is achieved.

All weigh scales, including fleece and live weight scales need to be calibrated at the start of each weighing session to ensure they are accurate.

4.3 Allocating ewes to mating groups

To ensure the genetic information generated by SGA is accurate, you need to identify clearly how your rams have been allocated to your ewes. By identifying which rams have been allocated to which ewes, the accuracy of the genetic performance of individual sheep within and between breeding groups will be maximised.

If you submit data that has sire ID recorded but no dam ID, the SGA analysis will assume that the dams have been equally allocated to the various sires - in other words, that the ewe mating groups have the same genetic merit. However, if specific ewes have in fact been selected to mate with particular sires (but the IDs of these ewes have not been recorded), then the accuracy of the breeding values could be reduced significantly. This will affect the breeding values of progeny and their sires and could also bias the calculated performance of all sheep in a group relative to other groups. To ensure the performance of sheep is not biased in this way, the mating allocation of rams to ewes is required to be correctly accounted for.

When a flock only records sire pedigree, all mating groups that have sire pedigree recorded must be mated to an equal allocation of ewes.

Procedures

Full pedigree recorded flocks (or tier of a flock)

All sheep born into a full pedigree flock (or tier of a flock) will have full pedigree recorded and submitted to SGA.

(i) Ewes with full or sire pedigree can be mated selectively to a ram or NAM or SIB syndicate (4.3 v) of rams.

(ii) Ewes that are not recorded with full or sire pedigree in the SGA database need to be allocated equally to all mating groups.

Sire only pedigree flock (or tier of a flock)

(iii) Ewes within a flock (or tier of a flock) recorded only with sire pedigree need to be allocated equally to all mating groups, i.e., the genetic merit of ewes in a mating group need to be the same for the traits recorded by the flock (or tier).

A random draft of ewes is a satisfactory method to achieve an equal allocation of ewes. A random draft alternatively allocates sheep filing through a draft into the number of mating groups required. Counting mating groups out the gate is not a satisfactory way of achieving an equal allocation.

Flock with no pedigree (or tier of a flock)

(iv) In a flock (or a tier of a flock) that does not record pedigree ewes can be mated selectively to rams. However, these flocks (or tiers of a flock) can only obtain FBVs because the flock is not linked genetically to other flocks.

Syndicate mating groups

(v) If ram-mating syndicates are identified in the pedigree records supplied to SGA they need to be defined by one of the following three options:

The correct coding of syndicates is critical to their effective use, eg. name option and year of drop.

Named = NAM:

NAM (short for name) syndicates are used when the identity of all rams in the syndicate is known and they are all recorded in the relevant SGA breed group, e.g., Terminal Sire, Merino, etc. The syndicate identification is recorded in the sire ID field of the dataset by a 16-digit ID, e.g., 5049672004NAM005. In this example, the last six digits identify the syndicate as the 5th NAM syndicate of this type within the particular flock and year.

The four-digit year section of the ID should be set as the year of drop minus one. In the example above, the actual year of drop was 2005 so the year in the ID is set at 2004. This ensures the sire and their progeny are not identified using the same year of birth, which would result in an error being recorded when the data are checked.

The ID of all the rams used in the syndicate need to be recorded in the 'Syndicate ID' area of the dataset using their 16-digit ID.

½ Sibs = SIB:

SIB syndicates are used when all rams in the syndicate have the same sire but the identity of the rams has not been recorded or the rams were not all recorded in the relevant

SGA breed group analysis. If the rams in the syndicate can be identified and have been recorded by SGA in the same breed group, the NAM option will establish the breeding value of the progeny more effectively and should be used in preference to the SIB option.

If the SIB option is used, the syndicate ID is recorded in the sire ID field in the dataset by using a 16-digit ID to identify the group of rams in the syndicate at that mating, e.g., 5049672004SIB002. In this example, the last six digits establish that this is the 2nd SIB syndicate in that flock and year. The four-digit year section of the ID should be set as the year of drop minus one. In this example, the year of drop was 2005 and the year is therefore set at 2004.

The sire of the rams in the syndicate is identified in the 'Syndicate ID' area of the dataset using its 16-digit ID.

A maximum of ten rams and/or sires can be used in a NAM or SIB syndicate.

Unknown = SYN

The SYN option is used when the syndicate cannot be recorded effectively as either a NAM or SIB syndicate. The syndicate is recorded in the sire ID field of the dataset by a 16-digit ID, e.g., 5049672004SYN007. In this example, the last six digits establish that this is the 7th SYN syndicate of this type in that flock and year. While SYN syndicates will be reported, they cannot be used in the analysis to improve the reliability of progeny breeding values, as is the case with NAM and SIB syndicates.

The syndicate needs to be identified in the 'Syndicate ID' area of the dataset by using the same 16-digit ID, e.g., 5049672004SYN007.

(vi) A flock can only be allocated a particular syndicate ID in one Management Group as this ensures the syndicate does not contribute to linkage between groups. A syndicate ID code should not be used more than once even if the same syndicate of rams is used in another mating because at any one mating the rams in the syndicate can sire a different proportion of the progeny.

A maximum of ten rams can be used in a NAM or SIB syndicate.

4.4 Managing mating

At mating, identify the mating group of ewes and record the ram/s joined to them to ensure the sire and dam ID of progeny can be recorded accurately.

Procedures

(i) At mating, identify the mating group of ewes and record the ram/s joined to them to ensure the sire and dam ID of progeny can be recorded accurately.

(ii) For flocks that submit birth weight and/or weaning weight:

When a joining lasts longer than 35 days it could be beneficial to submit the resulting progeny to SGA in separate Management Groups (4.8 i), so that the lamb birth dates within each Management Group are no more than 35 days apart. If lambing takes longer than 35 days and separate Management Groups are not created the SGA analysis will divide the lambs into groups when analysing birth and weaning weight so that the spread of their birth dates in the analysis is no greater than 35 days.

(iii) When the actual birth date of sheep in a Management Group is not recorded and mating is longer than 42 days, report any resulting progeny so that the spread of lambing is no longer than 42 days in a Management Group.

As a minimum, record the birth date of the Management Group as the average date of the Management Group's lambing period.

(iv) As far as possible, manage each mating group the same way – both before and during mating. The management of ewes mated by artificial insemination (AI) or embryo transfer (ET) recipient ewes need to be the same except for the procedure they undergo if their progeny are to be submitted as one Management Group along with naturally mated ewes.

(v) Submit a mating type record in the 'mate' type field for each progeny reported. If the natural mating is relevant no entry in the field is required. Record 'AI' or 'ET' if these mating types are used.

4.5 Managing pregnancy

During pregnancy all ewes whose progeny are to be submitted as a Management Group need to have the same nutrition and care.

Procedures

(i) Following mating and before lambing, all ewes whose progeny are to be submitted as a Management Group (4.8 i) need to have the same nutrition and care opportunity to ensure individual progeny are not advantaged or disadvantaged. Where this is not possible, allocate ewes randomly into separate groups (to ensure an even allocation of sires across groups) and record the groups in the data submitted as different Management Groups (4.8 i).

Management during pregnancy can impact on the lifetime performance of the ewe's progeny. While the last three months of pregnancy will have the largest impact, management during the entire period will still have an impact. If the management of individual ewes differs significantly during pregnancy, it is best to allocate these sheep into different Management Groups.

(ii) If ewes are separated into different paddocks for lambing then they need to be drafted into their mating groups as close as practical to lambing.

While lambing in different paddocks enables sire pedigree to be recorded accurately, it can also result in lambing groups receiving different management. To overcome this, choose paddocks so that each group of ewes and their progeny receive similar management.

(iii) If ewes are separated into different paddocks for lambing, they should be combined as soon as possible after lambing into as few groups as possible (preferably one) to reduce paddock differences. It is important to realise that paddock differences can have a significant effect on sheep performance even when these differences are not apparent.

Lambs should be combined and their Management Group identified as soon as practical but no later than 14 days after the end of the lambing period.

Ewes that are pregnancy scanned and separated into different groups so they can be managed according to their pregnancy status need to be submitted as separate Management Groups (4.8 i). It should be remembered that each of these Management Groups will require their own effective linkage (4.15).

(iv) If DNA is to be used to assign pedigree and sire ID is to be obtained by separating ewes into appropriate paddock groups, then these groups need to receive the same or similar management.

(v) ET-recipient ewes and foster mothers that have relevant SGA performance records should have their ID recorded within the data submitted to SGA. If recipient ewes and foster mothers of progeny in a Management Group do not have relevant SGA records, they need to all be one breed and preferably be of similar breeding i.e., one bloodline. In addition, they need to either all be maiden (up to 1.5 years of age) or all adult age (older than 1.5 years).

Lambs should be combined and their Management Group identified as soon as practical but no later than 14 days after the end of the lambing period.

4.6 Ear tagging

Use ear tags with a high retention rate and preferably tag all lambs in both ears to ensure their identity is maintained over their lifetime.

Recording sire and dam pedigree will improve the accuracy of breeding value estimates and the linkage within and between flocks.

When the sire of the dam is supplied for the SGA analysis, it is possible to account accurately for maternal effects on performance. For example, by recording the sire of the dam the maternal performance of a lamb's mother can be separated from the lamb's own performance.

Breeders in Australia should note that by 1st January 2006 a NLIS property identification code (PIC) needs to be displayed on an ear tag as required by NLIS.

The maximum lambing period for a Management Group is 42 days.

Procedures

(i) Where possible the birth date of each lamb should be recorded. When it is not possible to record the actual birth date for each lamb then record a mean lambing date over a short period, such as 14 days. If this is not possible, as a minimum requirement record the mean date of the complete lambing period of the Management Group. The maximum lambing period for a management Group is 42 days.

(ii) When recording sire and dam pedigree it is preferable to ear tag the progeny within 24 hours of birth but no more than 14 days after a Management Group (4.8 i) has completed lambing with the exception of when DNA is to be used to assign pedigree.

When sire pedigree is recorded based on lambing paddock groups, this should be done before these paddock groups are amalgamated.

Full pedigree flock

(iii) For a flock (or tier of a flock) that is full pedigree recorded:

Ear tag and record the ID of each lamb and the ID of the lamb's dam. It is recommended that ear tagging and recording be done within 24 hours of birth to minimise ID errors associated with cross mothering. If ear tagging is done within 24 hours of birth it is also an advantage to record birth weight, birth type, and lambing ease score at the same time.

(iv) The sire ID of a lamb is based on the mating record of the ewe identified as its dam or on records from a paddock mating group that identify the lambs in a paddock as the progeny of a particular sire.

Sire pedigree only mating groups

(v) If a flock (or tier of a flock) is only recording their lamb's sire pedigree and ewes mated to different sires are lambed together, then the lambs should be ear tagged and recorded and their sire recorded, preferably within 24 hours. If ear tagging and sire pedigree is not recorded within 24 hours of birth, try to record sire pedigree within 21 days of birth but no longer than 14 days after lambing in the paddock group has finished. The sire of the lamb needs to be recorded before the lambing paddock groups are amalgamated.

(vi) When a lambing paddock group contains only ewes mated to one sire, a lamb's sire ID can be easily recorded using the paddock mating records, which will show which sire mating group is in which paddock.

Lambs need to be recorded before paddock groups are amalgamated.

DNA technology for assigning pedigree

(vii) When using DNA technology to assign pedigree, there is no need to record sire or dam at or after birth, however ear tags need to be applied when the DNA is sampled. If you choose to lamb in paddocks based on ewes mated to a particular sire (or a syndicate of sires) tags should be applied before paddock groups are amalgamated and the sire pedigree for lambs in a paddock should also be recorded.

(viii) DNA pedigree (and paddock records if necessary) needs to be assigned to progeny records submitted to SGA before submitting any of these progeny's performance data to SGA.

(ix) When you use DNA technology to assign pedigree to particular sires or dams all progeny in a Management Group that are bred by these sires or dams also need to be DNA tested and assigned their relevant pedigree. However, if only limited DNA testing is available, no pedigree should be assigned to these progeny.

DNA pedigree needs to be assigned before submitting progeny's performance data to SGA.

4.7 Recording from lambing to weaning

Procedures

(i) Each sheep needs to have their ID (4.1) and sex code [entire male (1), female (2), castrated male (3)] recorded in the dataset submitted to SGA.

Progeny that have dam pedigree recorded need to have the date their mating started recorded and submitted to SGA.

Where available, you should endeavour to submit sire and dam pedigree, birth date, birth and rearing type, dam age and/or weaning weight records to SGA for analysis. SGA breeders are encouraged to develop their breeding program so that as much pedigree and performance data as practical can be submitted.

Birth date is optional but recommended and should preferably be recorded on the day of birth or, if this is not possible, within a week of birth.

(ii) Dry: 'Dry' is an optional record that is highly recommended when dam pedigree is recorded. 'Dry' is recorded against a ewe that was mated but did not get in lamb. 'Dry' is recorded by creating a dummy lamb ID with the last six digits of the ID being DRY001 (for the first dry ewe in the flock identified in that year), DRY 002 (for the second dry ewe in the flock identified in that year), etc. The dummy lamb should have a Birth Type equal to 0 (zero) and a Rear Type equal to 0 (zero).

'Dry' and 'Dead' are highly recommended to be recorded when dam pedigree is recorded.

It is essential that within a year drop that no progeny - male or female - may have the same last six digits of their ID.

(iii) Dead: 'Dead' (dead at birth) is an optional record that it is highly recommended when dam pedigree is recorded. 'Dead' is recorded against a ewe that lambed but her lamb/s died in the period up to weaning. 'Dead' is recorded by creating a dummy lamb ID with the last six digits of the ID being DAB001 (for the first death identified in that flock that year), DAB002 (for the second death identified in that flock that year), etc. The dummy lamb should have a Birth Type equal to the scanning or lambing observation and a Rear Type equal to 0 (zero).

'Dry' and 'Dead' records will be used to calculate the observed Number Lambs Born, Number Lambs Weaned and Lambing Opportunity values for the dummy lamb's dam. The dummy lambs themselves will not be included in the breeding value analysis and will not attract a SGA charge.

It is essential that within a year of drop in a flock that no progeny may have the same last six digits of the ID even when they are dummy 'Dry' and 'Dead' IDs.

(iv) Birth weight: This trait is optional but highly recommended if lambs are recorded for full pedigree. Birth weight needs to be obtained within 24 hours of birth.

(v) Lambing ease score: While recording this trait is optional, the following scoring system needs to be used if it is recorded.

1. Unassisted - Use this score by observing the state of ewes during birth or by noting the state of a ewe and her offspring shortly after birth.
2. Easy pull – use this score if slight intervention is required at birth.
3. Hard pull – this score indicates significant human force was required to assist at birth.
4. Malpresentation.
5. Veterinary assistance.

(vi) Birth type: Like lambing ease, this trait is optional but the following scoring system needs to be used if it is recorded.

1. Single.
2. Twin.
3. Triplet.
4. Quadruplet (or greater number of lambs born).

(vii) Dam age: This trait is also optional but the following scoring system needs to be used if it is recorded.

1. Progeny with a dam that is up to 550 days old at lambing (up to 1.5 years old).
2. Progeny with a dam that is between 550 and 900 days old at lambing (1.5 to 2.5 years old).
3. Progeny with a dam that is from 900 days up to six years old (2.5 to 6 years old).
4. Progeny with a dam that is an adult ewe of six years of age or older.

(viii) Rearing type: This trait is optional but the following scoring system needs to be used if it is recorded:

0. No lambs reared.
1. Single lamb reared.
2. Twin lambs reared.
3. Triplet lambs reared.
4. Quadruplet (or greater number of lambs reared).

Please note that for ET matings rearing type will not contribute to the SGA analysis of the performance of the dam.

Orphaned and artificially reared lambs in a Management Group should be recorded as having a rearing type of 1. Orphaned lambs preferably should not have production traits recorded however, if production traits are recorded, they need to be recorded in a separate orphaned Management Subgroup.

(ix) Weaning (live) weight: Recording this trait is optional but highly recommended - it is an easy and inexpensive trait to measure and can be used to increase the accuracy of breeding values.

Weaning weight needs to be evaluated when the average age of progeny in a Management Group is between 42 and 120 days of age. While this trait is called 'weaning weight' lambs do not need to be weighed at weaning. If breeders want to obtain the most accurate maternal weaning weight, progeny should be weighed while dams have a good milk supply.

When a flock is recording live weight, weaning weight is an important weight to obtain because it represents the first opportunity to record a live weight Base Trait and define the Management Group for that trait.

If you have evaluated the fleece weight of a flock but have not recorded date of birth or birth and rear type, you can use a measure of weaning live weight to adjust for early age effects on fleece weight and thus improve the accuracy of fleece weight breeding values.

Please note that if you identify sheep as being in different Management Subgroups at weaning (or any older age) they cannot be treated as a single Management Group at a later age, even if they are managed together after weaning. See sections 4.8 ii and 4.8 iii for a more detailed discussion on Management Subgroups.

Weaning weight is optional to record but highly recommended - it is easy and inexpensive to measure and can be used to increase the accuracy of breeding values.

4.8 Management Group and Base Traits

Procedures

(i) When a breeder submits records to SGA for progeny they bred the progeny need to be separated into a group known as a 'Management Group'. Management Groups are essential to allow progeny to be accurately grouped for an SGA analysis. The grouping together of progeny with certain characteristics allows both environmental and genetic differences to be accounted for in the analysis.

In addition, the name given to a Management Group is used to describe the sheep being submitted to and reported by SGA.

A Management Group is a group of progeny with all of the following characteristics.

a. Born under similar management conditions at one site.
b. Born over a period that is no longer than 42 days.
c. Male or female progeny from one Breed Group.

Breeders may if they wish submit a dataset that contains both male and female progeny if they have been managed together up to the time when the records were taken. Male and female progeny are often managed together in the period when birth records and weaning records are taken.

Some breeders require additional Management Group records to ensure progeny are correctly grouped in the analysis. Additional Management Group records (Section 6 - Glossary - 'Group') are required to be submitted when,

a. Management Group contains more than one flock code (the first six digits of the 16-digit ID).
b. a Management Group contains more than one tier or section within a flock code that are considered to be different genetic groups.
c. a flock code is being evaluated at more than one site code.

Progeny bred using embryo transfer are recommended to be allocated into a different Management Group compared to the progeny that were not bred using embryo transfer but would otherwise have the characteristics to be allocated into the same Management Group. The exception to this recommendation is when the recipient dams in the embryo transfer program have ASBVs in the same Breed Group as the naturally joined dams. In this situation the progeny can just as effectively be included in the same Management Group as long as the dams are recorded and all the dams are managed appropriately - 4.4 and 4.5).

A management Group is a group of progeny

a. Born under similar management at a site

b. Born over a period no longer than 42 days

c. Male or female progeny from a breed group.

(ii) It is highly recommended that a Management Group should not be split into Management Subgroups until after all Base Traits (4.8 v) are evaluated. This is because if the Subgroups that are formed have a bias representation of a sire or dams progeny relative to the complete Management Subgroup, the Management Group and the flock's performance could as a result also be biased.

If progeny in a Management Group cannot continue to be managed in the same way up until all their Base Traits (4.8 v) are evaluated, then two or more Management Subgroups need to be established and recorded to ensure the analysis is more effectively conducted. The sheep recorded in the same Management Subgroup are required to have the same or similar management.

It is critical to have effective genetic linkage between Management Subgroups as well as between Management Groups (4.15).

Each Management Subgroup needs to be recorded within the Management Group by identifying them as 1, 2, etc in the Subgroup field in the dataset. The Subgroup field in the dataset is required to be completed the first time any records for the Management Group are submitted after traits are evaluated following the splitting of the progeny into different Subgroups.

If only a small proportion (less than 5%) of progeny are managed differently due to disease, illness or misadventure one option is to leave them in the same Management Group but not submit any further trait performance information on these progeny.

Please note if progeny are in different paddocks after weaning this will usually mean they are experiencing different management and therefore need to be considered for being split into different Management Subgroups. Paddock conditions can be deceiving and even when two paddocks 'look' the same they can in fact be very different – for example they may have different worm burdens.

If progeny in a Management Group can not continue to be managed in the same way then two or more 'Management Subgroups' need to be established.

(iii) While it is highly recommended that a Management Group should not be split into Management Subgroups until after all Base Traits (4.8 v) are evaluated there are two exception to this recommendation. These exceptions are when progeny are allocated into Subgroups based on,

a. birth type (4.7 vi) or rearing type (4.7 vii) records that results from a pregnancy scan of their dam or their birth or rear type obtained by observation or DNA at some time after birth.

b. dam age (4.7 vii).

If different Management Subgroups are required to be established before all the Base Traits (4.8 v) of the Management Group have been evaluated, the progeny should be split into the Subgroups as randomly as possible for the traits submitted.

When a Management Group is split into Subgroups before the group's Base Traits have been evaluated and these Subgroups are specially managed there is a high risk that the comparison between progeny in the different Subgroups will be significantly biased. This is because the SGA analysis will not be able to use the sire pedigree records correctly to remove the environmental effects between the Subgroups. The comparison between progeny in other Management Groups within the flock and between other flocks in the analysis could also be biased. An example of specially managed Subgroups is auction sale rams fed on high quality pasture versus private treaty sale rams fed on poorer quality pasture.

(iv) The date each trait was evaluated needs to be submitted to SGA along with the performance record. In addition, when fleece weight is submitted the date of the shearing prior to the evaluation shearing (or the average birth date if the sheep have not been shorn) is also required to be submitted. The date of the shearing allows the wool growth at the time of evaluation to be calculated.

Base traits

(v)

a. When live weight data for a Management Group is submitted to SGA, the Base Trait is weaning (live) weight or an older age live weight. Apart from the exemptions outlined in 4.8 (vi), the Base Trait performance for all progeny in a Management Group needs to be submitted.

b. When carcase traits for a Management Group are submitted to SGA, the Base Trait is fat and eye muscle depth at the early post weaning age or an older age. Apart from the exemptions outlined in 4.8 (vi) whichever is greater of the following two options needs to be submitted: all pedigreed sheep in the Management Group measured for carcase traits, or - 75% of the sheep in the Management Group with sire or dam pedigree.

c. When worm egg count (WEC) for a Management Group is submitted to SGA the Base Trait is WEC at the weaning age or an older age. Apart from the exemptions outlined in 4.8 (vi) whichever is greater of the following two options needs to be submitted: all pedigreed sheep in the Management Group measured for WEC, or 75% of the sheep in the Management Group with sire or dam pedigree.

d. When fleece weight for a Management Group is submitted to SGA, the Base Trait is greasy fleece weight the yearling age or an older age. Apart from the exemptions outlined in 4.8 (vi) Base Traits for all progeny in the Management Group need to be submitted.

e. When fibre diameter for a Management Group is submitted to SGA, the Base Trait is fibre diameter at the yearling age or an older age. Apart from the exemptions shown in 4.8 (vi) Base Traits for all progeny in the Management Group need to be submitted.

It is not compulsory to submit any trait to SGA – all traits are optional. Additional traits to the Base Traits also can be evaluated (see Table 4.1).

Progeny that are being culled can be submitted at no cost - 4.8 (viii) and 4.14 (iii).

It is not compulsory to submit any trait.

Progeny that are being culled can be submitted at no cost.

(vi) If you submit Base Trait measurements (4.8 v) for sheep in a Management Group they should not be submitted if they have been injured or mismothered to the extent that it affects their performance for the traits being submitted.

It is recommended that sheep outlined below in points g and h should be submitted for the Base Traits the group is being submitted for.

If a Base Trait is being submitted for a Management Group the following sheep do not need to be submitted. If sheep are not submitted they should not be included in the calculation of the proportion of sheep required to be evaluated for a Base Trait (4.8 v).

a. sheep that are injured or mismothered to an extent that it affects their performance for the traits being submitted.

b. sheep that have a gross abnormality (e.g., deformed jaw, reproductive fault).

c. sheep that don't meet a breed type characteristic (e.g., horns in a poll breed). When sheep that don't meet a breed type characteristic are not submitted all sheep that don't meet the characteristic in the group are required to not be submitted.

d. Merino, Dohne or SAMM sheep that have pigmented wool.

e. sheep that have been submitted but have died due to disease. misadventure before the Base Traits being submitted were evaluated.

f. sheep that have not been submitted for a trait due to a mistake or misadventure.

g. sheep that don't have a known sire or dam.

h. sheep that are considered unsuitable for a trait that the Management Group is not submitted for. A maximum of 10% of the progeny with sire or dam pedigree in the Management Group can be excluded on this basis.

If some progeny with pedigree are not submitted and this results in the average performance of the progeny of a sire or dam in the group being biased, the complete Management Group and the flock's performance could as a result also be biased. If progeny with pedigree are not submitted, this will also reduce the accuracy of the parents' breeding value.

(vii) Progeny identified as poor performers (except for the reasons outline above) should be retained until they have been evaluated for their Base Traits.

(viii) Sheep identified as 'culls' (CU) or 'commercial' (CO) before the first Base Trait is submitted will not attract a SGA service fee (4.14 iii). These records will be used in the SGA analysis to calculate breeding values but these sheep will not have breeding values reported.

Progeny identified as poor performers should be retained until they have been evaluated.

4.9 Trait evaluation

Table 4.1 is a summary of the traits that can be submitted to SGA. A tick in the table indicates that the trait can be evaluated at the age specified on that row. As new traits become available they will be posted on the SGA website and will be available from service providers. There are no compulsory traits and a breeder can choose to submit data for any of the trait ages marked with a tick.

The traits listed in Table 4.1 are those that can currently be submitted to SGA for the calculation of breeding values. The traits or ages that cannot currently be reported as breeding values are highlighted in blue - they are expected to be able to be reported by the end of 2007. Traits highlighted in red are the Base Traits - see 4.8 (v) and 4.8 (vi) for details.

TABLE 4.1 Summary of SGA traits and ages of evaluation

Ages used to describe the performance of various traits	Age of evaluation[1]	Live weight (kg)	Muscle & fat depth (mm)	Fleece traits[2]	Scrotal cricumference (cm)	Worm egg count (epg)	Type & structural traits[3]
Birth	Birth to 24 hours	✓					
Weaning	42-120 days (7-16 weeks)	✓				✓	
Early post weaning	120-210 days (4-7 months)	✓	✓		✓	✓	
Post weaning	210-300 days (7-10 months)	✓	✓	✓	✓	✓	✓
Yearling	300-400 days (10-13 months)	✓	✓	✓	✓	✓	✓
Hogget	400-540 days (13-18 months)	✓	✓	✓	✓	✓	✓
Adult	540 days or older (18 mths or older)	✓		✓			✓

[1] The average age of the sheep in the Management Group.

[2] Fleece traits: The minimum fleece growth at evaluation varies for different traits as follows: six months: fleece weight (kg); five months: fibre diameter (μm); coefficient of variation of fibre diameter (%); staple strength (N/ktex); staple length (mm), crimp frequency (crimps/cm), and the scored wool quality traits (fleece rot, fleece colour, fleece character and staple weathering).
Breeding values will not be reported for fleece traits at the post-weaning age until research on the value of post-weaning fleece traits and subsequent industry consultation is completed.

[3] Scored type and structural traits (face cover, neck/body development and feet/leg conformation are available - 4.13).

4.0 QUALITY ASSURANCE PROCEDURES

Trait evaluation needs to be carried out in an identical manner for all sheep in a Management Group.

Procedures

(i) Recording trait evaluation needs to be carried out in line with all relevant procedures and in an identical manner for all sheep within a Management Group.

Where relevant, muscle and fat scanners, fleece testers and WEC laboratories that meet SGA standards need to be used. Service providers that meet SGA standards can be obtained from the SGA website.

(ii) Trait performance needs to be submitted in the correct units (Table 4.1).

(iii) The date of the evaluation for each trait needs to be submitted. When more than one fibre diameter trait (e.g., fibre diameter and CV of fibre diameter) is evaluated from the same fleece sample, only one date needs to be submitted for these traits.

(iv) Except for birth weight, live weight measurements can only be evaluated when the sheep have been without feed and water for a minimum of two hours. Evaluate live weight to at least the nearest 0.5 kg and where practical evaluate birth weight to the nearest 0.1 kg.

(v) The impact of dam and birth effects on fleece weight at the post-weaning or yearling ages can be minimised by:

a. Submitting sire pedigree, birth type or rear type and birth date or;
b. Shearing lambs at least six months before evaluating for fleece weight or;
c. Submitting a weaning live weight.

(vi) Fleece traits - fleece weight, staple length, fibre diameter, staple strength and yield need to be evaluated when the average age of the group is a minimum of 300 days (ten months). In addition, when evaluating for fleece weight, a minimum of 180 days (six months) wool growth is required and for fibre diameter, staple length, crimp frequency, staple strength and yield sheep need to have a minimum 150 days (five months) wool growth.

Until research on the value of post-weaning fleece traits and subsequent industry consultation is completed, breeding values will not be reported for fleece traits at the post-weaning age. Breeders who wish to report breeding values (FBVs or ASBVs) in the short term will need to submit yearling or older age evaluations, i.e., the average age of the group needs to be a minimum of 300 days (10 months) of age at evaluation.

(vii) Wool quality traits (fibre diameter, CV of fibre diameter, staple strength, yield, etc) need to be evaluated by a fleece tester accredited for on-farm fibre measurement (OFFM). Please note that OFFM includes laboratory and on-farm evaluations.

(viii) Staple length and crimp frequency can be evaluated by an accredited fleece tester using a mid-side fleece sample. Alternatively, breeders can evaluate these traits using the following procedure. When evaluating staple length and crimp frequency on sheep use a straight but relaxed staple at the mid-side. Measure staple length in mm using a ruler (a 15 cm steel ruler is recommended) and crimp frequency using a crimp gauge. Measure three staples selected at random but equally distant from each other on the outer edge of an imaginary 100 mm diameter circle around the mid-side. Submit the average of the three measurements to SGA. If you use mid-side fleece samples, the three evaluations can be carried out equi-distant from each other on the edge of the sampled area. Evaluate crimp frequency at the base of the staple.

It is best to evaluate staple length and crimp frequency on sheep that have already had a shearing. However, if this is not practical, and staple length is evaluated on unshorn sheep, consider the staple tip as the point where the staple narrows to two thirds the width of the major section of the staple, rather than the end of the staple that is used for shorn sheep.

(ix) Muscle and fat depth needs to be evaluated by an accredited ultra-sound scanner. A live weight measured at the time of scanning needs to be submitted with muscle and fat depth measurements.

The recommended average group live weight and fat cover are:

Live weight - ram average 55 to 60 kg, ewe and wether average 45 to 50 kg.

Fat depth - at least 2 to 3 mm of measured fat cover at the 'C' site.

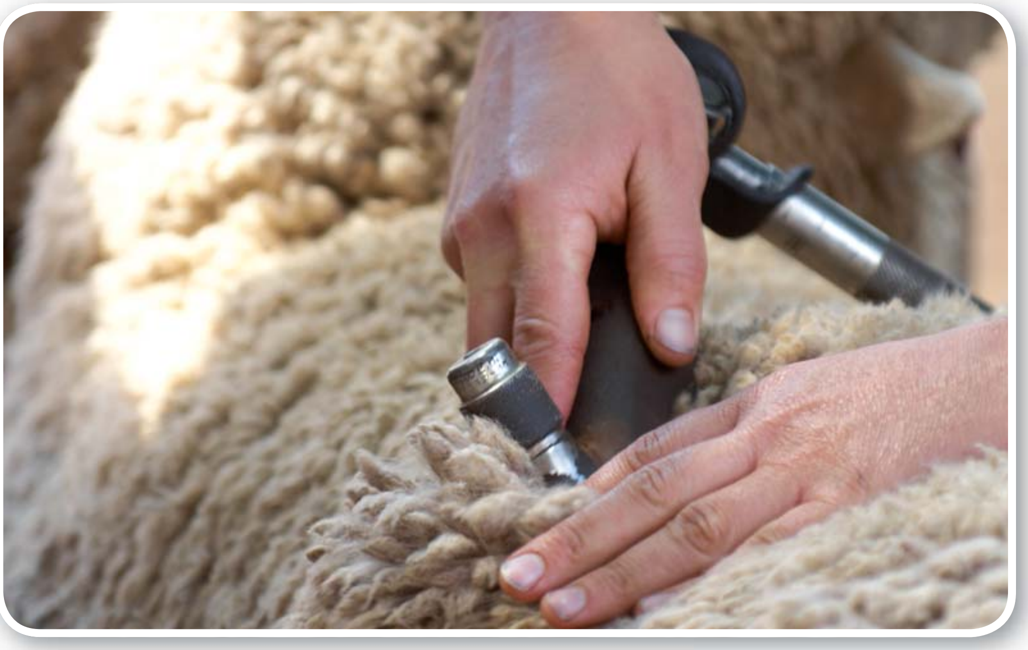
(x) Worm egg count (WEC) needs to be evaluated using the procedures outlined in 4.12 and by a laboratory that follows protocols defined by Nemesis.

(xi) Scrotal circumference needs to be measured at the largest circumference of the scrotum with the tape at right angles to the vertical axis of the scrotum. Breeders are recommended to submit a live weight evaluated on the same day as scrotal circumference, as this will assist the development of improved procedures for the evaluation of scrotal circumference and its effect on other traits and analysis procedures.

Do not submit a scrotal circumference record for rams with only one testicle but submit a Testicle Count on all rams with only one testicle as this information may help to understand the genetic relationships of this trait. Rams with only one testicle can be culled and submitted at no cost (4.14 iii).

(xii) When a sheep is injured do not submit data for any trait performance affected by the injury.

When a sheep is injured do not submit data for any trait performance affected by the injury.



4.10 Greasy fleece weight evaluation

Procedures

(i) When using scales, calibrate the weigh scales to within 0.1 kg of the standard weight at the start of each weighing session (4.2 iii).

(ii) Adjust the tare so the reading is zero.

(iii) Greasy fleece weight needs to be measured at a minimum of 300 days (ten months) of age and the sheep need to have a minimum of 180 days (six months) wool growth since the last shearing (4.9 vi). If chemical defleecing is used in conjunction with fleece trait evaluation it is important to account for the variation in fleece length that can occur.

(iv) Record the ear tag numbers at the time the sheep is being shorn.

(v) Either include the belly wool in the fleece weight for all the sheep in the Management Group or do not include the belly in the fleece weight for any of the group. It is preferable to include bellies in the fleece weight if possible.

(vi) Weigh the fleece before skirting.

(vii) Weigh and record the fleece weight to the nearest 0.1 kg.

Fleece weight needs to be measured at a minimum of 300 days of age and have a minimum of 180 days wool growth.

4.11 Fleece sampling and submitting for fibre measurement

Procedures

Fleece sampling

(i) For fleece samples, sheep should be a minimum of 300 days (ten months) of age and have 150 days (five months) of wool growth (4.9 vi) at the time of sampling. If chemical defleecing is used in conjunction with fleece trait evaluation it is important to account for the variation in fleece length that can occur - 4.9 (vi).

(ii) The fleece sample area should be about 100 mm X 100 mm in size.

(iii) Sample the fleece from either:

- a. The mid-side - over the third last rib, half-way between the mid-line of the back and the mid-line of the belly; or
- b. The pinbone - over the pinbone.

When evaluating fleece traits, use the same sample site and side for all sheep in a Management Group at a particular age.

Fleece sample at a minimum of 300 days of age and have 150 days of wool growth

(iv) If sampling at shearing, locate and mark the sampling site with a suitable marking substance on the standing sheep before shearing.

(v) If sampling at shearing, remove the sample on the board during or after shearing or during the skirting process on the wool-rolling table.

(vi) Shear the wool off the sample area as close and consistantly to the skin as possible using an appropriate apparatus. It is critical there are no second cuts if the sample is to be used to evaluate staple length, staple strength or crimp frequency.

(vii) If the sample is being sent off-farm, seal it in a bag labelled with the ear tag number of the sampled sheep using a permanent marker or barcode.

(viii) Follow other instructions provided by the fleece tester.

Packing and submitting fleece samples to a laboratory

(ix) Ensure each sample is clearly identified.

(x) Check that each sample bag is properly closed.

(xi) Prepare the laboratory submission form using the breeder's name and address, the name and contact telephone number of the person submitting the samples, and the number of samples submitted.

(xii) Write the tests required on the submission form, e.g., fibre diameter, yield etc.

(xiii) Pack the samples, add the laboratory submission form and address the container.

(xiv) Send the package to an accredited fleece tester.

Use an accredited fleece tester.

Consult a person with local expertise before carrying out a WEC evaluation program.

4.12 Worm egg count (WEC) evaluation

If you plan to evaluate sheep for WEC, you should consult a person who has local expertise in carrying out a WEC evaluation program. Animal care is particularly important as sheep health can be jeopardised if the evaluation is not carefully designed and monitored.

Procedures

(i) WEC is a Base Trait and as such there is a minimum requirement that needs to be achieved when evaluating for this trait - 4.8 (v) c.

Submit the total count of Strongyle eggs (this includes Trichostrongylus, Ostertagia, Haemonchus and other minor species whose eggs look similar on current egg counting technique). Although currently not used in the analyses submit an individual species count for Nematodirus if this count is available.

Additional evaluations can be submitted at a later age on all progeny or a sub-set of the group.

(ii) Time of evaluation - the immune system of the sheep needs to be stimulated by a worm challenge before genetic differences can be expressed. The optimum time for faecal sampling is determined by the seasonal rainfall conditions of the region where the sheep are being managed.

Summer rainfall area

Measure young sheep at least six weeks after weaning, so that they have been exposed to a worm challenge and maternal immunity has had time to dissipate. The best age to measure WEC is between six and 14 months.

Winter rainfall area

WEC measurements should be undertaken primarily between June and October to allow for the seasonal larval availability and seasonal variation in heritability. In practice the key to effective evaluation is monitoring the group to determine if there is adequate challenge.

Young sheep, between nine and 15 months of age, are preferred, however evaluation at a weaning age can be recommended when yearling and hogget evaluation are not giving adequate counts.

Measurements are possible in older sheep as long as they have high egg counts.

(iii) Level of infection - Under natural worm challenge, WEC can be measured after infection has built up to the level where there is sufficient variation between individuals. Sheep need to be monitored regularly until the WEC is high enough for sampling by obtaining random samples from the flock. The critical level of infection will vary between regions, depending on the worm species present, the condition of the sheep, the environmental conditions and the attitude of the breeder to risk of production losses from the worm burden.

Summer rainfall areas

Where Haemonchus is present the level of infection is 500-1000 eggs per gram (epg).

Winter rainfall areas

Where black scour and brown stomach worms predominate, sample when the level of infection reaches an average of 300 to 500 epg. If there is a distinct break to the season, this level of infection is often achieved 6-8 weeks after the break.

Most winter rainfall areas don't have significant numbers of Haemonchus, however when this is the case it is commonly recommended to use a narrow spectrum Haemonchus drench prior to the WEC evaluation. The removal of Haemonchus will ensure their high fecundity does not distort the egg count.

To ensure the Management Group has had sufficient challenge and that the most resistant sheep can be identified easily, have less than 10% of the sheep with zero egg counts.

Worm infections should not be allowed to build up to the stage where production and the welfare of the sheep are being compromised and it is strongly recommended that you organise for a flock health specialist to monitor the program. The inherent risks involved in allowing natural infections to progress to the desired level need to be considered, as responsibility for losses rest with the sheep breeder.

(iv) Number of measurements obtained - improvements in worm resistance can be achieved by evaluating one suitable WEC sample per sheep. However, if two measurements are used, evaluate the progeny at two separate infection cycles separated by a drench treatment.

Sire pedigree will assist greatly in genetic gain for worm resistance and it is highly recommended that a minimum of sire pedigree be submitted if selecting for WEC.

To ensure the most resistant sheep can be identified, have less than 10% of the sheep with zero egg counts.

4.13 Evaluating scored traits

Procedures

(i) Scored traits can be submitted to SGA if the evaluation is based on an SGA approved trait-scoring system. When photographic standards are included as part of the approved trait description they need to be used as the basis for the evaluation.

(ii) SGA approved trait-scoring systems include, AMSEA traits that are currently available and SGA trait scores under development that will be posted on the SGA web site as they are available.

Visual Breech Scores are under development by AWI for research and industry application. Breech Scores are expected to be added to the SGA web site in the near future and can then be regarded as approved SGA trait-scores.

AMSEA scored traits are currently fleece rot, fleece colour, fleece character, staple weathering, face cover, neck/body development and feet/leg conformation. The photographic standards for these traits are available on the Merino Superior Sires (MSS) site (http://mss.csiro.au). SGA are developing additional conformation scores and also a scoring system for temperament.

Use an approved trait-scoring system.

"Culls" can be submitted at no cost.

4.14 Castration and culling

Procedures

(i) When evaluating male progeny for Base Traits (4.8 v) it is highly reccommended that all the sheep submitted in a Management Group should be either entire or castrate. If only a proportion of the progeny are castrated before all of a Management Group's Base Traits are evaluated it is preferable that these progeny need to fit into a category that can be exempt from evaluation (4.8 vi). If sheep can be exempt (4.8 vi) and they are castrated before the Base Traits are evaluated their performance for any trait affected by castration must not be submitted.

(ii) If some progeny in a Management Group are castrated after (not before) the Base Traits have been evaluated and further evaluations are carried out on the castrated progeny these progeny need to be submitted as a separate Management Subgroup from the uncastrated progeny.

(iii) Sheep identified as 'culls' (CU) or 'commercial' (CO) before the first Base Trait is submitted will not attract a SGA service fee. While these records will be used in the SGA analysis to calculate breeding values, the breeding values will not be reported for the sheep identified as CU or CO. The CU and CO codes can be recorded in the 1st two digits of the sheep number section of the ID (last 6 digits of the ID) or in a 'Cull' field in the dataset.

4.15 Across-group and across-flock linkage

The SGA analysis calculates the degree of genetic linkage (common relatives) between flocks for each trait group – live weight, fleece, carcase, reproduction and WEC. The extent to which flocks are linked will determine whether the breeding values are reported as a FBV or as an ASBV.

When a flock has satisfactory linkage for a particular trait group, the genetic performance of the trait group will be reported as an Australian Sheep Breeding Value (ASBV). In addition, the accuracy of the ASBV will be reported and the results reported under the SGA logo and relevant brand name logo, e.g., MERINOSELECT, LAMBPLAN.

A trait without satisfactory genetic linkage across-flock will be reported as a Flock Breeding Value (FBV), not as an ASBV. FBVs will not be reported with trait accuracy. Management Groups reported only with FBVs can be reported under the SGA logo, however they cannot be promoted or sold using a brand name logo, e.g., LAMBPLAN or MERINOSELECT.

Procedures

(i) Genetic linkage between flocks is achieved when sires and/or dams that have progeny in one or more well linked flocks also have progeny in the flock that is being assessed for linkage. Sons and daughters of these sires or dams can also provide linkage when they have progeny in the analysis. Sires and dams that genetically link one flock to another flock are known as 'link' sires and dams. Sires and dams that have progeny in different management groups within a flock are also known as 'link' sires and dams.

(ii) As a guide a minimum of 30 progeny evaluated for each trait of interest is required to be bred by sire/s and/or dam/s in the relevant flocks or Management Groups (or 90 progeny of sons and daughters of link sires or dams) to achieve satisfactory linkage. Progeny of sires and dams providing the linkage between either flocks or Management Groups need to have been evaluated for the relevant Base Traits. This level of linkage is required between Management Groups (and where applicable between Management Subgroups) within flocks, as well as between flocks. While the reporting of ASBVs indicates that the required level of linkage has been achieved between flocks, it does not indicate that there is satisfactory linkage between all groups within the flock and it is the responsibility of a breeder who reports ASBVs to maintain satisfactory within-flock linkage.

Only linkage generated in the four most recently analysed years is used to calculate the across-flock linkage that is reported by SGA. This linkage determines if ASBVs are reported.

The number of progeny required to obtain ASBVs will depend on the design of the flock's breeding program. Please consult a genetic advisor to clarify the number of year drops that linkage will be based on and other requirements for a particular flock.

It is the responsibility of the breeder who is reporting ASBVs to maintain within flock linkage.

4.16 Breeders reporting SGA information

The procedures in this manual will ensure that breeders and their customers can identify information provided by SGA and differentiate between the genetic performance of sheep within and across-flocks.

Procedures

(i) When you complete a QA Check List and mark 'yes' for '4.16 Breeders Reporting SGA Information' you are indicating you will report SGA performance information in line with SGA requirements.

(ii) Breeders who provide information to customers from an SGA report may use the SGA logo to report and promote their sheep.

(iii) Breeders who provide information to customers need to define the performance of a trait in the same way it was reported by SGA - i.e., either as an ASBV along with its associated accuracy value or as an FBV.

(iv) Brand names or logos, such as MERINOSELECT and LAMBPLAN can only be used to promote sheep that have been issued with an ASBV for one or more traits. Breeders can promote their breeding program using a brand name logo or the SGA logo.

(v) The performance of all sheep can be reported relative to the breeder's personalised indexes or one or more industry standard indexes.

(vi) Sheep whose identity and genetic performance have been submitted to SGA can only be reported publicly by the breeder submitting data when:

a. The breeder owned (or part owned) the sheep (or held ownership rights to the genetic material of the sheep) at the time of evaluation in the case of performance records or the time of mating in the case of sires and dams or;

b. The breeder has obtained genetic material from the sheep (e.g., semen, embryos) that has no public reporting restrictions or;

c. The breeder has written permission from the owner to report publicly the SGA performance of the sheep or;

d. The SGA performance of the sheep has already been reported publicly by SGA or its owner.

Unless otherwise notified, SGA may report publicly the performance data of sheep deemed to be trait leaders from each breed group. It is the responsibility of the owner of data submitted to SGA to notify SGA if they do not want to publicly report information from SGA. Similarly, if the owner of the data submitted to SGA is restricted or has become restricted (for any reason) from reporting publicly a particular sheep it is the breeders responsibility to notify SGA in writing.

Notify SGA if as a breeder you do not want SGA to publicly report one or more sheep in the records you have submitted.

4.17 Quality assurance procedures training

Training is an integral part of all QA systems. SGA can provide assistance with staff training. Please contact SGA for a list of advisors to assist you and your staff to develop and use the QA procedures in this manual.

Breeders who wish to submit data directly to SGA have until the 1 November 2007 to meet the standard required by SGA. SGA will conduct workshops to provide breeders and their staff with training. These workshops will be tailored to the experience level of the breeders attending and the type of data being provided.

Breeders will not be required to meet all QA procedures until 1 November 2007. Before this date all datasets submitted to SGA that do not meet all relevant QA procedures need to be reported via a data manager to obtain advice on how to meet these procedures.

" As a breeder who submits data to SGA, you need to ensure that any person responsible for carrying out the procedures in this manual has relevant training and is familiar with the relevant parts of the SGA Breeder's Quality Assurance Procedures Manual. "

Procedures

(i) As a breeder who submits data to SGA, you need to ensure that any person responsible for carrying out the procedures in this manual has relevant training and is familiar with the relevant parts of the SGA Breeder's Quality Assurance Procedures Manual.

(ii) All breeders who submit data to SGA are responsible that the data meets the standards required by SGA. Training which includes QA procedures will be available for breeders and their staff. The training workshops will be targeted at groups of breeders with a similar level of experience as much as possible.

5.0 QA CHECK LIST

All areas listed under the Procedures headings in Section 4 of this manual are the minimum standard that all breeders need to meet before data can be accepted into the SGA database.

All areas listed under the **Procedures** headings in Section 4 of this manual are the minimum standard that all breeders need to meet before data can be accepted into the SGA database. It is the breeder's obligation to have read, understood and met these minimum standards. To verify that a breeder has met the procedures they need to complete the following QA Check List for each dataset submitted (also see 2.2). The Check List can be completed quickly using either a computer or paper system.

How to complete the QA Check List

Please respond to each of the Section 4 procedures listed in the table below. Respond by marking the correct option from the following four options:

Yes - if the dataset being submitted has met all the relevant procedures listed under this heading in Section 4.

No - if the dataset being submitted has not met all the relevant procedures listed under this heading in Section 4.

NA - if none of the procedures under this heading in Section 4 are relevant to the dataset being submitted.

Help - if you are not sure if the dataset has met the requirements of a procedure in Section 4 or if you need help to better understand a procedure and its relevance. If you mark 'Help' please contact a data manager or genetic advisor to obtain the assistance you require.

If you are completing the Check List on paper, mark the correct option by ticking the circle to the right of the relevant heading. If you are completing the Check List using a computer 'click' on and mark the option circle you wish to select.

QA CHECK LIST 5.0

Section	Procedures	Yes	No	N/A	Help
4.1	Sheep identity records	○	○	○	○
4.2	Facilities and euipment	○	○	○	○
4.3	Allocating ewes to mating groups	○	○	○	○
4.4	Managing mating	○	○	○	○
4.5	Managing pregnancy	○	○	○	○
4.6	Ear tagging	○	○	○	○
4.7	Recording from lambing to weaning	○	○	○	○
4.8	Management Group and Base Traits	○	○	○	○
4.9	Trait evaluation	○	○	○	○
4.10	Greasy fleece weight evaluation	○	○	○	○
4.11	Wool sampling for fibre measurement	○	○	○	○
4.12	Worm egg count evaluation	○	○	○	○
4.13	Evaluating scored traits	○	○	○	○
4.14	Castration and culling	○	○	○	○
4.16	Breeders reporting SGA information	○	○	○	○
4.17	Quality assurance procedures training	○	○	○	○

I the undersigned declare that the sections I have made on this form are accurate.

Management Group submitted:- Flock/s:

Breed/s:

Year of drop: Month/s of birth:

Name:

Sign: Date:

Ph: Mobile:

Email:

6.0 GLOSSARY OF TERMS

In this manual the meanings of the words and phrases listed below apply throughout the manual.

Across-breed:
Comparison of sheep across different breeds within a breed group.

Across-flock:
Comparison of sheep across different flocks within a breed group.

AGBU:
Animal Genetics and Breeding Unit.

AI:
Artificial insemination.

ASBV:
Australian Sheep Breeding Value - the genetic performance (breeding value) reported by SGA that describes the across-flock, or across-breed (as applicable) performance of a sheep for a trait.

Australian sheep identification system:
This system provides a unique sheep identification (ID) for each sheep across all flocks (4.1).

Base traits:

a. When a Management Group is evaluated for live weight the Base Trait is:
Weaning (live) weight or an older age live weight.

b. When a Management Group is evaluated for carcase traits the Base Trait is:
Fat and eye muscle depth at early post weaning or an older age.

c. When a Management Group is evaluated for Worm egg count the Base Trait is:
Worm egg count at weaning or an older age.

d. When a Management Group is evaluated for greasy fleece weight the Base Trait is:
Greasy fleece weight at post weaning or older age.

e. When a Management Group is evaluated for fibre diameter the Base Trait is:
Fibre diameter at post weaning or an older age.

For more detail see 4.8 (v).

BLUP:
Best linear unbiased prediction. The statistical method used to calculate estimated breeding values such as ASBVs and FBVs.

Body weight (WT):
See Live weight

Brand name:
SGA reports sheep under two brand names and their associated logos. The Merino breed group is reported under the MERINOSELECT brand name and logo. All other breeds at this stage are reported under the LAMBPLAN brand name and logo. There is the opportunity for a breed/s to be reported under a unique brand name and logo.

Breeder:
A person who participates in SGA quality assurance procedures and genetic evaluation. In relation to data being submitted to SGA a 'breeder' is the person, organisation or business that is the legal owner of the data.

Breed group:
The breeds of sheep that are combined in an SGA analysis and report. At present there are four segments of the SGA database – Merino, terminal, maternal and SAMM – and within these there are one or more breed groups. The complete list of breeds within a breed group is located on the SGA web site - www.sheepgenetics.org.au.

Merino
All breeds in the Merino segment of the data base are analysed and reported as one breed group. The breeds included are Merino, Poll Merino and Rambouillet. Sheep need to be no less than the 4th cross of these breeds to be reported in the Merino breed group. SAMM and Dohne Merino are not included in the Merino breed group.

Terminal
All breeds in the terminal segment of the database are analysed and reported as one terminal breed group. The breeds include, for example, Dorset Horn, Poll Dorset, Texel, Suffolk and White Suffolk.

Maternal
Each of the breeds in the maternal segment of the database are analysed and reported as a different breed group. The breed groups include, for example, Border Leicester, Coopworth, Corriedale, Australian Finnsheep, and East Friesian.

SAMM
South African Mutton (or Meat) Merinos from different countries are analysed and reported as one SAMM breed group.

Breeding objective:
The goals of the breeding program – a combination of the traits to be selected for and the desired direction.

Breeding value:
A breeding value describes a sheep's genetic performance expressed in terms of the expected genetic performance of its offspring. The breeding value is calculated by a BLUP analysis that can include information on the sheep's own performance and/or its relative's performance. A breeding value is used in this manual as a general term to describe either an ASBV or an FBV.

Clean fleece weight (CFW):
Greasy fleece weight multiplied by the yield of the fleece sample.

Crimp frequency:
Measured crimps per inch at the mid-side along a standard length of the staple using a crimp gauge or as measured by an accredited fleece measurement laboratory.

CTSE:
Central Test Sire Evaluation.

C site:
45 mm from the centre of the spine at the 12th/13th rib, where eye muscle and fat depth is measured by an accredited muscle and fat ultra-sound scanner.

Dam:
A female sheep with progeny data analysed in a particular SGA analysis.

Data Manager:
A person, organisation or business (not defined as a breeder) who provides a service required by a breeder to prepare and submit the breeder's data to SGA in a way that meets QA procedures.

Dataset:
Data provided to SGA for sheep in one or more Management Groups.

Ear tag:
An attachment to the ear of a sheep which, with the assistance of inscriptions on the tag and/or the tag's colour and/or an electronic signal, enable a sheep to be identified within a Management Group and, in some cases, between flocks and breeds.

Ear tag information is readable and/or interrogated electronically. At present, ear tags are the major method used to identify sheep but other devices are also being used, such as electronic implants or rumen capsules. In this manual the term 'ear tag' covers these alternative identification methods.

Environment:
All non-genetic influences that affect a sheep's performance.

ET:
Embryo transfer

Eye muscle depth (EMD):
The depth of eye muscle (Longissimus dorsi) measured at the 'C' site.

Ewe (or female progeny):
A female sheep that does not have progeny in a particular SGA analysis.

Faecal egg count (FEC):
See Worm egg count (WEC)

Fat depth (FAT):
The depth of subcutaneous fat measured at the 'C' site.

FBV:
Flock Breeding Value. The genetic performance (breeding value) reported by SGA that describes the within-flock performance of a sheep for a trait. FBVs can, but do not necessarily allow comparison of sheep across Management Groups within the flock.

Fibre diameter (FD):
Average fibre diameter of a representative sample of wool from a sheep.

Fibre diameter coefficient of variation (CV):
The standard deviation (SD) of fibre diameter (the distribution of fibre diameter) divided by the mean (average) fibre diameter and expressed as a percentage.

Flock:
All the sheep described by a particular breed and flock section of an ID (Flock Code).

Flock code:
see Group.

Flock group:
see Group.

Genetic Advisor:
A person, organisation or business (not defined as a breeder) who provides a service required by a breeder to advise them on genetic aspects of their breeding program.

6.0 GLOSSARY OF TERMS

Genetic correlation:
The genetic relationships that exist between traits.

Genetic group:
see Group.

Genetic linkage:
When two or more flocks share common genes.

Genetic parameters:
The complement of heritabilities, genetic and phenotypic correlations, variance and adjustment factors used in an SGA analysis.

Generation interval:
The time interval between generations, defined as the average age of parents when their progeny are born.

Genotype:
A combination of the genes of a sheep.

GR site:
110 mm from the centre of the spine at the last long rib.

Greasy fleece weight (GFW):
The weight of greasy wool shorn from the sheep before skirting. As long as all sheep at the fleece weighing of a Management Group are treated the same the belly wool can be either included or excluded.

Group:
Group records are required to adequately describe contemporary and genetic grouping of sheep records in the SGA analysis. The group types that need to be submitted to SGA are as follows:

Flock Code
The combined breed and flock sections (the first six digits) of the 16-digit Australian sheep identification (4.1).

Flock Group
A flock group has one or more flock codes that are considered by the breeder to have a comparable genetic group. A flock group will generally only have one flock code but in a small percentage of situations will be more than one.

A flock group can have one or more site codes. A flock code can only exist within a single flock group.

A flock group that contains a single flock code is not required to submit a flock group because in this case the flock group will default to the flock code. If more than one flock code is present in a flock group the group needs to be assigned a code (FG1, FG2, etc)

Site code
Site codes are relevant when a flock group is evaluated at different 'sites'. Sites are locations that are geographically remote from each other. Sites are independent of flock codes and flock groups and therefore two or more breeders can share a site code.

A flock group that is only evaluated at one site is not required to submit a site code because in this case the site code will default to the flock group. However, if a flock group is evaluated at more than one site a site code is required. A general name such as the property name can be used as the site code however it is preferable to use the property identification code (PIC) of the property that is most relevant to the site.

Genetic group
Genetic groups are segments of a flock code (or tiers within a flock code) that, for the traits submitted, are considered to be of significantly different genetic standard.

The vast majority of flock groups will contain a single genetic group.

All sheep can be assigned a genetic group however, where full pedigree exists the assigned genetic group is not used in the SGA analysis.

A genetic group is not applied across flock groups or across flock codes within a flock group.

If more than one genetic group is present in a flock group then each genetic group is assigned a code (GG1, GG2, etc). If only one genetic group is present no code should be submitted.

Genetic groups should only be assigned when there are significant genetic differences within a single flock code or tiers within a flock code. For example, genetic groups would be applied when separate fine and superfine lines are bred within a particular flock code.

Genetic group codes will be used only for SGA analysis and will not be publicly reported in a way that identifies a breeder or individual sheep.

Management Group
When a breeder submits data to SGA the sheep need to be separated into a group known as a 'Management Group'. A Management Group is used to group sheep accurately for an SGA analysis. In addition, the name of the Management Group is used to describe the sheep being submitted and reported.

A Management Group is a group of sheep with all the following characteristics:

a. Born under similar management conditions at one site.

b. Born over a period that is no longer than 42 days.

c. Male or female progeny from one Breed Group. Breeders may submit data that contains both male and female progeny if they have been managed together up to the time when the records were taken. Male and female progeny are often managed together in the period when birth records and weaning records are taken.

Some breeders require additional Management Group records to ensure sheep are correctly grouped in the analysis. Additional Management Group records (see 'Group') are required to be submitted when,

a. a Management Group contains more than one flock code (first six digits of the 16-digit ID).

b. a Management Group contains more than one tier or section of a flock that are considered to be different genetic groups.

c. a flock code is evaluated at more than one site code.

Management Subgroup

If sheep in a Management Group cannot continue to be managed the same way, then two or more Management Subgroups need to be established and recorded to ensure the analysis is correctly carried out.

Each Management Subgroup needs to be recorded within the Management Group by identifying them 1, 2, etc in a Subgroup field. Subgroup records need to be submitted the first time after traits have been evaluated following the establishment for the Subgroups. These codes are only applied by SGA within a Management Group

Heritability:
The average proportion of the difference between sheep (after adjusting for known non-genetic influences) that can be passed on to their progeny.

ID:
Australian sheep identification system 16-digit identification number (4.1).

Live weight (WT):
The weight of a live sheep in Kilograms.

Management Group:
see Group.

Management Subgroup:
see Group.

Merino Superior Sires (MSS):
Publications and activities conducted by Australian Merino Sire Evaluation Association (AMSEA).

Micron:
One millionth of a metre.

Nemesis:
Research and extension project carried out to establish an understanding of the genetics of sheep worm resistance. Nemesis guidelines were the basis for the worm egg count QA standards in this manual and the standards for the measurement of worm egg count. Also see worm egg count.

OVIS:
The name of the BLUP software used to calculate SGA breeding values (ASBVs and FBV).

Phenotype:
The observable performance for a given trait, as measured or scored for a sheep.

Progeny test:
A comparison between the progeny of a group of sires that were mated to randomly selected females. Pregnant females and progeny for all sire groups are run under identical conditions for the period of the test.

Quality:
The ability of a product or service to satisfy its customers.

Quality assurance (QA):
What you need to demonstrate so a product or service will satisfy your customers.

6.0 GLOSSARY OF TERMS

Quality assurance system:
The organisational structure, processes and procedures necessary to ensure the QA intentions and direction are met and the quality of a product or service is assured.

Ram (or male progeny):
An entire male sheep that does not have progeny data analysed in a particular SGA analysis.

Scored traits:
Those characteristics of a sheep that are evaluated subjectively – by hand and/or eye – relative to a set of standards. (4.13)

Selection:
The choice of sheep to be used as parents.

Selection accuracy:
The correlation between true breeding value and estimated breeding value. Selection response is directly proportional to selection accuracy.

Selection criteria:
The traits used to evaluate sheep for a particular breeding objective.

Selection differential:
The difference between the average phenotypic or genetic merit of the selected parents and the average merit of the group from which they came.

Selection index:
A calculation that weights and combines the performance of a sheep for two or more traits to give an overall index value for that sheep. An index value can be used to assist selection for the breeding objective defined by the index. SGA will produce index values by combining ASBVs and/or FBVs.

Selection response:
The effect of selection on the merit of progeny or later descendants, measured as a deviation of the merit expected if parents had been chosen at random, rather than by selection on a trait or combination of traits.

Service provider:
Data manager or genetic advisor who meets the standard required by SGA.

Shearing:
The removal of wool from a sheep by machines, blades or chemical defleecing. The latter can affect the calculation of age and wool growth due to difference in the wool growth being harvested.

Sire:
An entire male sheep that has progeny analysed in a particular SGA analysis.

Site code:
see Group.

TGRM:
Total Genetic Resource Management. TGRM is computer software used to optimise genetic gain and inbreeding.

Tier:
A section of the ewes within a flock group that has been selected for mating and is considered to be of a different genetic standard compared to other sections of the flock group.

Trait:
Traits current able to be submitted or that are reported are described in Table 4.1 in section 4.9 of this manual. A trait name, for example live weight, is often accompanied by a description of the age of evaluation of the trait (also listed in Table 4.1). Reports list both the trait and the age to provide a clear definition of the information reported. The abbreviation of an 'age and trait' is presented by adding the abbreviation for the 'age' in front of the 'trait' abbreviation. For example, hogget (live) weight is recorded as 'HWT'. The current SGA traits and ages are in the tables at the end of this glossary.

Worm egg count (WEC):
A measurement of intestinal parasite load to evaluate worm resistance that is obtained by counting the number of parasite eggs per gram (epg) in a sheep faecal sample collected and measured to Nemesis standards.

Yield:
The proportion of a fleece sample remaining after relevant washing.

Table 6.1 Age names, abbreviations

Age Name	Abbreviation (upper case)	Average age of the group*	Approximate age in weeks or month
Birth	B	birth to 24 hours	
Weaning	W	42 to 120 days	6 to 17 weeks
Early post weaning	E	120 to 210 days	4 up to 7 months
Post weaning	P	210 to 300 days	7 up to 10 months
Yearling	Y	300 to 400 days	10 up to 13 months
Hogget	H	400 to 540 days	13 up to 18 months
Adult	A	540 days or older	18 months or older

*Management Group

Table 6.2 Trait names and abbreviations

Trait Name	Abbreviation (upper case)	Units Submitted	Units Reported
Live weight	WT	kg	kg
Maternal weaning weight	MWWT	Not submitted	kg
Eye muscle depth	EMD	mm	mm
Fat depth	FAT	mm	mm
Greasy fleece weight	GFW	kg	%
Clean fleece weight	CFW	kg	%
Fibre diameter	FD	um	um
Coefficient of variation of FD	FDCV	%	%
Staple strength	SS	N/ktex	N/ktex
Staple length	SL	mm	mm
Worm egg count	WEC	%	%
Number of lambs born	NLB	0 to 4	%
Number of lambs weaned	NLW	0 to 4	%
Scrotal circumference	SC	cm	cm

7.0 QUICK SEARCH

QUICK SEARCH allows you to quickly find a section in the manual that relates to a term of interest to you – the terms are listed alphabetically.

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