DNA microarray analysis of gene expression in eutopic endometrium from patients with endometriosis

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INTRODUCTION: Endometriosis, a condition in which the uterus lining tissue appears and flourishes outside the uterus, is a progressive disease that causes diverse symptoms such as pelvic pain, menstrual pain, and infertility. Pathogenesis of the endometriosis is very complex and the etiology is still unclear. However, the exact molecular mechanism of the development of endometriosis has not been elucidated. It has recently been proposed that there are differences between the endometrial tissues of women with endometriosis and those of normal women, and these may be the cause of infertility in these patients.
OBJECTIVE: The objective of this study was to examine that endometrial gene expression in late secretory phase endometrium differs between patients with and without endometriosis.
METHODS: Five patients with laparoscopically proven advanced-stage endometriosis and 5 controls underwent endometrial biopsy in the late secretory phase. Analysis of eutopic endometrial gene expression was performed using Affymetrix gene arrays and differentially expressed genes were assigned to gene ontology groups based on overrepresented analysis using DAVID software.
RESULTS: Microarray data were obtained for 5 control samples and 3 samples from the patients with endometriosis. However, during Affymetrix GeneChip® analysis, the array data of two patients that may be biological outliers were excluded. Four hundred sixty two genes were identified as up-regulated such as matrix metalloproteinase 10 (MMP10), cytochrome P450 family 24 subfamily A polypeptide 1 (CYP24A1), matrix metalloproteinase 3 (MMP3), chemokine (C-C motif) ligand 20 (CCL20), Rho family GTPase 1 (RND1), interleukin 1-beta (IL1B), and insulin-like growth factor binding protein 1 (IGFBP1), while 643 genes were down-regulated in all endometriotic samples. A lot of genes related with metabolic process, cellular ketone metabolic process and ncRNA metabolic processing were included. Expression patterns of selected five genes were validated by quantitative real time PCR.
CONCLUSIONS: The results of this analysis support that the eutopic endometrium from patients with advanced-stage endometriosis has distinct gene expression profile from eutopic endometrium of control without endometriosis.

Keywords : Endometriosis, Eutopic endometrium, Microarray, Gene expression profiling
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