Differential expression of peroxisome proliferator-activated receptor γ, fatty acid synthase, and hormone-sensitive lipase in fat-tailed and thin-tailed sheep breeds

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ABSTRACT. Tail fat content affects meat quality, and it varies in different sheep breeds. Theoretically, lipid metabolism contributes to variation in tail fat content. Tail length, tail width, and tail girth were measured in live Tong sheep (with both short fat tail and long fat tail), Shaanbei fine wool sheep (long thin tail), Tan sheep (short fat tail), Kazakh sheep (hip fat tail), and Tibetan sheep (short thin tail). The expression levels of genes related to tail adipose tissue lipid metabolism were investigated, which included lipogenetic genes (*PPARγ* and *FAS*) and lipolytic gene (*HSL*). Differences were observed ($P < 0.05$) in *PPARγ* mRNA expression levels in the different breeds; *FAS* mRNA expression levels did not differ ($P > 0.05$) in Tong sheep with short fat tail, Tong sheep with long fat tail, Shaanbei fine wool sheep, and Tibetan sheep; *HSL* mRNA expression levels were not different ($P > 0.05$) in Tong sheep. PPARγ and HSL protein expression levels differed ($P < 0.05$) between the different breeds; FAS protein expression levels were different ($P < 0.05$) in Tong sheep with long fat tails, Tan sheep,

Kazakh sheep, and Tibetan sheep, but did not differ (P > 0.05) in Tong sheep with short fat tails and Shaanbei fine wool sheep. These results provide useful information to further understand the function of *PPARγ*, *FAS*, and *HSL* in sheep tail lipid metabolism, which should be applicable to studies on the regulation of fat deposition and improvement of meat quality.