Correlation between methylation of the E-Cadherin gene and malignancy of prostate cancer

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ABSTRACT. Prostate cancer is a common malignant tumor in males with an unclear pathogenic mechanism. As one epigenetic regulation mechanism, DNA methylation of the whole genome and specific gene(s) plays critical roles in pathogenesis, progression, diagnosis, and treatment of prostate cancer. The E-Cadherin gene is involved in cell metabolism and has been suggested to be related with malignancy of multiple tumors. This study investigated the correlation between E-Cadherin methylation and malignancy of prostate cancer. Gradient concentrations of 5-Aza-CdR (5, 10, and 20 μM) were used to treat the prostate cancer cell line (LNCaP), and mRNA level of E-Cadherin was detected by reverse transcription-polymerase chain reaction (RT-PCR). A total of 82 prostate cancer patients were recruited to detect the methylation status of the promoter region of the E-Cadherin gene by pyrophosphate sequencing. Real-time fluorescent quantitative PCR
(qRT-PCR) was employed to determine mRNA levels of E-Cadherin. Methylation and mRNA levels of E-Cadherin were analyzed by the SPSS software. With elevated concentrations of 5-Aza-CdR, mRNA levels of E-Cadherin gradually increased. DNA methylation levels of tumor tissues were significantly elevated with increased Gleason score (P < 0.05) and tumor-node-metastasis stage (P < 0.05) but were not related to age, smoking habits, or alcohol consumption (P > 0.05). DNA methylation level was negatively correlated with mRNA expression of the E-Cadherin gene. Methylation in tumor tissues was significantly higher than that in tumor adjacent tissues (P < 0.05). DNA methylation level of the E-Cadherin gene could be an important predictive index for malignancy of prostate cancer.

**Key words:** DNA methylation; Prostate cancer; E-Cadherin gene