

THE INFORMATION NUCLEUS – A NEW CONCEPT TO ENHANCE SHEEP INDUSTRY GENETIC IMPROVEMENT

N.M. Fogarty¹, R.G. Banks², J.H.J. van der Werf³, A.J. Ball², J.P. Gibson³

¹CRC for Sheep Industry Innovation, NSW Department of Primary Industries, Orange, NSW 2800

²Meat and Livestock Australia, C/- University of New England, Armidale, NSW 2351

³School of Rural Science, University of New England, Armidale, NSW 2351

SUMMARY

The Information Nucleus is an innovation for sheep industry improvement that is a program of the new CRC for Sheep Industry Innovation. It will allow breeders to quickly exploit new technology and molecular information to achieve more rapid genetic improvement in the industry. Key young industry sires are progeny tested for an extensive range of traits in widely differing environments. Genetic information will be generated on new traits and those that are difficult to measure commercially. Some of the benefits will flow immediately to industry through enhanced accuracy of Australian Sheep Breeding Values (ASBVs) for current and new traits. The longer term benefits to industry will flow from development of sheep genomic technologies such as whole genome scans and molecular breeding values combined with existing quantitative ASBVs. The Information Nucleus involves mating 100 sires to 5000 ewes annually across 8 sites over the range of sheep production environments in Australia. The progeny represent the major Merino and crossbred types in the industry and will be evaluated for a wide range of growth, carcass, meat, wool, reproduction and parasite resistance traits.

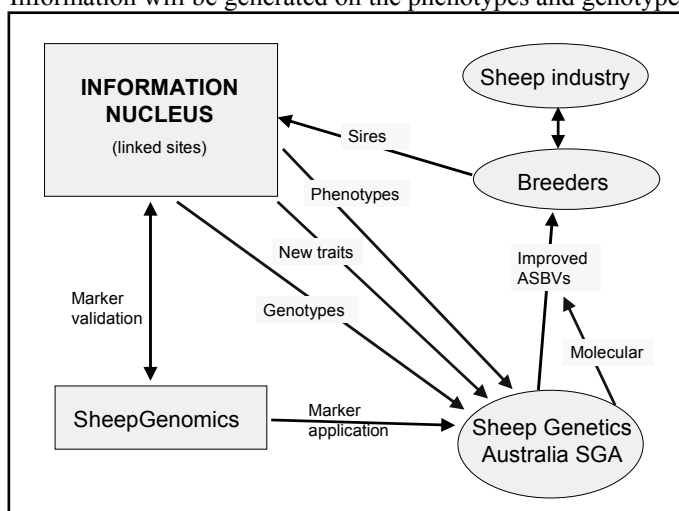
INTRODUCTION

The Information Nucleus (IN) is a major component of the new CRC for Sheep Industry Innovation that has recently obtained Commonwealth funding for 7 years. The IN is an innovation that will provide next generation information to the sheep industry. The concept, first outlined by Banks *et al.* (2006), integrates sophisticated genetic design and analysis with comprehensive measurement of biological and production parameters. It will allow breeders and commercial producers to quickly exploit new technology and molecular information to achieve more rapid genetic improvement in their flocks and across the whole sheep industry. The IN will also provide the base for core research activities in other CRC programs and enhance the application of results from these programs by industry. The three other research programs in the CRC that will be closely integrated with the IN are: Transforming Sheep and their Management, Next generation Wool Quality and Next generation Meat Quality. This paper further develops the design and outlines implementation of the IN.

CONCEPT AND OBJECTIVES

The IN progeny tests key young industry sires for an extensive range of traits in widely differing environments. It operates as a series of flocks at research sites around Australia that are directly linked to breeders and industry through the Sheep Genetics Australia (SGA) database. Information on progeny from the IN flocks will be added to the SGA database to enhance the accuracy of Australian Sheep Breeding Values (ASBV) on animals used by industry (Brown *et al.* 2006). The IN will work closely with Sheep Genomics (Oddy *et al.* 2005; Hynd 2006) to provide information on genetic

markers and validate their utility for industry sheep in a range of environments. The linkages between the IN and the industry breeders, the Sheep Genomics program and SGA are illustrated in Figure 1. Information will be generated on the phenotypes and genotypes of animals directly related to industry



flocks, potential genetic markers will be validated and collaborative research undertaken and applied. Genetic information will be generated about new and novel traits and traits that are difficult or expensive to measure commercially on-farm that are related to breeding objectives for wool and meat quality, parasite resistance and reproductive fitness. This will provide genetic parameters for traits such as wool UV colour stability and human nutritional characteristics of meat and attributes that result in easier care of sheep.

Figure 1. Industry linkages for the Information Nucleus

The IN will capture the power of high density whole genome molecular marker technologies developed by Sheep Genomics that can genotype animals for many traits simultaneously. These high density marker assays based on single nucleotide polymorphisms (SNP) will be validated in the IN. The associations of SNP data with animal performance for a range of traits will be estimated and the algorithms developed to predict breeding values from the molecular data. The methodology will also be developed to combine this molecular and the quantitative information into breeding values that will be delivered to industry through SGA. Gene marker discoveries can be validated in sheep with different genetic backgrounds in a range of environments where they may have different expression.

The specific objectives of the IN include:

- estimation of genetic parameters (heritability, genetic correlations)
- validation of gene markers
- estimation of management effects/treatments
- estimation of genotype x environment interactions
- prediction of whole genome selection and genotyping
- link directly to industry breeding through enhanced ASBVs

DESIGN

There are wide ranging objectives for the IN although the main criteria for the design are generally synergistic. Estimation of quantitative genetic parameters with reasonable precision requires measurement of approximately 5000 animals that are the progeny of 100-120 sires (40-50 offspring per sire) with the sires being randomly sampled from the relevant population. For marker validation about 2000 animals from each sub population need to be tested and should be randomly sampled from a large

number of unrelated sires and dams. Sires need to be used across environments to evaluate genotype x environment interactions and management treatments need to be allocated across families. There is always some compromise between the number of animals and costs involved and the accuracy of results. The broad design adopted involves mating by AI approximately 100 sires annually to 5000 ewes across several sites that are representative of the major sheep production environments. Complete balancedness in sire usage across sites is attempted. The matings are planned for 5 years with linkage of sires across years and further optimisation of the design as results become available.

Key industry sires from several breeds, generally 2-3 years of age, are mated to Merino and crossbred ewes. The progeny represent the major production types in the industry of Merino (MxM), Border Leicester X Merino (BLxM) and Terminal first cross (TxM) and second cross (TxBLM) progeny. The progeny will be evaluated for a large number of growth, carcass, meat, wool, reproduction and parasite resistance traits. The production systems involve the MxM and BLxM ewe progeny being retained for natural mating on at least 2 occasions to evaluate reproduction, lamb production and maternal traits as well as wool traits. The BLxM ewes will be first mated at 7 months of age to evaluate puberty and early lambing performance, whereas the MxM ewes will be first mated at 19 months. The MxM wethers will be retained for shearing at about 10 months, with half then slaughtered as lambs at a target average carcass weight of 21 kg. The other half will be retained for another year and adult shearing to further evaluate wool traits. All other crossbred progeny (TxM, BLxM wethers and TxBLM) will be slaughtered at a target average carcass weight of 21 kg to evaluate growth and carcass traits. These lambs will be slaughtered in collaborating abattoirs where the CRC Meat program will undertake extensive sampling and evaluation of a wide range of new meat traits. The approximate annual numbers of sires and predicted progeny for the various breeds are shown in Table 1.

Generally young sires are selected from within the Merino, Border Leicester (maternal) and terminal sire breeds based on a combination of several attributes:

- High genetic merit for production traits, with significant divergence for key traits e.g. worm resistance, birth weight, leanness, fibre diameter, staple strength, staple length
- Genetic diversity so that a broad range of bloodlines, strains and breeds are sampled
- Linkage to the SGA database including potential future industry influence

Table 1. Approximate annual numbers of sires, ewes mated and progeny of various breeds

Sires and breed	Ewes (breed)	Total (breed)	Progeny	
			Retained ewes	Slaughtered
40 Merino (M)	2000 (M)	1500 (MxM)	750	750
20 Border Leicester (BL)	1000 (M)	750 (BLxM)	375	375
40 Terminal (T)	1000 (M)	750 (TxM)	-	750
	1000 (BLM)	750 (TxBLM)	-	750
Total	5000	3750	1125	2625

IMPLEMENTATION

The IN is run on research sites operated by 5 of the parties in the CRC, with 3 split flocks across 2 sites. The 8 sites in NSW (Cowra, Trangie and Armidale), Victoria (Hamilton and Rutherglen), SA (Turretfield and Struan) and WA (Katanning) cover the spectrum of sheep environments in Australia.

Breeding Program Design Initiatives

The first matings occurred in early 2007 so that progeny are available for evaluation in the research programs in the first year of operation of the CRC. The short time between confirmation of the CRC funding and mating and limited availability of semen and resources meant the numbers of ewes and sires mated in 2007 were slightly reduced. There will be 5 years of sire matings with the final mating scheduled for autumn 2011.

Management of the various sites will be consistent with Lifetime Wool guidelines (Behrendt 2006) and good industry practice for the area, with e-sheep technology and precision management (Rowe 2003) implemented. The IN will provide base resources for the other CRC research programs. These include animals of known genetic background for evaluation of growth, carcass, wool, reproduction and disease resistance. The range of locations and environments provide opportunities for road testing, demonstration and application of technologies from these programs and a point of contact with a wide range of producers.

CONCLUSIONS

The Information Nucleus is an innovation that will contribute to increased genetic improvement in the sheep industry. It will provide genetic information on new traits and those that are difficult to measure that affect meat and wool quality and ease of management of sheep as well as capture the power of whole genome molecular marker technologies. Some of the benefits will flow immediately to industry through enhanced accuracy of the ASBVs provided by SGA, as the progeny test data will be included in routine SGA genetic evaluations in industry. The longer term benefits to industry will flow from development of sheep genomic technologies such as molecular EBVs combined with existing quantitative ASBVs for various traits and validation of individual gene tests developed by Sheep Genomics (Hynd 2006).

ACKNOWLEDGEMENTS

The IN is run with support of the Australian Government's Cooperative Research Centres Program, Australian Wool Innovations Ltd. and Meat and Livestock Australia. Considerable staff and resources are also provided by the parties at each site: NSW Department of Primary Industries, University of New England, Department of Primary Industries Victoria, SA Research & Development Institute and the Department of Agriculture and Food WA. The support of Sheep Genetics Australia in sourcing sires and the breeders who provided semen is appreciated.

REFERENCES

- Banks, R.G., van der Werf, J.H.J and Gibson, J.P. (2006) *Proc. 8th Wld. Congr. Genet. Appld. Livest. Prod.* Belo Horizonte, Brazil, August, CD-ROM Communication 30-12.
- Behrendt, R. (2006) *2006 Agribusiness Sheep Update*, Department of Agriculture Western Australia, July, Perth WA, CD-ROM.
- Brown, D.J., Ball, A.J., Huisman, A.E., Swan, A.A., Atkins, K.D., Graser, H-U., Banks, R., Swan, P. and Woolaston, R. (2006) *Proc. 8th Wld. Congr. Genet. Appld. Livest. Prod.* Belo Horizonte, Brazil, August, CD-ROM Communication 05-03.
- Hynd, P.I. (2006) *Proc. 8th Wld. Congr. Genet. Appld. Livest. Prod.* Belo Horizonte, Brazil, August, CD-ROM Communication 05-06.
- Oddy, V.H., Longhurst, T.J., Nicholas, F.W., Maddox, J.F. and McDonagh, M.B. (2005) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **16**: 209.
- Rowe, J. (2003) *Wool Technol. Sheep Breed.* **51**: 121.