final report

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Sheep Genetics – Genomics Pilot Project II

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Sheep CRC
Report on Pilot Projects I, II & III and Large Scale Genotyping Project
August 23rd 2013

1. Introduction

Since the commencement of the Information Nucleus Program in 2007, young rams over a range of bloodlines have been selected on the basis of high levels of performance in at least one trait to be used in the Information Nucleus Flock.

The Information Nucleus comprises eights flocks of ewes across Australia, with a total of 5000 ewes, mated to 100 industry sires annually for 5 years to generate a diverse range of phenotypes and massive amounts of genetic information with which to develop new and improved breeding values, genomic relationships and tests for use by industry.

Sheep CRC has undertaken 4 pilot projects in 2010, 2011 and 2012 to assist with development of these genomic tests for industry. The pilot projects – I, II and III and Large Scale Genotyping allowed the CRC to work with AGBU and Sheep Genetics to fine tune;

- The application of the tests
- Logistics for ordering, payment, sample handling, processing and reporting
- Data integration and analysis
- Reporting formats to breeders
- Working with breeders to model the cost/benefit and improvements in genetic gain that could be achieved with genomic testing.

The pilot projects also provided an opportunity to support breeders undertaking genomic testing for the first time, who were unsure of the processes, requirements or likely outcomes.

Pilot Projects I and II acted as pre-cursors to the more substantial pre-commercial trials in Pilot Project III and the Large Scale Genotyping project. The bulk of this report will relate to the outcomes of Pilot Project III and the Large Scale Genotyping Project (LSGP).

2. Pilot Project I

Pilot Project I demonstrated that data from the 50k SNP-chip can be used in conjunction with conventional genetic parameters to predict breeding values with sufficient accuracies to be of value for early ram selection decisions, including long to measure traits such as adult fleece weight. The Pilot involved some 200 breeders and more than 360 young sires from across Australia having their DNA information incorporated with pedigree and performance data into Research Breeding Values, or RBVs. These RBVs have been produced for a range of existing and new LAMBPLAN - MERINOSELECT traits.

3. Pilot Project II

Pilot Project II was conducted during 2011/12 to build on the learnings from the first pilot and test protocols to form the basis of a future commercial DNA testing service for the Australian sheep industry.

Breeders were encouraged to enter up to 10 Terminal Sires or 20 Merinos. Pilot Project II participants were selected from breeders of the major breeds (Merino, Poll Dorset, White Suffolk, Border Leicester) who use Sheep Genetics (LAMBPLAN or MERINO SELECT); with preference for those involved in Pilot Project I, with at least Bronze Quality data. These requirements were based on the fact that the genomic data was to be combined with pedigree and performance data and computational capability was only established for the LAMBPLAN and MERINOSELECT data bases. 650 rams were entered, with the genomics tests providing information on a range of wool, meat and parasite traits for young rams.

Logistics and sample turnaround times were improved compared to the first Pilot by using blood cards. Participants were provided with more accurate predictions for a broader range of traits with RBVs turned around in 12 weeks. As there was still an element of research involved participants were offered a subsidised rate of $50 per test to participate.

4. Pilot Project III

Pilot Project III built on the earlier trials, providing genomic prediction for new traits including dressing percentage and lean meat yield, together with traits for meat eating quality such as intramuscular fat and shear force that are difficult and expensive to measure. Producers were offered a SNP test for parentage at $17/test; a SNP test for Merino poll/horn for $17/test; and the 50k SNP test for prediction of genomic breeding values for sires at a cost of $50/test (excl GST). In total 1500 50K SNP tests were made available and the project was fully subscribed.

5. Large Scale Genotyping Project

The large scale genotyping project was undertaken to encourage breeders to trial the implementation of genomic testing within their breeding programs. Breeders were encouraged to test a cohort of 2012 drop ram lambs with a view to making early selections which reduces generation interval, positively impacting on the rate of genetic gain. In total 11 breeders and breeder groups participated in the project using 1296 x 50 K tests. In May 2013 the breeders were invited to a workshop to share their experiences and discuss the latest developments with genomic testing. The agenda and workshop reports are provided in Appendix 4a and 4b. Important outcomes of the workshop included;

- The potential for increased genetic gain was highlighted in the scenario modelling presented by Stephen Lee
- Breeders shared their experiences and application of genomic testing with the group
- A range of breeder case studies and scenario modelling needs were identified for Stephen Lee to undertake
- The group committed to meeting again in August 2013 to review further modelling and scenario analysis
- A series of written case studies will be prepared from Stephen Lee's work with breeders.

6. Test Numbers

Table 1 provides a summary of the numbers and types of tests undertaken in each of the Pilot Projects. (Please note that the Parentage & Poll tests are still ongoing so their numbers are not final, report as at 12/08/2013.)

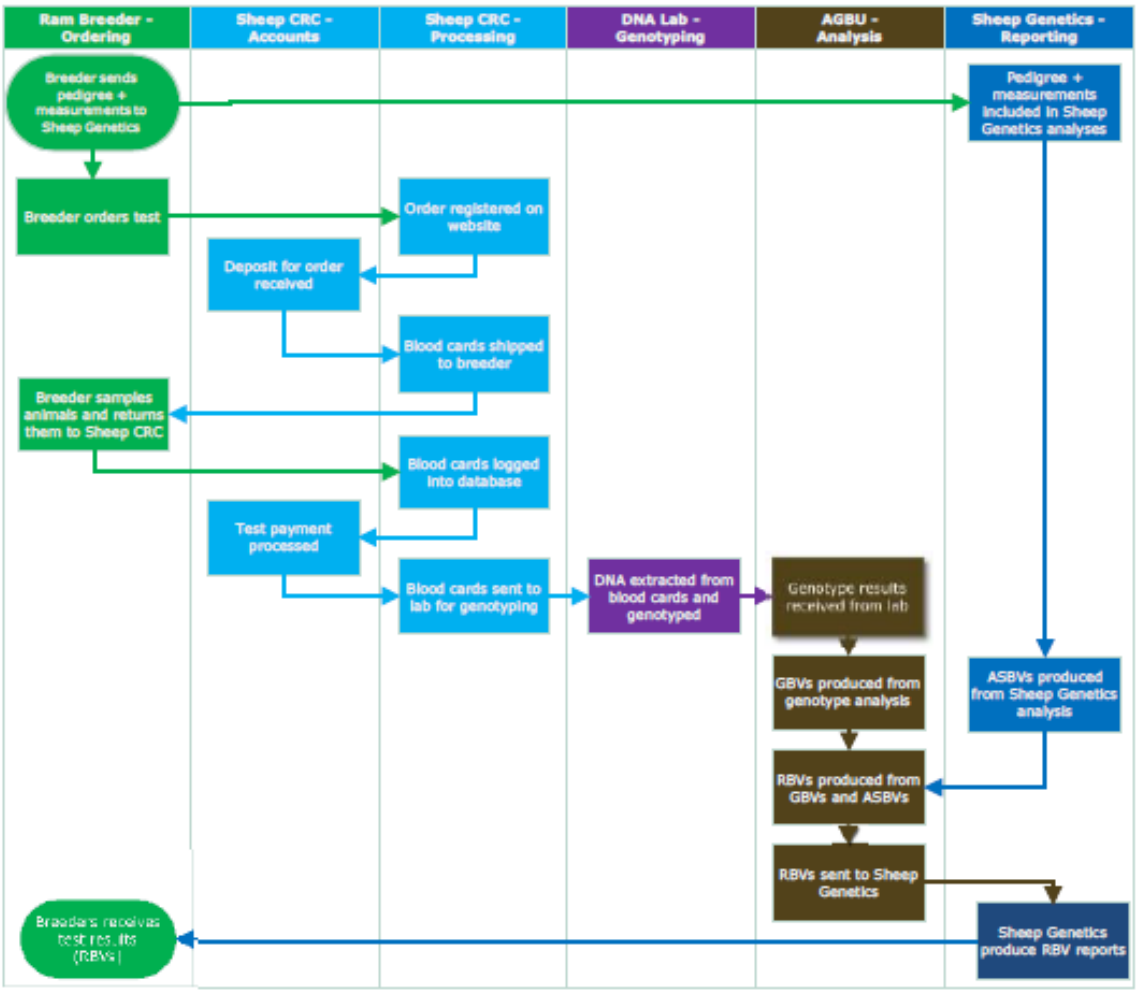
Table 1: Test numbers for Pilot Projects

Test	PP I	PP II	PP III	LSGP
50K	**361**	**806**	**1,462**	**1296**
Parentage - Commercial			14,749	
Parentage - Research			10,155	
TOTAL PARENTAGE			**24,904**	
Poll - Stud Merino Breeders			163	
Poll - Wiltipoll			230	
Poll - Merino			788	
TOTAL POLL			**1,181**	

7. Logistics and Process Overview

Figure 1: is a process map that describes the steps and processes involved in undertaking genomic testing in Pilot Project III and LSGP.

Figure 1: Process Map for Genomic Testing in PPIII and LSGP



The Operations Manual (Appendix 2) provides a detailed description of the processes and logistics of;

- Ordering
- Payment
- Sample collection
- Sample processing
- Sample dispatch
- Data return and reporting

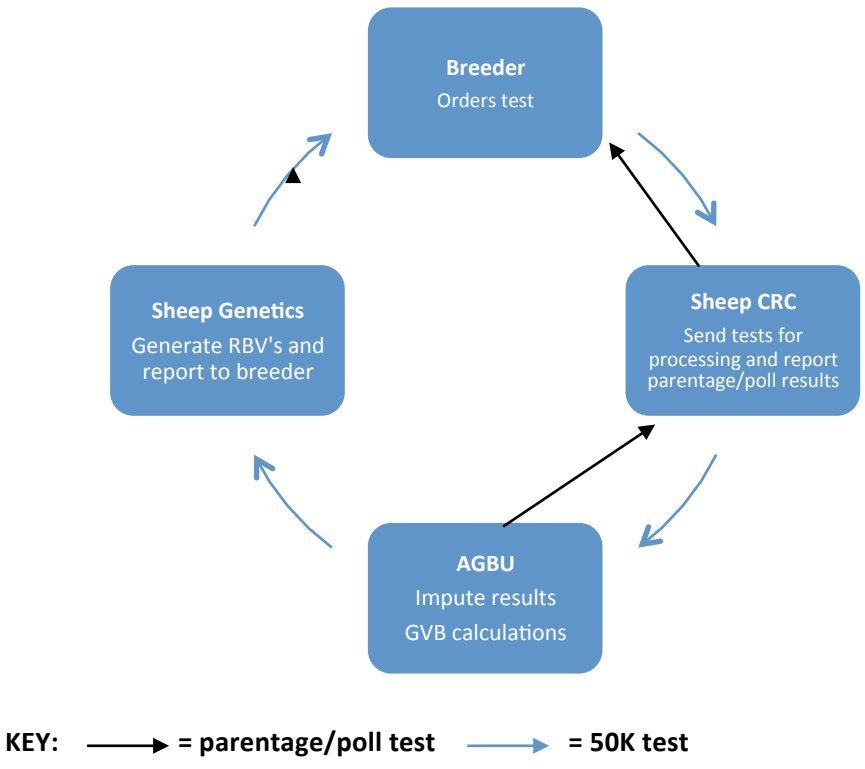
It serves as an invaluable guide to all personnel working to provide the service to industry. The Operations Manual will be regularly updated to keep pace with system improvements as they arise.

Appendix 3 provides copies of the information and registration sheets that were provided to breeders undertaking parentage, poll or 50 K genomic testing.

8. Interactions (CRC / AGBU / SG / Breeders)

The genomic testing process involves interactions between the breeder, the Sheep CRC, AGBU and Sheep Genetics. The diagram in Figure 2 explains the interactions required for delivery of genomic tests to industry. The Sheep CRC is responsible for breeder communication and reporting results to breeders for parentage/poll tests. Sheep Genetics staff are responsible for reporting RBV's, however Sheep CRC staff are jointly responsible for following up issues, such as sheep not being entered in the Sheep Genetics database.

Figure 2: Interactions between organisations to deliver genomic tests



9. Timelines for Genomic Testing

Average times for each stage of the genomic testing process are described below.

1. Sending out blood cards
   Under the current prepayment system blood cards are sent to the breeder within 2 days of ordering.
2. Entering blood cards into the database
   For a 'normal' order with no issues approximately 350 parentage/poll cards can be entered per day, and approximately 250 50K cards per day (these take longer due to the 16 digit ID's). As most orders are well under these numbers most orders with no issues are entered within 2 days.
3. Sending cards to Geneseek
   Once payment has been made by the breeder and cards are entered in the database approximately 800 cards can be sent to Geneseek each day.
4. Geneseek lab processing times
   The average processing time, from when the tests are posted to the when the results are returned has been 28 days/order. Geneseek will not process cards until they have a full batch so delays can occur here when small amounts of cards are sent. A batch is 96 cards for parentage/poll orders and minimum of 24 in multiples of 12 for 50K orders.
5. Reporting to growers
   Parentage results go through quality control and into the parentage test and then results are reported to growers. This takes 2 days with no issues. 50K tests go through an imputation then into a GVB calculation then are merged with the next OVIS run and reported as RBV's to growers by Sheep Genetics. Quality control takes a few hours, the imputation runs over night and the GVB calculation takes a day. As results have to fit in with the timing of Sheep Genetics runs time to report to growers can take up to 4 weeks.
6. Longest and shortest times for each stage of the process
   i. Sending out blood cards -there are usually no issues in sending out blood cards once an order has been placed, blood cards are all sent out within 2 days.
   ii. Entering blood cards into the database - if there is a query with the blood cards returned, the breeder will be contacted prior to entering in the database. Once this is resolved cards are entered within a day.
   iii. Sending cards to Geneseek - delays can occur here if the breeder has not paid for the tests. Cards are not sent to Geneseek until they are paid for. Geneseek will not process the cards until they have a full 'batch'. This is 96 for parentage/poll tests and 24 for 50K tests. The range of processing times from the time the tests are posted to the time the results get back has been 10-64 days. There were large delays over the Christmas / New Year period with some postage parcels delayed in customs for 30 days.
   iv. Reporting to growers – if there are issues with the results orders can take up to 3 days to be finalised before reporting. The main issue is animals that had a 50K test not being entered in the SG database, therefore RBV's are not able to be generated.

10. Dealing with problems, complaints and slow turn around

The main complaints from breeders have been:

- The time taken to receive results
- Test failures and non-assignment

The main reasons for delays have been:

- Breeder not labelling cards correctly – including not identifying which sheep are lambs, which are Sires etc
- Breeder not returning poll/horn scores (SMB & WPT orders only)
- Breeder not paying invoice promptly
- No 16 digit ID provided on 50K blood cards
- Sheep not entered in SG database for 50K tests
- Problems/test failures with genotyping results received from Geneseek
- Non assignment of parentage in the test results
- Person requesting test not the breeder of the animal
- Delays in postage over Christmas period
- Geneseek processing times have not always been within the agreed 10 day period – possibly due to waiting for a full batch
- Reporting issues – industry sires have not been reported to breeders

Table 2 provides information on the number of test failures and non-assignment of parentage

Test	Total tests	Failures – number	Failures – %	Non assignment – number	Non assignment - %
50K – INF, INF2 and Industry Sires	14,633	301	2.1		
50K – PP I, II and III and LSGP	3,925	22	0.6		
Parentage – Research flocks	10,155	143	1.4	149	1.5
Parentage – Commercial tests	14,749	92	0.6	62	0.4
Poll	1,181	27	2.2		

A number of measures have been implemented to address these issues:

1. Turns around times have been clearly communicated on the online ordering system and verification emails so breeders have more realistic expectations.
2. New blood card design will help avoid card labelling errors
3. A new Client Relationship Management system integrated between Sheep CRC genomics staff and SG staff will help with more effective communication and dealing with issues promptly.

4. The test results have been connected to the order number instead of the breeder, so the person who ordered the tests now receives the results.(i.e. if the blood card is sent in by someone other than the breeder it is reported to the breed / flock that belongs with the order number)
5. The verification sent to breeders on entering the data now highlights for 50K tests any animals not in the SG database. This ensures the breeder and genomics staff are aware of the problem and can follow it up.
6. The database has been fixed so Industry Sires test results are now be reported to the breeder.
7. The main reason genotyping and parentage test failures was due to poor samples such as contamination of the blood card by bacteria or mould or inadequate blood on the card. This has been dealt with on a case by case basis. In the majority of cases the Sheep CRC has paid for the animals to be retested. In one case, where the breeder had 29 failures the costs or re-testing were shared between the breeder and the CRC. The protocol clearly explains how to collect blood and dry the cards correctly to minimise contamination.
8. Non assignment of parentage has occurred in a small number of cases. The Parentage Test uses three different analyses to increase the accuracy of the parentage assignment. The Maximum Likelihood Algorithm checks the likelihood of an animal being the parent, compared with the "average parent" and the second most likely parent. The result of the ML test is cross checked against i) the number of opposing homozygotes and ii) correlations between genotypes. Usually these tests are consistent (80% of the time), but occasionally there are inconsistencies.

   The main reasons for non-assignment were;
   - Parent not in the test batch
   - Genotype is borderline (failure is <50% call rate or >60% heterozygosity)
   - Too closely related parents

   The test was designed for testing batches of more than 50 progeny with several candidate parents. The test is not suitable to confirm assignment of one or a few offspring with only one candidate sire. The rules for assigning parentage, with confidence, are that batches have to be larger than 50 progeny and contain at least 2 potential sires/parents. For small batches and confirmation of individual matches (parent + offspring) the recommendation would be to use a test with more markers ie 12 K test.

   Other recent improvements;
   - Discounting information from SNPs that often have a high genotype error
   - Using breed or batch specific allele frequencies for the comparison with an "average parent"

   has decreased the number of problems with non-assignment.
9. Poll Tests
   There were some early issues with failure of the Poll test (16.2%) as a result of a poor call rate on the second SNP. This was corrected in mid-July when GeneSeek changed the chemicals used in the process. The failure rate on the poll test has now dropped to (0.07%).

A list of Frequently Asked Questions and suggested responses is provided in Appendix 1.

11. Recommended timelines for communication with industry

The current turnaround times of 6 weeks for poll/parentage testing and 10 weeks for 50K testing are achievable except when there are insufficient card numbers to make up batches, as has happened at the end of the Pilot Project III. It is recommended that breeders are advised the postage is delayed over Christmas/New Year and to get orders in by the end of November, or expect longer turnaround times.

12. How could we make the process faster?

As breeders get used to the process, delays due to incorrect procedures and breeder error will be minimised. The requirements are clearly communicated in the protocols, however a checklist to be sent with the cards would be useful.

If possible research project cards could be kept to fill batches where breeders send in small numbers of cards. This would minimise delays at Geneseek waiting for full batches.

Currently there is no alert system in place if test results have not been returned within the required timeframe. This would be a useful enhancement to the database.

Obviously if the test was available in Australia postage time would be reduced considerably.

13. Improvements to the process as a consequence of the pilot projects

Listed below is a summary of improvements / changes that were made during the course of Pilot Project III for operational, logistical or administration reasons.

- Originally cards were purchased by breeders for $3 per card. The word deposit was added to the order form and invoices as breeders who had unused blood cards from previous pilot projects often became confused and thought that they didn't have to pay for the full amount of the test. (December 2012)
- The split payment system ($3 on ordering of cards, balance of test charged on return of cards with blood) was changed to a full test amount charged upfront. (January 2013)
- The Blood Collection protocol that is sent with the cards upon initial ordering had edits regarding labelling the cards with the 16 digit Sheep Genetics Animal ID for 50k testing as this was not clearly stated in the original version.
- The Blood card has been re designed.
    - The signature & date were removed.
      A number of items were added:
    - Check boxes for Sire, Dam & Progeny
    - the animal ID was split into the 6 digit Sheep Genetics breed & flock number followed by the Year of Birth & the 6 digit Animal ID
    - The logos were removed and a section was made for the EID barcode if breeders wished to put it on the cards.
    - The instructions on the back of the card were slightly improved.

- The order form that is sent with the cards had the following improvements:
    - Following the upfront payment system being implemented the payment details were removed.
    - A number of questions in particular for Parentage tests were added regarding any close relationships within sires and all potential sire's being submitted.
    - A place for the breeder to sign was added and a box for how many cards they had remaining.
    - A note was added that all animals submitted for 50k testing were required to be in either the LAMBPLAN or MERINOSELECT databases.
    - A sentence was added with the expected turnaround times for the tests (i.e. 6 weeks for Parentage / Poll & 10 weeks for 50k testing).
- The online order form on the Sheep CRC website had the following change made:
    - The 6 digit SG breed & flock was made a compulsory field for 50k orders.
- A number of changes were made to the database throughout the project:
    - A number of reports were developed including a genetic contract report, unpaid cards & unpaid tests, to assist with reporting and number analysis.
    - A sentence was added to the verification email regarding that animals submitted for 50k testing were required to be in the LAMBPLAN or MERINOSELECT databases.
    - A sentence was added to the verification email with the expected turnaround time for the tests (i.e. 6 weeks for Parentage / Poll & 10 weeks for 50k testing)
    - When animals were entered in the database for 50k testing they were cross referenced with the last run of the SG database to check if they had been submitted, if they were not in the database, the animal was then identified by an * on the verification email to the breeder & SG were also notified.
    - To check to see if an animal had been genotyped before a search field was added.
    - A date field was added for when results were reported to breeders
    - Each order placed by a breeder has that breeders 6 digit breed & flock number identified on all animals put in the database under that order. This has eliminated issues with breeders submitting animals that they have not bred and therefore not receiving the results for that animal.
    - 2 fields were added on the database for returned unused cards & destroyed cards for reporting purposes.
- Genotyping Failure Reports for 50k tests are forwarded to breeders as soon as the genotyping results are returned from Geneseek.
- With the upfront payment system implemented, issues that are still being worked through are:
    - In some cases cards have been sent to breeders to speed up the process before any payment is received, should this be the future policy. (Please note that cards are not sent to Geneseek until payment is received)

14. Further Development Requirements

- Upon initial ordering, an invoice has been raised for the amount of tests ordered. This has caused complications when the breeder returns less than what they have paid for and a credit note must be issued. The system would be improved with an initial order being raised in the accounting system, but the invoice not raised until confirmation of how many cards will be returned.

- The recommendations for Parentage Testing will be modified to reflect the risk of non-assignment will small batch sizes and potential parent numbers. With a batch size of less than 50 progeny and only one potential sire the 12K Test is recommended. Alternatively the Parentage Test can be used and then any non-assigned animals can be re-tested using the more expensive 12 K test.
- For individual matches of one progeny and their sire the 12K test is recommended.
- Develop a checklist to be sent out with the bloodcards
- Where possible, retain research project cards to fill small batches sent in by breeders. This will minimise delays at Geneseek waiting for full batches to run tests
- Develop an alert system within the database for for test results have not been returned within the required timeframe.

Appendix 1: Frequently Asked Questions

Logistics

1. Why is there such a long turnaround time?
   Blood cards are sent by airmail to a company based in the USA called Geneseek. It averages around 7-10 days for postage to clear customs and reach Geneseek. Sometimes there are delays in customs especially over holiday periods such as Christmas. Geneseek normally return results in 10-20 days, which we then analysis before reporting to you.

   You should allow 10 weeks turnaround time for 50K tests and 6 weeks for parentage and poll.

   To make the process as quick as possible you should;
   - *Pay for your tests up front*
   - *Ensure that blood cards and paper work have correct 16 digit IDs*
   - *Ensure that the animals being tested are entered into SG database at the same time as you send of the card, with pedigree if you have it.*

2. Why do the Poll and Parentage tests come back in 6 weeks but the 50K SNP tests take 10 weeks.
   The 50K SNP test results need to be combined with your data in LAMBPLAN or MERINOSELECT to generate Research Breeding Values (RBVs). It takes some additional time to do this analysis and appropriate checking, and to fit in with the SG run timing.

3. How do I get a blood sample from the ear?
   Refer to the blood collection protocol in your blood card pack. You need a set of manicure pliers to cut the base of the ear and create a blood flow; these can be brought from a chemist. Ensure that you wash the pliers with antiseptic after each animal.

4. Can I submit semen samples instead?
   No, this test is only set up for handling blood cards.

5. Why do I have to pay for the test before I get the result? Do I have to pay for genotyping failures?
   The CRC has paid for a large number of tests in advance. It is necessary for us to collect the funds from breeders prior to paying Geneseek. Please note that the CRC is providing a significant subsidy on tests in this pre-commercialisation trial.

   In the current pilot project the Sheep CRC have in some cases offered retests at no charge. But in the future yes you will be required to pay for genotyping failures depending on the reason for the failure. Please refer to the Genotyping Failure Policy. Test failures are usually due to insufficient blood or contamination. It is important you collect enough blood to soak through the blotting paper, and that cards are dried correctly. Please refer to the protocol when collecting blood.

6. Do you send the test results to Sheep Genetics?
   In order to generate an RBV from the 50K SNP the data must be sent to Sheep Genetics. For the Parentage and Poll tests the results will be sent directly to you. It will be up to you as the breeder to submit any parentage or poll data to Sheep Genetics.

7. What is a test failure?
   A test failure occurs when a sample cannot be analysed by Geneseek due to contamination of the blood sample with mould or dirt or some other substance. If there is insufficient blood on the card the sample will also be unsuitable for analysis. It is imperative that you follow the protocol provided for collecting and preparing blood cards for DNA testing.

Poll Test

1. Why are there two prices $17 from CRC and $10 through AASMB?
   CRC has made a special offer to AASMB members in order to collect information on the prevalence of the PP genotype in the population and to gather visual horn scores for the animals tested. Stud merino breeders are allowed 10 animals each at $10, more animals can be tested at $17 if required.

2. Why isn't it a Yes/No result?
   This SNP is not the direct marker, or the actual gene causing polled status. However, it is highly associated with polled and horn phenotypes, and is closely linked to the polled gene in this region, which has been independently confirmed in other studies.
   This means that while using this SNP does not result in a simple 'yes/no' outcome, sires with the "PP" genotype will produce significantly more offspring with polled status than sires a 'heterozygous' "PH" genotype or the "HH" genotype.
   As it is a predictive test. See Fact Sheet for more information.

3. Can I test non-Merino breeds?
   Yes the test has been successfully used on Wiltipolls this year.

Parentage Test

1. What is the accuracy of the test?
   a. With blood cards for all sires, dams and progeny (>50 progeny in the batch and at least 2 sires) assignment would be greater than 99%.

   b. With blood cards for all sires and progeny (>50 in the batch, and at least 2 candidate sires) assignment would be greater than 99%.

   c. With blood cards for all dams and progeny (>50 progeny in the batch) assignment would be greater than 99%.

   d. With a highly related or inbred flock.
      The recommendation would be to use the Parentage Test and then re-test any progeny not assigned with the 12K test.

e. A small flock or small sample size (<50 progeny and < 2 potential parents)
The test was designed for batches of more than 50 progeny and 2 or more potential parents. The risk of non-assignment with small batch sizes and few parents is greater. In this situation the recommendation would be to use the Parentage Test and then re-test anything that is not assigned using the 12 K test.

For individual matches of parents and offspring use the 12 k test.

2. Will I get the Poll result of my animals with the Parentage test and will it cost me extra?
Yes, the horn / poll result will be provided with your Parentage results at no extra charge.

3. Can I sample my Sires first and then sample the Progeny later (or vice versa)?

Yes you can sample the Sires / Dams / Progeny in separate Groups. When returning the cards please let us know what animals and order number they are to be matched to.

4. Can I use the test for maternal pedigree if I already know the sire through single sire mating or AI?
Yes, you will need to test all potential dams and all progeny.

5. Can I use the test for paternal pedigree if I already know the dam from pedigree matchmaker?
Yes, you will need to test all potential sires and all progeny.

6. Can I use the test for matching ewes with lambs that fail with Pedigree Matchmaker?
Yes, but will need to test all potential dams and lambs that did not get assigned through Pedigree Matchmaker.

7. Do I need to pay to match progeny to Sires that have been previously genotyped?
You will be charged the test cost ($17) for each progeny and you will need to identify the Sires that have been previously genotyped when returning the progeny cards.

8. If I would like a parentage test on an animal I am 50k testing, will this cost extra?
In this current Pilot Project, we have been doing parentage tests on animals that have been 50k tested at no charge. In the future it is likely that parentage tests / verification on 50k tested animals will incur a small administration fee.

9. I want to be able to match future progeny to Sires/Dams/Progeny I am testing now, will this be possible?
Yes, this will be possible in most cases. It is important that the animal ID is accurate. The best option is for all to be matched to a 16 digit ID. If this isn't possible we need as much information as possible on each animal – e.g. year drop, sex and animal ID that in the future you will be able to identify.

10. What is non- assignment of the test result?

In a small number o f cases the test is unable to assign parentage to the animal sampled. The main reasons for non-assignment are;

- *A blood card has not been provided for all the potential parents of the progeny. The test cannot allocate progeny to parent unless all potential parents are either in the test batch (blood card) or have been previously tested and their individual identification number is provided.*
- *The analysis result does not meet the accuracy/certainty criteria established by geneticists for reporting*
- *The parents are too closely related and it is not possible to differentiate between potential parents*
- *In a small number of cases the candidate group size is too small for the algorithms to provide an accurate result*

It is imperative that all potential parents are provided to get assignment of parentage. It is possible to re-test animals that have not been assigned with a 12 K test.

50k SNP

1. Why can't I test my Dorpers, Dohnes, SAMMs, Texels, Suffolk, East Friesians, Corriedales, Coopworths?
   It is a numbers game; we don't have enough measured animals of breed 'X' to provide reliable RBVs. The current cost of the tests at the moment (>$100) and the numbers of animals required to be measured and genotyped for a breed within a resource flock is not feasible at the moment. It is likely tests will become cheaper in the future which will provide opportunities for smaller breeds to participate in genomics.
   However, they need to have a lot of animals measured and genotyped so it is best to encourage as many people to participate in LAMBPLAN with good records, so that in the future you can sample the young sires and relate them to the data in LAMBPLAN.That way, within the breed there will be a critical mass of samples with measured progeny when the cost of genotyping becomes more useful.

2. What is the "critical mass" of animals that need to be measured in the database to make genomic testing feasible for smaller breeds in the future.
   For a minimum accuracy you need 2,000 genotyped individuals with a phenotype or about 600 sires with 40 progeny each.

3. Can I get results for animals that I have bought as well as bred?
   Yes, when you place an order, all animals that you send blood cards in for under your order number will be reported to the Breed / Flock code that is linked to your order number. Therefore it is essential to provide us with your correct Breed / Flock.

4. If I have bought an animal that has been genotyped before can I have a copy of the animal's RBV's?
   You should be able to obtain a copy of the RBV's from the breeder or previous owner. If not, we will forward you a change of ownership form that you will need to fill out before we can report the RBV's results to you. We do not automatically track ownership; you do need to notify us.

5. Can any sheep get RBV's?
   No, RBVs can only be generated for the four major breeds (Merino, Poll Dorset, White Suffolk and Border Leicester) and for sheep that are in the Sheep Genetics databases – LAMBPLAN and MERINOSELECT or that you intend to enter.You need to be a member of LAMBPLAN or MERINO SELECT.

Appendix 2: Operations Manual

Provided in a separate file.

Appendix 3: Information Sheets

Provided as separate files – examples of these are all in the operations manual
Information sheets for Parentage, Poll and 50K
Registration sheets sent back with data

Appendix 4a: Agenda from Large Scale Genotyping Project Workshop

Large Scale Genotyping in Breeders Flocks
Workshop Number 2
Botany Room Level 1
Stamford Hotel – Sydney Airport
11.30 am May 7th to 2.30 May 8th

Facilitator – Lu Hogan

Purpose:

The workshop is an opportunity to;

- share breeder experiences using genotyping to date
- explore the opportunities and issues associated with implementing genotyping into breeding programs
- discuss the latest developments from R&D
- identify future R&D needs

Day 1 – Tuesday May 7th

	Time	Item	Presenter
1.	11.30	Welcome and Introduction • Summary of issues raised for the workshop	James Rowe
		What has happened so far	
2.	12.00	Breeder Reports on Experiences – covering the following; i. Selection of animals for testing ii. Management groups and data collection iii. How did you use the RBVs? iv. What did or will you do differently as a result of having the RBVs? v. Did you use pedigree and/or poll test results as well? vi. Experiences with the logistics – sample collection, processing with CRC, getting back the results vii. What additional information/support do you need?	Each breeder or breeder group to have 15 minutes Centre Plus MerinoLink AMSEA Hazeldean Super Borders
	1.00	Lunch	
3.	1.30	Continuation of Item 2 Breeder Reports on Experiences – covering the following; i. Selection of animals for testing ii. Management groups and data collection iii. How did you use the RBVs? iv. What did or will you do differently as a result of having the RBVs? v. Did you use pedigree and/or poll test results as well? vi. Experiences with the logistics – sample collection,	Each breeder or breeder group to have 15 minutes Ruby Hills Super Whites Bundilla Pooginook Meat Elite

		processing with CRC, getting back the results vii. What additional information support do you need?	
4.	2.30	Genomics and JIVET i. Selection of animals for testing ii. Management groups and data collection iii. How did you use the RBVs? iv. Using JIVET v. Experiences with the logistics – sample collection, processing with CRC, getting back the results vi. What additional information support do you need?	Andrew Michael and Stephen Lee
	3.00	Afternoon Tea	
		Application to Breeding Programs	
5.	3.30	Usefulness of RBVs • Accuracy with and without genomic tests at 6 and 18 months – current recommendations for application to breeding programs	Andrew Swan
6.	4.15	Incorporating genotyping into current breeding programs (Case study approach) i. Management groups and phenotypic data collection – what might we lose using small numbers of ram lambs in early matings - Sam ii. Weighing up the cost:benefit – reducing generation interval versus loss of accuracy iii. Moving to genomic testing only – no phenotypic data collection. Is this possible in the future?	Sam Gill and Stephen Lee
7.	5.30	Individual meetings - breeders, geneticists.	
8.	6.30	Dinner	

Day 2 – Wednesday May 8th

9.	8.00	Individual meetings - breeders, geneticists.	
10.	9.30	Recap on Day 1 – anything you want to discuss further or need clarification on	
		What happens in the future?	
	10.15	Morning Tea	
11.	10.45	The CRC extension bid – engagement of breeders	James Rowe
11.	11.15	Further research needs – what are the key questions? Key messages for industry?	All
12.	11.45	Future arrangements for DNA testing – who, logistics, costs, turnaround times, breeder support, chip development	Sam Gill
	12.45	Lunch and Close	

Appendix 4b: Report from Large Scale Genotyping Project Workshop

Workshop Report
Large Scale Genotyping in Breeders Flocks

7th and 8th May 2013
Sydney Stamford Hotel

Attendees: James Rowe, Lu Hogan, Rob Banks, Sam Gill, Andrew Swan, Daniel Brown, Sam Clark, Geoff Lindon, Ben Swain, Tom Silcock, Sally Martin, Mark Mortimer, Andrew Burgess, Murray Long, Rick Baldwin, Andrew Michael, Dale Price, Andrew Heinrich, Steve Milne, Stephen Lee, Rodney Watt, John Sutherland, Peter Amer, Roger and Diane Trewicke, Allan Casey, Anne Ramsay, Phil Clothier, Marg Shedden, Fiona McLoughlin

Apologies: Craig Wilson, Matthew Coddington, Jim Litchfield, Wayne Pitchford, Ian Robertson, Bill Webb, Julius van der Werf, Tim de Mestre, Warren Russell, Philip Attard, Neil Johnston, George Carter

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1. **Presentations**
   All presentations are provided as pdfs in separate files
   - James Rowe
   - Centre Plus
   - MerinoLink
   - AMSEA
   - Hazeldean
   - $uperBorder$
   - Bundilla
   - Meat Elite
   - Super Whites
   - Stephen Lee
   - Andrew Swan
   - Sam Gill