

SCANNING CHROMOSOME 9 FOR QTL UNDERLYING MILK PRODUCTION TRAITS IN SPANISH CHURRA SHEEP

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INTRODUCTION

In recent years, the advent of DNA molecular technologies, specifically PCR, and the appearance of microsatellites as an abundant source of highly polymorphic markers has boosted the generation of linkage maps in sheep and other livestock species (Beattie, 1994 ; Crawford *et al.*, 1995 ; de Gortari *et al.*, 1998 ; Maddox *et al.*, 2001). The availability of these genetic maps jointly with other genomic resources (segregating populations, large insert libraries, radiation hybrid maps, comparative maps, preliminary transcript maps, etc.) has opened the possibility to map by linkage analysis and identify by positional cloning economic trait loci in livestock (Andersson, 2001).

In outbreed populations “daughter design” and “granddaughter design” are well-accepted schemes to identify marker-QTL associations in large half-sib dairy populations resulting from the use of artificial insemination (Neiman-Sorensen and Robertson, 1961 ; Weller *et al.*, 1990). Both familiar designs have been used mainly in dairy cattle with excellent results (Georges *et al.*, 1995 ; Coppieters *et al.*, 1998 ; Ron *et al.*, 2001). In dairy sheep these investigations show larger limitations when compared with dairy cattle. The different production systems applied in each local breed imply lower population sizes with relatively recent implantation of selection schemes. These circumstances do not permit, in most of the cases, a granddaughter design, and the limited size of half-sib families in a daughter design results in a low statistical power of the study. However, many experiments are currently being undertaken searching for QTL in dairy sheep and first results in Churra sheep have already been reported (Diez-Tascón *et al.*, 2001).

Churra sheep is one of the most important dairy sheep in Spain, with a population size of about 800,000 pure-bred animals. A selection scheme for milk production began in 1985 (De la Fuente *et al.*, 1995) on the basis of artificial insemination and progeny test program. The objective of the present study was to identify possible QTL affecting milk production traits in chromosome 9 of Spanish Churra sheep using a daughter design.

MATERIAL AND METHODS

Pedigree material. A total of 807 ewes belonging to 7 half-sib families were analyzed in a daughter design for associations between markers and putative QTL. Average number of daughters per sire was 115 with a range of 65 to 144.

Genotyping and map construction. DNA was isolated from blood samples using standard procedures and transferred to a 96 microwell format. A set of eight microsatellite markers (*OARCP9*, *RHJI*, *MCM42*, *MAF33*, *CSSM66*, *ILSTS011*, *BMS1694*, *MCM63*) was compiled from previously published maps of ovine chromosome 9 (Crawford *et al.*, 1995 ; de Gortari *et al.*, 1998). PCR amplification was carried out in fluorescence-labeled primers and genotypes were interpreted upon a «four colours one-lane» technologie using an ABI377 automatic sequencer. The CRIMAP v. 2.4 program (Green *et al.*, 1990) was used for map construction. Information content mapping was performed according to Kruglyak and Lander (1995).

Phenotypic data and QTL mapping. Three milk production traits were analyzed: milk yield, protein percentage and fat percentage. The quantitative measurements used were daughters' yield deviations (YDs); estimated as weighted averages of ewes' performances expressed as deviations from the population mean. Before averaging, performances were adjusted for the fixed environmental effects described by Diez-Tascón *et al.* (2001). QTL analysis was performed using multi-marker regression (Knott *et al.*, 1996). Chromosomal wise significance levels were determined through permutation (Churchill and Doerge, 1994).

RESULTS AND DISCUSSION

The eight markers were positioned on ovine chromosome 9 yielding a map of 117.7 cM (Kosambi). The mean bracket size was 16.8 cM ranging from 10.1 to 22.4 cM. Figure 1 shows the marker map obtained and the information content for chromosome 9. The information content was over 60% along the entire chromosome.

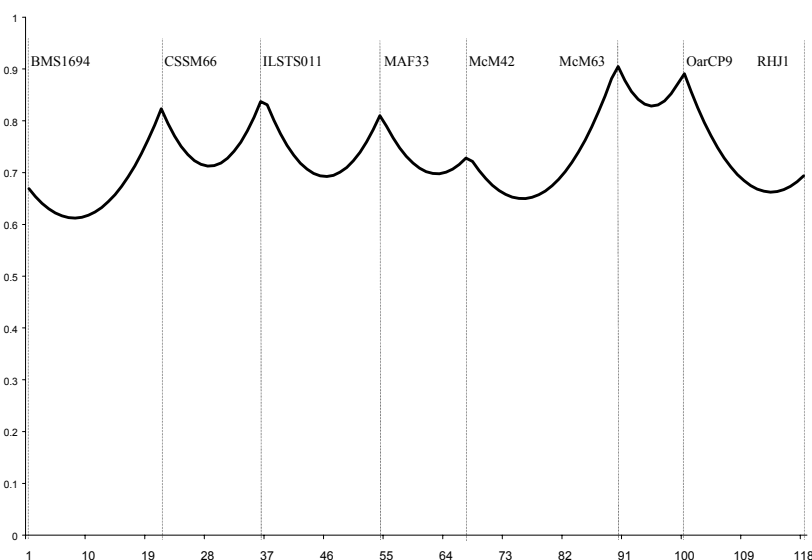


Figure 1. Information content map of ovine chromosome 9

Figure 2 shows the multimarker regression test statistic curves along the map obtained from the across families analysis for milk yield, protein percentage and fat percentage. The analysis revealed in the telomeric region of chromosome 9 (in the bracket limited by OarCP9 and RHJ1 markers) an effect upon fat percentage that exceeded the 5% chromosomewise threshold, suggesting the presence in this region of a QTL influencing this trait.

Regression estimates of QTL allele substitution effects on YDs were obtained in each family at position where F-ratio reached its maximum. The estimates of substitution effects ranged from -0.43% to 0.41% for fat percentage.

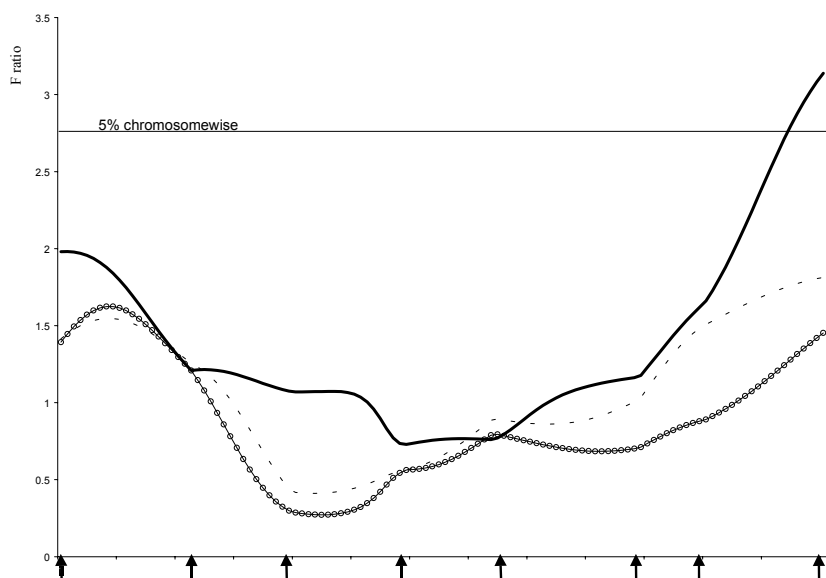


Figure 2. Test statistic curves from the analysis across families for milk yield (---), protein percentage (—○—) and fat percentage (—)

CONCLUSION

The investigation of ovine chromosome 9 for the presence of QTL affecting milk production traits, through the use of a daughter design in Spanish Churra sheep, indicated a location close to the telomeric region with a significant influence on milk fat percentage.

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