Abstract

The enzyme, acetyl-CoA acetyltransferase 2 (*ACAA2*), which is encoded by the ACAA2 gene, catalyzes the last stage of beta-oxidation of fatty acids. During the early stages of lactation there are growing energy needs for liver gluconeogenesis, which are met primarily by the beta-oxidation of fatty acids, thereby, leading to increased acetyl-CoA levels (Vernon, 2005). Orford et al. (2012) were the first to study the single nucleotide polymorphisms (SNPs) of the *ACAA2* gene, which may correlate with the productive characteristics of the milk of Chios' sheep. In their investigation, sequencing and genotyping of the *ACAA2* gene were performed in sheep for the first time and showed that there is a SNP (C/T) in exon 10 of the 3 "untranslated region" (untraslation region, UTR) of the gene. The results of this research revealed that the heterozygous CT genotype and homozygous TT genotype were associated with high milk production in sheep, while the CC genotype was associated with low milk production. The findings of the above study provided the basis for further investigation of the ACAA2 gene of Chios' sheep. Polymorphism is likely to affect gene expression in both liver and udder. Therefore, this project aims to study the expression of the three different genotypes, CC, TT and CT, in liver and udder of Chios' sheep, and investigate the different expression between the two alleles, T and C, of heterozygous sheep (CT). We used control methods for (a) the expression of the three genotypes, CC/TT/CT (Real-Time PCR) and (b) the expression between the two alleles, T and C, of CT heterozygotes (Taqman Real-Time PCR). Our results show that the level of expression of the TT genotype is larger than that of the CC genotype. The differential expression of the two alleles, T and C, showed no statistically significant difference in their expression. There is a need for further studies to determine the molecular mechanism that is responsible for the difference in the expression of the two genotypes.