

New Zealand Society of Animal Production online archive

This paper is from the New Zealand Society for Animal Production online archive. NZSAP holds a regular annual conference in June or July each year for the presentation of technical and applied topics in animal production. NZSAP plays an important role as a forum fostering research in all areas of animal production including production systems, nutrition, meat science, animal welfare, wool science, animal breeding and genetics.

An invitation is extended to all those involved in the field of animal production to apply for membership of the New Zealand Society of Animal Production at our website www.nzsap.org.nz

[View All Proceedings](#)

[Next Conference](#)

[Join NZSAP](#)

The New Zealand Society of Animal Production in publishing the conference proceedings is engaged in disseminating information, not rendering professional advice or services. The views expressed herein do not necessarily represent the views of the New Zealand Society of Animal Production and the New Zealand Society of Animal Production expressly disclaims any form of liability with respect to anything done or omitted to be done in reliance upon the contents of these proceedings.

This work is licensed under a [Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License](http://creativecommons.org/licenses/by-nc-nd/4.0/).



You are free to:

Share— copy and redistribute the material in any medium or format

Under the following terms:

Attribution — You must give [appropriate credit](#), provide a link to the license, and [indicate if changes were made](#). You may do so in any reasonable manner, but not in any way that suggests the licensor endorses you or your use.

NonCommercial — You may not use the material for [commercial purposes](#).

NoDerivatives — If you [remix, transform, or build upon](#) the material, you may not distribute the modified material.

<http://creativecommons.org.nz/licences/licences-explained/>

Genetic analysis in sheep using hypervariable DNA probes

I.F. HERMANS, G.K. CHAMBERS AND T.W. JORDAN

Victoria University, Wellington

ABSTRACT

Hypervariable DNA probes can be used to detect a series of polymorphic markers that are stably inherited and potentially useful in genetic analysis. We have determined the amount of informative polymorphism that would be revealed by these probes if genetic crosses were to be created within and between flocks of Romney sheep selected for resistance and susceptibility to facial eczema.

Keywords Hypervariable DNA; genetic analysis; sheep, facial eczema, polymorphism

INTRODUCTION

Genetic analysis requires a study of the segregation patterns of polymorphic genetic markers. Cloned DNA sequences can be used as markers for the presence of DNA polymorphism. Hypervariable DNA loci are particularly polymorphic as a result of individual variation in the number of repeats of a core DNA sequence. These loci are dispersed throughout the genome and can be grouped into families according to the type of core sequence they possess. Using the Southern hybridisation technique it is possible to detect a whole family of hypervariable DNA fragments using a single radioactive DNA probe containing the common core sequence. It can be assumed that each hybridised DNA fragment represents a single genomic locus which is inherited in a Mendelian fashion (Jeffreys, 1986).

For hypervariable DNA polymorphism to be informative in a genetic cross, both parents must be carrying different alleles for a particular locus, i.e. DNA fragments of different lengths. Following meiosis, the segregation pattern of each allele can be compared to that of the other marker alleles or a given trait. Linked markers have similar segregation patterns.

Animals from facial eczema resistant and susceptible Romney flocks were assessed for the amount of informative DNA polymorphism revealed by three hypervariable DNA core sequence probes.

MATERIALS AND METHODS

Animals were made available from MAF Ruakura resistant and susceptible Romney sheep flocks. DNA was prepared from six animals from each flock, restricted with either *HinfI* or *HaeIII* and electrophoresed through 0.85% agarose. The DNA was transferred to Hybond N membranes (Amersham) and hybridised with one of three hypervariable DNA probes: 33.15 (Jeffreys, 1986); M13 (Vassart *et al.*, 1987); alpha-globin 3'HVR (Fowler *et al.*, 1988).

RESULTS

Animals from the facial eczema resistant and susceptible flocks were assessed for the amount of informative DNA polymorphism revealed by three hypervariable DNA probes. The following points were considered:

1. What was the average number of scorable hypervariable DNA fragments detected per individual (Table 1)?
2. When two DNA fingerprints were compared, what proportion of scorable hypervariable DNA fragments were of identical length in both (Table 2)?
3. If two randomly selected animals were mated, how many scorable loci would prove to be informative in segregation analysis (Table 3)?

TABLE 1 Average number of scorable loci

M13 <i>Hinf I</i>	M13 <i>Hae III</i>	3'HVR <i>Hinf I</i>	3'HVR <i>Hae III</i>	33.15 <i>Hinf I</i>
13.0±3.7	11.5±1.7	10.5±1.6	8.4±1.5	7.0±1.4

TABLE 2 Proportion of hypervariable DNA bands that were of identical length

	M13 <i>Hinf I</i>	M13 <i>Hae III</i>	3'HVR <i>Hinf I</i>	3'HVR <i>Hae III</i>	33.15 <i>Hinf I</i>
Resistant	0.49	0.43	0.63	0.53	0.57
Res x Sus.	0.44	0.62	0.64	0.51	0.61
Susceptible	0.49	0.56	0.70	0.62	0.68

TABLE 3 Number of informative scorable loci per mating

	M13 <i>Hinf I</i>	M13 <i>Hae III</i>	3'HVR <i>Hinf I</i>	3'HVR <i>Hae III</i>	33.15 <i>Hinf I</i>
Resistant	6.5±1.9	4.0±1.0	4.0±0.6	3.2±0.7	3.0±0.6
Res x Sus.	7.3±2.0	4.1±0.6	3.8±0.6	4.1±0.7	2.7±0.5
Susceptible	6.4±1.9	4.9±0.7	3.2±0.7	3.4±0.6	2.2±0.4

DISCUSSION

For the three hypervariable DNA probes assessed the mean number of scorable hypervariable loci ranged from 7-13. If crosses were within the facial eczema flocks, 2-6 loci would prove to be informative per mating. If crosses were made between these flocks, 2-7 loci would prove to be informative per mating.

DNA fingerprints are complex to interpret and we have shown that only a small number of loci will prove informative in these flocks. In contrast, the same three DNA probes reveal 20-30 informative loci per mating in humans (Jeffreys, 1986). Adopting a strategy of linkage analysis with hypervariable DNA probes in these flocks would require development of more probes.

REFERENCES

- Fowler S.; Gill P.; Werrett D.J.; Higgs D.R. 1988. Individual specific DNA fingerprints from a hypervariable region probe: alpha-globin 3'HVR. *Human Genetics* 79: 142-146.
- Jeffreys A.J. 1986. Highly variable minisatellites and DNA fingerprints. *Biochemical Society Transactions* 15: 309-317.
- Vassart G.; Georges M.; Monsieur R.; Brocas H.; Lequarre A.S.; Christophe D., 1987. A sequence in M13 phage detects hypervariable minisatellites in human and animal DNA. *Science* 235: 683-684.