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SHORT NOTE [NOTA CORTA]

DETECTION OF QTL AFFECTING FLEECE TRAITS ON CHI 19 IN ANGORA GOATS

[DETECCIÓN DE QTL QUE AFECTAN LOS CARACTERES DE LA LANA EN CHI 19 EN CABRAS DE ANGORA]

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SUMMARY

Some previous studies have indicated the presence of genes or gene families involved in fleece traits in different species. The aim of the present study was to search Quantitative Traits Loci (QTL) associated with fleece qualitative and quantitative traits on goat chromosome (CHI) 19. The population analyzed had a total of 727 kids from 17 Angora bucks. Nine phenotypic fleece traits were recorded. An interval analysis was performed under a half-sib model using the QTL Express program. Our results confirm a QTL for Coefficient of Variation of Average Fiber Diameter (CVAFD) and we found new QTL for Staple Length (SL) and Greasy Fleece Weight (GFW). Further investigations should concern diminishing the confidence interval increasing the number of kids in existing families and making a fine mapping on the candidate region.

Key words: *Fleece traits, Angora goat, QTL, Microsatellites*

INTRODUCTION

In recent decades, the molecular biology techniques developed have made possible to construct comprehensive marker maps in different species which allow mapping of Quantitative Traits Loci (QTL) influencing economically important traits, including fleece and wool traits. Some previous studies have indicated the presence of genes or gene families involved in fleece traits in sheep (reviewed by Purvis and Franklin, 2005), and the hair in human (Rogers et al., 2004) and mice (Pruett et al., 2004). In a genome screen for QTL in Angora goats, Cano et al. (2003, 2007), reported the first results on putative QTL affecting Coefficient of Variation of Average Fiber Diameter (CVAFD), percentage of fiber kemp (KEMP), percentage of Discontinuous Medullated Fibers (DISC) and Staple Length (SL). The aim of this study was to identify QTL affecting fleece traits in the interstitial region on CHI19, using microsatellites and enlarged families in Angora goats.

MATERIALS AND METHODS

Animals and Phenotype Traits. The population analyzed had a total of 727 kids from 17 Angora bucks. The number of half-sib offspring per buck ranged between 10 to 85 kids. The population was created in seven batches (years 2000 to 2005).

Mid-side fleece samples were taken from kids at 4 and 11 months of age. Eight phenotypic fleece traits were recorded, at 4 months old (^{1}) and at 11 months old (^{2}): Average Fiber Diameter (AFD; µm), Coefficient of Variation of AFD (CVAFD; %), the percentage of fiber with diameter over 30 µm (F30), percentage of kemp fiber (KEMP; %), percentage of Continuous Medullated Fibers (CONT; %), percentage of Discontinuous Medullated Fibers (DISC; %), Staple Length (SL; mm), the Average Curvature of Fiber (ACF; deg/mm) and Greasy Fleece Weight (GFW, kg-recorded only at 11 month old).

Microsatellite genotyping. The DNA isolation and PCR conditions were the same as described by Cano et al. (2007). Five microsatellite markers distributed over 25 cM on chromosome CHI19 were used (IDVGA46, LSCV36, BP20, MAF48 and OarFCB193) from the available web goat genetic map (http://locus.jouy.inra.fr/). PCR products were then run on a ABI3130xl Genetic Analyser sequencer (Applied Biosystems). Raw data were analysed with Genemapper v4.0 software (Applied Biosystems).
Statistical Analysis. An interval analysis was performed under a half-sib model using the QTL

Express program (Seaton et al., 2002), at: http://qtl.cap.ed.ac.uk/. The fixed effects included in the analysis were: sex, year of birth (2000 - 2005), birth type (single or twin) and flock (8 levels). To estimate the confidence intervals (CI) of the QTL locations the LOD drop-off method developed by Lander and Botstein (1989) was used.

RESULTS AND DISCUSSION

According to the web genetic map the interval between the markers used was in average 6.25 cM (from 4 to 9). Table 1 shows only the traits with significant effects under the "one QTL model" at P<0.05 chromosome-wise level on CHI19.

Figure 1 shows the plot of the F-statistics significant traits found in CHI19. These results allow us to confirm a QTL affecting CVAFD in Angora goat on CHI19 (Cano et al., 2003). Besides, we found two new putative QTL affecting SL[1] and GFW[2] on CHI19**.** Taking into account the homology between sheep and goat maps (Maddox et al., 2005) and the conserved segments between the human and ruminant (Schibler et al., 1998), the QTL found here could be related with keratin-associated proteins (KRTAP) and keratin (KRT) genes family as pointed out by McLaren et al. (1997) and Roger et al. (2001). McLaren et al. (1997) mapped several high-glycine-tyrosine keratin-associated proteins and keratin (KRTAP1, KRTAP3 and KRT1) genes on sheep chromosome 11 (OAR11). In human, keratin (KRT) gene domains were assigned to bands q21 and q22 on chromosome 17 (HSA17) (Roger et al., 2004). These bands show homology to the interstitial region of CHI19 (Schibler et al., 1998). The putative QTL reported here, could be related with those KRT and KRTAP genes family. KRT and KRTAP genes could be good candidates for the associated QTL on CHI19.

Further investigations should concern diminishing the confidence interval increasing the number of kids in existing families and making a fine mapping on the candidate regions before these results can be used in breeding via Marker Assisted Selection (MAS).

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Table 1. Significant effects for the one-QTL model at the P<0.05 chromosome-wise level on CHI19.

Putative QTL	CVAFD[1]	SL[1]	GFW[2]
Closest marker	**MAF48**	**IDVGA46**	**MAF48**
Position (cM)	49	28	50
Length CI[a]	12	~11	~15
F-statistic	2.3	2.1	2.7
Number of informative families	3	3	1
QTL variance (%)	8.1	7.6	9.3
Effect/SD	0.9/1.1/1.4	1.1/1.1/1.3	1.4

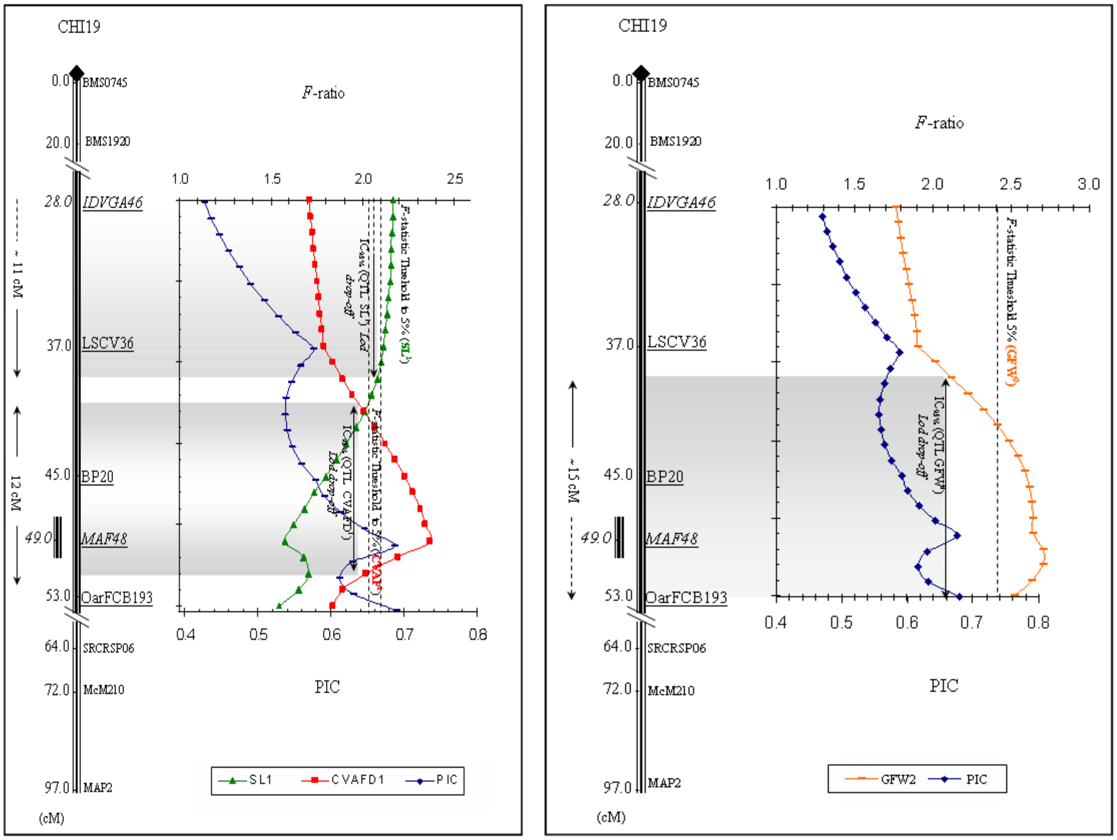
Chromosome-wise *F*-statistic threshold at the P<0.05 level QTL, as determined by permutation test 10.000 iterations, each 2 centi-Morgan (cM).

(a) 95% LOD drop-off confidence interval (CI) in cM.

[1] Fleece samples taken at 4 month

[2] Fleece samples taken at 11 month

Figure 1. Map of the F-statistics depicting the positions of putative QTL (4 and 11 months of age) in Angora goat on CHI19 on the chromosome (CHI) the markers used. The level is provided for P<0.05 (dashed line) chromosome-wise significance.



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