Session 14 barton.ludek@vuzv.cz

# The association of stearoyl-CoA desaturase (*SCD1*) and sterol regulatory element binding protein-1 (*SREBP-1*) genotypes with the adipose tissue fatty acid composition in Fleckvieh cattle

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## Introduction and objective

It is generally accepted that the fatty acid (FA) composition of dietary fat from meat and dairy products is affected by a number of nutritional and genetic factors. Stearoyl-CoA desaturase (SCD) is an enzyme responsible for the conversion of saturated fatty acids (SFA) into monounsaturated fatty acids (MUFA). It is also involved in the endogenous production of the cis-9 trans-11 isomer of conjugated linoleic acid (CLA). The *SCD1* gene coding for this enzyme is regulated by sterol regulatory element binding proteins (SREBPs). The objective of this study was to associate the polymorphisms in *SCD1* and *SREBP-1* genes with the FA composition of intramuscular and subcutaneous fat in Fleckvieh bulls.

## Material and methods

Genomic DNA was obtained from 370 Fleckvieh bulls fattened under identical feeding and housing conditions and slaughtered at a similar age. Genotyping for the *SCD1* (SNP 878C>T) and *SREBP-1* (84-bp Ins/Del) polymorphisms was performed using a polymerase chain reaction method with the previously described primers (Taniguchi et al., 2004; Hoashi et al., 2007). Muscle and subcutaneous fat samples were collected from the *m. longissimus thoracis* and the brisket, respectively. The fatty acid profile (g/100 g of total FA) of intramuscular and subcutaneous fat was determined using a gas chromatography method.

## Results

### Allele and genotype frequencies

| Gene | Polymorphism | Region | No. individuals | Allele notation/ frequencies | | Genotype notation/ frequencies | | |
|---|---|---|---|---|---|---|---|---|
| SCD | SNP 878C>T | Exon 5 | 370 | A<br>0.5554 | V<br>0.4446 | AA<br>0.3216 | AV<br>0.4676 | VV<br>0.2108 |
| SREBP-1 | 84-bp Ins/Del | Intron 5 | 370 | L<br>0.9203 | S<br>0.0797 | LL<br>0.8486 | LS<br>0.1432 | SS<br>0.0081 |

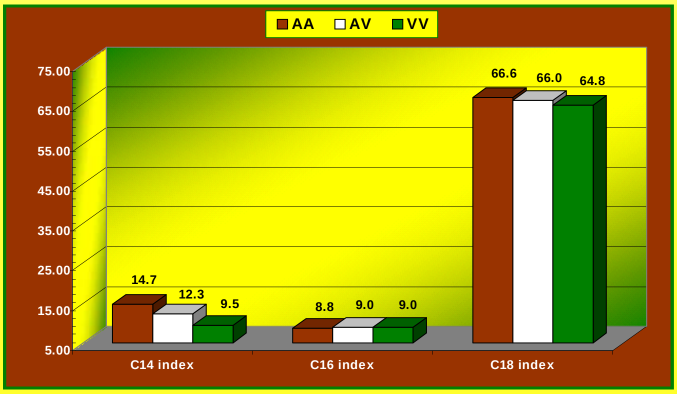
### Effect of the studied polymorphisms on the fatty acid profile of intramuscular fat

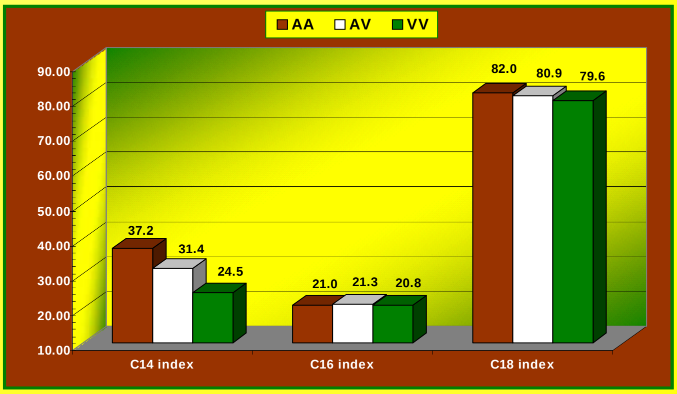
| | SCD1 (SNP 878C>T) | | | | SREBP-1 (84-bp Ins/Del) | | |
|---|---|---|---|---|---|---|---|
| | AA | AV | VV | P-value | LL | LS | P-value |
| | (n=118) | (n=172) | (n=77) | | (n=314) | (n=53) | |
| C14:0 | 2.57 | 2.55 | 2.66 | NS | 2.58 | 2.60 | NS |
| C16:0 | 26.1 | 25.9 | 26.4 | NS | 26.0 | 26.2 | NS |
| C18:0 | 18.6 | 19.1 | 19.6 | ** | 19,0 | 19.5 | NS |
| C14:1 cis-9 | 0.45 | 0.36 | 0.28 | *** | 0.37 | 0.38 | NS |
| C16:1 cis-9 | 2.55 | 2.58 | 2.62 | NS | 2.59 | 2.51 | NS |
| C18:1 cis-9 | 37.1 | 37.1 | 36.1 | * | 37,0 | 36.5 | NS |
| C18:1 trans-11 | 0.98 | 0.94 | 0.94 | NS | 0.94 | 0.99 | NS |
| CLA cis-9, trans-11 | 0.26 | 0.26 | 0.24 | NS | 0.25 | 0.26 | NS |
| SFA | 47.3 | 47.5 | 48.7 | ** | 47.6 | 48.3 | NS |
| MUFA | 42.9 | 42.9 | 41.8 | * | 42.8 | 42.1 | NS |

### Effect of the studied polymorphisms on the fatty acid profile of subcutaneous fat

| | SCD1 (SNP 878C>T) | | | | SREBP-1 (84-bp Ins/Del) | | |
|---|---|---|---|---|---|---|---|
| | AA | AV | VV | P-value | LL | LS | P-value |
| | (n=50) | (n=75) | (n=25) | | (n=129) | (n=21) | |
| C14:0 | 2.85 | 2.95 | 3.07 | NS | 2.93 | 2.98 | NS |
| C16:0 | 24.7 | 24.9 | 24.7 | NS | 24.7 | 25.3 | NS |
| C18:0 | 10.0 | 10.5 | 11.4 | * | 10.6 | 9.89 | NS |
| C14:1 cis-9 | 1.68 | 1.37 | 1.02 | *** | 1.37 | 1.70 | ** |
| C16:1 cis-9 | 6.58 | 6.73 | 6.56 | NS | 6.58 | 7.10 | NS |
| C18:1 cis-9 | 45.0 | 44.5 | 44.3 | NS | 44.7 | 44.1 | NS |
| C18:1 trans-11 | 0.83 | 0.84 | 0.89 | NS | 0.85 | 0.79 | NS |
| CLA cis-9, trans-11 | 0.52 | 0.51 | 0.49 | NS | 0.51 | 0.50 | NS |
| SFA | 37.4 | 38.3 | 39.1 | NS | 38.1 | 38.1 | NS |
| MUFA | 57.6 | 56.7 | 55.9 | NS | 56.8 | 56.9 | NS |

*** $P<0.001$ ** $P<0.01$ * $P<0.05$ NS – not significant





C14 index = C14 : 1 *cis* – 9 / (C14 : 0 + C14 : 1 *cis* - 9) . 100, C16 index = C16 : 1 *cis* – 9 / (C16 : 0 + C16 : 1 *cis* - 9) . 100, C18 index = C18 : 1 *cis* – 9 / (C18 : 0 + C18 : 1 *cis* - 9) . 100

## Conclusion

It was demonstrated that the polymorphism in the *SCD1* and *SREBP-1* genes existed in Fleckvieh cattle. The *SCD1* polymorphism (SNP 878C>T) was associated with proportions of several FA and FA indices in intramuscular and subcutaneous fat.

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