

BIOINFORMATIC ANALYSIS OF TRANSCRIPTOMIC DATA IDENTIFIES miRNAS RELEVANT FOR ENDOMETRIOSIS PATHOGENESIS

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Introduction and Objectives: To identify miRNAs relevant to endometriosis pathogenesis by means of a bioinformatic analysis of validated transcriptomic data
Methods: Putative regulating miRNAs were identified by matching previously published and validated transcriptomic data to miRWalk 2.0 database. This database provides a list of all known miRNAs controlling gene expression. These miRNAs were then quantified in endometriotic tissue by qRT-PCR. Total RNA was extracted from endometriotic tissue and eutopic endometrium of five patients afflicted with isolated painful endometrioma. TaqMan®Advanced miRNA Assays (ThermoFisher Scientific) were used for miRNA quantification both in eutopic and ectopic endometrium.
Results: Twenty-six miRNAs were identified as potentially responsible for abnormal gene expression in ectopic endometrium as compared to eutopic endometrium. Among these 26 miRNAs, 8 (30%) were previously cited in published literature. Seventeen genes, such as HSPA1B, AGO1 or Ki67, were controlled by 10 newly identified miRNAs or more. Gene interaction enrichment are significant for those genes ($p < 0.001$) meaning that they interact with each other in a structured gene network. Quantification of these miRNAs is currently underway and will be showed at the congress.
Discussion and Conclusion: Bioinformatics is an original tool able to identify putative miRNAs that may control gene expression in endometriotic lesions and contribute to its development.

Keywords : epigenetics, gene expression, endometriosis, miRNA
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