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TITLE

DNA-METHYLATION IN UTERINE MYOMA

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ABSTRACT

Purpose:to investigate the pathogenetic importance of DNA methylation in the development of fibroids (gene ESR1?, gene PgR-B and gene WIF1 in fibroids compared to the normal myometrium.

The tissue samples. In a prospective study samples of myoma node biopsies myometrium are examined, the samples were obtained during the conservative myomectomy or hysterectomy in 30 patients aged 35 to 52 years. The control group included samples of biopsies of normal myometrium taken from the same patients.

First was Isolation of DNA according to standard protocol.

Carrying out PCR. 50 ng of bisulfite-converted DNA was collected for subsequent "touchdown" PCR amplification using Polymerase Mix GoTaq® HotStartGreenMasterMix (Promega, USA) primer

Sequencing was carried out in the center of collective use "Gene" at the on Institute of Molecular Biology of V.A. Engelhardt RAS based on standard protocol using forward primers and kit reagents ABI PRISM® BigDye ™ Terminator v. 3.1.

Statistical analysis of the results of sequencing were performed using software DNA Sequencing Analysis Software version 5.1 and QUMA resource: quantification tool for methylation analysis. DNA methylation level was evaluated qualitatively (presence / absence).

Results and discussion

We have identified particular DNA methylation : hypomethylation of ESR1?(10% vs 90%, p = 0.0273), hypomethylation of PgR-B (6,67% vs 93,33%, p = 0.03253) and hypermethylation WIF1 factor (73.33% vs 26.67%, p = 0.032).

WIF1 methylated gene epigenetically silent, it is not capable of encoding functionally active protein WIF1 - inhibitor WNT-canonical signaling cascade. As a result of WNT-signaling pathway becomes active and thus forming a mechanism triggered myoma tumors.

The findings can be considered as yet another step towards understanding the formation of abnormal cellular mechanisms of the pathogenesis of uterine fibroids

INSTITUTE

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