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Intermediate and high-risk prostate cancer methylation analysis

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Introduction

Prostate cancer (PC) is one of the most important socially significant oncological diseases in men. When disease is detected the question arises as to the choice of treatment tactics [1]. Treatment may consist of surgery, hormone therapy, or both. As a rule, determination of risk group is based on criteria such as TNM parameters, Gleason score, PSA level [2, 3, 4]. Considering above criteria and risk group a therapeutic concept is chosen. However, in practice these criteria are not enough to choose a therapeutic concept [2]. Additional markers of diagnosis are needed to optimize the choice of therapy.

The aim of research is to identification differentially methylated CpG sites as possible diagnosis markers PC.

Results

In this study we found out 1056 differentially methylated CpG sites between high and intermediate risk groups. From those we selected the most interested CpG sites that are in regulatory regions:

CpG sites	chr	position	annotation
cg17687367	13	79936801	ENSR00000064172 (promoter flank)
cg26874611	5	168147884	ENSR00000776896 (enhancer)
cg06989693	5	41409252	ENSR00000753523 (promoter flank)
cg02226810	6	1605117	ENSR00000191969 (promoter)
cg07736716	8	85379411	ENSR00000332061 (transcription factor binding site) ENSR00000860893 (transcription factor binding site)

Methods

This work included PC samples methylation data of The Cancer Genome Atlas (TCGA) project. Either high (23 cases) or intermediate (103 cases) risk PC cases are involved into the cohort. Risk groups were determinate based on TNM parameters, Gleason score and PSA level.

Differential methylation analysis was performed in statistical environment R using EdgeR and BiSeq packages. The Mann-Whitney test, beta-regression and logistic regression models were used for statistical analysis.

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References

[1] Chang A.J., Autio K.A., Roach M., Scher H.I. (2014) High-risk prostate cancer-classification and therapy. Nat Rev Clin Oncol. 11(6):308-23. doi: 10.1038/nrclinonc.2014.68.

[2] Gerhauser C., Favero F., Risch T., Simon R., Feuerbach L., Assenov Y., et al. (2018) Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell. 10;34(6):996-1011.e8. doi: 10.1016/j.ccell.2018.10.016.

[3] Hurwitz L.M., Cullen J., Kim D.J., Elsamanoudi S., Hudak J., Colston M., et al. (2017) Longitudinal regret after treatment for low- and intermediate-risk prostate cancer. Cancer. 1;123(21):4252-4258. doi: 10.1002/cncr.30841.

[4] Serrano N.A., Anscher M.S. (2016) Favorable vs Unfavorable Intermediate-Risk Prostate Cancer: A Review of the New Classification System and Its Impact on Treatment Recommendations. Oncology (Williston Park). 30(3):229-36.