Transcript analysis of a goat mesenteric lymph node by deep next-generation sequencing

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ABSTRACT. Deep RNA sequencing (RNA-seq) provides a practical and inexpensive alternative for exploring genomic data in non-model organisms. The functional annotation of non-model mammalian genomes, such as that of goats, is still poor compared to that of humans and mice. In the current study, we performed a whole transcriptome analysis of an intestinal mucous membrane lymph node to comprehensively characterize the transcript catalogue of this tissue in a goat. Using an Illumina HiSeq 4000 sequencing platform, 9.692 GB of raw reads were acquired. A total of 57,526 lymph transcripts were obtained, and the majority of these were mapped to known transcriptional units (42.67%). A comparison of the mRNA expression of the mesenteric lymph nodes during the juvenile and post-adolescent stages revealed 8949 transcripts that were differentially expressed, including 6174 known genes. In addition, we functionally classified these transcripts using Gene Ontology (GO) and the Kyoto Encyclopedia of Genes and Genomes (KEGG) terms. A total of 6174 known genes were assigned to 64 GO terms, and 3782 genes were assigned to 303 KEGG pathways, including some related to immunity. Our results reveal the complex

transcriptome profile of the lymph node and suggest that the immune system is immature in the mesenteric lymph nodes of juvenile goats.

Key words: Transcriptome; RNA-seq; Lymph; Goat