Effective Regulatory Pathways and Hub Genes in HCoV-229E Pathogenesis: RNA-Seq Data Analysis

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ABSTRACT

Introduction: Human coronavirus 229E (HCoV-229E) infects humans and bats. It is associated with various respiratory symptoms, ranging from the common cold to terrible outcomes such as pneumonia and bronchiolitis. Understanding the molecular biology and gene function after infection with coronaviruses is crucial for developing appropriate strategies for prevention and treatment. This study aimed to investigate the transcriptomic changes in response to the infection with HCoV-229E and identify hub genes and significant regulatory pathways involved in the host cell response to this infection.

Methods and Materials: RNA-Seq data was downloaded, and differentially expressed genes (DEGs) were identified in the infected and untreated samples. Pathway enrichment and gene ontology analysis were carried out using the DAVID web tool, while the protein-protein interaction network was generated using the Cytoscape software. The Cytohubba plugin of Cytoscape software was utilized to identify hub genes.

Results: A total of 946 genes were identified as having differential expression, with 717 genes upregulated and 229 genes downregulated. Major pathways associated with upregulated genes were the IL-17 signaling pathway, TNF signaling pathway, and Legionellosis. The most significant pathways associated with downregulated DEGs included complement and coagulation cascades, coronavirus disease (COVID-19), and drug metabolism (cytochrome P450). The most significant biological process terms for the upregulated genes was inflammatory response. Fifteen hub genes were identified, all associated with inflammatory and immune responses, as well as cytokine storms.

Conclusion and Discussion: Identifying DEGs could be a practical approach for recognizing potential therapeutic targets to develop effective drug delivery systems against HCoV-229E infection. The Potential drugs predicted in this study mainly aim to decrease the severity of inflammatory response and inhibit coronavirus replication. Common mechanisms and genes were identified with various categories of coronaviruses, including SARS-CoV-2. Understanding these mechanisms and identifying these genes can offer valuable insights into preventing and treating diseases caused by these viruses.

Keywords: Coronaviruses, RNA-Seq, SARS-CoV-2