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QUANTITATIVE TRAIT LOCI FOR FLEECE TRAITS IN BALUCHI SHEEP

[LOCI DE CARACTERISTICAS CUANTITATIVAS DE CARACTERES DE VELLON DE OVEJAS BALUCHI]

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SUMMARY

Three sheep chromosome regions (OAR1, OAR5 and OAR25) were selected to study quantitative trait loci (QTL) segregating for wool traits in Baluchi sheep, an indigenous sheep breed in Iran. A total of 503 progeny from 13 half-sib families were genotyped for 15 microsatellite markers. The data were collected from Research Centre on Baluchi breed from 2009-2010. Wool traits were corrected for fixed effects of birth-year, sex, herd, and litter size. The average number of progeny per sire was 38 and ranged between 16 and 59. The QTL analyses were performed using regression-based interval mapping. The results revealed 7 QTL on OAR1 for type fiber traits (hetero-type, kemp and true wool percent in fleece), coefficient of variation of fiber diameter, greasy and clean fleece weight and staple length, 2 QTL on OAR5 for hetero-type wool percent and clean fleece, and 6 QTL on OAR25 for type wool traits, greasy and clean fleece weight and coefficient of variation of average fiber diameter.

Key words: DNA markers; QTL mapping;Baluchi sheep; fleece traits.

RESUMEN

Se seleccionaron tres regiones del cromosoma de ovejas (OAR1, OAR5 and OAR25) para estudiar los rasgos cuantitativos del loci (QTL) seleccionados para rasgos de lana en ovejas Baluchi, una raza de oveja endémica de oveja mejorada en Iran. Un progenie total de 503 de 13 familias de medios hermanos fueron genotipados para 15 marcadores de microsatelites. Los datos fueron colectados del centro de investigaciones sobre la raza Baluchi durante 2009-2010. Los rasgos de lana fueron se corrigieron para fijar efectos del año al nacimiento, sexo, rebaño y tamaño de camada. El promedio de numero de progenie por padre fue de 38 y con un rango entre 16 y 59. El análisis de QTL se desarrolló utilizando una regresión basada en un intervalo de mapeo. Los resultados revelaron 7 QTL sobre OAR1 para el rasgo de tipo de fibra (tipo hetero,Kemp y porcentaje verdadero de lana en el vellón), coeficiente de variación de diámetro de fibra, grasosa y vellón limpio, longitud de la grapa, 2 QTL sobre OAR5 para tipo hetero porcentaje de lana y vellón limpio y 6 QTL sobre OAR25 para rasgos de lana, grasa y peso vellón limpio y coeficiente de variación de promedio de diámetro de fibra.

Palabras clave: Marcadores de ADN; mapeo de QTL; ovejas Baluchi; Rasgos de vellón.

INTRODUCTION

Genomic research and the detection of quantitative trait loci (QTL) provide an opportunity to investigate the underlying genetic mechanism and improve the understanding of the biology of economically important traits. Although, some of wool traits have moderate to high heritability (Fogarty, 1995), because of antagonistic correlations among wool traits and also between wool and growth traits, there is a great interest in the study of genes of major effect and identifying QTLs to improve wool quality and hence, production efficiency.

In recent years, the construction of comprehensive marker maps in different species has been feasible

through using techniques of molecular biology (Vaiman et al., 1996; Schibler et al., 1998; Maddox et al., 2001). These techniques allow mapping of quantitative trait loci (QTL) influencing economically important traits, including fleece and wool traits. Microsatellite makers from these maps are being used to identify inheritance patterns of linked segments of the genome in structured pedigree populations. Associations of marker allele with phenotype of interest indicate the presence of quantitative traits loci (QTL). The development of efficient and robust linear regression methods to detect and mapping of QTL in simple and complex pedigree (Haley and Knott, 1992; Knott et al., 1998; de Koning et al., 2001) have made it possible to locate the chromosomal regions influencing traits of interest.
Identifying genes affecting quantitative trait loci (QTL) of economically importance traits in livestock species has the potential to significantly increase the accuracy of predicted breeding values and to reduce the generation interval which consequently would increase the rate of genetic progress (Spelman and Bovenhuis, 1998; Dekkers and Hospital, 2002). QTL mapping also opens the possibility of studying genes and causal polymorphisms for traits of agricultural importance (Seaton et al., 2006).

The total sheep population of Iran is 54 million heads which consisted of 27 breeds and ecotypes (ASRI, 2004). The Baluchi sheep is one of the most frequent breeds, which constitutes about 30 percent of the total sheep population of Iran. It plays an important role in meat and wool production (648000 tons meat and 81000 tons wools) in the area (ASRI, 2004). The wool yield is being used for carpet production. The coat color in this breed is white and has been adapted to the harsh local climate condition.
The objective of the present study was to identify QTL affecting sheep wool production and wool quality in a half-sib design in Baluchi sheep, through the analysis of specific regions of chromosomes 1, 5 and 25.

MATERIALS AND METHODS

Animal and phenotype traits

The experimental population for the QTL study was 503 individuals belonging to 13 paternal half-sib families of Baluchi sheep from two flocks at Research Center of Baluchi sheep located in north-east of Mashhad, Iran. The average family size was 38 offspring per sire, ranging from 16 to 59. The data were collected in two consecutive years (2009 and 2010).

Wool production and wool quality traits were recorded on sire's progeny. Mid-side fleece samples were taken from individuals at 15-17 months of age and staple length (SL, mm) and greasy fleece weight (GFW, g) were measured. Then, after washing, wool samples were analyzed in a laboratory (based on textile standard) for determining clean fleece weight (CFW, g), clean wool yield (YLD, %), average fiber diameter (AFD; µm), coefficient of variation of AFD (CVAFD; %), percentage of Kemp fiber and continuous medullated fibers (KEMP; %), percentage of discontinuous medullated fibers (HET; %) and percentage of true wool (TRUE, %).

Wool trait records were analyzed by least squares analysis of variance (SAS, 2009) to identify known fixed effects including birth-year, sex, litter size, flock, shearing date and birth weight (as covariate) with significance ($p<0.05$) and such effects were included in the mixed model for variance component estimation. Further, (co)variance components were estimated with mixed model by DMU 5.0 (Madsen et al., 2011) from single-trait analyses using animal model:

$$y = X\beta + Za + e$$

In this model, y was a vector of observations for different wool traits, β was vector of fixed effects influencing traits, α was the direct additive effect with the normal distribution $N(0, A\sigma_\alpha^2)$, where **A** is the additive relationship matrix and σ_α^2 is the additive genetic variance and e was a randomly distributed vector of residuals. X and Z were the corresponding incidence matrices relating observation to the respective fixed effects and random animal effects. Because most of traits had not normal distribution their data were transformed (arcsine was used for YLD and natural logarithm for CVAFD, TRUE, HET and KEMP) for improvement of residual distribution.

Microsatellite genotyping

Fifteen microsatellite markers from the available web-based sheep genetic map (www.thearkdb.org/arkdb/) on chromosomes 1, 5 and 25 were used. Chromosomal region studied in the present study is given in Figure 1. Our linkage analysis covered specific regions on OAR1 (8 microsatellites from 80.8 to 234.6 cM), OAR5 (4 markers from 12.8 to 95.7 cM) and OAR25 (3 markers from 0 to 52.6), with an average distance between markers of 19.2, 20.7 and 17.5 cM, respectively.

Blood samples of thirteen sires and their progeny were collected from the jugular vein in tubes with k3-EDTA 5% as anticoagulant. The blood samples were frozen at -20 ºC. The DNAs was extracted from refrigerated blood using a DNA extraction kit (CinnaGen Co., Iran). Purity of all extracted DNA

was assessed by calculating the 260/280 nm ratios using Nano drop machine. PCR amplifications were carried out in 25µl reactions with 20-50 ng genomic DNA as template. Reaction mixtures contained *Taq* DNA Polymerase, dNTP, Tris-HCL, KCL and MgCl2. The cycling protocol was as follows: An initial denaturation step at 95 ^{0}C for 10 min, followed by 35 cycles with the following steps: 94^{0}C for 30s, 48-62^{0}C for 55s and 72^{0}C for 30s. The reactions were terminated by a final extension step at 72^{0}C for 10 min. The primer, amplification conditions and other information were obtained from the Roslin Institute (University of Edinburg) website (www.roslin.ed.ac.uk/). Amplification products were electrophoresed on 6 and 8% denaturing polyacrylamide gels and the DNA bands were visualized by silver staining.

In the first step, all sires were genotyped for all microsatellite markers and then the offspring were genotyped for those markers heterozygous in their sire. Dams were not genotyped. Allele size was calculated using 20 bp DNA ladder (In the rage 0f 100-200bp). The scanned gels were visually scored independently by two researchers and the results incorporated in a database containing maker genotype and phenotypic data.

QTL analysis

Single trait QTL analysis was performed by multi-marker regression (Knott et al., 1996; Elsen et al., 1999) using GridQTL software (Seaton et al., 2006). Each of the adjusted phenotypes was regressed on the inheritance probabilities, at each location along each chromosome for each family. For each regression an F-ratio ($p<0.05$) of the model including the phase probability versus the same model without the phase probability was calculated. The best estimated position for a QTL in each family, for each trait, was taken to be the location with the largest F-ratio. Appropriate F-statistic thresholds for chromosome-wise type 1 error rate were generated by permutation test of 10,000 iterations (Churchill and Doerge, 1994). Confidence interval for the location of QTL was calculated by bootstrapping (Visscher et al., 1996) with 10,000 resamples.

RESULTS

Family phenotypic means and their standard deviations are shown in Table 1. Phenotypic and genetic estimates of wool traits in the overall Baluchi sheep population are presented in Table 2. Some of wool traits showed medium to high heritability.

This study detected QTL for wool traits on three chromosomes (Table 3 and Fig. 2-6). Chromosome 1 showed segregation of seven putative QTL at position 91.8, 92.8, 93.8, 93.8, 95.8, 151.8 and 227.8 affecting CFW, GFW, CVAFD, SL, TRUE, KEMP and HET traits, respectively ($p<0.01$ chromosome-wise significance level for GFW and KEMP and $p<0.05$ chromosome-wise significance level for CFW, CVAFD, TRUE, HET and SL).

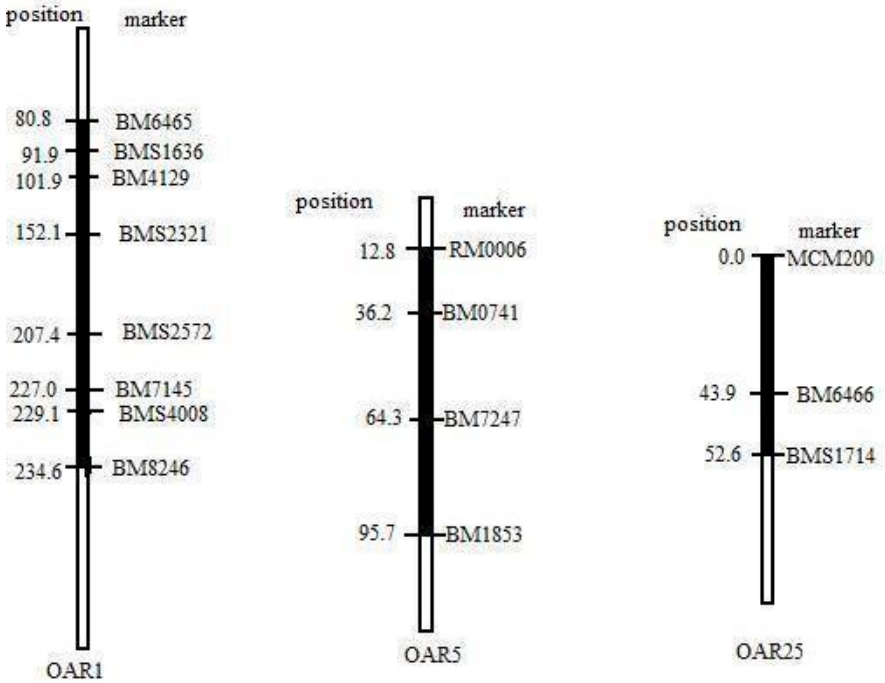

Figure 1.Chromosomal regions studied for QTL

Table 1. Family phenotypic mean ± standard deviation (SD) for wool traits in Baluchi sheep.

Family (size)	GFW (g)	YLD (%)	CFW (g)	SL (cm)	FD20 (%)	FD30 (%)	FD40 (%)	FD50 (%)	FDUP50 (%)	AFD (µm)	CVAFD (%)	HET (%)	KEMP (%)	TRUE (%)
1001 (59)	1245.6	73.7	991.7	6.69	0.60	0.24	0.09	0.05	0.02	24.8	41.9	0.03	0.02	0.95
SD	5.20	1.34	4.92	0.40	0.12	0.08	0.05	0.03	0.02	0.78	1.01	0.02	0.02	0.15
1062 (51)	1410.5	70.5	1050.9	6.54	0.56	0.26	0.07	0.04	0.06	25.8	47.2	0.03	0.03	0.94
SD	6.09	1.62	6.24	0.49	0.14	0.10	0.05	0.04	0.05	0.98	1.32	0.03	0.03	0.19
1314 (43)	1492.9	71.7	1150.5	7.14	0.63	0.23	0.08	0.03	0.02	23.9	43.6	0.03	0.01	0.96
SD	7.30	1.81	7.23	0.57	0.17	0.10	0.06	0.04	0.03	1.04	1.41	0.04	0.03	0.21
1369 (38)	1325.0	72.0	1041.4	6.83	0.61	0.24	0.09	0.05	0.02	24.2	41.5	0.03	0.02	0.96
SD	7.43	1.90	7.22	0.58	0.17	0.11	0.07	0.05	0.03	1.1	1.44	0.04	0.03	0.22
1414 (37)	1313.8	71.6	993.2	6.92	0.52	0.29	0.10	0.05	0.04	26.4	40.9	0.03	0.03	0.95
SD	6.73	1.76	6.57	0.55	0.15	0.11	0.07	0.05	0.04	1.07	1.33	0.03	0.03	0.20
1433 (45)	1421.1	73.4	1073.4	6.81	0.62	0.23	0.08	0.04	0.03	24.0	43.4	0.03	0.01	0.96
SD	6.12	1.49	5.7	0.45	0.14	0.08	0.05	0.04	0.03	0.85	1.15	0.03	0.02	0.17
1584 (16)	1241.2	73.5	900.8	6.21	0.64	0.23	0.08	0.04	0.02	23.7	41.1	0.02	0.01	0.97
SD	8.54	2.08	7.28	0.60	0.19	0.12	0.07	0.05	0.03	1.18	1.55	0.03	0.03	0.24
2310 (34)	1474.1	74.3	1083.4	7.92	0.53	0.26	0.11	0.06	0.04	26.6	43.5	0.03	0.03	0.94
SD	7.39	1.88	7.18	0.61	0.16	0.11	0.07	0.05	0.04	1.13	1.44	0.04	0.04	0.21
2338 (29)	1278.3	71.1	927.8	6.75	0.55	0.28	0.08	0.05	0.04	25.8	41.1	0.03	0.02	0.96
SD	7.45	1.84	6.65	0.57	0.16	0.12	0.06	0.05	0.04	1.11	1.40	0.03	0.03	0.21
2348 (30)	1458.3	73.5	1136.4	6.95	0.61	0.22	0.08	0.06	0.03	24.7	41.2	0.03	0.02	0.95
SD	7.8	1.87	7.36	0.58	0.17	±0.10	±0.06	±0.05	±0.03	±1.08	±1.40	±0.04	±0.03	±0.21
2365 (34)	1558.6	71.5	1130.7	7.26	0.58	0.25	0.07	0.04	0.06	25.1	45.1	0.03	0.02	0.95
SD	7.33	1.73	6.86	0.55	0.16	0.10	0.05	0.04	0.05	1.02	1.37	0.03	0.03	0.20
2382 (36)	1808.3	68.2	1256.5	7.26	0.60	0.25	0.09	0.04	0.02	24.3	41.9	0.02	0.01	0.97
SD	8.68	1.76	7.56	0.57	0.17	0.11	0.06	0.04	0.03	1.05	1.38	0.03	0.03	0.21
2413 (38)	1373.3	70.2	997.9	6.83	0.59	0.24	0.09	0.05	0.02	24.9	41.4	0.03	0.02	0.95

Family (size)	GFW (g)	YLD (%)	CFW (g)	SL (cm)	FD20 (%)	FD30 (%)	FD40 (%)	FD50 (%)	FDUP50 (%)	AFD (µm)	CVAFD (%)	HET (%)	KEMP (%)	TRUE (%)
SD	6.76	1.67	6.31	0.52	0.15	0.15	0.06	0.04	0.03	0.99	1.28	0.03	0.03	0.19
Mean (490)	1410.3	72.0	1055.5	6.92	0.59	0.25	0.09	0.05	0.03	24.9	42.7	0.03	0.02	0.95
SD	24.62	0.43	19.37	0.08	0.008	0.01	0.00	0.00	0.00	0.19	0.45	0.00	0.00	0.00

Greasy fleece weight, GFW; Clean fleece weight, CFW; Clean wool yield, YLD; Average fiber diameter, AFD; Coefficient of variation of AFD, CVAFD; The percentage of fiber with diameter under 20 µm, FD20; The percentage of fiber with diameter between 20 to 30 µm, FD30; The percentage of fiber with diameter between 30 to 40 µm, FD40; The percentage of fiber with diameter between 40 to 50 µm, FD50; The percentage of fiber with diameter up 50 µm, FDUP50; The percentage of hetero type wool, HET; The percentage of medullated wool, KEMP; The percentage of true wool, TRUE.

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QTL for different traits were mapped to similar regions of the chromosome and this may suggest that the same gene(s) might be involved in the control of the traits. In chromosome 1, QTL for GFW, CFW in the small distance and QTL for CVAFD and SL were mapped in similar regions on OAR1 (Figure 2)

The two QTL segregation on chromosome 5 were related to HET and CFW at 87.8 cM with effects from 0.67 to 3.8 phenotypic standard deviations for HET in 2348 and 2382 families and an effect of 0.97 phenotypic standard deviation for CFW in 2382 families ($p<0.05$).

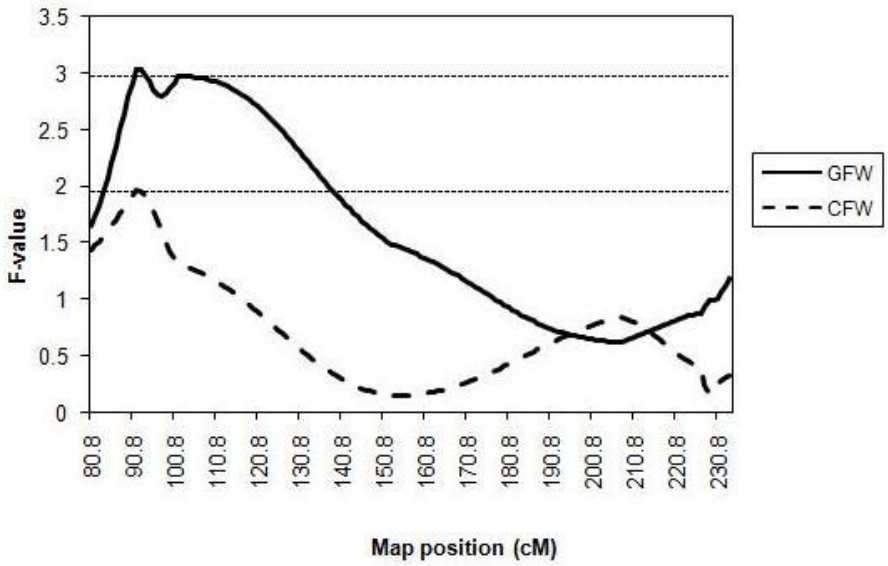

Figure 2. The F-value profile obtained from across family analysis for greasy fleece weight (the solid line) and clean fleece weight (the dash line) on sheep chromosome 1. The lower and upper horizontal dotted lines represent 5% and 1% chromosome-wide significant levels of linkage, respectively.

Table 2. Summary of phenotypic and genetic parameters of fleece traits in Baluchi sheep.

Traits	Average	SD	MIN	MAX	δ^2a	R	h^2	S.E.(h^2)
GFW	1519	0.544	100.0	4400	10634	43836	0.195	0.08
YLD	72.35	7.795	45.19	91.95	6.0303	19.647	0.235	0.01
CFW	1103	0.432	72.00	3549	6973.6	28146	0.198	0.01
SL	6.998	1.550	3.375	15.00	0.9999	1.0742	0.482	0.18
AFD	25.11	3.555	17.43	38.98	1.8313	3.8434	0.322	0.07
CVAFD	42.87	8.280	20.80	83.85	9.1300	59.300	0.133	0.11
HET	0.026	0.028	0.000	0.228	0.8332	0.43515	0.650	0.23
KEMP	0.021	0.025	0.000	0.230	0.8332	0.43510	0.650	0.25
TRUE	0.954	0.042	0.708	1.000	0.8682	0.4632	0.650	0.44

Minimum, MIN; Maximum, MAX; Additive genetic variation, δ^2a; Residual error, R; Heritability, h^2
Standard error of heritability, S.E.

There was a highly significant QTL on OAR25 affecting HET, KEMP, TRUE and GFW. Six QTL related to wool traits were detected on this chromosome, i.e. GFW at 23cM with effects from 0.75 to 0.57 phenotypic standard deviations for 1414 and 1314 families ($p<0.01$), TRUE at 28 cM with effects from 0.91 to 1.35 phenotypic standard deviations for 1001, 1414 and 1062 families ($p<0.01$), KEMP at 32 cM with effects from 1.06 to 1.96 phenotypic standard deviations for 1414 and 1062 families ($p<0.01$), HET at 42 cM with effects from 0.33 to 4.17 phenotypic standard deviations for 2413, 1001 and 1414 families, CFW at 46cM with effects from 0.55 to 0.79 phenotypic standard deviations for 2310 and 1414 families ($p<0.05$) and CVAFD at 52cM with effects from 0.92 to 1.21 phenotypic standard deviations for 1001 and 2310 families ($p<0.05$) (Figure 3, 5 and 6).

Significant results for the two-QTL models are presented in Table 4. For GFW two QTL were detected but they were located very close to each other and could be one QTL. Also two-QTL model for CVAFD and HET were significant.

Confidence interval for all QTL situations included the complete region studying on chromosome. The effect/standard deviation ranged from 0.33 to 5.34 phenotypic standard deviations and is shown in the last column of Table 5.

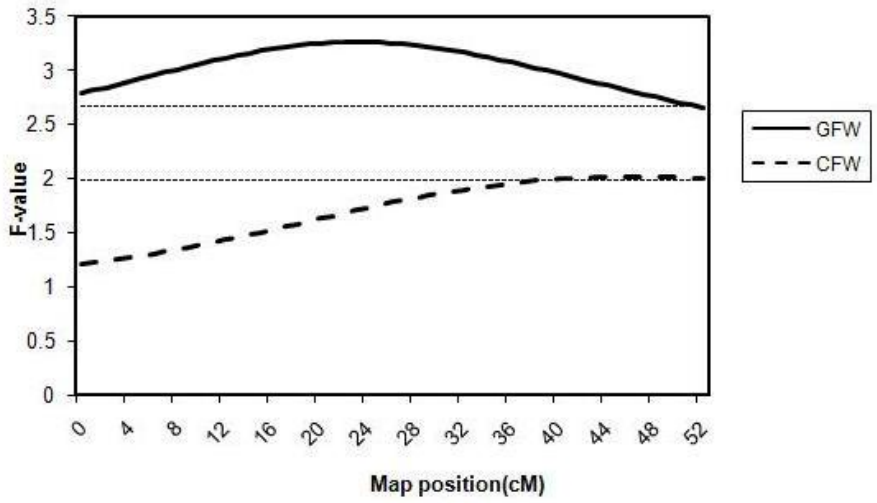

Figure 3. The F-value profile obtained from across family analysis for greasy fleece weight (the solid line) and clean fleece weight (the dash line) on sheep chromosome 25. The lower and upper horizontal dotted lines represent 5% and 1% chromosome-wide significant levels of linkage, respectively.

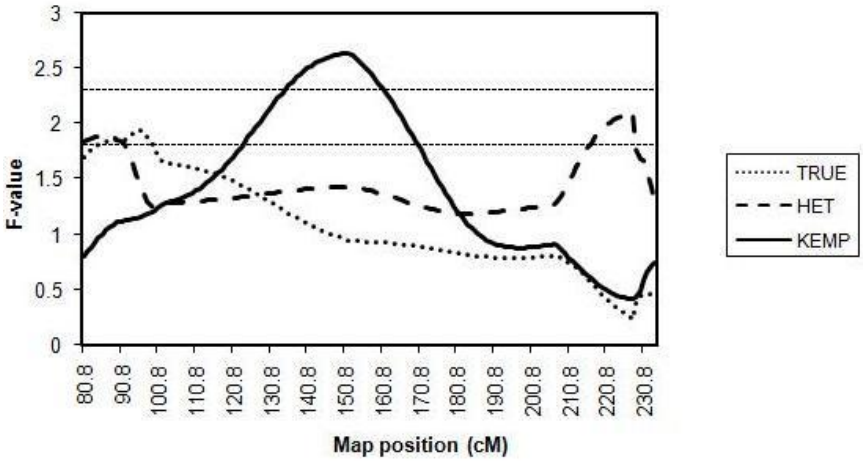

Figure 4. The F-value profile obtained from across family analysis for KEMP (the solid line), TRUE (the square dot line) and HET (the dash line) on sheep chromosome 1. The lower and upper horizontal dotted lines represent 5% and 1% chromosome-wide significant levels of linkage, respectively.

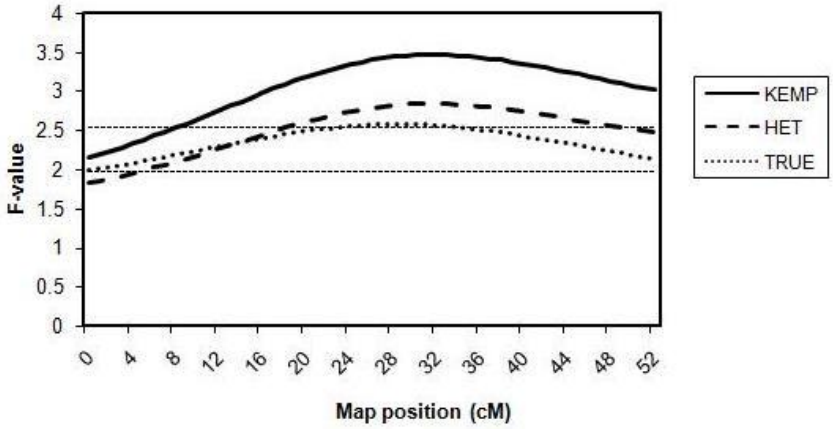

Figure 5. The F-value profile obtained from across family analysis for KEMP (the solid line), TRUE (the square dot line) and HET (the dash line) on sheep chromosome 25. The lower and upper horizontal dotted lines represent 5% and 1% chromosome-wide significant levels of linkage, respectively.

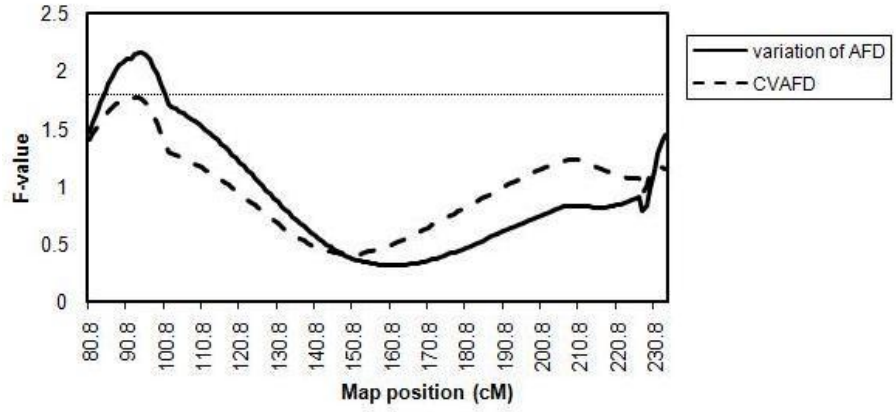

Figure 6. The F-value profile obtained from across family analysis for variation of fiber diameter (AFD), and coefficent of variation of fiber diameter (CVAFD) on sheep chromosome 1. The horizontal dotted line represent 5% chromosome-wide significant level of linkage.

Table 3. Summary of QTL segregation for wool traits in Baluchi sheep

OAR	Position	Trait	F-value	Family	Effects± S.E.	Nearest marker	Effect/SDp[a]
1	227.8	HET	2.11**	2310	0.71±0.34	BM7145	3.69
				2382	0.78±0.35		4.33
				1433	0.78±0.29		1.56
	151.8	KEMP	2.64**	1433	1.97±0.76	BMS2321	5.34
				1001	0.87±0.26		1.47
	95.8	TRUE	1.95*	2348	0.56±0.31	BMS1636	0.59
				2413	0.46±0.21		0.48
				1314	0.42±0.20		0.44
	93.8	CVAFD	1.76*	1062	23.52±11.25	BMS1636	0.5
				1314	22.12±9.92		0.51
				2310	18.29±10.29		0.42
	92.8	GFW	3.11**	1314	841.97±218.55	BMS1636	0.56
				1414	540.86±262.84		0.41
	91.8	CFW	1.95*	1314	567.60±260.34	BMS1636	0.49
				2413	483.08±221.91		0.48
				2310	468.52±240.19		0.43
	93.8	SL	1.71*	2413	3.34±1.54	BMS1636	1.28
				2310	3.016±1.69		1.26
				1314	3.29±1.63		1.23
5	87.8	HET	1.97*	2348	1.14±0.36	BM1853	3.8
				2382	1.21±0.54		0.67
	87.8	CFW	2.09*	2382	1215.78±402.1	BM1853	0.97
25	42	HET	2.33**	2413	0.075±0.03	BM6466	4.17
				1001	0.056±0.025		2.0
				1414	0.024±0.01		0.33
	32	KEMP	3.46**	1414	0.051±0.01	BM6466	1.96
				1062	0.034±0.01		1.06
	28	TRUE	2.57**	1001	1.29±0.61	BM6466	1.35
				1414	0.86±0.42		0.91
				1062	0.86±0.40		0.91
	52	CVAFD	2.18*	2310	39.91±17.97	BMS1714	0.92
				1001	50.73±30.11		1.21
	23	GFW	3.26**	1414	989.13±272.28	BM6466	0.75
				1314	849.42±335.25		0.57
	46	CFW	2.01*	1414	547.12±230.11	BM6466	0.55
				2310	857.43±473.14		0.79

* and ** = Genome-wise significant level ($p<0.05$ and $p<0.01$, respectively).
a = QTL effect in phenotypic deviation units.

DISCUSSION

In the present study, we reported several putative QTL for wool traits on chromosome 1 (seven QTL related to HET, KEMP, TRUE, GFW, CFW, CVAFD and SL), chromosome 5 (two QTL related to CFW and HET) and chromosome 25 (Six QTL related to HET, KEMP, TRUE, GFW, CFW, and CVAFD) in Baluchi sheep.

The putative QTLs affecting hetero-type (HET), kemp and true wool percentage were observed on chromosome 1. The position of the putative QTLs related to these traits was far from others. The results suggested that these traits could be controlled by different set of genes. Two QTL were detected for GFW and CFW on chromosome 1, i.e. close to BMS1636 marker. The short distance between these QTLs, and the high genetic and phenotypic correlation between GFW and CFW traits in the present study (r_g= 0.89 and r_p=0.91), suggested that these QTLs could be a single QTL with the same effect on both traits.

A QTL influencing coefficient of variation of fiber diameter on chromosome 1 was also detected. Cano et al. (2007) detected a putative QTL for CVAFD at position of 96 cM on chromosome 1 in Angora goat. Due to homology of sheep and goat (Maddox, 2005) it is confirmed that a QTL related to fiber diameter is

at this position of chromosome. Also, a putative QTL related to staple length was detected close to the QTL responsible for wool yield. Beh et al. (2001) also detected a putative QTL on chromosome 1 related to staple length.

In sheep, there are several reports available for the linkage between genes and QTL in wool production traits (Ponz et al., 2001, Bray et al., 2002, Purvis and Franklin, 2005). The putative QTL for wool traits found in Baluchi sheep on chromosome 1 could be related to keratin (KRT) and keratin-associated protein (KRTAP) family genes as pointed out by McLaren et al. (1997).

The Kemp fibers are large modulated fibers with a latticed deficient in sulphur. OAR1 harbors one of the keratin-associated-protein clusters (KAP, KAP7 and KAP8) involved in the formation of matrix surrounding cortex wool micro fibrils (McLaren et al., 1997; Ede et al., 1995; Parsons et al., 1993). Another important wool follicle protein, i.e. trichohyalin (THH), encoded by a single gene, was also mapped in chromosome 1 (McLaren et al., 1997). A linkage between this keratin cluster gene and fiber diameter in a merino half-sib was observed (Parsons et al., 1994) confirming that KAP cluster genes are strong candidates for the wool quality traits studied in Baluchi sheep.

In this study, two QTL on chromosome 5 were detected which are related to clean fleece weight and hetero-type wool percent traits. In Angora goat a QTL for Kemp wool percent trait on the position of 20 cM was detected (Cano et al., 2007). Two keratin family genes (KRT8 and KRT1B) have been assigned to chromosome 5 in sheep, goat and cattle (Fries et al., 1991; Schibler et al., 1998; Pinton et al., 2000), all of them could be related to those QTLs found here on chromosome 5 of Baluchi sheep.

Significant QTLs affecting several wool traits were observed on chromosome 25 suggesting the evidence of a gene with major effect on wool traits. Ponze et al. (2001) in INRA401 breed have described three QTLs related to AFD, CVAFD and staple length traits. Allain et al. (2006) in a Lacaune × Sarda backcross detected four QTLs for fleece characteristics on OAR25, including greasy fleece weight at position of 17 cM, mean diameter at position of 2 cM, coefficient of variation of diameter fiber at position of 4 cM and medullated fiber percent at position of 7 cM. In this study, putative QTLs for CVAFD, GFW, CFW, and Kemp were detected at positions of 52, 23, 46, 35 and 32 cM on this chromosome, respectively. Therefore, these results and others confirm that there is a gene or genes with major effect on chromosome 25 which are responsible for wool production and wool quality traits.

CONCLUSION

The study has been successful in detecting QTL in Baluchi sheep populations, and contributes to the understanding of chromosomal region that explain part of the variability of wool quality traits in Baluchi sheep especially in chromosome 1 and 25. The QTL effects raged from 0.33 to 5.34 in units of phenotypic standard deviation, thus the experiment had only a power to detect medium to large QTL. The QTL involved in wool traits, might allow considerable improvement in the response to selection.

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