ANGUS BEEF FATTY ACID COMPOSITION (MUFA AND CLA) RELATED WITH THE G.878TC SCD GENE POLYMORPHISM.

Karla Inostroza[1], Giovanni Larama[1], Silvana Bravo[1], Néstor Sepúlveda[1]

1Facultad de Ciencias Agropecuarias, Centro de Tecnología e Innovación de la Carne. Universidad de La Frontera, Temuco, Chile

*nestor.sepulveda@ufrontera.cl

Abstract – The beef is a source of protein, fat and minerals for humans and is composed of a series of structures that provide nutritional and biochemical properties. A single nucleotide polymorphism (SNP) in the SCD gene (g.878TC) that influences the fatty acid composition in cattle was identified. The aim of this study was to determine the presence of the SNP g.878TC in beef meat using the PCR -RFLP technique. It was used a sample of 100 Aberdeen Angus steers raised and slaughtered in the Araucanía Region (Chile). According to the fatty acid composition there is a positive relationship between the CC genotype and fatty acid content of MUFA and CLA present in the Longissimus dorsi muscle of Angus steers. Therefore, the SNP g.878TC could be considered as a genetic marker for selection of animals Aberdeen Angus, with a composition of healthier fatty acids

I. INTRODUCTION

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 [1]. 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 [2].

The Estearoyl 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. Taniguchi et al [3], identified 8 SNPs in the SCD gene, 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.

II. MATERIALS AND METHODS

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 -80ºC. 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. ACCTGGCTGGTGAATAGT GCT-5'-3'and5' – TCTGGCACGTAACCTAATACCCT-3', with which a gene 170pb region was amplified: one set based on the sequence available in GenBank (Access No.AF285607) 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 [4]. The FA methyl esters were analyzed on a gas chromatography. The standard mixture of fatty acid components 37 FAME mix (C4-C24, Supelco, USA) for identification of fatty acids was used. Furthermore, the standard octadecadienoic, Acid , Methyl Ester Conjugated (CLA Sigma, USA) for identification of the isomers of conjugated linoleic acid. All fatty acids were quantified using calibration curves using Methyl Nonadecanoate fatty acid (Sigma, USA) as internal standard.

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 ($P < 0.05$).

III. RESULTS AND DISCUSSION

The genotype and allele frequencies described in Table 1. Frequency of the SNP allele g.878TC C is in the range described by Taniguchi et al [3] and Milanesi et al [5] in their studies with beef cattle. Inostroza et al [6], 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 [3,6]. In this study, CC animals (Table 2) 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)

Table1. Genotypic and allelic frequency for g.878TC SNP

	Genotype		
	TT	TC	CC
Genotypic frequency	0.33	0.43	0.22
Allelic frequency	T= 0.54	C=0.46	

Table 2. Relationship g.878TC SNP with the FA (mg/g) in Angus steers

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

IV. 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.

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REFERENCES

1. Lichtenstein, A., Kenndy, E, Barrier, P., Danford, D, Ernst, N, Grundy, S., Leveille, G., Van Horn, L., Williams, C., Booths., S. Dietary fat consumption and health. Nutr. Rev., 56:3-9, 1998.
2. Keating, A., Kennelly, J., Zhao, F. Characterization and regulation of bovine stearoyl CoA desaturase gene promoter. Biochem. Biophys. Res. Commun., 344:233-240, 2006.
3. Taniguchi, M., Utsugi, T., Oyama, K., Mannen, H., Kobayachi, M., Tanabe, Y., Ogino, A., Tsuji, S. Genotype of stearoyl CoA desaturase is associated with fatty acid composition in Japanese black cattle. Mamm. Genome., 14:142-148, 2004.
4. Folch, J., Ascoli, I., Lees, M., Meath, J., Lebaron,F. Preparation of lipids extracts from brain tissue. J Boil. Chem., 188:833-841, 1951.
5. Milannesi, E., Nicoloso, L., Crepaldi, P., Stearoyl CoA desaturase (SCD) gene polymorphism in Italian cattle breeds., J. Animal Breed. Genet., 125:63-67, 2008.
6. Inostroza, K., Scheuermann, E., Sepúlveda, N. 2013. StearoylCoA desaturase and fatty acid synthase gene polymorphisms and milk fatty acid composition in Chilean Black Friesian cows. Rev. Colomb. Cienc. Pecu. 26:263-269.