DNA hypermethylation as a predictor of PSA recurrence in patients with low- and intermediate-grade prostate cancer.


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Abstract

BACKGROUND: DNA CpG island hypermethylation causes gene silencing and is a common event in prostate carcinogenesis and progression. We investigated its role as a possible prognostic marker in patients with PCA Gleason score ≤7.

PATIENTS AND METHODS: We used a quantitative, methylation-specific PCR to analyze methylation patterns at five gene loci (APC, GSTP1, PTGS2, RARbeta and TIG1) in 84 prostate cancer (PCA) tissues (Gleason Score ≤7). Methylation was correlated with established clinico-pathological parameters (preoperative PSA, pathological Gleason score, extraprostatic extension, seminal vesicle penetration, lymph node involvement, surgical margins and age) and PSA recurrence.

RESULTS: DNA hypermethylation was frequently detected at APC (95.2%), GSTP1 (84.5%), PTGS2 (100%), RAR-beta (81.0%) and TIG1 (95.2%). DNA hypermethylation was correlated with Gleason Score (p=0.027; PTGS2) and lymph node involvement (p=0.024; RARbeta). High methylation levels at RARbeta (p=0.023) was a significant predictor of PSA recurrence following radical prostatectomy.

CONCLUSION: The analysis of DNA hypermethylation provides prognostic information in prognosis of low- and intermediate-grade PCA.

KEYWORDS: DNA hypermethylation, PTGS2, Prostate cancer, RARB, methylation, prognosis

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