Streszczenie w języku angielskim

High-grade Serous Ovarian cancer is clinically significant gynecological neoplasm due to five-year relative survival rate of approximately 50%.

The aim of the study was to assess the dominant energy substrate transport mechanism, the analysis of the relationship between gene expression and clinical, biochemical parameters and to verify whether genomic aberrations could predict clinical outcomes using the Cancer Genome Atlas (TCGA) dataset.

The study group consisted of 27 females (surgeries were performed between 2017-2021). 23 of them presented stage III or IV according to FIGO.

Total RNA was extracted from the frozen HGSC tissues. To evaluate the expression of the mRNA, quantitative real-time polymerase chain reaction (qRT-PCR) was performed. Results were compared to control group which included 14 patients.

The increased expression of the genes *GLUT1* (glucose transporter type 1), *FABPpm* (membrane fatty acid binding protein), *MCT4* (monocarboxylate transporter), *SNAT1* (sodium-coupled neutral amino acid transporter type 1) was observed, while the expression of *CD36/SR-B2* (translocase fatty acids), *FATP1* (fatty acid transport protein 1), *FABP4* (fatty acid transport protein 4), *GLUT4* (glucose transporter type 4), *ASCT2* (alanine, serine, cysteine transporter type 2) and LPL (lipoprotein lipase) was diminished. The upregulation of *SNAT1* transcript level was found. Therefore, no single preferred energy substrate has been identified, but the results suggest the predominance of glucose and lactate over fatty acids and the potential role of glutamine in the progression of ovarian cancer.

The expression of the analyzed genes did not correlate with the clinical stage of cancer according to the FIGO classification, invasion of lymph nodes or greater omentum. Based on the analysis of TCGA data, overall survival was shorter in patients with high *FABP4* and *LPL* levels, while high *TFAM* (mitochondrial transcription factor) expression was associated with a better prognosis. Moreover, due to increased *MCT4* expression, ovarian cancer cells may maintain a favorable acidic environment, which could be related cancer aggressiveness. Positive correlations were found between *FABPpm* expression and BMI, *GLUT1* and plasma glucose concentration, and *LAT1* (neutral cellular amino acid transporter) and tumor volume. Obesity in patients from the study group was associated with higher expression of *FABPpm*, *PGC-1 α* (peroxisome proliferator-activated receptor γ coactivator 1α) and *FASN* (fatty acid synthase).- compared to patients with BMI <30/m^2.

Overall, the results and the analysis of data from the TCGA database confirm significant differences between the metabolism of healthy and ovarian cancer cells. Further research should be conducted to determine the potential clinical use of these outcomes and development of prospective therapeutic inhibiting agents to impede ovarian cancer cells' proliferation and metastasis.