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P269. Identification of global transcriptome abnormalities in eutopic endometria of women with endometriosis: potential biomarkers of endometriosis

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Context: The current study was performed to test the hypothesis that differential gene expression in the eutopic endometrium between women with endometriosis and controls could be used to allow a better understanding of the pathogenesis of endometriosis and the development of a semi-invasive diagnostic test for endometriosis.
Objective: To identify the genes, the expression of which in the eutopic endometrium of the proliferative phase differs in patients with endometriosis compared to that in the eutopic endometrium of the proliferative phase of women without endometriosis.
Methods: Eutopic endometrium pipelle biopsy specimens were obtained directly intraoperatively before hysteroscopy, with subsequent endometrectomy and histological examination. Total RNA was isolated from the specimens. An expression profile was subsequently obtained by microarray hybridization using the GeneChip Human Exon 1.0 ST Arrays (Affymetrix, USA) according to the manufacturer's protocol. The mRNA levels of the candidate genes in the eutopic endometrium of the proliferative phase were determined by quantitative RT-PCR.
Patients: Two patient groups (7 women with endometriosis (a study group) and 7 women without endometriosis (a control group)) were examined. In the next stage of the study, the mRNA levels of the candidate genes in the eutopic endometrium of the proliferative phase were determined from 71 women with endometriosis (a study group) and 46 women without this disease (a control group) by quantitative RT-PCR.
Interventions: None.
Main Outcome Measures: The eutopic proliferative endometrium of the women with endometriosis (a study group) showed increased expression of 27 genes and decreased expression of 17 genes (the microarray measures the expression level of a total of 14318 transcripts) as compared with that from the women without endometriosis (a control group). According to quantitative RT-PCR, expression FOS, EGR-1, FOSB and ZFP36 genes significantly increase in eutopic endometrium of proliferative phase from women with endometriosis.
Conclusions: All these genes are encountered in the works on eutopic endometrial expression; thus, our results are largely consistent with the published data, which makes these genes promising biomarkers for endometriosis. These genes may be promising potential biomarkers to create quantitative RT-PCR-based diagnostic systems for the determination of mRNA levels in eutopic endometrium.

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