Abstract

Introduction: preeclampsia is an important cause of maternal and perinatal morbidity-mortality throughout the world. Its etiopathogenesis still remains an enigma; however, the advances made in genomics and proteomics promise early identification of the disease or the risk of suffering from it. Objective: thoughts on the most promising advances in genomics and proteomics regarding the pressing goal of early detection and/or prediction of preeclampsia risk. Conclusions: two functional polymorphisms, one on the ACE gene (I/D) and another one in the COMT gene (Val158Met) are the most promising results of genomics for identifying women at genetically higher risk of developing preeclampsia during pregnancy. Proteomics has identified SERPINA-1 as a useful biomarker for detecting preeclampsia in the urine of pregnant women at least 10 weeks before clinical manifestations as well as the need for early termination of pregnancy. Such recent progress in genomics and proteomics adapted to clinical practice might reduce the impact of this disease on maternal health.

Keywords

Genomics, proteomics, maternal health, pregnancy, preeclampsia, angiotensin converting enzyme (ACE), catechol-O-methyltransferase (COMT), SERPINA-1.