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COMPARATIVE TRANSCRIPTOME ANALYSIS OF LIVER TISSUES IN BACTRIAN CAMEL (*Camelus Bactrianus*)

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ABSTRACT

In the present study, comparative transcriptome sequencing was used to compare liver tissue transcriptome profiles between domestic bactrian camel (BCL), cattle (CL) and sheep (SL). The RNA-seq data from these two groups revealed that 3254 genes were differentially expressed between the BCL and CL groups, 2426 genes were found to differ significantly in expressional levels between BCL and SL. Pathway analysis revealed that the differentially expressed genes between the BCL and CL belong to non-alcoholic liver disease, bile secretion, as well as metabolic related pathway such as fatty acid metabolism and degradation, xenobiotics by cytochrome P_{450}, drug metabolism-cytochrome P_{450}, and drug metabolism-other enzymes; between the BCL and SL groups. A complete dataset of bactrian camel liver tissue using RNA-seq will facilitate the understanding of the unique biological characteristics of bactrian camels and supply essential information towards further studies on the genomes of bactrian camel and other ralated mammals.

Key words: Bactrian camel, orthologous gene, RNA-seq, transcriptome