A genome scan to detect QTL affecting dairy traits in a dairy sheep backcross Sarda x Lacaune population

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RIASSUNTO – Individuazione di QTL per le produzioni lattee in una popolazione backcross Sarda x Lacaune – *Si presentano i risultati preliminari della ricerca di QTL per le produzioni lattee in una popolazione backcross Sarda x Lacaune attraverso un panel di marcatori microsatelliti sparsi in tutto il genoma ovino. Sono stati individuate le posizioni significative almeno alla soglia chromosome –wise del 5%. Le posizioni interessanti sono risultate 5 per la quantità di latte, 4 per il tenore in proteine e 3 per il tenore in grasso.*

KEY WORDS: dairy sheep, backcross, QTL, milk traits.

INTRODUCTION – Recently in Mediterranean countries as France, Italy and Spain, dairy sheep selection has been efficiently oriented towards milk yield and milk composition. More attention has been now paid to traits related to the reduction of production costs (milkability, functional traits, longevity), health (resistance to mastitis or parasitic diseases), safety of food (reduction in contaminants) and quality (milk fatty acids composition). Therefore, research combining classical quantitative approach and QTL detection is needed, either on-farm by implementing experimental recording schemes, or in experimental flocks especially for traits costly to record. In this framework, two complementary QTL detection projects have been implemented in France and Italy: one based on crossbreeding between Sarda and Lacaune breeds (Carta *et al.*, 2002) and the other based on purebred granddaughter families of French dairy sheep breeds (Schibler *et al.*, 2002). In this paper, first results of a genome scan based detection of QTL affecting milk traits in first lactation in the Sarda x Lacaune backcross population are presented.

MATERIAL AND METHODS – In 1998, 14 elite Lacaune rams were mated by AI to 100 Sarda ewes to produce F1 rams. Among those, 10 sons of different Lacaune sires were mated to 3,000 Sarda ewes to procreate 967 backcross females born in 1999 and bred in an experimental farm in Sardinia. 887 milk yield (MY), fat and protein content (FC and PC) total 1st lactation records were calculated starting from TD records fortnightly collected. A panel of 127 microsatellites to enable a quite complete scan of the autosomic sheep genome was used. Most of the genotypings have been carried out in multiplex using an ABI377-96 automatic sequencer. A total of 125,064 genotypings were available. Prior to the QTL analysis, phenotypes were adjusted for different combinations of fixed effects specific for each milk trait. The main factors were the milking length, the lambing period class and the number of lambs born. Across family single trait QTL analysis was carried out by within-sire linear regression (Knott *et al.*,1996) using the following model:

$$Y_{ij} = s_i + (2p_{ij}\text{-}1)a_i + e_{ij}$$

where Y_{ij} is the individual phenotype adjusted as described above, s_i is the sire, p_{ij} is the probability

of inheriting one defined QTL allele from sire i for the daughter j given the marker information, a_i is the substitution effect of the putative QTL carried by the sire i, and e_{ij} was the residual, assumed to be normally distributed with a zero expectation and a heterogeneous variance σ^2_{ei}. The most likely phase for each sire was retained and the probability that each progeny received one or the other chromosomal segment was estimated at every position using a 1 cM step. The rejection thresholds were estimated by within-family permutations as proposed by Churchill and Doerge (1994), for each trait using 10,000 permutations.

RESULTS AND CONCLUSIONS – An important heterogeneity between families of the phenotypic means and residual variability was detected (Table 1).

Table 1. Family means and residual standard deviation (rsd) for milk traits (1st lactation).

Sire	N of daughters	MY (l)		PC (%)		FC (%)	
		Mean	rsd	Mean	rsd	Mean	rsd
1	96	195	32.00	4.84	0.26	6.53	0.45
2	91	199	34.75	4.87	0.23	6.35	0.38
3	112	192	26.76	4.93	0.24	6.70	0.42
4	101	224	29.41	4.83	0.26	6.35	0.38
5	76	159	41.46	5.01	0.26	6.62	0.46
6	102	207	31.02	5.12	0.31	6.81	0.47
7	78	231	37.39	5.03	0.23	7.14	0.43
8	80	231	27.04	4.60	0.22	6.29	0.34
9	83	162	31.70	5.06	0.22	6.75	0.40
10	68	180	38.38	4.99	0.24	6.83	0.41

Table 2. Descriptive statistic of the genome scan.

OAR	TL	ASL	NM	INF	OAR	TL	ASL	NM
1	346	307	15	61	14	118	93	5
2	306	300	12	53	15	124	51	2
3	315	247	10	54	16	87	71	4
4	134	126	6	52	17	122	98	4
5	150	95	3	64	18	122	89	4
6	157	123	6	58	19	72	57	4
7	145	107	6	39	20	87	32	3
8	126	61	3	58	21	75	60	5
9	126	82	4	67	22	83	62	3
10	100	86	4	69	23	73	33	2
11	127	80	5	38	24	97	14	2
12	102	96	6	59	25	69	-	-
13	137	102	5	46	26	70	63	4

Table 3. OAR, map position, closest marker and chromosome-wise significant level of QTL findings

Trait	OAR	Pos. (cM)	Closest marker	P <	Trait	OAR	Pos. (cM)	Closest marker	P <
MY	1	244	LSCV06	0.050	PC	16	28	BM1225	0.050
MY	3	196	BMC1009	0.001	PC	18	78	OARHH47	0.050
MY	16	42	MAF214	0.010	PC	26	38	CSSM43	0.050
MY	20	28	BM1258	0.010	FC	1	254	MAF109	0.060
MY	22	0	BMS0651	0.050	FC	3	37	ILSTS045	0.050
PC	1	114	MCM058	0.010	FC	20	56	OARHH56	0.001

Results of genome scan are summarized in Table 2. For each chromosome the Table reports the total length in cM (TL), the length of the analysed segment (ASL) the number of analysed markers (NM) and the average percentage of informative meioses (INF). The coverage of the sheep genome was not completely attained, especially in some chromosomes where ASL or INF were not yet adequate. The QTL results for MY, PC and FC in 1st are reported in Table 3 by listing all locations significant or close to significance at least at the chromosome-wise type I error level of 0.05 (*i.e* with 3.75= 25*3*0.05 type I errors expected by chance under the null hypothesis). This first analysis confirms that the Sarda x Lacaune backcross design is adequate to detect QTL of quite large effect. More precise results will be available by 2003 by adding data from 2nd and 3rd lactations and densifying the markers panel. Further on, new traits of economic interest such as somatic cell count, parasite resistance, udder morphology and milkability will be analysed. The number of families showing within-family significant LRT ranged from 1 to 4, suggesting that QTL are still segregating in purebred populations. QTL effects ranged from 18 to 41 litres for MY, from 0.11 to 0.22% for PC and from 0.16 to 0.45% for FC. In particular, two positions reached a high level of significance: in OAR 3 for MY and in OAR 20 for FC.

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