COMPARATIVE TRANSRIPTOME RESEARCH IN HU SHEEP HYPOTHALAMUS ASSOCIATED WITH PROLIFICACY

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Hu sheep is unique in China, the world famous prolific sheep breeds, with early sexual maturity, a seasonal breeding and prolificacy. This study aims to investigate the key functional genes associated with prolificacy by a hypothalamus transcriptome analysis. We performed RNA-seq and bioinformatics analysis between Hu sheep with high prolificacy (H, n=3, litter size=3 for three consecutive lambing) and low prolificacy (L, n=3, litter size=1 for three consecutive lambing), then the expression levels of differentially expressed (DE) genes in the hypothalamus tissue were verified by real-time reverse transcription quantitative PCR (qRT-PCR). By comparing and analyzing transcriptome data, 56 DE genes were obtained, 24 of them were up-regulated and 32 of them were down regulated between the H and L group. GO classification and annotation analysis showed that these DE genes are closely related to biological processes such as organ development, signal transduction and transcriptional regulation. Meanwhile, molecular events such as DNA binding, protein binding and ATP binding are also involved. KEGG pathway analysis showed that the neural signal pathway, GABA signaling pathway might play an important role in hypothalamus regulation of ovulation and follicular development. The qPCR analysis of 5 randomly selected DE genes were consistent with sequencing results. This study provides a basis for further explanation of the basic molecular mechanism of hypothalamus, but also provides a new idea for a comprehensive understanding of prolificacy characteristics in Hu sheep.

Key words: Hu sheep; hypothalamus; transcriptome; qRT-PCR