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TITLE

METHYLATION PROFILE OF INHIBITORS OF METALLOPROTEINASES IN ENDOMETRIOSIS.

AUTHOR/S

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ABSTRACT

Context: Endometriosis is a presence of endometrium outside of uterine cavity. Widely accepted explanation is occurrence of retrograde menstruation, which is followed by invasion of endometrial explants to peritoneum. It has been proven that endometrial implantation is augmented by dysregulation of matrix metalloproteinases (MMP) and their inhibitors and by increased extracellular matrix (ECM) turnover.

Objective: The aim of the study is to describe methylation profile of inhibitors of metalloproteinases in ectopic lesions and eutopic endometrium in affected and control individuals.

Methods: Tissue samples were collected, DNA was isolated and treated by bisulfite conversion and specific promoters were amplified. Afterwards, libraries were prepared using Illumina Nextera® DNA Library Preparation Kit and Next Generation Sequencing was performed.

Patients: 20 patients in reproductive age without endometriosis and 20 patients in reproductive age with laparoscopically confirmed endometriosis.

Interventions: Samples of eutopic endometrium were collected by hysteroscopy. Samples of ectopic endometrium were collected during laparoscopic surgery. All procedure were performed because of medical indications and informed consent was collected according to Bioethics Committee opinion.

Main Outcome Measures: Methylation rate of CpG island regulating inhibitors of metalloproteinases: TIMP 1-4 and RECK.

Results: Changes in methylation profile between investigated groups is described.

Conclusions: Epigenetic modification of genes involved in ECM remodeling seems to be important factor in development of endometriosis. Differences in certain CpG motifs methylation rate results in altered gene expression level what can unleash MMP activity and EMC remodeling. Further investigation of the role of specific CpG methylation status modification on pathogenesis of endometriosis is warranted.

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