

## Identification of Common Genes, miRNAs, and Transcription Factors through Comprehensive Network Analysis for Enhanced Management of Gastritis and Stomach Cancer

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### Abstract:

Gastritis is a chronic inflammatory condition of the gastric mucosa and a proven precursor to stomach cancer which is one of the most common causes of cancer-related mortality in the world as a result of late diagnosis. Genetic and epigenetic changes promote the inflammation to malignancy. The proposed research employs the network-based method of bioinformatics to determine widespread genes, microRNAs (miRNAs), and transcription factors between the conditions to manage them better in the clinic. Gastritis and stomach neoplasma-related genes were scanned in the Comparative Toxicogenomics Database (CTD), and the top 200 genes with inference scores were selected; the intersection of the two was identified. NetworkAnalyst 3.0 created gene-miRNA interaction studies, stomach tissue-specific coexpressions, and transcription factor-gene studies, which identified overlapping pathways in NF-KB signaling, cell cycle regulation, apoptosis, and oxidative stress. Hub miRNAs regulate several disease genes post-transcriptionally, whereas progression stage is driven by master transcription factors, such as MYC, RELA, and STAT3, as observed in dense network clusters and stomach-specific modules. These molecular signatures explain the inflammation-cancer transformation and thus, can be used as biomarkers of early detection, prognosis, and treatment. Attacking such regulators aids in precision medicine, that is, personalized treatments to prevent disease cascades and improve outcome. They should be further clinically validated in the future to be translated into practice to bridge the gap between gastritis and stomach cancer at a molecular level to develop more advanced diagnostics and interventions.

### Keywords:

Gastritis, stomach cancer, network analysis, miRNA, transcription factors.