MT1G Hypermethylation Is Associated with Higher Tumor Stage in Prostate Cancer

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Abstract

Purpose: Zinc is an essential trace element as a component of several metalloenzymes involved in critical physiologic processes, including cell growth and proliferation. Although in normal prostate tissue zinc levels are high, there is a marked decrease in prostate cancer. Metallothioneins control the bioavailability of zinc and one isoform, MT1G, was reported down-regulated in prostate cancer. Here, we investigated whether promoter methylation might cause MT1G silencing in prostate cancer.

Patients and Methods: The MT1G promoter was assessed by quantitative methylation-specific PCR on prospectively collected tissue samples from 121 patients with prostate cancer, 39 paired high-grade prostatic intraepithelial neoplasia (HGPIN), 29 patients with benign prostatic hyperplasia, 13 normal prostate tissue samples from cystoprostatectomy specimens, and prostate cancer cell lines. The methylation levels were calculated and were correlated with clinical and pathologic variables. Reverse transcription-PCR was done in cell lines to assess MT1G mRNA expression before and after demethylating treatment.

Results: MT1G promoter hypermethylation was found in 29 of 121 prostate cancer, 5 of 39 HGPIN, 3 of 29 benign prostatic hyperplasia, and 0 of 13 normal prostate tissue samples. No significant differences in methylation frequencies or levels were found (P = 0.057, for both). Methylation levels were found to correlate with tumor stage but not with Gleason grade. MT1G hypermethylation was more frequent in prostate cancer that spread beyond the prostate capsule. All prostate cancer cell lines tested showed MT1G promoter methylation, but no differences in expression were apparent after demethylation.

Conclusions: Our findings suggest that MT1G promoter methylation is associated with tumor aggressiveness in prostate cancer and it might be a marker of locally advanced disease. (Cancer Epidemiol Biomarkers Prev 2005;14(5):1274–8)

Introduction

Zinc is an essential trace element as a component of several metalloenzymes involved in critical physiologic processes, including cell growth and proliferation, osteogenesis, immu-

nity, and antioxidant activity (1). In a normal prostate gland, zinc levels are high and heterogeneously distributed (2). Because these levels are significantly reduced in malignant prostate tissue (2, 3), a putative prostate cancer–protective effect has been credited to zinc supplements, although no definitive evidence has been provided thus far (1). Indeed, an association between supplementary doses of zinc over 100 mg/d and increased risk for advanced prostate cancer has been recently reported (4).

The bioavailability of zinc is controlled by metallothioneins, a class of low molecular weight proteins with metal-binding and antioxidant properties (5). Human metallothioneins are encoded by a family of genes located at chromosome 16q13 (6, 7) and some of the isoforms seem expressed in an organ-dependent manner (8). In several human cancers, metallothionein expression was found to correlate with cell proliferation, tumor progression, and drug resistance (9). In prostate cancer, an association between tumor grade and expression of metallothioneins has been reported, using immunohistochemical analysis (10). However, the antibody used cross-reacts with different isoforms not allowing for a discriminative expression analysis. Interestingly, the gene transcribing for one of those isoforms, MT1G, was found down-regulated in high-grade (Gleason grade 4 and 5) prostate adenocarcinomas (11), but the mechanism of gene silencing remains elusive. Remarkably, in papillary thyroid carcinoma, MT1G down-regulation was reported mediated by promoter methylation (12). Because hypermethylation of cancer-related genes is a common event in prostate cancer (13, 14), we hypothesized that this epigenetic alteration might be responsible for MT1G down-regulation in prostate adenocarcinoma.

Herein, we sought to characterize quantitatively the promoter methylation status of MT1G in tissue specimens from primary prostate cancer, paired high-grade prostatic intraepithelial neoplasia (HGPIN) lesions, benign prostatic hyperplasia (BPH), and normal prostate tissue. Relationships between methylation levels and frequencies and clinicopathologic variables were further assessed. Additionally, prostate cancer cell lines were used to test whether MT1G promoter methylation was associated with altered expression.

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Note: R. Henrique and C. Jerónimo contributed equally to this study and should be regarded as joint first authors.

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Materials and Methods

Patients, Sample Collection, and DNA Extraction. Primary tumors from 121 patients with clinically localized prostate adenocarcinoma (stages T1c and T2, according to the tumor-node-metastasis staging system; ref. 15), consecutively diagnosed and primarily treated with radical prostatectomy at the Portuguese Oncology Institute, Porto, Portugal, were prospectively collected. In 39 radical prostatectomy specimens with prostate cancer, a HGPIN lesion was identified and collected for further analysis. For control purposes, nonneoplastic prostate tissue samples were obtained from 29 randomly selected patients with BPH that underwent transurethral resection of the prostate and also from 13 prostates that did not harbor prostate cancer collected from cystoprostatectomy specimens of bladder cancer patients (normal prostate tissue). All tissue specimens were promptly frozen immediately after surgery and stored at −80°C for further analysis. Five-micrometer-thick sections were cut and stained for the identification of the areas of prostate cancer (i.e., the index or dominant tumor), HGPIN, BPH, and normal tissue. Then, the tissue block was trimmed to maximize the yield of target cells (>70% of target cells). Subsequently, an average of fifty 12-μm-thick sections were cut and every fifth section was stained to ensure a uniform percentage of target cells and to exclude contamination from neoplastic cells in normal and BPH tissue samples. DNA was extracted from all samples with phenol/chloroform and precipitated with ethanol (16).

Histologic slides from formalin-fixed, paraffin-embedded tissue fragments were obtained from the same surgical specimens and assessed for Gleason grade (17) and tumor-node-metastasis stage (15) by two pathologists (R.H. and C.L.) blinded to clinical and methylation analysis data. Relevant clinical data were abstracted from the clinical records. The Institutional Review Board of Portuguese Oncology Institute, Porto approved these studies and permission to test these clinical data were abstracted from the clinical records. The Institutional Review Board of Johns Hopkins University approved these studies and permission to test these clinical data were abstracted from the clinical records. The Institutional Review Board of Johns Hopkins University approved these studies and permission to test these clinical data were abstracted from the clinical records.

Cell Culture Conditions and Demethylating Treatment. Human prostate cancer cell lines LNCaP, DU-145, PC-3, and 22Rv1 were obtained from American Type Culture Collection (Rockville, MD) and cultured in RPMI 1640 (Invitrogen, Carlsbad, CA) supplemented with 10% fetal bovine serum for isolation of DNA and RNA. The cells were split to low density (5 × 10^5) per T-25 flask) 12 to 24 hours before treatment. Then, cells were treated at days 1 and 4 with 5 μmol/L 5-aza-2’-deoxycytidine (Sigma, St. Louis, MO) and 100 μmol/L of 50% acetic acid–dissolved stock. Cells were harvested at day 5 and processed for DNA and RNA extraction.

Bisulfite Treatment and Quantitative Methylation-Specific PCR. Sodium bisulfite conversion of unmethylated (but not methylated) cytosine residues to uracil of genomic DNA obtained from patient tissue samples and cell lines was done as described previously (18). Four micrograms of DNA were used for the chemical treatment. DNA samples were then purified using the Wizard purification resin (Promega, Madison, WI), treated again with sodium hydroxide, precipitated with ethanol, resuspended in 200 μL of water, and stored at −80°C.

The modified DNA was used as a template for real-time fluorogenic quantitative methylation-specific PCR (QMSp). The primers and probes used for the target gene (MT1G, Genbank accession no. J03910) and the internal reference gene (β-actin, ACTB) were, respectively, (sense) 5’-TGGCAAGGGGTTGTGTGTCG-3’ (antisense) 5’-CCAGCGCTTAAATCGCACAACCA-3’; (probe) 6FAM-5’-GGATCCGCACTAACATACAGGC-3’-TAMRA and (sense) 5’-GTGTTAGGGAGGTGTTTGAAGT-3’; (antisense) 5’-AACAATAAACCCTACTCCTCCCTA-3’; (probe) 6FAM-5’-ACCACACCCACACAAATAACACACAC3’-TAMRA. To determine the relative levels of methylated promoter DNA in each sample, the values of the target gene were compared with the values of the internal reference gene to obtain a ratio that was then multiplied by 1,000 for easier tabulation (MT1G/ACTB × 1,000).

Fluorogenic QMSP assays were carried out in a reaction volume of 20 μL in 384-well plates in an Applied Biosystems 7900 Sequence Detector (Perkin-Elmer, Foster City, CA). PCR was done in separate wells for each primer/probe set and each sample was run in triplicate. The final reaction mixture consisted of 600 nmol/L of each primer (Invitrogen); 200 nmol/L probe (Applied Biosystems, Foster City, CA); 0.75 unit of platinum Taq polymerase (Invitrogen); 200 μmol/L each of dATP, dCTP, dGTP, and dTTP; 16.6 mmol/L ammonium sulfate; 67 mmol/L Trizma; 6.7 mmol/L magnesium chloride; 10 mmol/L mercaptoethanol; 0.1% DMSO; and 3 μL bisulfite-converted genomic DNA. PCR was done using the following conditions: 95°C for 2 minutes followed by 50 cycles at 95°C for 15 seconds and 60°C for 1 minute. Each plate included multiple water blanks, a negative control, and serial dilutions of a positive control for constructing the calibration curve on each plate. Leucocyte DNA collected from healthy individuals was used as negative control. The same leucocyte DNA was methylated in vitro with SssI bacterial methyltransferase (New England Biolabs, Inc., Beverly, MA) and used as positive control.

A given sample was considered positive for MT1G hypermethylination when amplification was detected in at least two of the triplicates of the respective QMSP analysis. The QMSP threshold was determined for each run adjusting the best fit of the slope and R^2 using the calibration curve.

RNA Extraction and Conventional Reverse Transcription-PCR. Total RNA was extracted from all prostate cancer cell lines using RNeasy kits (Qiagen, Valencia, CA) and it was reverse transcribed by random primers (Invitrogen) according to manufacturers’ protocol. cDNA was amplified by PCR with primers spanning several exons to avoid amplification of DNA: for MT1G, 5’-GCCAGCTCTGCAAGTGCAA-3’ (sense) and 5’-CTCTCCGATGCCCTTTGGC-3’ (antisense), which amplify a 119-bp product; for glyceraldehyde-3-phosphate dehydrogenase, 5’-TCTTCCAGGACGGAGATCCC-3’ (antisense), which amplify a 274-bp product. Reverse transcription-PCR for glyceraldehyde-3-phosphate dehydrogenase served as a positive control. Each cDNA sample (1 μL) was used as a template for PCR reaction, done as previously described (19). In brief, one cycle at 94°C for 5 minutes, 30 cycles at 94°C for 30 seconds, 58°C for 20 seconds, and 72°C for 30 seconds, with final extension of 5 minutes at 72°C. Electrophoresis of the PCR products was carried out on 2% agarose gels, stained with ethidium bromide, and visualized by UV fluorescence. Non-template control served as negative control. To confirm the efficiency of the demethylating treatment, the expression of TIG-1 was analyzed before and after treatment with 5-aza-2’-deoxycytidine (20).

Statistical Analysis. The Shapiro-Wilk’s W test allowed for the examination of the appropriateness of a normal distribution assumption for each of the variables (data not shown). Then, the median and interquartile range of the methylation ratios for each group of samples was determined and analyzed using nonparametric tests (i.e., the Kruskal-Wallis one-way ANOVA followed by the Bonferroni-adjusted Mann-Whitney U test when appropriate). For this comparison test among four groups of tissue samples, the nonadjusted statistical level of significance of P < 0.05 corresponds to a Bonferroni-adjusted statistical significance of P < 0.0125. Differences in methylation frequencies among prostate cancer, HGPIN, BPH, and normal
Results

Clinical and Pathologic Data. Tissue samples from 121 prostate adenocarcinomas, 39 HGPIN lesions, 29 BPH, and 13 normal tissue samples were tested. The clinical and pathologic characteristics of the patients are depicted in Table 1. Although prostate-specific antigen levels were higher in patients with prostate cancer (P = 0.004), there was considerable overlap with BPH cases. Statistically significant differences in patient’s age were detected among the three groups of patients (P = 0.003). The Mann-Whitney U test disclosed a significant difference only between the median age of BPH and prostate cancer patients (P = 0.0006).

MT1G Promoter Methylation in Prostatic Tissues and Clinicopathologic Correlations. The frequency of MT1G promoter methylation in normal prostate tissue and prostate lesions is displayed in Table 2. Although the frequency of this epigenetic alteration was higher in prostate cancer, no statistically significant differences among the four groups of tissue samples were noted (P = 0.057).

We further analyzed the methylation levels of MT1G in all tissue samples. The distributions of MT1G methylation levels in BPH, HGPIN, and prostate cancer are depicted in Fig. 1. Median methylation levels and respective interquartile ranges were 0 (0–0) for prostate cancer, HGPIN; BPH, and normal prostate tissue and significant differences were not found among the four groups of tissue samples (P = 0.057). In three HGPIN lesions with MT1G promoter methylation, the respective prostate cancer was also methylated; whereas in the remaining two cases of methylated HGPIN, the paired prostate cancer was unmethylated.

In prostate cancer tissue samples, no correlation was found between age or prostate-specific antigen levels and MT1G methylation status of tumors at the MT1G promoter was significantly higher in cases with extraprostatic extension (pT3 and pT4) than in localized tumors (pT2; P = 0.049).

MT1G Promoter Methylation and RNA Expression in Prostate Cancer Cell Lines. Prostate cancer cell lines LNCaP, DU-145, PC-3, and 22RV1 were found methylated at the MT1G locus and the methylation levels were 75.6, 61.3, 107.4, and 40, respectively. Reverse transcription-PCR showed that all cell lines expressed MT1G mRNA (Fig. 2). After demethylating treatment, no difference in the size and intensity of the bands was apparent. The demethylating treatment was effective as MT1G was reexpressed in prostate cancer cell line PC-3 (Fig. 2), as previously reported (20).

Discussion

The aim of this study was to determine the promoter methylation status of MT1G in tissue specimens from primary prostate cancer, paired HGPIN lesions, BPH, and normal prostate tissue using a highly sensitive and specific method.
Moreover, this epigenetic change might be a marker of locally advanced disease and could be useful as a stage predictor in prostate cancer.

In conclusion, our data suggests that acquisition of $MT1G$ promoter methylation is associated with tumor aggressiveness. Moreover, this epigenetic change might be a marker of locally advanced disease and could be useful as a stage predictor in prostate sextant biopsies.
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