

## **Effect of SCD SNPs on milk production traits of Jersey cows (Brief Report)**

### **Auswirkungen der SCD SNPs auf die Milchleistungmerkmale bei Jersey Kühen (Brief Report)**

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### **Background**

Studies concerning associations between candidate gene polymorphisms and milk production traits in cattle are carried out on a large scale (CITEK *et al.* 2007, KULIG 2005). Stearoyl-CoA desaturase (SCD) is the enzyme involved in conversion of saturated fatty acids into monounsaturated fatty acids. The gene encoding SCD was mapped to bovine chromosome 26 (CAMPBELL *et al.* 2001), where some QTLs for fat yield and other milk production traits as well as for somatic cells count (SCC) were also identified. Some of the SNPs identified within the *SCD* were significantly associated with fatty acid composition in milk and in carcass fat tissue (MOIOLI *et al.* 2007, TANIGUCHI *et al.* 2004). The effect of genotypes on milk production traits and SCC in cattle has not been reported so far. The aim of this study was therefore to establish possible associations between two SNPs in the *SCD* and milk production traits and SCC in Jersey cows.

### **Procedure**

The analysed polymorphic sites localised in exon 3 of the *SCD* gene were as follows: G/A and C/T transitions in positions 10153 and 10329, respectively (GeneBank acc. no. AY241932). The latter SNP results in an alanine-to-valine substitution in the polypeptide sequence. The *SCD* genotypes were identified according to TANIGUCHI *et al.* (2004).

#### *Primer sequences*

SCD10153-F	5'-GTG TCC TGT TGT GCT TCA TCC TGC C-3'
SCD10153-R	5'-AAT ATT CTC TCG GGG GTT GAT GGT CTT G-3'
SCD10329-F	5'-ATG TAT GGA TAC CGC CCT TAT GAC-3'
SCD10329-R	5'-TTC TGG CAC GTA ACC TAA TAC CCT AAG C-3'

Next, a statistical analysis of associations between the SNPs and milk traits (milk yield, kg; fat content,%; protein content,% and SCC, ln) was performed. A total of 1 315 test-day observations for the above traits were obtained monthly from 180 Jersey cows belonging to one herd. The analysis was carried out using the GLM (STATISTICA 2006); the genotype, number of consecutive lactation (1-5), season of lactation (1-4), month of lactation (1-14), cow as a random factor nested within genotype (1-180) were defined in a linear model.

## Results

In the studied herd of Jersey cows, all the possible *SCD* genotypes were identified. The most frequent alleles for each SNP were as follows: A – 0.76 for 10153G/A and C – 0.74 for 10329C/T. Seven out of nine possible combined genotypes were found, the three most frequent being AA-CC – 0.47, GA-TC – 0.38 and AA-TC – 0.08. As regards the physiological function and/or chromosomal localisation, the *SCD* might be considered as a candidate gene for milk fat traits. Unfortunately, no associations were found between the studied polymorphisms and fat content in milk of the studied cows (data not shown). Similarly, in terms of milk yield and protein content, the differences between the respective *SCD* genotypes were statistically non-significant. Although, the study results show statistically significant differences in the mean SCC values in cows with different 10329C/T genotypes (Table 1). The TT cows were characterised by a significantly ( $P \leq 0.01$ ) higher ln SCC in milk compared with the CC and TC cows. The difference between the TT and CC individuals averaged 0.528395 while the difference between the TT and TC cows was lower (0.450844). As regards the 10153G/A polymorphism, no significant differences were found in this study between the genotypes and SCC. Moreover, an analysis of the combined genotype data showed no statistically significant differences among cows with different genotypes in relation to the trait under study.

Table 1

Means and standard deviations of SCC in cows with different *SCD* genotypes

*Mittelwerte und Standardabweichungen der SCC bei Kühen mit verschiedenen SCD-Genotypen*

Polymorphism	Genotype	N	ln SCC
10153G/A	AA	1315	5.192585 ± 1.145354
	GA	1119	5.196667 ± 1.191726
	GG	111	5.439986 ± 1.144766
10329C/T	CC	1217	5.148583 ± 1.116710 <sup>A</sup>
	TC	1237	5.226134 ± 1.195735 <sup>B</sup>
	TT	91	5.676978 ± 1.307258 <sup>AB</sup>
10153G/A-10329C/T	AA-CC	1123	5.155977 ± 1.111552
	AA-TC	192	5.406706 ± 1.308770
	GA-CC	94	5.060250 ± 1.179212
	GA-TC	1001	5.182552 ± 1.179711
	GA-TT	24	6.319666 ± 1.225492
	GG-TC	44	5.429670 ± 0.944374
	GG-TT	67	5.446761 ± 1.266089

N = number of test-day records. The means in columns marked with the same superscript letter differ significantly at  $P \leq 0.01$ .

The presented results suggest that the *SCD*-10329C/T genotypes might contribute to a decreased SCC in Jersey cattle; cows with C allele should be preferred in selection programmes. Therefore, the *SCD* could be proposed as a candidate gene for SCC. Nevertheless, further studies will be necessary to confirm the result.

## References

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