GENOMICS FOR THE AUSTRALIAN SHEEP INDUSTRY: FROM DESIGN TO DELIVERY

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SUMMARY

This paper tells the story of translating a scientific concept to commercial scale use of game changing genomic technology within a period of just 6 years. It has involved close collaboration between researchers and end-users of the technology, facilitated by the resources and cooperative structure of the Sheep CRC. The paper explores some of the challenges encountered and the ways in which these challenges were addressed. Key elements of success were considered to be (i) delivery via existing modes, i.e. using estimated breeding values (EBVs) provided through Sheep Genetics, as breeders were familiar with the terminology and source of information; (ii) the delivery of EBVs for new traits created a huge amount of excitement, especially for terminal breeders (they do not have this in most other places, usually same traits); and (iii) the close engagement of breeders as potential end-users of the new technology.

THE INFORMATION NUCLEUS PROGRAM

The project was designed in 2006 when it became clear that searching for genes of major effect in extensive livestock had been largely unproductive and that a whole genome approach in the form of genomic selection was likely to be a more useful approach. The aim was to create a resource for estimating genetic parameters for new traits that could potentially be added to a breeding program using genomic selection, and at the same time serve as a reference population that could be used to predict genomic breeding values of young industry sires, both for existing traits and for those new traits that were considered. This was a world first design in which progeny of sires selected to maximise diversity and genetic potential were measured for the broadest range of traits considered to have commercial or scientific relevance (Banks *et al.* 2006). The size of the Information Nucleus (IN) was chosen to achieve both clear proof of concept but also to have useful accuracy of genomic prediction – even for new traits that had not previously been measured (Van der Werf *et al.* 2010)

Detailed protocols for measurement of each trait were developed by each discipline group across a range of institutions to ensure that all data were collected using identical procedures. Achieving agreement on protocols, submission of data, checks on accuracy and payment details across 6 organisations required a full time project coordinator as well as a database manager but this degree of engagement turned out to be a key to the success of the project. Rapid transfer of data to a central database, prompt data checking and a well-coordinated team of analysts delivered quick feedback of new information to a range of stakeholders as well as providing the basis for a number of research publications. IN data flowed into the database of Sheep Genetics to become part of the national system for genetic evaluation and to add to accuracy of estimated breeding values (EBVs) of many industry sires. Moreover, within a few years, EBVs for new traits were released, and with genotype information based on the 50K Ovine chip (Illumina Inc., San Diego, CA, USA) genomically enhanced EBVs could be released for new traits that had not been measured before on-farm. Figure 1 summarises the flow of data collection across discipline areas as well as its analysis, interpretation and processing to facilitate commercial delivery of new information to ram breeders. It also shows the extremely important step of a pre-determined 'route

to market' through the existing Sheep Genetics organisation with the infrastructure, expertise and industry credibility to introduce new breeding values and introducing the use of genomic information.
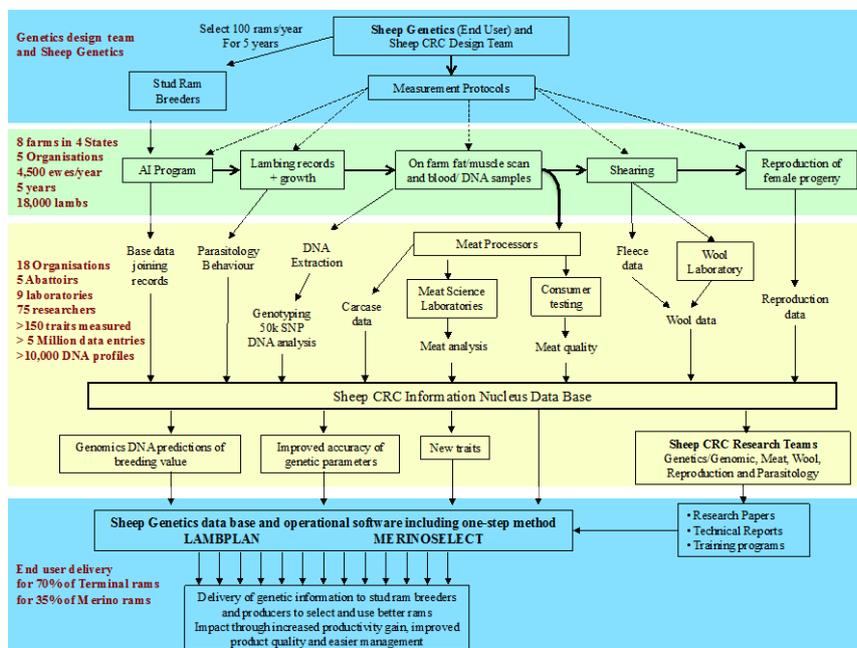

Figure 1. Diagram summarising Information Nucleus program data collection and interpretation

END-USER ENGAGEMENT

   A key component of the success of this initiative has been the early engagement with end-users and maintaining their interest and participation throughout the program. The first step was to work with leading ram breeders to encourage them to provide semen from leading young rams representing a wide range of genotypes from all major breeds. Commitment by breeders to collect semen and provide it to the CRC at significantly discounted rates, was matched by an undertaking by the research team to provide accurate estimates of breeding values on these rams based on their progeny for a very wide range of traits. Ram breeders could see information on their rams changing each fortnight through updates to the Sheep Genetics web site. This near real-time availability of new information provided an unexpected benefit in that breeders were able to provide valuable feedback to the researchers whenever new data entry resulted in unexpected changes to breeding values. This resulted often in adjustment of protocols and data checking routines.

   Breeders became comfortable about the reliability of the IN data and its value in contributing to EBVs for new traits. Many of the sires used in the Information Nucleus program were then widely used in industry to link into other evaluations such as young sire programs. This in turn brought further information into the national database for the rams being used in the Information Nucleus and rapidly expanded the impact of the program. The fact that genomic breeding value from the IN program were separate from Sheep Genetics estimates of Australian Sheep Breeding

Values (ASBVs) for industry rams allowed unbiased validation and the ability to produce unbiased blended breeding values.

The extensive range of measurements on existing and new traits provided the resource material for researchers working in many areas of biology and genetics. For example, the impact of the current breeding program on meat quality traits became clarified and new EBVs gave tools to the industry to turn around any potentially negative correlated selection responses. An improved understanding of the biology of meat quality and delivery of EBVs for new traits created a lot of excitement - particularly for terminal breeders.

COMMUNICATION

From the commencement of the program there has been a well-structured communication plan to keep all stakeholders well informed of the progress, e.g. via letters to breeders who had supplied rams; quarterly newsletters to all organisations involved in the Sheep CRC; and regular media releases with information on significant developments.

Awareness of the potential use of genomic technologies in the dairy and beef industries was a benefit as well as a potential risk. The communication plan was therefore structured in a way that built on the background knowledge from other industries without over-selling the potential benefits. Communicating a time-frame for delivery of new genomic technologies needed a careful balance between maintaining a sense of urgency for the research team and realistic industry expectations.

Field days and the appointment of industry advisory groups played an important role in connecting local producers and ram breeders with the program.

ESTIMATING BENEFITS AND COSTS

Initial estimates of benefits of genomic selection to the Australian sheep industry were reported by Van der Werf (2009) and Banks and Van der Werf (2009). A project initiated by Meat and Livestock Australia set out to document potential benefits of using genomic technologies to individual breeders. This project developed a number of case studies in conjunction with leading ram breeders. Through workshops with the group and with detailed analysis and modelling with each breeder the case studies provided guidelines for cost effective strategies for genotyping and some insight in the price structure needed to make the new technologies commercially attractive to ram breeders. It also provided guidelines for breeders to consider when planning their investment in genomic testing.

GENOMIC PILOT PROJECTS

In early 2010, just 3 years into the project, it became clear that the genomic predictions of breeding values were sufficiently accurate to warrant industry scale testing of the new technology. A subsidized genomic test ($50/test) was offered to clients of Sheep Genetics and a total of 460 rams were tested. One of the major challenges in this first pilot project was the complexity of end-to-end sampling, analysis and reporting. Setting up new protocols for each component of the process was a big job and there were also delays due to a very extensive review of the new genomic breeding values prior to their release.

In 2011 the second pilot project was advertised at the same price of $50/sample. At this stage there was a greater range of traits able to be predicted and increased accuracy for all traits offered. A total of 860 rams were tested and all results were reported well within the 12 week turnaround time specified at the time the tests were offered. Feedback on the service and on the value of the results to breeders was generally positive. In this second trial, DNA sampling was via blood cards, which proved to be a lot more efficient than earlier ear punches or nasal swaps. The sample tracking system was much smoother, and the analysis pipeline was now setup to communicate

much more efficiently with the large industry phenotype and pedigree database, as well as the CRC database with genotypic and phenotypic information from the reference population.

In 2012 the third pilot project was advertised in two parts, one for small-scale sampling (between 10 – 20 tests per breeder) and a commercial scale genotyping/breeding component in which breeders and groups of breeders working together could order up to 200 tests. The cost per test was again set at $50. The 3,000 tests allocated to the 2012 project were fully subscribed within three weeks. An on-line ordering system worked well and many aspects of the sample handling and reporting were also fully automated.

An important component of the 2012 pilot project has been the technical support provided for the 11 breeders participating in the 'commercial scale' component. Each breeder, or group of breeders, has had access to a range of specialist geneticists during planning workshops as well as one-on-one access to a consultant able to help optimise the design of their breeding program to take advantage of genomic information. These case studies will be available for others to use in modifying current breeding programs to include genomic information.

The main benefit of the pilot projects has been to prepare ram breeders and Sheep Genetics for commercial scale application of genomic technology. A second benefit has been the collection of additional genomic information on a wider range of industry rams that have subsequently been widely used and thoroughly measured. This information has been valuable in terms of improving accuracies for some of the more difficult to measure traits such as number of lambs weaned.

CONCLUSIONS - COMMERCIAL TESTING AND FUTURE CHALLENGES

In 2013 a commercial service is being offered by Sheep Genetics based on a combination of a "standard density" SNP test (12k SNP) in combination with the use of 50k SNP tests on some key flock sires. The commercial cost of the test will be around $50 and is consistent with subsidised prices paid in previous years in the pilot projects.

Sheep Genetics client base directly covers approximately 80% of rams produced for prime lamb production and over 30% of Merino rams. It is expected that the results and benefits of the new genomic technologies extend through a large proportion of the rams evaluated through the Sheep Genetics program and therefore through the Australian sheep industry. In large part the benefit of this initiative is a result of the relatively short lead-time from initiating the research to commercial availability of the new product.

Funding of an ongoing resource flock program to maintain genomic prediction accuracies for difficult to measure traits is currently provided through MLA. There is the possibility of increasing numbers of breeders electing to use only genomic information or reducing the amount of data collected in commercial breeding programs. A sustainable financial model is needed whereby a fair value is determined for physical data collection and/or a margin imposed on genomic tests to cover ongoing maintenance of genomic prediction accuracies.

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