

عنوان مقاله:

The Comparative Analysis of Gene Expression Profiles in Lymph Node Cells of Naturally BLV-infected and Uninfected Bovine

محل انتشار:

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خلاصه مقاله:

Bovine leukemia virus (BLV) is the etiologic agent of enzootic bovine leucosis (EBL) for the bovine host. In this study to examine gene expression changes in the manifestation of the EBL malignancy, four pooled RNA samples (three RNAs in each sample) were applied for transcriptome sequencing using RNA-seq technique. Differential expression analysis was done to compare the infected bovine group with the healthy bovine group using DESeq2 package in R software. Furthermore, functional gene ontology (GO) term and KEGG pathway enrichment analysis were established using the DAVID online database to identify involved GO terms and pathways in the host response to BLV infection. Our results suggested that 371 up- and 72 downregulated genes were involved in EBL with statistically significant threshold $\log_2\text{foldchange}$ (LFC) = 1 and false discovery rate (FDR) <0.05 that were enriched in 74 biological processes and 20 KEGG pathways. Most of identified genes were associated with cancer, especially B-cell malignancies. The glycolysis/glycogenesis metabolic process is activated in B cells that confers growth and survival advantages in tumor and dysregulated CXCL10, IL17R, BTK, CDK4 and SYK genes known as valid biomarkers to increase the proliferation of malignant cell. The outcomes can provide a list of involved genes in the malignancy and .help to screen candidate genes for cancer therapy in the future

کلمات کلیدی:

BLV, EBL, transcriptome, RNA-Seq, Gene Ontology

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