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

