

Identification of Key Molecular and Regulatory Signatures in Late-Onset Preeclampsia Using Integrated Bioinformatics Analysis

Forouzan Amerizadeh,

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

Background: Late-onset preeclampsia (LOPE) is a pregnancy complication characterized by complex placental molecular alterations whose regulatory mechanisms remain incompletely understood. Transcriptomic analysis of placental tissue may provide insight into genes and regulatory pathways associated with disease development. This study aimed to identify differentially expressed genes and explore their functional, network, and transcriptional regulatory characteristics in LOPE.

Methods: The publicly available placental microarray dataset GSE74341 was obtained from the Gene Expression Omnibus (GEO) database. Gene-expression profiles from eight women with late-onset preeclampsia and five gestational age-matched term controls were compared using GEO2R and the limma framework. Multiple-testing correction was performed using the Benjamini–Hochberg method, and adjusted $P < 0.05$ was considered statistically significant. Significant genes were subjected to Gene Ontology (GO)-based functional characterization and protein–protein interaction network analysis. Network topology and potential molecular modules were further investigated using CytoCluster. In parallel, promoter sequences of selected genes were analyzed for potential regulatory motifs, with motif comparison and functional characterization performed using Tomtom and GOMO.

Results: Transcriptomic comparison identified 383 significantly altered probes between LOPE placental samples and term controls, comprising both increased and decreased expression patterns. Functional and network-based analyses indicated that the identified molecular alterations were distributed across multiple biological processes and interaction networks. Promoter-level analysis further suggested the presence of potentially shared regulatory elements among selected differentially expressed genes.

Conclusion: Integrated analysis of GSE74341 revealed distinct placental transcriptional alterations associated with late-onset preeclampsia. Combining differential expression, functional annotation, network clustering, and promoter regulatory analysis provides a framework for identifying candidate molecular mechanisms potentially involved in LOPE and warrants further validation in independent cohorts.

Keywords: Late-onset preeclampsia; Transcriptomics; Bioinformatics