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Comparison of circulating miRNAs expression alterations in matched serum and tissue samples during Gestational diabetes mellitus progression

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<u>Abstract</u>

Objectives: MicroRNAs (miRNAs) are an emerging class of small non-coding RNAs implicated in wide variety of cellular processes. The purpose of this study was to evaluate the altered expression of selected miRNAs between non-glucose tolerant (NGT) and Gestational diabetes mellitus (GDM) mother matched maternal blood serum (MB), Cord blood serum (CB) and Placental tissue samples (Pl).

Methods: Twenty serum and matched placental tissues samples (MB n = 10, CB n = 5, and Pl n = 5) were selected, for isolation of miRNA fraction. Stem-loop RT-qPCR was used for quantitative expression of selected miRNAs, followed by target prediction, Gene Ontology analysis and pathways identification. Target genes were further verified in vitro by RT-qPCR.

Results: In NGT vs GDM comparison, all five miRNAs namely let 7a- 5P, miR7-5P, miR9-5P, miR18a-5P and miR23a-3P were found to be significantly overexpressed (p < 0.05) with comparatively higher expression of miR 7 and miR 9 in all three samples namely MB, CB and Pl. Comparative fold change expression analysis revealed higher expression of these miRNAs in MB followed by placenta and cord blood samples of GDM as compared to controls. Target prediction and pathway enrichment analysis revealed the MAPK signaling, Insulin signaling, JAK-STAT signaling, and Type II diabetes mellitus as major pathways regulated by these altered miRNAs. Major target genes namely NRAS, RAF1, IL6R, PGC1A, IRS1 and IRS2 were found to be downregulated in GDM.

Conclusion: Higher expression of these miRNAs particularly miR7 and miR9 in GDM mothers lead to down-regulation of their target genes involved in inflammatory and insulin metabolism which provide insights into the molecular mechanism that underlie GDM. These miRNAs can be used as non-invasive diagnostic markers for early detection of GDM.



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