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Hair follicle transcriptome profiles during the transition from anagen to catagen in Cashmere goat (*Capra hircus*)

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ABSTRACT. Previous molecular genetic studies of the goat hair life cycle have focused primarily on a limited number of genes and proteins. To identify additional genes that may play important roles in hair follicle cycle regulation, Illumina sequencing technology was used to catalog differential gene expression profiles in the hair growth cycle (anagen to catagen) of goat, comparing the primary hair follicle with the secondary hair follicle. There were 13,769 and 12,240 unigenes assembled from the reads obtained from primary hair follicle and secondary hair follicle, respectively. Genes encoding keratin proteins and keratin-associated proteins were the

most highly expressed. A total of 5899 genes were differentially expressed in anagen *vs* catagen primary hair follicles, with 532 genes up-regulated and 5367 genes down-regulated. A total of 5208 genes were differentially expressed in anagen *vs* catagen secondary hair follicle, including 545 genes that were up-regulated and 4663 genes that were down-regulated. Numerous hair growth genes are expressed in the goat hair follicle, of which 73 genes showed co-up-regulation in both hair follicles during the anagen stage. Many of these up-regulated genes, such as *STC2*, *VEGFR*, and *ROR2*, are known to be transfactors in the process of cell differentiation and in the cell cycle. The differential gene expression profiles between primary hair follicles and secondary hair follicles obtained provide a foundation for future studies examining the network of gene expression controlling hair growth cycle in Cashmere goat.

Key words: Cashmere goat; Gene expression; Hair growth cycle; Transcriptome

