**20.Overexpression of miR-200b-3p in Menstrual Blood-Derived Mesenchymal Stem Cells from Endometriosis Women**

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Abstract

The key relationship between Sampson's theory and the presence of mesenchymal stem cells in the menstrual flow (MenSCs), as well as the changes in post- transcriptional regulatory processes as actors in the etiopathogenesis of endometriosis, are poorly understood. No study to date has investigated the imbalance of miRNAs in MenSCs related to the disease. Thus, through literature and in silico analyses, we selected four predicted miRNAs as regulators of EGR1, SNAI1, NR4A1, NR4A2, ID1, LAMC3, and FOSB involved in pathways of apoptosis, angiogenesis, response to steroid hormones, migration, differentiation, and cell proliferation. These genes are frequently overexpressed in the endometriosis condition in our group studies. They were the trigger for the miRNAs search. Therefore, a case-control study was conducted with MenSCs of women with and without endometriosis (ten samples per group). Crossing information obtained from the STRING, PubMed, miRPathDB, miRWalk, and DIANA TOOLS databases, we chose to explore the expression of miR-21-5p, miR-100-5p, miR-143-3p, and miR- 200b-3p by RT-qPCR. We found an upregulation of the miR-200b-3p in endometriosis MenSCs (P = 0.0207), with a 7.93-fold change (ratio of geometric means) compared to control. Overexpression of miR-200b has been associated with increased cell proliferation, stemness, and accentuated mesenchymal-epithelial transition process in eutopic endometrium of endometriosis. We believe that dysregulated miR-200b-3p may establish primary changes in the MenSCs, thus favoring tissue implantation at the ectopic site.

Keywords: Endometriosis; MenSCs; Menstrual blood; RT-qPCR; miR-200b-3p.