LOCATIONS OF QTLs AFFECTING FLEECE TRAITS IN ANGORA GOATS ON CHROMOSOMES 1 AND 5


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INTRODUCTION
Several previous studies have indicated the presence of gene or gene families involved in fleece traits in sheep (reviewed by Cockett et al., 2001 and Purvis and Franklin, 2005), the hair in rabbit (Powell et al., 1995; Allain, D. et al., 2004), in human (Rogers et al., 2000; van Steensel et al., 2000) and in mice (Pruett et al., 2004).

In a genome screen for QTLs in Angora goats, Cano et al. (2003), reported the preliminary results on putatives QTLs for Standard Deviation of Average Fiber Diameter (SDAFD), Coefficient of variation of AFD (CVAFD) and the proportion of fiber with diameter over 30 µm (F30).

The aim of this study was to confirm the location of a QTL on chromosome (CHI) 1 and the location of a new QTL on CHI5 using new microsatellites and enlarged families in Angora goats.

MATERIALS AND METHODS
Animals and Phenotype Traits. The population analyzed had a total of 418 kids from 10 Angora bucks. The number of half-sib offspring per buck ranged between 26 to 73 kids. The population was created in five batches (years 2000 to 2004).

Mid-side fleece samples were taken from kids at 4 months of age. Fleece samples were analyzed at the Textile Fibers Laboratory of INTA Bariloche. Eight phenotypic fleece traits were recorded: 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) and the Average Curvature of Fiber (ACF; deg/mm).

Microsatellite genotyping. The DNA isolation, microsatellite genotyping and PCR conditions were the same as described by Cano et al. (2003).

All bucks were genotyped for 11 microsatellite on CHI1 and CHI5 from the available web goat genetic map (http://focus.jouy.inra.fr/cgi-bin/lgbc/mapping/common/intro2.pl?BASE=goat); 6 markers on CHI1 (ILSTS004, BM1312, LSCV06, CSSM32, CSSM19 and BM3205) and 5 markers on CHI5 (OarFCB005, LSCV25, BMS1248, ILSTS034 and BM2830). Every offspring was subsequently genotyped for every marker which buck was heterozygote.

Statistical Analysis. An interval analysis was performed under a half-sib model (Knott et al., 1996) 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, 2001, 2002, 2003 or 2004),
birth type (single or twin) and flock (8 levels). Appropriate F-statistic thresholds for chromosome wise type 1 error rate were generated by permutation test of 10,000 iterations (Churchill and Doerge, 1994; Doerge and Churchill, 1996). 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

In Table 1 phenotypic data (means and standard deviations) for the 10 families are shown.

<table>
<thead>
<tr>
<th>Family</th>
<th>Traits</th>
<th>AFD (µm)</th>
<th>CVAFD (%)</th>
<th>F30 (%)</th>
<th>KEMP (%)</th>
<th>CONT (%)</th>
<th>DISC (%)</th>
<th>SL (mm)</th>
<th>ACF (deg/mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (26)</td>
<td>24.1±2.6</td>
<td>27.8±2.7</td>
<td>17.9±11.3</td>
<td>0.9±1.0</td>
<td>1.3±1.0</td>
<td>0.8±0.9</td>
<td>89.9±17.7</td>
<td>34.7±22.4</td>
<td></td>
</tr>
<tr>
<td>2 (73)</td>
<td>23.4±1.8</td>
<td>27.4±3.8</td>
<td>12.5±8.6</td>
<td>2.9±3.3</td>
<td>4.1±6.8</td>
<td>1.9±3.6</td>
<td>90.0±11.0</td>
<td>34.3±3.6</td>
<td></td>
</tr>
<tr>
<td>3 (31)</td>
<td>23.3±1.8</td>
<td>29.4±3.9</td>
<td>13.2±8.3</td>
<td>1.2±1.2</td>
<td>2.9±3.2</td>
<td>1.7±2.3</td>
<td>69.0±13.5</td>
<td>34.3±1.8</td>
<td></td>
</tr>
<tr>
<td>4 (28)</td>
<td>22.7±1.1</td>
<td>28.7±2.5</td>
<td>11.3±5.2</td>
<td>0.9±0.9</td>
<td>2.3±2.0</td>
<td>0.6±0.9</td>
<td>76.0±16.0</td>
<td>33.7±2.0</td>
<td></td>
</tr>
<tr>
<td>5 (42)</td>
<td>23.2±1.6</td>
<td>26.7±2.7</td>
<td>12.2±7.2</td>
<td>2.7±2.7</td>
<td>4.4±5.7</td>
<td>2.5±3.5</td>
<td>96.1±10.9</td>
<td>32.7±2.8</td>
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</tr>
<tr>
<td>6 (67)</td>
<td>24.1±1.9</td>
<td>26.6±3.4</td>
<td>15.0±7.9</td>
<td>1.4±2.5</td>
<td>2.4±3.4</td>
<td>1.4±2.4</td>
<td>140.0±46.3</td>
<td>31.7±5.4</td>
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</tr>
<tr>
<td>7 (56)</td>
<td>24.1±2.1</td>
<td>28.3±3.1</td>
<td>16.8±10.0</td>
<td>1.6±2.4</td>
<td>3.3±3.8</td>
<td>1.5±2.0</td>
<td>114.9±39.1</td>
<td>28.3±2.1</td>
<td></td>
</tr>
<tr>
<td>8 (35)</td>
<td>24.1±2.6</td>
<td>29.7±3.6</td>
<td>18.6±10.3</td>
<td>1.8±3.4</td>
<td>11.2±11.6</td>
<td>5.5±6.8</td>
<td>-</td>
<td>31.6±4.1</td>
<td></td>
</tr>
<tr>
<td>9 (29)</td>
<td>23.6±1.6</td>
<td>26.6±2.3</td>
<td>12.7±5.6</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>33.7±3.6</td>
<td></td>
</tr>
<tr>
<td>10 (31)</td>
<td>23.0±1.6</td>
<td>25.7±2.9</td>
<td>10.2±6.0</td>
<td>0.5±1.5</td>
<td>7.2±8.7</td>
<td>3.4±5.0</td>
<td>110.0±30.7</td>
<td>23.0±1.6</td>
<td></td>
</tr>
</tbody>
</table>

(n) Progeny numbers by families. AFD, Average Fiber Diameter; CVAFD, Coefficient of Variation of AFD; F30, the proportion of fiber with diameter over 30 µm; KEMP, kemp fiber; CONT, Continuous Medullated Fibers; DISC, Discontinuous Medullated Fibers; SL, Staple Length; ACF, Average Curvature of Fiber. - : data not available

Based on the web genetic map and with the markers used in both chromosomes, the intermarker interval was in average 25.2 cM (for CHI1 30.6 cM and for CHI5 18.5 cM) and we covered 31.6% and 95% of the CHI1 and CHI5 chromosome length respectively. In Table 2 are shown only the traits with significative effects under the “one QTL model” at P<0.05 chromosome-wise level on CHI1 and CHI5.

In the Figure 1 are shown the plot of the F-statistics for all traits analyzed in each chromosome. With our results now we can confirm a QTL affecting CVAFD on CHI1. Taken 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 for CVAFD could be related with those keratin (KRT) and keratine-associated protein (KRTAP) family genes as pointed out by McLaren et al. (1997).

<table>
<thead>
<tr>
<th>Trait</th>
<th>CHI1</th>
<th>CHI5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Closest marker</td>
<td>BM1312</td>
<td>LSCV25</td>
</tr>
<tr>
<td>Position (cM)</td>
<td>92</td>
<td>20</td>
</tr>
<tr>
<td>Confidence Interval (cM)</td>
<td>42-90</td>
<td>12-40</td>
</tr>
<tr>
<td>F-statistic</td>
<td>2.6</td>
<td>2.3</td>
</tr>
<tr>
<td>F-threshold</td>
<td>2.2*</td>
<td>2.0*</td>
</tr>
<tr>
<td>Number of informative families</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>QTL variance (%)</td>
<td>6.6</td>
<td>6.0</td>
</tr>
<tr>
<td>Effect/SD</td>
<td>1.6/1.1</td>
<td>0.9/1.1</td>
</tr>
</tbody>
</table>
CVAFD, Coefficient of Variation of AFD; KEMP, kemp fiber. Chromosome-wise $F$-statistic threshold at the *$P<0.05$ level QTL, as determined by permutation test 10,000 iterations, each 4 centi-Morgan (cM). \(^{(A)}\) 95% LOD drop-off confidence interval.

![Figure 1. Map of the $F$-statistics depicting the positions of putative QTL in Angora goat by chromosome. On the chromosome (CHI) the markers used. The level is provided for $P<0.05$ (dashed line) chromosome-wise significance.](image)

On chromosome 1, in sheep, several high-glycine-tyrosine keratin associated proteins ($KRTAP6.1$, $KRTAP7$, $KRTAP8$) genes were mapped by McLaren et al. (1997). The same authors also mapped on chromosome 1 an important wool follicle protein trichohyalin ($THH$) encoded by a single gene.

On CHI5 a putative QTL for KEMP was found. This QTL is segregating in two families and could be related with those keratin ($KRT$) and keratine-associated protein ($KRTAP$) family genes as pointed out by McLaren et al. (1997) in sheep.

Again, based on genetic map homologies the $KRT2$, $KRT2.13$ and $KRT2.10$ genes (McLaren et al., 1997) mapped on chromosome 3 in sheep, four keratin family genes ($KRT8$ and $KRT1B$) assigned to chromosome 5 in cattle (Fries et al., 1991), and one of these genes $KRT$ 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 CHI 5. Moreover, in sheep, it has been previously demonstrated a linkage between high-glycine-tyrosine keratin gene loci and wool fibre diameter (Parsons et al., 1994). Thus $KRT$ and $KRTAP$s gene could be good candidates for the associated QTL on both CHI 1 and CHI5.

CONCLUSION

Our results confirm a QTL for CVAFD on CHI 1 in Angora goats and we found a new QTL for KEMP on CHI5. Nevertheless, new families, increased number of kid in extant families and a fine mapping on the candidate regions should be the next steps to carry out.

REFERENCES


Fries, R., Threadgill, D.W., Hediger, R., Gunawardana, A., Blessing, M., Jorcano, J.L.,
*Mamm. Genome* 8: 938-940.
Pruett, N.D., Tkatchenko, T.V., Jave-Suarez, L., Jacobs, D.F., Potter, C.S., Tkatchenko, A.V.,
114: 464-472.
901-915.