

Integrated Transcriptomic and Regulatory Network Analysis Identifies Candidate Molecular Signatures Associated with Endometriosis

Forouzan Amerizadeh,

1. Department of Internal Medicine, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Background: Endometriosis is a chronic gynecological disorder characterized by ectopic growth of endometrial-like tissue and is frequently associated with pelvic pain and infertility. Despite extensive investigation, the molecular mechanisms underlying endometriosis remain incompletely understood. This study aimed to identify differentially expressed genes and explore their functional, network, and transcriptional regulatory characteristics in endometriosis.

Methods: The publicly available microarray dataset GSE7305 was obtained from the Gene Expression Omnibus (GEO) database. The dataset includes gene-expression profiles from 10 endometriosis samples and 10 normal endometrial controls. Differential expression analysis was performed using GEO2R based on the limma framework. Multiple-testing correction was conducted using the Benjamini–Hochberg method, and genes with adjusted $P < 0.05$ and an absolute log2 fold change ≥ 1 were considered significantly differentially expressed. Identified genes were subjected to Gene Ontology (GO)-based functional characterization and protein–protein interaction network analysis. Network organization and potential molecular modules were further investigated using CytoCluster. In parallel, promoter sequences of selected differentially expressed genes were analyzed for potential regulatory motifs, with motif comparison and functional annotation performed using Tomtom and GOMO.

Results: Results: Differential expression analysis identified 2,860 significantly altered probes between endometriosis and normal endometrial tissues after multiple-testing correction. These alterations included both upregulated and downregulated expression patterns. Subsequent functional annotation, interaction-network analysis, and promoter-level regulatory assessment were used to explore the biological and regulatory characteristics of the identified molecular signature. Network clustering further supported the presence of potentially coordinated molecular modules associated with endometriosis.

Conclusion: Integrated transcriptomic, functional, network, and promoter analyses of GSE7305 identified candidate molecular signatures potentially associated with endometriosis. These findings provide a hypothesis-generating framework for understanding disease-related molecular alterations and warrant validation in independent cohorts and experimental studies.

Keywords: Endometriosis; Transcriptomics; Bioinformatics