Potential biomarkers associated with poor prognosis for locally advanced prostate cancer without lymphatic dissemination

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Motivation and Aim: Prostate cancer (PC) is a major cause of cancer-related deaths in men worldwide. Locally advanced prostate cancer (LAPC) is characterized by invasion of the prostatic capsule without evidence of nodular or distant metastatic spread. Patients within this clinical category have different risks of recurrence [1, 2]. Our study is aimed at identifying novel prognostic biomarkers for LAPC, which will lead to optimization of treatment and development of appropriate clinical recommendations.

Methods and Algorithms: We performed bioinformatics analysis of The Cancer Genome Atlas (TCGA) project RNA-Seq data using the computational resources of EIMB RAS "Genome" center (http://www.eimb.ru/rus/ckp/ccu_genome_c.php); 130 samples (only derived from Caucasian patients) of LAPC without lymphatic dissemination were divided into two groups depending on the cancer prognosis (favorable or unfavorable). In the analysis, the genes previously identified by published data as potential prognostic biomarkers were considered.

Results: Additional eight genes, that are characterized by differential expression, were found. Increased expression of *TWIST1*, *TUBB3*, and *CHAT* and decreased expression of *CYP1B1*, *IGSF1*, *EDN3*, *MSMB*, and *SERPINA3* were detected in the group of patients with poor prognosis in comparison to one with favorable prognosis. These genes are involved in the key processes of carcinogenesis, such as angiogenesis, proliferation and migration of tumor cells (*CYP1B1*, *EDN3*, *TWIST1*, *TUBB3*, and *CHAT*), as well as with disturbance of regulation of signaling cascades (*IGSF1*, *SERPINA3*, and *MSMB*).

Conclusion: Thus, we identified a number of genes as potential prognostic biomarkers associated with poor prognosis of LAPC without lymphatic dissemination.

References
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