After lung and breast cancer, colorectal cancer is the third most commonly diagnosed cancer in the world and the second highest mortality rate. A small proportion of colorectal cancers are hereditary and develop from Lynch syndrome or familial adenomatous polyposis (FAP). However, the vast majority of cases are sporadic colorectal cancers associated with older age, low physical activity, improper diet and spontaneous changes at the molecular level.

The process of colon cancer formation lasts for many years and its development is most often caused by adenoma. Among the factors that may influence the neoplastic transformation of the normal colon epithelium, elements of the TGF-β signaling pathway are mentioned, which are important from the point of view of cell growth regulation, differentiation, migration and apoptosis. This pathway includes receptors and SMAD mediating proteins that transmit information to the nucleus where the expression of target genes is regulated.

The subject of the study was to evaluate the relative expression levels of the *ACVR2A* and *TGFB1* genes that are components of the TGF-β pathway, and the *RUNX3* gene encoding one of the nuclear transcription factors. For this purpose, the real-time PCR method was used, and in the case of the *TGFB1* gene an additional qualitative assessment of *CpG* island methylation of the promoter region was performed by using the MS-PCR technique. The material for the study was tissue fragments acquired perioperatively from 84 patients with histopathologically confirmed colorectal cancer.

The results obtained in the study in connection with demographic and pathological features showed higher relative levels of the *ACVR2A* gene transcript in rectal cancers compared to the colon and cecum. This may indicate its involvement in the development of end-colon cancers. In the case of the *TGFB1* gene, higher relative mRNA levels were observed in patients with low clinical advancement according to the Astler-Coller (II^o) and TNM (I^o) classifications than in patients with the most progressive cancers that suggest its significant role in the early stages of tumor development. Additionally, higher relative expression levels of *TGFB1* were confirmed in tumors with stage T1 and T2 compared to T3 as well as in non-metastatic colorectal cancers (M0). This may indicate the inhibitory effect of *TGFB1* on the growth and proliferation of cells, weakening their migratory capacity and initiating the process of distant metastasis. Moreover, the presence of lymphocytes in the neoplastic tissue and the lack of blood vessel invasion by cancer cells were associated with higher relative transcript levels of this gene, which may confirm the protective role of the *TGFB1*

in the process of distant metastasis.

It was not possible to verify the method of regulating the *TGFB1* gene expression by assessing the methylation within the promoter region, therefore further analyzes should aim at establishing the mechanisms regulating this process. Their determination could contribute to the development of new treatment strategies or become a new prognostic tool in colorectal cancer.