



Comparative analysis of the liver tissue transcriptomes of Mongolian and Lanzhou fat-tailed sheep

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ABSTRACT. Research on gene regulation has been made possible with the help of RNA sequencing applications such as RNA-Seq technology for high-throughput sequencing platforms. Recent studies have explored the transcriptomes from different tissues of domestic animals using RNA-Seq technology, but little research has been done to study the transcriptomes of breeds of sheep having different adipose tissue deposition mechanisms, such as Mongolian and Lanzhou fat-tailed sheep. In this study, Mongolian and Lanzhou fat-tailed sheep were selected as experimental breeds, and six libraries (three libraries per breed) were constructed. A total of 286 Mb of high-quality reads was obtained, and three-quarters of the reads were mapped to the reference genome per library. In addition, there were 16,257, 16,186, 16,254, 16,827, 16,437, and 15,761 known reference genes in the six constructed libraries (LCL1, LCL2, LCL3, MCL1, MCL2, and MCL3, respectively). Seven genes were differentially expressed: four were upregulated and three were downregulated in liver tissue between the MCL and LCL groups; 65,303, 65,442, 63,426, 76,267, 69,853, and 57,439 potential cSNPs were detected in the six libraries, respectively,

with the G/R substitution occurring most commonly. There were 24,239, 22,283, 22,457, 26,635, 27,093, and 18,700 alternate splicing (AS) events in the six libraries. Intron retention was the most common AS event, followed by alternative 3' splice sites. These results indicate that there are many differences in the liver transcriptomes of Mongolian and Lanzhou fat-tailed sheep breeds. Such results may provide fundamental information for further research on defining the sheep genome.

Key words: Sheep; Liver tissue; RNA-Seq; Transcriptome