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Expression profile of CD81 gene transcripts in colorectal cancer

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Background: The activity profile of alternative promoters may be an indicator of tumor characteristics. Alternative promoters of CD81 gene were shown to be differentially active in colon and rectal cancer tissue. The promoter active in colon and rectal cancer gives rise to transcripts CD81-205 and CD81-215, while the promoter active in normal gut mucosa gives rise to transcripts CD81-203 and CD81-213. This study aimed to analyze the relative abundance of the CD81 gene transcripts in colorectal cancer. **Material and Methods:** Transcripts generated from two alternative promoters of CD81 gene were analyzed by qPCR in the following sets of samples: human colon cell lines grown as 3D spheroids (non-malignant HCEC-1CT and malignant DLD1, HCT116 and SW620); ten pairs of tumor and non-tumor tissue samples from patients with colon cancer; five pairs of tumor and non-tumor tissue samples from patients with rectal cancer. The total expression of CD81 gene was analyzed as well. **Results:** Analyzed transcripts were represented with low frequency in the total amount of CD81 gene transcripts (0.2-3.3% for cell lines; 0.2-15.3% for colon tissue; 0.3-19.1% for rectal tissue). In non-malignant cell line HCEC-1CT, an approximately equal level of the transcripts of both promoters was shown. In the malignant cell lines and all analyzed tissue samples, the relative abundance of transcripts CD81-205 and CD81-215 was higher than transcripts CD81-203 and CD81-213. **Conclusions:** These findings showed the biomarker potential of the CD81 gene alternative transcripts and indicate their potential role in colorectal cancer. Increased transcript abundance in both tumor and non-tumor tissue samples in comparison to the cell lines indicates their stromalorigin.
Keywords: biomarker, cancer, colon, rectum

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Genetic polymorphisms of enzymes involved in redox homeostasis can influence survival in smokers and overweight patients with prostate cancer

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Background: Prostate cancer (PC) represents a major cause of mortality in developed countries. Nevertheless, due to disease heterogeneity, in certain cases, prognosis can be difficult to anticipate. It is believed that oxidative damage can also affect prostate carcinogenesis. Genetic single nucleotide polymorphisms (SNPs) of enzymes involved in redox homeostasis can lead to oxidative damage and contribute to patients' shorter overall survival. The aim of this study was to investigate whether SNPs of glutathione peroxidase 1 (GPX1 rs1050450), superoxide dismutase 2 (SOD2 rs4880) and regulatory antioxidant protein nuclear factor erythroid 2-related factor 2 (Nrf2 rs6721961) stratified by different age groups and acquired risk factors (obesity, hypertension, and smoking status) can affect overall survival. **Material and Methods:** Total of 235 patients with histologically confirmed prostate cancer treated at the Institute forOncology and Radiology of Serbia and the Urology Clinic of the Clinical Center of Serbia in Belgrade were included in the study. The epidemiological data was collected from standard questionnaires and patients' medical records. Isolated DNA from whole blood was used for quantitative polymerase chain reaction (qPCR) to detect SOD2 and GPX1 gene polymorphisms and polymerase chain reaction with confronting two-pair primers (PCR-CTTP) to detect Nrf2 gene polymorphism. The follow-up time was up to 98 months or death, whichever came first. At the end of the follow-up, 76 patients died, 146 were alive and 13 were lost. Patients were stratified in groups by obesity observed by body mass index (BMI), smoking status, presence/absence of hypertension and age. **Results:** In the overweight group of patients (BMI 25-29.9) shorter survival was observed for carriers of Nrf2*C/C genotype compared to carriers of at least one variant Nrf2*T allele (78 vs 91 months; p=0.022). In smokers, patients with variant GPX1*T/T genotype