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Sheep map: The New Zealand programme to map the sheep genome

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ABSTRACT

Sheep and their products contribute significantly to the New Zealand economy. A map of the sheep genome would accelerate the future genetic improvement of sheep by enabling loci for agriculturally and economically important traits to be identified and manipulated. Such a map would also contribute to the development of gene maps of cattle, goats and deer.

The core of the New Zealand programme comprises two research groups (DSIR and MAF Technology) located at Palmerston North and Dunedin respectively.

Keywords Sheep, physical mapping, linkage mapping.

INTRODUCTION

The primary goal of Sheep Map is to foster, co-ordinate and undertake research to identify, characterise and select for genes responsible for traits of agricultural and economic importance to meet the future needs of the New Zealand sheep industry. Ultimately, the programme’s effort may extend to the manipulation and transfer of genes of importance.

The underlying foundation of Sheep Map is that an accelerated rate of genetic improvement of sheep and the quality of their products will only come from an understanding of the function of the genome which is based, in turn, on the knowledge of its architecture and organisation.

OBJECTIVES

Four major objectives have been identified:

1. The construction of a primary map consisting of 200 markers, evenly spaced across the sheep genome, using physical and linkage mapping techniques.

2. High resolution mapping and sequencing of specific regions of the sheep genome containing genes which have been identified as having major agricultural or economic importance.

3. The establishment of a computerised system to manage mapping data, information and resources.

4. The application of Sheep Map to the genetic improvement of sheep through the development of gene testing and selection procedures.

RESEARCH PRIORITIES

Cytogenetics (DSIR)

The focus of this programme is to standardise banding procedures as well as the classification and nomenclature of ambiguous sheep chromosomes through the use of Robertsonian translocation marker chromosome. Homologies with cattle and goat chromosomes will also be standardised. Robust in situ hybridisation protocols for routinely mapping autologous and heterologous probes to sheep chromosomes are being established. A highly repeated ribosomal DNA probe has been mapped by in situ hybridisation, and several medium and single copy probes are in the process of being localised on specific sheep chromosomes.
Use of Anchor Probes (DSIR and MAF Technology)

This aspect of Sheep Map is proceeding in two directions:

1. Identification and characterisation of mapped anchor probes of human, bovine and murine origin which from comparative mapping information are likely to be located on the three metacentric and five known Robertsonian fusion chromosomes in sheep.

2. Screening for hybridisation stringency and polymorphisms against sheep genomic DNA to select at least two probes for in situ hybridisation to each sheep chromosome. The other probes will be used for Southern blotting to DNA from somatic cell hybrids and from sheep/goat hybrids backcross offspring.

Generation of Interspecies Hybrids (DSIR)

Two collaborations form the backbone of this aspect of the programme:

1. With the Eleanor Roosevelt Institute for Cancer Research, Denver, USA, a hybrid cell panel is being constructed by fusing sheep leucocytes with selected hamster auxotrophs.

   About 30 such hybrid cell lines are being amplified and characterised cytogenetically and biochemically.

2. With the DSIR Grasslands Embryology group and the Department of Animal Science, Massey University, attempts are being made to produce backcross offspring from a fertile female Geep (goat X sheep hybrid) by follicular oocyte harvesting, in vitro fertilisation and maturation.

Generation and Scoring of Polymorphic Probes (MAF Technology)

This approach constitutes the linkage mapping component of Sheep Map. It is proceeding by screening heterologous probes for length polymorphisms using various restriction enzymes and a panel of sheep DNA. Suitable probe and enzyme combinations are being scored across single trait selection families (Booroola and Inverdale high fecundity lines) and analysed for linkage. Isolation of mini- and micro-satellite sequences from sheep DNA and analysis in single-trait selection families for linkage is continuing. Over 30 polymorphic markers have been identified to date.

RESOURCES

Sheep Map is strategically placed to draw upon and contribute to the expertise and skills in molecular biology within DSIR, MAF Technology and the universities and make use of the extensive breeding flocks held by these institutions. The programme is funded by New Zealand Government grants through the Ministry of Research, Science and Technology to the Department of Scientific and Industrial Research and the Ministry of Agriculture and Fisheries. A panel of gene mapping experts from Australia, USA and UK proves operational and strategic advice to the programme.

Additional information may be obtained by contacting the authors.