

A DESIGN AIMING AT DETECTING QTL CONTROLLING WOOL TRAITS AND OTHER TRAITS IN THE INRA401 SHEEP LINE.

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SUMMARY

An experimental population comprising 30 sires families of 40 halfsibs / sire were used for a QTL detection experiment in a composite sheep line of 50percent Romanov (prolific breed) and 50percent Berrichon du Cher (meat breed). Genetic variability of wool traits was evaluated using an animal model. A first set of 7 out of a total of 64 marker genes was tested on wool traits. Marker gene within sire effect were tested. Heritability and genetic correlations between wool traits (WFD: wool fibre diameter; CVFD: wool coefficient of variation of fibre diameter; SL: staple length) were high: 0.51 to 0.75. Fleece pigmentation score (FPS) had a high heritability (0.72) but was not genetically correlated to other wool traits. A marker located on chromosome 3 had a significant effect on CVFD, SL and FPS within 3, 5 and 4 families respectively, and another located on chromosome 4 had a significant effect on CVFD in 2 families indicating their potential linkage to QTL's.

INTRODUCTION

A QTL detection experiment was organised in a synthetic sheep line (INRA401) between 1994 and 1996. The first aim of this experiment was the search for loci influencing salmonellosis susceptibility and in particular the test of possible effect of polymorphism(s) at the NRAMP1 locus, known to control early infectious step of intracellular pathogens in the mouse (Vidal *et al.*, 1995). Other recorded traits were relative to wool quality, prolificacy, growth and carcass value. We present here the principles of the scheme, and the first results obtained on the wool traits.

MATERIAL AND METHODS

Experimental design.

Population. INRA401 was created in 1969 in France. It is a composite line of 50pcent Romanov (prolific breed) and 50pcent Berrichon du cher (meat breed). The line was considered as a new breed at the 4th intercross generation and closed after 1989 (Ricordeau *et al.*, 1992). The population size reaches 40 000 individuals in 1996, 1700 of the ewes being bred in a nucleus located in an INRA experimental farm (« Domaine de la Sapinière », near Bourges). Selection objectives are mostly maternal traits (prolificacy, growth of the lambs between 10 and 30 days) and meat production traits. This population was chosen as support

for a QTL detection experiment considering its polymorphism and the opposite behaviour of its component breeds concerning salmonellosis resistance (Lantier *et al.*, 1990).

An experimental resource population comprising 30 sire families of 40 halfsibs was created in three batches (autumn 1993 and 1994 : 15 sires, 30 progeny/sire, spring 1993 : 30 sires, 10 progeny/sire, autumn 1993 : 15 sires, 30 progeny/sire). Simulations showed that this "daughter design" should allow the detection of a 1 standard deviation effect QTL located near a biallelic marker locus with a 90 percent power.

Traits. The main traits were indirect measurements of salmonellosis susceptibility. After a number of preliminary experiments, the following protocol was applied : lambs were vaccinated with the vaccinal *Salmonella abortus ovis* strain Rv6 at about 100 days of age (constant weight of 37 and 31 kg for males and females, respectively), and their blood, spleen and popliteal lymph nodes were sampled at slaughtering 10 days later for the measurement of bacterial colonization and antibody responses.

Mid side wool samples were taken from a total of 1292 lambs at 3 months of age. Staple length (SL) was measured. Then after a washing treatment, wool samples were analysed in a textile laboratory (ITF, France) by Optical Fibre Diameter Analyser (OFDA) for determining mean fibre diameter (WFD) and coefficient of variation of fibre diameter (CVFD) according to IWTO-47-95 standard method (1995). OFDA results were based on measurement of 4000 fibre snippets. A single score was allocated for the extend of pigmentation over the fleece (FPS). Score 1 (white coloured fleece), score 2 (white with a few sparse brown patches), score 3 (a mixture of white and brown pigmented patches), score 4 (a mixture of brown and black pigmented patches), score 5 (black and near black pigmented fleece). This score have also been registered on most of the ewes and rams of the flock from 1980.

All lambs were weighed at birth and 45 days of age and at slaughtering. Carcass characteristics were measured at the abattoir, comprising dressing percentage, carcass length and width, conformation score, external fat depth, fat score, area of loin-eye muscle.

Markers. Markers of NRAMP locus have been made available in sheep (Pitel *et al.*, 1996), with 2 microsatellites within or very closed to the gene. A first panel of 64 microsatellites from the sheep or bovine species has been set up after being tested as multiplexes for amplification and polymorphism with sheep DNA's. A first set of 7 markers, located on ovine chromosomes 2, 3, 4, 5, 12 and 13 has been tested on the 1200 lambs, their dam and sire (OarFCB020, MAF050, HUI625, OarAE129, BMC1009, MCM218 and IL2RA located on the sheep genetic map by Crawford *et al.*, 1995).

Estimation of genetic parameters and QTL's detection

The estimates of variance components for prolificacy, milking ability, wool traits and fleece pigmentation score were obtained by using VCE, a multivariate multi model REML variance component estimation (Groeneveld, 1996) with an animal model. The random part of the model included a direct additive genetic effect of the animal on all analysed traits, plus a

maternal additive genetic effect on 10-30d daily growth rate and a permanent environmental effect on prolificacy as up to 6 lambing performances were recorded per ewe.

The following linear mixed model was used:

$$Y_i = X_i \beta_i + Z_i a_i + K_i m_i + W_i p_i + e_i$$

where

Y_i is a vector of animal records for the i^{th} trait,

β_i is a vector of fixed effects for the i^{th} trait consisting of sex, year-management group, ewe parity, dam parity, number of suckling lambs, birth-suckling pattern and age at wool sample.

a_i is a random vector of direct additive genetic effects of animals for the i^{th} trait,

m_i is a random vector of maternal additive genetic effects for the i^{th} trait,

p_i is a random vector of permanent environmental effects of ewes for the i^{th} trait,

e_i is a random vector of residuals for the i^{th} trait.

X_i , Z_i , K_i and W_i are corresponding matrices for trait i .

Detection of QTL on fineness, coefficient of variation of fibre diameter, staple length and fleece pigmentation score was undertaken by using a fixed model variance analysis. For each trait and each marker, this model included same known fixed effects as previously for estimation of genetic parameters, plus two additional fixed effects : a sire effect and the within sire effect of the marker allele received by a progeny from its sire (Neimann-Sorensen and Robertson, 1961).

RESULTS AND DISCUSSION.

Genetic variability of wool traits are shown in table 1. Heritability estimates of wool traits are high (from 0.52 for SL to 0.75 for CVFD), and genetic correlations between wool traits are positive and moderate. These heritability estimates are a little higher than expected or observed in literature but in agreement with most of studies in sheep (Fogarthy, 1995). No earlier estimations have been ever made on this INRA 401 sheep which has never been selected for wool traits. Heritability estimate of FPS is very high with no significant genetic correlation between fleece pigmentation score and the other wool traits (table 1).

Table 1. Estimates of heritability (h^2 on diagonal), genetic correlations (above diagonal), mean fibre diameter (WFD), c.v. of fibre diameter (CVFD), staple length (SL) and fleece pigmentation score (FPS)

h^2	WFD	CVFD	SL	FPS
WFD	0.62	0.51	0.58	0.22
CVFD		0.75	0.56	0.03
SL			0.52	0.18
FPS				0.72

Heritability and common environment ratio of prolificacy are low (0.08 and 0.09 respectively). Milking ability heritability of ewe evaluated as the maternal genetic components of 10-30d average daily growth is high (0.25) with a low lamb heritability (0.13). These estimations are in agreement with previous studies. Genetic correlations between most of wool traits and the 2 other important traits *i.e.* prolificacy (range: 0.11 - 0.34) and 10-30d average daily growth (range: -0.30 - 0.03) are low and non significant. These results would justify that wool traits can be improved by selection without any major effect on prolificacy, milking ability and growth rate which remain the main selection goals in the INRA401 sheep.

BMC1009 marker (Chr. 3) had a significant within sire effect on CVFD ($p < 0.05$), SL ($p < 0.01$) and FPS ($p < 0.05$). According to the marker allele transmitted by their heterozygous sire, significant differences were observed within 3, 2 and 5 offspring respectively. These within family sire differences extended from 0.8 to 1.3 sd.. Because microsatellite BMC1009 has been located close to the keratin gene KRT2 (Maddox *et al* 1996, Size *et al.*, 1996), this gene could be a good candidate for the BMC1009 associated QTL. Other results have previously demonstrated a linkage between high-glycine-tyrosine keratin gene loci and wool fibre diameter (Parsons *et al* 1994). Another marker, MCM218 (Chr. 4) had a significant effect on CVFD ($p < 0.05$) within 4th offspring. Polymorphism at this loci have been recently studied (Hulme *et al* 1996) but up to now no linkage was observed with a wool trait. Our results would indicate that BMC1009 and MCM218 markers located on different chromosomes are linked to different QTLs controlling wool traits. These results are consistent with initial simulations which have shown that such a "daughter design" should allow detection of 1 standard deviation effect QTL located near a biallelic marker locus.

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