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TITLE

PLACENTAL MICRORNA EXPRESSION IN PREGNANCIES COMPLICATED BY GESTATIONAL DIABETES MELLITUS AND PREECLAMPSIA

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ABSTRACT

Background and aims:The incidence of gestational diabetes mellitus (GDM) has increased over the world. Relevant studies are of importance because GDM is associated with unfavorable perinatal outcomes including preeclampsia (PE), preterm labor, fetal macrosomia and long-term effects – a high risk of metabolic syndrome and type 2 diabetes mellitus. The aim of study was to determine changes next generation sequencing (NGS) of the placental miRNAs expression profiles between pregnancies of patients with GDM with and without PE.

Methods:The study was performed on placenta samples from four groups of women: patients with GDM (n= 2), PE (n=4), GDM with PE (n=4) and with normal pregnancies (n=6). miRNA expression profiles in placentas were investigated using an Ion Torrent sequencing system. Sequencing data were processed using a comprehensive analysis pipeline for deep miRNA sequencing (CAP-miRSeq). Statistical analysis was performed with Statistica 10.0 (StatSoft, Inc., Tulsa, OK, USA).

Results:A total of 27 miRNAs ($P<0.01$) exhibited altered expression patterns in the GDM with PE placentas, when compared with those in the PE placentas. Only one his-miR-451a of the 27 miRNAs, the difference in expression was significant ($FDR<0.05$). Comparative analysis of the expression profile of miRNAs in the GDM placentas and PE placentas were found differences 53 microRNA expression of which were reliable differences in the expression of hsa-miR-4532 ($p <0,0001$ FDR = 0.0008), hsa-miR-34c-5p ($p <0,0001$, FDR = 0.0083), and hsa-miR-193b-5p ($p <0,0001$, FDR = 0.0139) in pregnancy complicated by GDM, without the development of PE.

Conclusions:The present results suggest that GDM and PE is associated with specific alterations in the placental miRNA expression pattern, and therefore, provide novel targets for further investigation of the molecular mechanisms underlying GDM and PE pathogenesis.

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