

Differential-expressed proteins of the myometrium at uterine myoma

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Introduction. Relevance of studying of metabolic processes in the uterine myoma is caused by its high prevalence, and also negative influence on the state of health and reproductive function of women. In the development of this pathology is of great importance may have impaired production of proteins that play an important role in all cellular processes. Timely detection of proteomic imbalance in myometrium will allow to make prognosis and to determine adequate tactics of management of patients with uterine myoma.

The aim of this research is the analysis of proteomic spectrum of samples of a myomatous node, pseudocapsule and intact myometrium of women of reproductive age.

Materials/Patients and methods. Proteomic analysis of the samples was carried out in 11 women using the two-dimensional electrophoresis (1st dimension: IPG-strip, pH 3-10, 17cm; 2nd dimension: 8-16% polyacrylamide gel) with the subsequent silver staining of protein and analysed using PDQuest v7 software (BioRad) and matrix-assisted laser desorption/ionization time-of-flight mass-spectrometry of peptides extracted from gel. Proteins were identified using the Mascot program of the peptide sequences and a search of the Swiss-Prot and NCBI databases. Mann-Whitney U-test used to determine statistical significance of differences.

Results. The development of the uterine myoma is followed by a modification of the expression of proteins with different regulatory and structural functions in comparison with normal tissue of the myometrium, moreover the expression orientation for a number of proteins is opposite. Proteins with down-regulated expression are involved in the formation of the structure and functioning of the cytoskeleton in the processes of intra - and intercellular transport and protein folding. Among them β -tropomyosin, α -actin-1, heat shock protein 70 kDa, annexin A2, transgelin. Down-regulation of expression membrane protein annexin A2, which plays an important role in the regulation of cytoskeleton structures and actin remodeling, indirectly affects the processes of cell migration. A decrease in the production of transgelin in the cells of the myoma compared with normal myometrium can support proliferation tumor cells and reduces their sensitivity to apoptosis, contributing to the prolongation of the longevity of these cells.

Proteins with increased expression include desmin, peroxiredoxin 2, 14-3-3 epsilon protein, protein Erp29 involved in cell proliferation, signal transduction, redox reactions and other processes. The overexpression of 14-3-3 epsilon protein may lead to increased apoptosis by influencing the activity of transforming growth factor- β and tumor necrosis factor- α . Changes in the production peroxiredoxin 2, a key regulator of cell invasion and metastasis, contribute to the development of these processes. Analysis of up-regulated protein indicates its relationship with the degree of proliferative activity of smooth muscle cells. A certain dependence of proteomic spectrum from the time of detection of myoma and histological analysis detected not only for myomatous node, but also for pseudocapsule with the increased expression of the protein Erp29 and desmin.

Conclusion. Changes in the composition of proteins in the myometrium (especially increased expression) are pathogenetic important for development of the uterine myoma and their identification can promote optimization of conservative methods of treatment.

Keywords : myoma, proteomic analysis

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