Session 24 Poster 8

Forage quality in ewe diets determines fatty acid profile and lipogenic gene expression in *Longisimus dorsi* of suckling lambs

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The aim of this study was to investigate whether forage quality in ewe diets affects IMF fatty acid profile and the expression of genes related with fat metabolism in l. dorsi muscle from suckling lambs of Churra Tensina sheep breed. The effect of ewe diet on the expression of some lipogenic (LPL, ACACA, FASN, FABP4, DGAT1, SCD, PRKAA2), and transcription factors genes (SREBP1, PPARG, PPARA and CEBPB) was also studied. Twenty-four lambs were used for IMF fatty acid profile determination and gene expression studies: HAY group lambs (n=12) and GRE group lambs (n=12) were raised by ewes receiving meadow hay and grazing green forage, respectively. When lambs reach 10-12 kg live weight were slaughtered and sample of l. dorsi was used for IMF fatty acid profile and gene expression studies. The fatty acids profile and gene expression levels were determined. Statistical analysis were carried out using the SPSS 15.0, using GLM. The relationship between gene expression and FA indicators was determined using stepwise linear regression analysis. GRE lambs promoted the formation and deposition of vaccenic (C18:1 n-7), CLA and PUFA n-3 in L. dorsi from their suckling lambs (P<0.05). Significant statistical differences were found in SCD gene expression (P=0.04), and CEBPB was at the limit of significance (P=0.05). Relative gene expression of SCD was 0.22 lower in lambs from GRE group compared to HAY group. While CEBPB gene expression was 1.31- fold higher in GRE group compared to HAY group. Regression analysis showed that SCD and CEBPB gene expression in suckling lambs are modulated by PUFA n-6/ n-3 ratio. Higher levels of n-6/n-3 stimulate SCD expression and inhibited CEBPB gene expression in HAY group lambs.