Identification and Preliminary Validation of Biomarkers Associated with Mitochondrial and Programmed Cell Death in Preeclampsia

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Abstract

(1) Background: The role of mitochondrial and programmed cell death (mtPCD)-related genes in the pathogenesis of preeclampsia (PE) remains poorly understood. (2) Methods: This study investigates the role of mtPCD genes in the pathogenesis of PE through bioinformatics and experiments. DE-mtPCD was identified as potential biomarkers from GSE10588 and GSE98224 datasets, then validated. Hub genes were defined using SVM, LASSO, and Boruta, considering their consistent expression as biomarkers. Their performance was evaluated using nomogram and ANN models. Biomarkers were utilized for localization, functional analysis, regulatory network construction, and drug prediction. Validation was done clinically using RT-qPCR. (3) Results: Four genes (SLC25A5, ACSF2, MFF, and PMAIP1) were identified as biomarkers distinguishing PE from normal groups. Functional analysis revealed their involvement in various pathways. Immune analysis showed connections between immune cells and biomarkers. Additionally, a regulatory network was constructed based on the biomarkers and database predictions. The result revealed that KCNQ1OT1 regulated ACSF2 expression by modulating hsa-miR-200b-3p. And drug predictions like clodronic acid were made. RT-qPCR confirmed altered gene expression in PE. (4) Conclusion: These four mtPCD-related biomarkersmay play an important role in the development of PE, providing new insights into the diagnosis and development mechanisms of PE.

Keywords

Mitochondrial, Programmed Cell Death, Preeclampsia, Bioinformatics, Database, PT-PCR