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Poster Presentations

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Evaluation of miRNAs involved in patients with endometriosis as diagnostic and therapeutic biomarkers using bioinformatics analysis

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Background: Endometriosis is one of the most common reproductive diseases in women. About 10% of women are pregnant, and about 50% of women between the ages of 30 and 50 and between 30 and 50% of women experience pelvic pain or infertility due to endometriosis. There are several treatments available for people with endometriosis, but facilitating and optimizing early detection of the disease can help manage its treatment. miRNAs are important regulatory molecules at the cellular level that control the expression of many genes due to their inhibitory effect. miRNAs can be found in human secretions. Therefore, these regulatory molecules can be used as diagnostic biomarkers for endometriosis.

Objective: This study examined the ectopic and eutopic tissue data of patients with endometriosis and isolated the miRNAs in the extracellular matrix.

Materials and Methods: In this study, using bioinformatics analysis, we first isolated the appropriate data through the GEO database. We then uploaded the hypex gene to examine the signal path in the Enrichr database and the KEGG library. We loaded the genes involved in important pathways into the STRING database and measured their protein network. We then used the Targetscan database to obtain miRNAs.

Results: 700 low-expression genes were selected with LogFC < 2. These genes played a more prominent role in complement and coagulation cascades, cell adhesion molecules, TGF-beta, and Hedgehog signaling pathways. Of these pathways, 34 genes were involved in this pathways and extracellular matrix. After the examination, the hsa-miR-4800-3p, hsa-miR-4473, hsa-miR-614, hsa-miR-4671-3p, and hsa-miR-3659 miRNAs were identified more clearly.

Conclusion: Finally, this study showed that miRNAs, between ectopic and eutopic tissues, were significantly identified and could be found in the serum or plasma samples of patients with endometriosis.

Key words: *Endometriosis, Biomarkers, Bioinformatics analysis, Micro RNAs.*