Prediction efficiency of PITX2 DNA methylation for prostate cancer survival

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ABSTRACT. This study determined the level of PITX2 methylation in prostate cancer and benign tissues and its relationship with the postoperative survival rate. Forty-four patients with prostate cancer who underwent radical prostatectomy and 43 patients with benign prostatic hyperplasia were selected. DNA was extracted from the tissues and PITX2 methylation status was quantitatively analyzed by using the EpiTect MethyLight method. The median follow-up time of the patients was 63 months and was used to analyze the relationship between PITX2 methylation status with tumor stage and survival rates. Median PITX2 gene expression in benign tissues was 1.46, which was higher than that of tumor tissues with a median of 0.01 (P < 0.001). The median methylation in the controls was less than 0.001%, while the median methylation in the test group was 23.3% (P = 0.000). The number of patients with low methylation level in T2 stage was 15, which was more than that in T3 and T4 stages (8 patients); while the number of patients with high methylation levels in T2 stage was 6, which was less than that in T3 and T4 stages (15 patients) (P = 0.035). The PITX2 gene expression level in prostate cancer tissues was lower than that in benign
tissues. A higher degree of PITX2 DNA methylation was associated with higher tumor stage and lower survival rates. PITX2 DNA methylation presents a good predictive value for prostate cancer survival.

**Key words:** DNA methylation; Prostate cancer; PITX2; Survival