

# Network Creation and Comparison From MicroRNAs Extracted From Peripheral Blood Of Primigravidae Submitted Or Not To Psychosocial Intervention

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## Abstract

Environmental disturbance during the initial phases of human development, especially the gestational period, brings consequences that can last the offspring lifetime. Among these environmental problems, the mother's exposition to different stressors is correlated to a significant increase in the offspring's risk of developing various adversities, including cognition problems, emotional reactivity, impaired sociability and psychiatric disorders. The here proposed study is part of a randomized double-blind psicossocial intervention for primigravidae in socioeconomic vulnerability. Notwithstanding, there is a lack of knowledge on the possible biological markers of the intervention. Taking this into account, the present study has the goal to associate an important epigenetic factor, the microRNA, which has its expression associated to the period mentioned and disturbances along it, with the intervention. To this end, a comparison between two interaction networks microRNAs-mRNA will be performed. The complex networks are going to be created using the differentially expressed microRNAs from two gestational times. One network will be created using the differentially expressed microRNAs between the baseline (T0) and 30 weeks of gestation (T1), extracted from placental exosomes from peripheral blood of pregnant submitted to psychosocial intervention (cases), and the other network from differentially expressed microRNAs from the same moments (T0 and T1), collected from mothers not submitted to the intervention (controls). After the microRNA differential expression results from the RT-qPCR, a target prediction will be executed, using only experimentally validated targets, and the two networks containing the miRNAs and its target genes are going to be created on Cytoscape. The databases for experimentally validated targets are going to be extracted from miRTarBase, TarBase and miRwalk2.0. Different measurements collected from each network individually, using global topological properties and graph entropy are going to be compared to obtain a unique global value that represents the graphical differences between the two networks created.

Funding: Fundação Maria Cecília Souto Vidigal, Grand Challenges Canada, FAPESP e CNPq