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Short Communication: Quantitative Trait Loci Affecting the Somatic Cell Score on Chromosomes 4 and 26 in Italian Holstein Cattle

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ABSTRACT

This work aimed to confirm previously reported quantitative trait loci (QTL) affecting the somatic cell score (SCS) in dairy cattle on *Bos taurus* autosomes (BTA) 4 and 26. A granddaughter design with selective genotyping was implemented that included half-sib families from 12 male lines of Italian Holstein cattle. The animals were genotyped for 5 microsatellite markers each on regions of BTA 4 (average marker spacing 9.42 cM) and BTA 26 (average marker spacing 5.26 cM), previously reported by other authors as carrying QTL for somatic cell count. Quantitative trait loci analyses were performed using interval mapping by regressing sire breeding values for SCS onto genotype probabilities at 1-cM intervals along the 2 chromosome regions. Breeding values for SCS were estimated for the whole population using a test-day repeatability animal model. Results were not significant on a chromosome basis, but a possible QTL was found at BM4505 on BTA 26, confirming this region for further studies of QTL affecting SCS in the Italian Holstein population.
Key words: somatic cell score, quantitative trait loci, microsatellite

In several independent studies, QTL with major effects on SCS have been identified on BTA 4 (Zhang et al., 1998; Klungland et al., 2001) and BTA 26 (Ashwell et al., 1997; Zhang et al., 1998; Heyen et al., 1999). The objective of this study was to confirm the presence in these regions of QTL affecting SCS in Italian Holstein cattle families.

The experimental model was a classic granddaughter design (Weller et al., 1990). It included 12 sire families, chosen as having large between-sons variability in SCS. The 12 sire families included a total of 5,192 sons. Bull breeding values for SCS were estimated on granddaughter records by the Italian Holstein Association (ANAFI) using a test-day repeatability animal model (Samorè et al., 2001). Bull breeding values are more reliable than simple daughter phenotypic data, because they are estimated using information from a large number of daughters and because they take into account environmental and dam effects. A selective genotyping model (Darvasi and Soller, 1992) was used to reduce genotyping costs. A total of 270 sons were chosen from the high and low tails of the family distributions of the 12 sires, including all sons deviating from the family mean by more than 1 SD in either direction.

All 12 sires and 270 sons were genotyped for 5 polymorphic microsatellites on BTA 4 (BL1030, MAF50, RM188, BMS1840, and BM885) and 5 polymorphic microsatellites on BTA 26 (BM1314, HAUT27, BM4505, TGLA429, and BMS882). The markers were selected from the USDA map (http://www.marc.usda.gov), on the basis of their map position and informativity, or on the basis of their previously reported linkage with QTL. The average marker spacings were 9.42 and 5.26 cM on chromosomes BTA 4 and BTA 26, respectively. Published PCR protocols were adjusted to optimize performance. All PCR products were separated by electrophoresis in 4.2% denaturing polyacrylamide gels on an ABI Prism 377 DNA Sequencer equipped with Genescan and Genotyper software (Applied Biosystems, Foster City, CA). Statistical analyses were performed by QTL Express software (Seaton et al., 2002), with the interval mapping for multiple markers set at 1 cM in half-sib families, as described by Knott et al. (1996). The regression model included breeding values for SCS and probabilities of individuals inheriting allele 1 or allele 2 from the common parent, estimated on genotypes. The reliability of the SCS breeding values was included as a weight.

An F-test ratio was calculated to test the presence of a QTL at 1-cM intervals. One thousand resamples were selected for bootstrapping to determine the 95% confidence intervals for linkage analyses within the 12 families.

On a chromosome-wide basis, neither of the 2 chromosomes showed a significant effect. On BTA 4, the F-test ratio had a value of 1.2, whereas the threshold for significance at $P = 0.05$ was $F = 2.0$. However, there was some evidence for the existence of a QTL very close to

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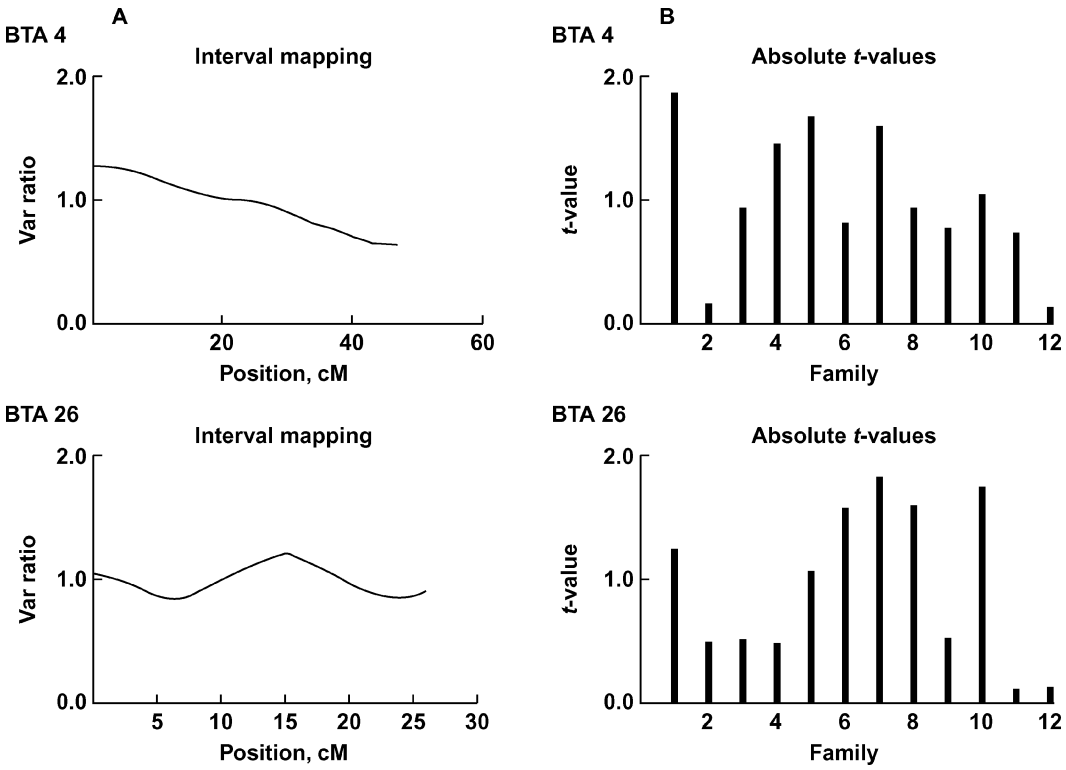

Figure 1. (A) Interval mapping graphic showing the *F*-ratios for 1 QTL at each location (1-cM intervals; with 0.00 representing the most centromeric marker) vs. no QTL; (B) absolute *t*-values for each family indicating the strength of evidence for a QTL at the location estimated in the across-family analysis.

marker BL1030 (at 3.1 cM). The significant QTL effect at RM188 reported by Zhang et al. (1998) and Klungland et al. (2001) was not confirmed in this study. On BTA 26 the *F*-test ratio had a value of 1.27, whereas the threshold for significance at $P = 0.05$ was $F = 2.0$.

Table 1. Map position of markers on *Bos taurus* autosomes 4 and 26 according to the USDA map, and references of previously reported linkages for QTL affecting SCS[1]

Marker	Map position, cM	Reference for SCS (***)
BTA 4		
BL1030	3.1	Zhang et al. (1998) Klungland et al. (2001)
MAF50	24.7	
RM188	41.7	
BMS1840	47.4	
BM885	50.2	
BTA 26		
BM1314	24.8	Heyen et al. (1999)
HAUT27	31.3	
BM4505	39.7	Ashwell et al. (1997)
TGLA429	50.6	Zhang et al. (1998)
BMS882	51.1	

[1]USDA map available at http://www.marc.usda.gov.

***$P \leq 0.001$.

However, there was evidence of the existence of a QTL very close to marker BM4505 at 39.7 cM (Table 1, Figure 1). This confirms the QTL previously reported by Ashwell et al. (1997) and by Zhang et al. (1998). On the same chromosome, 2 more regions affecting SCS were reported by other authors: one centromeric, close to marker BM1314 (Ashwell et al., 2004) and another telomeric (Zhang et al., 1998). Neither of these regions was confirmed in the present study. It should be noted that aside from the different methods and the level of significance, all these studies confirmed associations between SCS and a QTL close to the BM4505 locus on BTA 26. The evidence for involvement of this chromosomal region in different populations adds confidence and indicates the region as of potential interest for finer analysis in the Italian Holstein population.

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