

## FATTY ACID COMPOSITION (MUFA AND CLA) RELATED WITH THE G.878TC SCD GENE POLYMORPHISM IN ABEERDEEN ANGUS STEERS

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The composition of the fatty acids (FA) in meat is of great importance in the human diet. There are polyunsaturated and monounsaturated fatty acids (MUFA and PUFA) whose intake is reported as beneficial for a healthy diet. In addition, beef is of great importance as a functional food because it is an important source of conjugated linoleic acid (CLA), which has a key role in human health. The Esteroyl CoA desaturase (SCD) catalyzes the biosynthesis of monounsaturated fatty acids (MUFA), and also causes the endogenous synthesis of major isomer of conjugated linoleic acid (CLA) cis-9, trans-11 CLA. 8 SNPs in the SCD gene has been identified, among which is mentioned primarily g.878TC SNP, which causes an amino acid substitution from valine to alanine in the protein. The aim of this study was to determine the relationship of polymorphism g.878TC with the composition of MUFA and CLA in longissimus dorsi muscle of Angus cattle breed. The study was conducted with 100 Angus steers from the Region of Araucania, Chile, and slaughtered with an average age of 12 months and 263±18 kg weight of carcasses. 100 g were collected from the central portion of the muscle Longissimus dorsi of each channel two days after slaughter and stored at -80°C. Subsequently, genomic DNA from each sample with genomic DNA mini Kit ISOLATE (Bioline, USA) was extracted commercial kit. The presence of SNP g.878TC was determined by PCR-RFLP and was designed primers SCD. The PCR reaction was performed using DNA Polymerase enzyme Paq5000 (Agilent Technologies, USA). The PCR products were digested with the restriction enzyme SATI (Fermentas, USA). The FA of the L. dorsi muscle samples were extracted by the method described by Folch et al. (1951). The FA methyl esters were analyzed on a gas chromatography. Statistical Analysis. Estimated marginal means (±SE) were determined using a general linear model including the fixed effect of genotype, age and weight. The average values were then subjected to multiple comparison test (Tukey) and determining differences (P <0.05). The genotype were TT= 0.33; TC=0.43; CC=0.22 and allele frequencies were T=0.54 and C=0.46. Frequency of the SNP allele g.878TC C is in the range described by Taniguchi et al. (2004) and Milanesi et al. (2008) in their studies with beef cattle. Inostroza et al., (2013), state that there is an effect of genetic variation on the total amount of fatty acids in milk. The SNP g.878TC is positively related to the content of monounsaturated fatty acids, and significantly affects the amount of myristoleic fatty acids (C14:1), oleic (C18:1) and CLA (Taniguchi et al, 2004; Inostroza et al., 2013). In this study, CC animals (Table 1) genotype have a higher total content of monounsaturated fatty acids (MUFA) than with genotype TT animals (P <0.05). Moreover, high values of CLA are linked to the presence of the CC genotype, as myristoleic fatty acids (C14:1), palmitoleic (C16:1), cis-10-heptadecanoic (C17:1), elaidic (C18:1n9t) and oleic (C18:1n9)

**Conclusion.** The composition of fatty acids in Angus steers beef, is influenced by polymorphisms present in genes associated with FA synthesis. It is also established that the g.878TC SNP may be a possible genetic marker for selection of animals with higher amounts of MUFA and CLA, and therefore, a composition of healthier fatty acids.

**Acknowledgements.** Dirección Investigación Universidad de La Frontera,

Table 1. Relationship g.878TC SNP with the FA in Angus steers

Fatty Acid	Genotype		
	TT	TC	CC
C14:1	0.25±0.03 <sup>b</sup>	0.33±0.03 <sup>b</sup>	0.58±0.04 <sup>a</sup>
C16:1	1.15±0.22 <sup>b</sup>	1.61±0.19 <sup>b</sup>	3.36±0.25 <sup>a</sup>
C17:1	0.12±0.02 <sup>b</sup>	0.19±0.02 <sup>b</sup>	0.42±0.03 <sup>a</sup>
C18:1n9t	0.49±0.20 <sup>b</sup>	1.03±0.17 <sup>b</sup>	1.81±0.23 <sup>a</sup>
C18:1n9c	8.42±1.23 <sup>c</sup>	12.41±1.06 <sup>b</sup>	23.36±1.41 <sup>a</sup>
CLA <sup>1</sup>	0.16±0.06 <sup>b</sup>	0.33±0.05 <sup>b</sup>	0.83±0.07 <sup>a</sup>
MUFA <sup>2</sup>	10.43±1.47 <sup>c</sup>	15.57±1.27 <sup>b</sup>	29.53±1.69 <sup>a</sup>
MUFA: SFA <sup>3</sup>	0.80±0.02 <sup>b</sup>	0.88±0.02 <sup>a</sup>	0.92±0.02 <sup>a</sup>

**Sesión: Regulación Génica del Metabolismo Lipídico.**