Novel Early Prediction Modalities for Pregnancy-Related ComplicationsBased on MicroRNA Biomarkers and Maternal Clinical Characteristics

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Background: We were interested if it would be feasible to develop efficient cost effective early predictive models for identification of women at increased risks of adverse pregnancy outcomes based on a selection from 6 cardiovascular disease associated microRNAs (miR-181a-5p, miR-20a-5p, miR-146a-5p, miR-574-3p, miR-1-3p, and miR-16-5p), whose altered expression was observed in particular pregnancy-related complications.

Methods: Mirna gene expression was studied retrospectively in peripheral venous blood samples derived from singleton Caucasian pregnancies diagnosed with gestational hypertension (GH), preeclampsia (PE), HELLP syndrome, fetal growth restriction (FGR), small for gestational age fetuses (SGA), gestational diabetes mellitus (GDM), preterm birth in the absence of other pregnancy-related complications, late miscarriage, stillbirth and normal term pregnanciesusing real-time RT-PCR. These microRNAs were further combined with selected maternal clinical characteristics representing risk factors for individual pregnancy-related complications. In addition, first trimester screening for PE and/or FGR, and first trimester screening for spontaneous preterm birth, both by FMF algorithm, may be added to the models, since these two independent variables slightly increased a detection rate of pregnancies at risk of development of GH, PE, HELLP syndrome, FGR, SGA, preterm birth, and GDM.

Results and Conclusion: The models based on the combination of 6 microRNAs and maternal clinical variables have a very high predictive potential for identification of women at increased risks of adverse pregnancy outcomes (GH: 69.88% cases, PE: 83.33% cases, HELLP: 92.86% cases, FGR: 73.17% cases, SGA: 81.08% cases, GDM on therapy 89.47% cases, late miscarriage: 84.85% cases, and stillbirth 91.67% cases at 10.0% FPR)and may be implemented into the routine first trimester screening programmes.

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