

miRNAs Expression Profiling of Preeclamptic Pregnancies

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Preeclampsia (PE) is one of the most studied pregnancy complication and human pregnancy-specific syndrome characterized by hypertension ($\geq 140/90$ mmHg or mean arterial pressure ≥ 105 mmHg) and proteinuria (≥ 300 mg of protein in 24-h urine collection or $\geq 1+$ protein on urine dipstick) that occurs after 20 week of pregnancy. Aberrant expression of some miRNAs in placenta caused pathogenesis of PE with altering key processes in placental development as lead to limited proliferation and shallow invasion of trophoblast cells, as well as insufficient remodeling of maternal spiral arteries and defective angiogenesis. The role of posttranscription regulation in preeclampsia is largely unknown. MicroRNAs (miRNAs) regulate the expression of nearly 30% of all the human genes and participate in all fundamental cell processes. Transcriptional analysis of miRNAs shows that human placenta expresses more than 600 miRNA species, including placenta-specific ones with high level of expression during different stage of pregnancies. miRNAs have emerged as key regulators of gene expression stability implicated in cell proliferation, apoptosis, and development.

Using microarray profiling of human miRNAs (1368 probe) were measured in samples collected from 18 PE cases and 18 NT. The analysis indicated that 406 of these miRNAs in all placentas and 42 of these miRNAs in all maternal plasma were expressed. The relative expression of 12 miRNAs (P 0.05 and 2-fold) in

maternal plasma (hsa-miR-191*, hsa-let-7b*, hsa-let-7f-1*, hsa-miR-1539, hsa-miR-23c, hsa-miR-33b*, hsa-miR-425*, hsa-miR-4313, hsa-miR-550a, hsa-miR-933, hsa-miR-877* and hsa-miR-1183) were differentially expressed in PE and NT.

Results showed that there were differentially expressed placenta and maternal plasma miRNAs in patients with PE and control cases. These plasma miRNAs might be used as notable biomarkers for diagnosis of preeclampsia.