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QTL affecting conformation traits in Angora goats

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Abstract

A genomic screen for quantitative trait loci (QTL) affecting conformation traits was performed by genotyping 288 Angora goats offspring from 8 half-sub families with 76 microsatellite markers. The following traits were recorded: weaning weight (WW, Kg); stature (S, cm); chest depth (CD, cm); shoulder width (SW, cm); rump length (RL, cm); rump width (RW, cm); head length (HL, cm); head width (HW, cm); shin circumference (SC, cm); chest circumference (CC, cm) and body length (BL, cm). Data were analyzed using the *QTL Express* program. A total of 5 QTL were detected in five chromosomes with chromosome wide significance level. For the 11 analysed traits the results were: evidence of two possible QTL for HL were found in chromosomes 1 and 4, a putative QTL for trait CD was found in chromosome 2, evidence for BL was found in chromosome 8 and a possible QTL was found for trait CC in chromosome 9. The results reported here show the existence of chromosomal regions in Angora goats involved in conformation traits and represent the first in depth search in some specific-genome sections in order to identify and characterize the genetic variability involved in these traits.

Keywords: QTL; Conformation traits; Angora goats; Microsatellites

1. Introduction

Body weight or size in general has long been considered as a paradigm for quantitative inheritance. It is normally distributed and seems to be controlled by many genes, each with relatively small additive effects on the phenotype (Falconer and Mackay, 1996).

The development of molecular biology techniques and the application of these techniques to farm animals have progressed rapidly in the last years and have opened new perspectives for gene identification of underlined quantitative traits. Dense marker maps and advanced statistical methods have made it possible to search for quantitative trait loci (QTL) over the whole genome and have allowed the measurement of individual gene effects on complex morphological traits.

Studies aimed at detecting QTL for growth and conformation traits in cattle have been successfully conducted in the last years (Stone et al., 1999; Schrooten et

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al., 2000; Casas et al., 2003; Kim et al., 2003; Boichard et al., 2003; Hiendleder et al., 2003). In goats a comprehensive genetic linkage map has been developed (Vaiman et al., 1996; Schibler et al., 1998) and due to the high homology with cattle genetic map some QTL could be found to be homologous between both species, cattle and goat.

In Angora goats, putative QTL affecting fleece traits were reported by Cano et al. (2007). Making use of the resource created by the Angora Dispersed Nucleus in Argentina (Abad et al., 2002) an experiment was designed in order to search for QTL affecting conformation traits. We present here the results of an initial genome-wide scan, using 76 microsatellite markers in 8 half-sibs Angora goat families for 11 conformation traits.

2. Materials and methods

2.1. Animals and conformation traits

The population analyzed was the same as reported by Cano et al. (2007). At weaning, the following conformation traits were recorded: weaning weight (WW) expressed in kilograms; stature (S); chest depth (CD); shoulder width (SW); rump length (RL); rump width (RW); head length (HL); head width (HW); shin circumference (SC); chest circumference (CC) and body length (BL), all of them measured in centimetres. All conformation traits were taken by the same operator and follow the methodology by Herrera et al. (1996).

2.2. Microsatellite genotyping

DNA isolation, microsatellite panel from the goat genetic map (Vaiman et al., 1996; Schibler et al., 1998) and PCR conditions were described by Cano et al. (2007).

2.3. Statistical analysis

Analyses were done with the program *QTL Express* (Seaton et al., 2002—http://qtl.cap.ed.ac.uk/).

The fixed effects, sex, year of birth (2000–2001), birth type (single or double) and flock effects (8 levels) were included in the model. Appropriate *F*-statistic thresholds for chromosome wise type I error rates were generated by permutation test of 10,000 iterations (Churchill and Doerge, 1994). Confidence intervals were calculated by Boostrap analysis (Visscher et al., 1996). Estimates of QTL contributions to the QTL variance (%) were estimated in an analysis across family. The effect/standard deviation were calculated as the QTL effect scaled in within informative family analysis.

3. Results

In Table 1 phenotypic measurements (means and standard deviations) for the eight families progenies are shown.

In the first step a panel of 120 microsatellites was run in the 8 bucks. After taking account of the polymorphic information content (PIC) (Botstein et al., 1980), the allele number and heterozygocity by microsatellite, a set of 76 markers were selected to genotype the 288 offspring in 21 autosomes.

Number of markers used, chromosome length, proportion of sire heterozygous and marker name by chromosome are show in Table 2.

Based on the goat genetic map (Vaiman et al., 1996; Schibler et al., 1998 http://locus.jouy.inra.fr) the esti-

Table 1
Phenotype data (means ± S.D.) of the progeny of the eight Angora goat families

Trait	Family 1 (25)	Family 2 (71)	Family 3 (28)	Family 4 (24)	Family 5 (42)	Family 6 (31)	Family 7 (41)	Family 8 (26)
WW (kg)	18.7 ± 4.5	18.3 ± 3.1	17.3 ± 3.4	15.6 ± 1.8	19.2 ± 3.8	19.9 ± 2.7	18.0 ± 4.0	16.5 ± 5.7
S (cm)	46.4 ± 3.7	47.3 ± 3.9	43.6 ± 4.9	41.8 ± 3.6	46.4 ± 4.1	46.6 ± 3.8	44.1 ± 3.7	46.5 ± 4.0
CD (cm)	21.2 ± 2.0	21.1 ± 2.0	19.9 ± 2.0	20.0 ± 2.5	21.8 ± 1.6	21.7 ± 1.3	21.0 ± 1.5	20.7 ± 1.8
RL (cm)	15.0 ± 1.7	16.0 ± 1.1	14.1 ± 1.9	13.8 ± 1.4	16.2 ± 1.5	16.5 ± 1.1	16.3 ± 1.3	15.9 ± 2.0
RW (cm)	11.0 ± 1.0	11.1 ± 1.7	11.0 ± 1.2	10.2 ± 1.1	11.3 ± 1.2	12.0 ± 1.0	11.7 ± 1.1	12.1 ± 1.3
SW (cm)	15.0 ± 1.5	14.9 ± 1.5	14.1 ± 1.9	14.6 ± 1.3	15.0 ± 1.7	15.2 ± 1.3	15.3 ± 1.8	15.6 ± 2.6
HL (cm)	15.2 ± 0.9	15.2 ± 1.4	14.9 ± 1.7	15.4 ± 1.7	15.7 ± 1.7	14.8 ± 1.2	15.0 ± 1.4	14.7 ± 2.1
HW (cm)	10.5 ± 1.6	10.2 ± 0.5	10.0 ± 0.7	10.0 ± 0.4	10.1 ± 0.4	10.4 ± 0.5	10.3 ± 0.7	10.2 ± 0.8
SC (cm)	6.9 ± 0.6	7.1 ± 0.5	6.7 ± 0.4	7.0 ± 0.7	7.0 ± 0.4	7.3 ± 0.5	7.3 ± 0.6	7.7 ± 0.4
CC (cm)	66.9 ± 8.5	66.8 ± 5.2	62.3 ± 6.3	61.1 ± 5.3	67.2 ± 5.6	68.2 ± 5.0	67.7 ± 5.1	65.5 ± 9.2
BL (cm)	56.9 ± 4.9	54.8 ± 4.3	53.0 ± 5.3	52.5 ± 3.9	54.6 ± 4.8	54.5 ± 4.3	54.8 ± 4.6	55.2 ± 5.4

(*n*) Progeny numbers; WW, weaning weight; S, stature; CD, chest depth; RL, rump length; RW, rump width; SW, shoulder width; HL, head length; HW, head width; SC, shin circumference; CC, chest circumference; BL, body length.