Detection Of QTL Affecting Fleece Traits On CHI5 In A Backcross Angora x Creole Goats In Argentina - Preliminary Results

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Introduction

Some previous studies have indicated the presence of genes or gene families involved in fleece traits in sheep (reviewed by Purvis and Franklin, 2005). Compared to with other livestock species, there is very limited published literature on QTL identification in goat populations. A genome examination for QTL in Angora goats conducted by Cano *et al*. (2007) and Marrube *et al*. (2007) reported the first results on putative QTL affecting fleece and conformation traits. Recently, in a partial genome examination Mohammad Abadi *et al*. (2009) also reported putative QTL affecting growth and cashmere yield in Rayini goats.

A QTL detection experiment was organized in a backcross Angora x Creole goats resource population. Angora and Creole goats breeds differ for fleece characteristics. The Angora goats have a single hair coat and the mohair fiber is highly valued due to its resistance, flexibility, softness and luster. The Creole goats have a double hair coat: cashmere, fine and short seasonal down coat and coarser and longer guard hair. In this study, we report the results obtained in the search of QTL affecting fleece traits on chromosome 5 (CHI5) in a backcross goats population resource.

Material and methods

Experimental design. The backcross used was generated as follow: 5 Angora rams were mated at random with 23 Creole goats producing 35 F1 kids. In the next year 5 F1 male were mated with 140 Creole female to procreate 354 backcross kids. The population was created in three batches (years 2006 to 2008).

Fleece traits measurements. Mid-side fleece samples were taken from kids at 6 months of age. Fleece samples were analyzed at the Textile Fibers Laboratory of INTA Bariloche. Thirteen phenotypic fleece traits were recorded, average fiber diameter (AFD), coefficient of variation of AFD (CVAFD), proportion of fibers over 30 microns (F30), continuous medullated fibers (CONT), discontinuous medullated fiber (DISC), kemp fiber (KEMP), down diameter (DD), hair diameter (DP), down proportion (PD), average curvature of fiber (ACF), staple length (SL), greasy fleece weight (GFW) and clean fleece weight (CFW).

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DNA markers and genotyping. The DNA isolation, microsatellite genotyping and PCR conditions were the same as described by Cano *et al.* (2009). A panel of twelve microsatellite markers distributed over 50 cM on chromosome CHI5 were used (*BM0321*, *GLYCAM1*, *OarFCB005*, *ILSTS022*, *KRT*, *KRT2.13*, *BMS1898*, *KD103*, *OarVH130*, *LSCV25*, *BMS1248* and *LSCV11*) from the available web goat, sheep and cattle genetics map (http://locus.jouy.inra.fr/; http://rubens.its.unimelb.edu.au/; http://www.thearkdb.org). Every offspring and their parents were genotyped for every marker.

Statistical analyses. An interval analysis was performed under a backcross design (Knott *et al.*, 1994) 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 (2006, 2007 or 2008) and birth type (single, twin or triplets). Appropriate *F*-value thresholds for chromosome wise type 1 error rate were generated by permutation test of 10,000 iterations (Churchill and Doerge, 1994). When a QTL reached at least the suggestive significance level bootstrap approach (Visscher *et al.* 1996) was used to estimate the 95% confidence interval using 2000 bootstrap resamples.

Results and discussion

The phenotypic data (mean, standard deviation, minimum and maximum) for each trait are shown in Table 1.

Table 1: The fleece traits measured in the population (N=354)

Trait	MEAN	SD	MIN	MAX
AFD (μm)	22.36	1.38	17.13	26.65
CVAFD (%)	35.02	4.93	22.52	54.45
F30 (%)	9.64	3.91	1.20	29.00
CONT (%)	2.50	2.35	0	16.67
DISC (%)	0.49	0.56	0	6.33
KEMP (%)	1.11	1.09	0	10.00
DD (μm)	20.42	1.05	16.02	23.50
DP (μm)	42.77	3.55	34.04	56.16
PD (%)	68.79	8.74	39.11	94.24
ACF (^{0}/mm)	37.07	3.19	28.50	57.40
SL (mm)	81.54	11.63	51.00	124.30
GFW (kg)	8.06	1.88	2.70	19.70
CFW (kg)	6.69	1.53	2.10	16.30

AFD, average fiber diameter; CVAFD, coefficient of variation of AFD; F30, proportion of fiber over 30 microns; CONT, continuous medullated fibers; DISC, discontinuous medullated fiber; KEMP, kemp fiber; DD, down diameter; DP, hair diameter; ACF, average curvature of fiber; SL, staple length; GFW, greasy fleece weight; CFW, clean fleece weight.

Based on the web genetic map the interval between the markers used, was in average 4.8 cM and we covered 76 % the chromosome length. Table 2 shows only the traits with significative effects under the model “one QTL model” at P<0.05 chromosome-wise level on CHI5.

In Figure 1 the plot of the *F*-value for all traits analyzed in chromosome CHI5 is shown.

We found four putative QTL affecting AFD, F30, GFW and CFW (centromeric region) on CHI5. Taken account the homology between sheep and goats map (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 (KRT) family genes as pointed out McLaren *et al*. (1997).

Table 2: Significant effects for the one QTL model at the P<0.05 chromosome-wise level on chromosome 5.

Trait	Psition (cM)	*F*-value	CI	ADD ± SE	Var (%)
AFD (µm)	5	7.90	0 – 37	- 0.32 ± 0.11	1.94
F30 (%)	8	7.05	0 – 50	- 0.29 ± 0.10	1.71
GFW (kg)	8	7.10	4 – 37	- 0.29 ± 0.11	1.73
CFW (kg)	5	7.50	4 – 37	- 0.31 ± 0.11	1.83

AFD, average fiber diameter; F30, proportion of fiber over 30 microns; GFW, greasy fleece weight; CFW, clean fleece weight. CI, 95 % confidence interval using 2000 bootstrap resamples. ADD, additive effect on mean. If the allele substitution effect is positive then the effect of the homozygous QTL genotype is larger than the effect of the heterozygous genotype Var (%), percentage of trait variance explained by QTL.

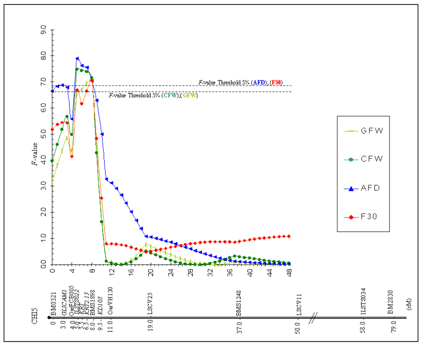

Figure 1: Map of the F-value depicting the positions of putative QTL in a backcross Angora x Creole goats on CHI5. On the chromosome (CHI) the markers used. The level is provided for P<0.05 (dashed line) chromosome-wise significance.

Compared with other livestock species; there is very limited published literature on QTL identification in goat populations. Recently, Mohammed Abadi *et al.* (2009) reported putative QTL affecting cashmere yield on three candidates regions previously reported by Cano *et al*. (2007).

In sheep several reports of linkage between genes and QTL with wool production traits are available (Purvis and Franklin, 2005; Allain *et al.,* 2006; Bidinost *et al.,* 2008). In cattle, four keratin family genes (*KRT8* and *KRT1B*) have been assigned to chromosome 5 in cattle (Fries *et al*., 1991), and one of the these genes *KRT* was assigned to chromosome 5 in the goat (Schibler *et al.,* 1998; Pinton *et al.,* 2000), all of them could be related with those QTL found here on goat CHI5. Moreover, in sheep, a linkage between high-glycine-tyrosine keratin gene loci and wool fiber diameter has been previously demonstrated (Parsons *et al.,* 1994).

As was mentioned above, the coincident results reported by Cano *et al.* (2007) and Mohammed Abadi *et al*. (2009) and in other species, such *KRT* genes family could be the best candidates for the associated QTL on goat chromosome 5.

Conclusion

Significant QTL affecting AFD, F30, GFW and CFW was observed on chromosome 5 in a backcross Angora x Creole goats. The development and application of fine mapping and candidate gene approach methodologies have been progressing in experimental and commercial livestock populations. Fine mapping will shorten the size of the candidate chromosomal regions harboring the QTL detected in this study.

After fine mapping and identification of causative mutations in candidate gene, these QTL will have the potential to achieve additional genetic and economic gains by incorporating marker-assisted selection into breeding programs.

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