



ICPSE
2026

نوزدهمین کنفرانس بین المللی پژوهش های نوین در روانشناسی، علوم اجتماعی، علوم تربیتی و آموزشی

گرجستان - ۲۷ شهریور ۱۴۰۵ - آکادمی بین المللی علوم و مطالعات گرجستان

<http://icpse.ir>
info@icpse.ir

18 Septembre 2026 - TBILISI GEORGIA

Integrated Transcriptomic and Regulatory Analysis of Whole-Blood Gene Expression in Major Depressive Disorder

Forouzan Amerizadeh

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

Background: Major depressive disorder (MDD) is a heterogeneous psychiatric disorder associated with complex molecular and regulatory alterations. Peripheral blood transcriptomics provides an accessible approach for investigating disease-related molecular signatures. This study aimed to identify differentially expressed genes in MDD and explore their functional, network, and transcriptional regulatory characteristics.

Methods: The publicly available microarray dataset GSE98793 was obtained from the Gene Expression Omnibus (GEO) database. It includes whole-blood expression profiles from 128 individuals with MDD and 64 healthy controls generated using the Affymetrix Human Genome U133 Plus 2.0 Array. Differential expression analysis was performed using GEO2R based on the limma framework, with Benjamini–Hochberg correction for multiple testing. Genes with adjusted $P < 0.05$ were considered significant. Identified genes were further evaluated through Gene Ontology-based functional characterization, protein interaction analysis, network exploration, and promoter motif analysis to investigate potential regulatory signatures.

Results: Five genes remained significant after multiple-testing correction: SLC39A10, GZMK, RETN, MAFK, and PFKFB2, showing both upregulated and downregulated expression patterns. These genes were considered a focused molecular signature for exploratory downstream analyses. Owing to the limited number of significant genes, functional enrichment, interaction networks, and regulatory findings were interpreted as hypothesis-generating rather than confirmatory.

Conclusion: Whole-blood transcriptomic analysis of GSE98793 identified a small but statistically supported set of genes associated with MDD. Integrating differential expression with functional and regulatory analyses may provide complementary insights into peripheral molecular alterations in depression. Independent cohort validation and experimental studies are required to confirm the reproducibility and biological relevance of these findings.

Keywords: Major depressive disorder; GSE98793; transcriptomics; differential gene expression; promoter motif analysis