Characterization of Gene Expression Related to Milk Fat Synthesis in the Mammary Tissue of Lactating Yaks

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Summary

This research communication describes the mechanism of gene expression related to the synthesis of yak milk, which has special properties, including high milk fat and protein and low milk yield, as determined via quantitative reverse transcription polymerase chain reaction

(RT-qPCR), a powerful method of genetic expression analysis. In our study, significant up-regulation and % relative mRNA abundance during lactation were observed in genes related to fatty acid (FA) uptake from blood (*LPL, CD36*), intracellular transport (*FABP3*), intracellular FA activation of long- and short-chain FAs (*ACSS1, ACSS2, ACSL1*), *de novo* synthesis (*ACACA*), desaturation (*SCD*), triacyglycerol (TAG) synthesis (*AGPAT6, GPAM, LPIN1*), lipid droplet formation (*PLIN2, BTN1A1, XDH*), ketone body utilization (*BDH1, OXCT1*), and transcription regulation (*THRSP, PPARGC1A*). In particular, intracellular *de novo* FA synthesis (*ACSS2*, *ACACA,* and *FABP3*) and TAG synthesis (*GPAM*, *AGPAT6*, and *LPIN1*), whose regulation might be orchestrated as part of the gene network under the control of *SERBF1* in the milk fat synthesis process, were significantly more activated compared to levels in dairy cows. However, the genes involved in lipid droplet formation (*PLIN2*, *XDH*, and *BTN1A1*) were expressed at lower levels compared to those in dairy cows, where these genes are mainly controlled by the *PPARG* regulator. These phenomena seem to affect the characteristics of yak milk such that the fat content is high and the milk yield is low.