**22. Clues for Improving the Pathophysiology Knowledge for Endometriosis Using Serum Micro-RNA Expression**

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Abstract

The pathophysiology of endometriosis remains poorly understood. The aim of the present study was to investigate functions and pathways associated with the various miRNAs differentially expressed in patients with endometriosis. Plasma samples of the 200 patients from the prospective "ENDO-miRNA" study were analyzed and all known human miRNAs were sequenced. For each miRNA, sensitivity, specificity, and ROC AUC values were calculated for the diagnosis of endometriosis. miRNAs with an AUC ≥ 0.6 were selected for further analysis. A comprehensive review of recent articles from the PubMed, Clinical Trials.gov, Cochrane Library, and Web of Science databases was performed to identify functions and pathways associated with the selected miRNAs. In total, 2633 miRNAs were found in the patients with endometriosis. Among the 57 miRNAs with an AUC ≥ 0.6: 20 had never been reported before; one (miR-124-3p) had previously been observed in endometriosis; and the remaining 36 had been reported in benign and malignant disorders. miR- 124-3p is involved in ectopic endometrial cell proliferation and invasion and plays a role in the following pathways: mTOR, STAT3, PI3K/Akt, NF-κB, ERK, PLGF-ROS, FGF2-FGFR, MAPK, GSK3B/*β*-catenin. Most of the remaining 36 miRNAs are involved in carcinogenesis through cell proliferation, apoptosis, and invasion. The three main pathways involved are Wnt/*β*-catenin, PI3K/Akt, and NF-KB. Our results provide evidence of the relation between the miRNA profiles of patients with endometriosis and various signaling pathways implicated in its pathophysiology.

Keywords: endometriosis; miRNA; pathophysiology; pathways.