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De novo assembly and characterization of skin transcriptome using RNAseq in sheep (*Ovis aries*)

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ABSTRACT. Wool is produced via synthetic processes of wool follicles, which are embedded in the skin of sheep. The development of new-generation sequencing and RNA sequencing provides new approaches that may elucidate the molecular regulation mechanism of wool follicle development and facilitate enhanced selection for wool traits through gene-assisted selection or targeted gene manipulation. We performed *de novo* transcriptome sequencing of skin using the Illumina Hiseq 2000 sequencing system in sheep (*Ovis aries*). Transcriptome *de novo* assembly was carried out via short-read assembly programs, including SOAPdenovo and ESTScan. The protein function, clusters of orthologous group function, gene ontology function, metabolic pathway analysis, and protein coding region prediction of unigenes were annotated by BLASTx, BLAST2GO, and ESTScan. More than 26,266,670 clean reads were collected and assembled into 79,741 unigene sequences, with a final assembly length of 35,447,962 nucleotides. A total of 22,164 unigenes were annotated, accounting for

36.27% of the total number of unigenes, which were divided into 25 classes belonging to 218 signaling pathways. Among them, there were 17 signal paths related to hair follicle development. Based on mass sequencing data of sheepskin obtained by RNA-Seq, many unigenes were identified and annotated, which provides an excellent platform for future sheep genetic and functional genomic research. The data could be used for improving wool quality and as a model for human hair follicle development or disease prevention.

Key words: Sheep (*Ovis aries*); Skin; *De novo* assembly; Transcriptome; RNA sequencing

