

Expression profile of LncRNA ANRIL, miR-186, miR-181a, and MTMR-3 in patients with preeclampsia

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Abstract

Preeclampsia (PE) is a leading cause of maternal and neonatal morbidity and mortality worldwide. Several studies demonstrated the role of lncRNAs and miRNAs in the pathogenesis of preeclampsia; the aim was to detect the expression profiles of serum LncRNA ANRIL, miR-186, miR-181a, and MTMR-3 in patients with preeclampsia. The study included 160 subjects divided into 80 subjects considered as a control group, 80 patients with preeclampsia. We found that there was a significant difference between the preeclampsia and control groups with up-regulation of miR-186 median (IQR) = 4, 29 (1.35–7.73) ($P < 0.0001$), miR-181a median (IQR) = 2.45 (0.83–6.52) ($P = 0.028$), and downregulation of lncRNA ANRIL median (IQR) = 0.35(0.28–0.528) ($P < 0.0001$), MTMR median (IQR) = 0.32(0.155–1.11), ($P < 0.0001$). ROC curve of lncRNA ANRIL, miR-186, miR-181a, and MTMR-3 in preeclampsia patients showing the roles of these markers in the diagnosis of preeclampsia. In conclusion, serum LncRNA ANRIL, miR-186, miR-181a, and MTMR-3 could be promising biomarkers in the diagnosis of preeclampsia.