P3087 A functional variant in the promoter region of ovine *stearoyl-CoA desaturase* gene (*SCD*) affects gene expression and fatty acid profile in muscle. Laura González-Calvo and Laura Iguacel (CITA), Alfonso Bolado-Carrancio (Universidad de Cantabria), Elda Dervishi (University of Alberta), Mª Magdalena Serrano (INIA), Guillermo Ripoll, Francisco Molino, Mireia Blanco and Margarita Joy (CITA), José Rodriguez-Rey (Universidad de Cantabria) and Jorge Calvo (Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA) and ARAID)

This experiment was conducted to study the effect of the g.31A>C (GenBank acc. Number FJ513370) SNP, located in the promoter region of ovine SCD, on the transcription rate of this gene and fatty acid profile in two different muscles. Fifty Rasa Aragonesa male lambs were fed commercial concentrate. Lambs were slaughtered at 22–24 kg live-weight, and a piece of Semitendinosus and L. thoracis muscles were obtained for functional characterization, genotyping and a steak to determine fatty acid composition. Only palmitoleic acid (C16:1) and trans-octadecadienoic acid (C18:2 n-6tt) contents in Semitendinosus and L. thoracis, respectively, were affected by the SNP. To elucidate the functionality of this SNP, transcriptional activity and protein binding of the SCD were evaluated. The g.31A>C SNP was found to be associated with SCD gene expression in both muscles. Genotypes carrying C-allele showed a lower expression rate compare to genotypes carrying A-allele. Because of the lower expression of the genotypes carrying the C-allele, methylation analysis of a 199 bp region of the SCD promoter, which include the g.31A>C SNP, was performed to verify if the C-allele could be methylated. Sequence analysis of the bisulfite converted DNA confirmed that the amplified region was not methylated. EMSA suggested the presence of a specific binding and allelic differences in the interaction with nuclear proteins. The experiments showed that the C-allele oligonucleotide had higher binding than the A-allele. The in silico analysis

of transcription factor binding sites suggested that the nucleotide change could alter the affinity of the SP-1 (g.31A>C), AP-2 alpha (g.31C), WT1 (g.31C), NF-1 (g.31C) and C/EBP alpha (g.31A) nuclear proteins for the sequence including the g.31A>C polymorphism. However, EMSA supershift assay with anti-Sp1 revealed that SP1 nuclear protein was not interacting with this region of the SCD gene.

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ABSTRACT

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