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MicroRNA expression profiling in placenta and maternal plasma in early pregnancy loss

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Early pregnancy loss (EPL), is determined as the unintentional expulsion of an embryo or fetus prior to the 12th week of gestation. EPL frequency is ~15% in pregnancies. Fetal development and growth is associated with placental function and vessel development; therefore, the placental genome would represent a useful EPL model for epigenetic and genomic studies. An important factor of placental development and function is epigenetic regulation of gene expression. MicroRNAs (miRNAs) are the primary epigenetic regulators which have an important role in placental development and function. In the present study, maternal plasma and villous tissue were collected from 16 EPL cases during 6th-8th gestational weeks (GWs) and 8 abortions (control group) in 6th- 8th GWs. Detection of the differences in miRNA expression was performed using microarrays and dysregulated miRNAs were validated by RT-qPCR. miRNA microarray findings revealed that four miRNAs, including hsa-miRNA (miR-125a-3p, hsa- miR-3663-3p, hsa-miR-423-5p and hsa-miR-575 were upregulated in tissue samples. In maternal plasma, two miRNAs (hsa-let-7c, hsa-miR-122) were upregulated and one miRNA (hsa-miR-135a) was downregulated. A total of 6 out of 7 dysregulated miRNAs were validated using RT-qPCR. The aim this study was to detect dysregulated miRNAs in maternal plasma and villous cells and identify the target genes of dysregulated miRNAs and their associated pathways. The target gene analyses have revealed that the affected genes are primarily associated with cell migration, proliferation, implantation, adhesion, angiogenesis and differentiation and all are involved with EPL pathogenesis. Therefore, the present study may contribute to the understanding of the molecular mechanisms which lead to EPL.

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