SHEEP GENOMICS – CORE TECHNOLOGIES AND RESOURCES

V.H. Oddy[1], T.J. Longhurst[1], F.W. Nicholas[2], J.F. Maddox[3] and M. B. McDonagh[4]
Sheep Genomics (a joint venture between Australian Wool Innovation (AWI) and Meat and Livestock Australia (MLA)), [1]Meat and Livestock Australia, 165 Walker Street, North Sydney, NSW 2060, [2]The University of Sydney, NSW 2006, [3]Centre for Animal Biotechnology, University of Melbourne, Victoria 3010, [4]Victorian Department of Primary Industries, Werribee, Victoria 3030.

SUMMARY

Sheep Genomics (SG) has been established to draw together people, knowledge and physical resources to exploit genomic technologies for the benefit of the Australian sheep industry. A major start up activity has been to establish access to genomic resources and well characterized flocks to enable genome mapping. This paper describes the approach taken to develop these resources and make them available to an industry focused program.
Key words: genomics, sheep, gene mapping, gene expression, animal resources

INTRODUCTION

There is substantial interest in using genomic technologies for genetic improvement in livestock species. Initial products such as linked markers and causative single nucleotide polymorphisms (SNPs), are already in use in animal breeding (Barendse *et al.,* 2001; Grisart *et al*., 2004). As costs of genome technology reduce, alternate methods of screening for genetic improvement may become available such as expression arrays and rapid quantitative trait loci (QTL) screens (Kraft and Horvath 2003). These technologies will lead to tools to dissect a phenotype into causative mechanisms which should provide methods for more precise selection and higher rates of genetic gain.

Compared with cattle, where there is substantial world-wide investment in genomic tools, there are limited genomic resources for sheep. Sheep Genomics (SG, www.sheepgenomics.com), a joint investment between Meat and Livestock Australia, Australian Wool Innovation and ten different Research Organizations in Australia and New Zealand, was set up to overcome this limitation by bringing together relevant researchers to access, develop and apply genomic tools to important sheep industry traits that have in the past been difficult to address. These traits include host resistance to internal parasites and disease, efficiency of muscle growth, meat quality, quality attributes of wool, reproductive efficiency, and, eventually, mothering ability. Many of the traits can be measured only with considerable practical difficulty (late in life or in only part of the population or after death). Accordingly they are prime targets for a genomics approach. This paper outlines the approach taken by SG to develop genomics resources. A description of the SG host-resistance-to-parasites sub-program (Emery and Beh, 2005) is presented elsewhere.

Resources for sheep genomic research.
The primary resources desired for genomic research are the genomic sequence of the target species in regions of interest, and populations of animals that have wide variance in phenotype and genotype.