

# Preventive Effect of Colchicine on Severe Acute Pancreatitis in Rats Based on Comprehensive Bioinformatics Analysis

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## Abstract

**Purpose** Severe acute pancreatitis (SAP) is a life-threatening condition characterized by rapid progression and high mortality. While colchicine has shown potential in mitigating SAP-related inflammation, its underlying mechanisms remain unclear. This study aimed to explore the molecular mechanisms by which colchicine alleviates SAP in rats through comprehensive transcriptomic and bioinformatics analyses. **Methods** Transcriptomic sequencing was performed on pancreatic tissues from control (CON), SAP, and colchicine-treated (SAP+COL) rat groups. Differential gene expression analysis, Gene Ontology (GO), and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment were conducted to identify key pathways. A protein-protein interaction (PPI) network was constructed using the STRING database, and hub genes were identified through topological analysis. The expression of hub genes was validated via qRT-PCR and immunohistochemistry (IHC). Immune cell infiltration was analyzed using the xCELL algorithm, and correlations between hub genes and immune cells were assessed. **Results** The study identified seven hub genes associated with colchicine's protective effects: IL-6, Mmp9, Hif1a, Timp1, Mpo, Lcn2, and Thbs1. Colchicine significantly reduced the infiltration of macrophages and neutrophils in SAP tissues while increasing CD8+ T cell infiltration. Notably, Hif1a and Thbs1 showed strong positive correlations with macrophage and neutrophil infiltration, whereas Mmp9 exhibited a negative correlation with CD8+ T cell infiltration. GO and KEGG analyses revealed that these genes are involved in inflammatory and immune-related pathways, such as the TNF, NF- $\kappa$ B, and IL-17 signaling pathways. **Conclusion** Colchicine alleviates SAP by modulating the expression of key genes related to inflammation and immune response, particularly through its effects on macrophage, neutrophil, and CD8+ T cell dynamics. The identified hub genes (IL-6, Mmp9, Hif1a, Timp1, Mpo, Lcn2, and Thbs1) represent potential therapeutic targets for SAP, with Hif1a, Thbs1, and Mmp9 playing critical roles in immune cell regulation. These findings provide a theoretical basis for the clinical application of colchicine in SAP treatment.

## Keywords

Acute Severe Pancreatitis, Colchicine, Bioinformatics, Protein-Protein Interaction, Immune Cell Infiltration