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DNA HYPOMETHYLATION ON PERICENTROMERIC SATELLITE REGIONS SIGNIFICANTLY CORRELATES WITH LOSS OF HETEROZYGOSITY ON CHROMOSOME 9 IN UROTHELIAL CARCINOMAS

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ABSTRACT

Purpose: DNA methylation has important roles in genomic stability. Accordingly DNA hypomethylation on pericentromeric satellite regions may induce chromosomal instability through heterochromatin decondensation and chromosomal recombination enhancement. We elucidated the significance of aberrant DNA methylation on pericentromeric satellite regions during urothelial carcinogenesis.

Materials and Methods: We examined DNA methylation status on satellites 2 and 3 by Southern blotting and determined the allelic status of chromosome 9 using 6 microsatellite markers (D9S775, D9S925, D9S304, D9S303, D9S283 and D9S747) in 27 transitional cell carcinomas of the bladder, ureter or renal pelvis and corresponding noncancerous tissues.

Results: DNA hypomethylation on satellites 2 and 3 was detected in 2 (7%) and no (0%) noncancerous tissues, and in 11 (41%) and 12 (44%) urothelial carcinomas, respectively. DNA hypomethylation in urothelial carcinomas significantly correlated with histological grade ($p = 0.0012$ and 0.0043), invasion depth ($p = 0.0055$ and 0.0228) and morphological structure (papillary vs nodular, $p = 0.0161$ and 0.0297) for satellites 2 and 3, respectively. Loss of heterozygosity on at least 1 locus of chromosome 9 was detected in 14 urothelial carcinomas (52%). DNA hypomethylation on satellites 2 ($p = 0.0098$) and 3 ($p = 0.0034$) significantly correlated with loss of heterozygosity on chromosome 9.

Conclusions: DNA hypomethylation on pericentromeric satellite regions may participate in the development and progression of urothelial carcinomas by inducing loss of heterozygosity on chromosome 9.

KEY WORDS: urothelium; carcinoma, transitional cell; DNA methylation; chromosomal instability; loss of heterozygosity

DNA methylation has important roles in transcriptional regulation, chromatin remodeling and genomic stability.[1] Satellites 2 and 3, which are related families containing a frequent 5 bp repeat, are abundant in pericentromeric heterochromatin regions on chromosomes 1, 9 and 16, and heavily methylated in normal somatic cells.[2] DNA hypomethylation on such pericentromeric satellite regions may induce chromosomal instability through heterochromatin decondensation and chromosomal recombination enhancement.[3,4] DNA hypomethylation on satellites 2 and 3 has been reported to cause chromosomal instability, such as the formation of multiradiate chromosomes composed of chromosomes 1, 9 and 16, in ICF (immunodeficiency-chromosomal instability-facial anomalies) syndrome.[2]

In human cancers overall DNA hypomethylation accompanied by region specific hypermethylation is generally observed.[1] Aberrant DNA methylation may be involved in carcinogenesis by at least three possible mechanisms: induction of genomic instability as a result of decreased methylation level,[5–7] increased gene mutagenicity caused by deamination of 5-methylcytosine to thymine and repression of gene transcription through CpG island methylation in specific gene regulatory regions, including tumor suppressor genes.[1] For example, frequent chromosomal 1q copy gain with a pericentromeric break point has been reported in hepatocellular carcinomas showing DNA hypomethylation on satellite 2.[8]

The role of DNA hypomethylation in urothelial carcinomas is not fully understood, although aberrant hypermethylation on CpG islands around the promoter region and decreased expression of tumor suppressor genes, such as the *p16* and *E-cadherin* genes, have been reported.[9,10] In addition, loss of heterozygosity (LOH) on chromosome 9 is the most common genetic abnormality in urothelial carcinomas.[11] Consequently we focused on the clinicopathological significance of DNA hypomethylation on pericentromeric satellite regions in urothelial carcinomas and examined whether this hypomethylation is the underlying mechanism for LOH on chromosome 9 during human urothelial carcinogenesis.

MATERIALS AND METHODS

Patients and tissue samples. Paired specimens of primary urothelial carcinoma and corresponding noncancerous tissue were obtained from surgically resected specimens from 27 patients (U1 to U27) treated at National Cancer Center Hospital, Tokyo, Japan. The patients were 22 men and 5 women with a mean age ± SD of 67.6 ± 10.5 years (range 50 to 85).

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The primary tumor sites were the bladder, ureter and renal pelvis in 13, 5 and 9 patients, respectively. Based on histological examination 5 (19%), 10 (37%) and 12 (44%) tumors were classified as G1, G2 and G3–4 transitional cell carcinoma, while 11 (41%) and 16 (59%) were superficial (pTa and pT1) and invasive (pT2 to pT4), respectively.[12] Morphologically 21 tumors (78%) were papillary carcinoma and 6 (22%) were nodular carcinoma. Noncancerous specimens were obtained from the urothelium distant from the carcinoma.[13] In cases of widely spreading carcinomas in situ, as diagnosed histopathologically in preoperative biopsy specimens, the muscle layer of the bladder or the renal parenchyma was collected as noncancerous specimens since macroscopic examination cannot necessarily discriminate noncancerous urothelium from carcinoma in situ.

Southern blotting for pericentromeric satellite regions. High molecular weight DNA was isolated from fresh tissue samples by phenol-chloroform extraction and dialysis. DNA methylation status was assessed by digesting DNA with *Msp* I and *Hpa* II, which cut at the sequence CCGG. *Hpa* II does not cut when the internal cytosine is methylated. High molecular weight DNA (5 μg) was digested for 24 hours with 10 U *Msp* I or *Hpa* II/μg DNA. DNA fragments were separated by electrophoresis, transferred to nitrocellulose membranes and hybridized with ^{32}P labeled DNA probes. Previously described oligonucleotides were used as probes for satellites 2 and 3.[14]

Analysis of LOH on chromosome 9. Genomic DNA was amplified by polymerase chain reaction (PCR) using oligonucleotide primers for 6 microsatellite loci on chromosome 9, namely D9S775, D9S925, D9S304, D9S303, D9S283 and D9S747. Primer sequences were D9S775 (9p23) 5′-AAAGTAGCCATCCGTGTGT-3′ and 5′-GCTTTCTTTGATGGTTTACAG-3′, D9S925 (9p21–22) 5′-GTCTGGGTTCTCCAAAGAAA-3′ and 5′-TGTGAGCCAAGGCCTTATAG-3′, D9S304 (9p21) 5′-GTGCACCTCTACACCCAGAC-3′ and 5′-TGTGCCCACACACATCTATC-3′, D9S303 (9q21) 5′-CAACAAAGCAAGATCCCTTC-3′ and 5′-TAGGTACTTGGAAACTCTTGGC-3′, D9S283 (9q22) 5′-TGCTGGATTTCAGGTAGGG-3′ and 5′-ATGGTTATGCGGGTGTATTTCTC-3′, and D9S747 (9q32) 5′-GCCATTATTGACTCTGGAAAAGAC-3′ and 5′-CAGGCTCTCAAAATATGAACAAAAT-3′. The 5′ ends of forward primers were labeled with 6-carboxyfluorescein and PCR amplifications were performed with 20 ng genomic DNA. Subsequently PCR products were fractionated by electrophoresis (ABI 3100 sequencer, Applied Biosystems, Foster City, California) according to the manufacturer protocol. Data were analyzed with the GeneScan, version 3.7 computer program (Applied Biosystems). When 2 amplified bands per locus were detected in the noncancerous tissue specimen, the case was considered informative for LOH analysis. LOH was recorded when signal intensity for a tumor allele was decreased by more than 50% relative to the matched normal allele in informative cases, as described previously.[15–17] Replication error was identified by the presence of band shifts or the presence of novel bands in PCR products.

Statistics. Correlations between any 2 of DNA methylation status, allelic status and clinicopathological parameters were analyzed by the chi-square test with $p < 0.05$ considered significant.

RESULTS

DNA methylation status on pericentromeric satellite regions and its correlation with clinicopathological parameters. Figure 1 shows examples of Southern blotting. In 25 (93%) and all 27 (100%) noncancerous tissue specimens examined significantly larger DNA fragments were detected in *Hpa* II digests compared with *Msp* I digests at satellites 2 and 3, respectively, indicating that these regions were heavily methylated. In 11 (41%) and 12 (44%) urothelial carcinomas smaller fragments were detected in *Hpa* II digest compared with corresponding normal tissues or *Hpa* II digest showed almost the same hybridization pattern as the *Msp* I digest of the same sample and the corresponding normal tissue, indicating that these regions were hypomethylated. In almost all carcinoma samples in which DNA hypomethylation was detected hypomethylation occurred on satellites 2 and 3.

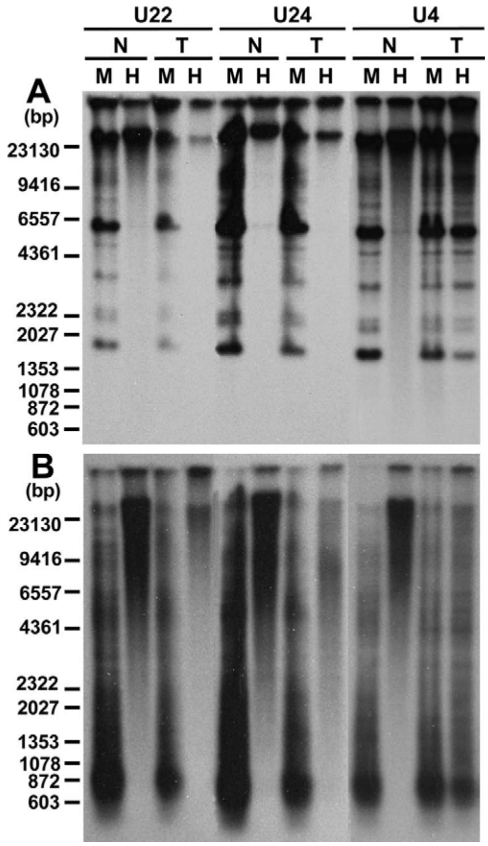

FIG. 1. Examples of Southern blotting for satellites 2 (*A*) and 3 (*B*) in cases of urothelial carcinoma. Methylation status was assessed by digesting DNA with *Msp* I (*Lane M*) and *Hpa* II (*Lane H*). DNA fragments were separated by electrophoresis, transferred to nitrocellulose membranes and hybridized with ^{32}P labeled DNA probes. Larger bands were detected in lane H compared with lane M in all noncancerous tissue (*N*), and in U22T and U24T, indicating that satellite 2 region was heavily methylated (*A*). In U4T lane H showed same hybridization pattern as lane M, indicating that this region was hypomethylated. (*B*) In all noncancerous tissues, and U22T and U24T satellite 3 region was heavily methylated, whereas this region was hypomethylated in U4T. *T*, cancerous tissue.

DNA hypomethylation on pericentromeric satellite regions significantly correlated with histological grade (chi-square test p = 0.0012 and 0.0043), invasion depth (chi-square test p = 0.0055 and 0.0228) and morphological structure (papillary vs nodular chi-square test p = 0.0161 and 0.0297) for satellites 2 and 3, respectively (table 1), but not with age or gender (data not shown).

Allelic status of chromosome 9 and its correlation with clinicopathological parameters. Figure 2 shows examples of electropherograms of PCR products. Figure 3 shows the results of LOH analysis. Table 2 lists the incidence of LOH on each locus. LOH for at least 1 marker was found in 14 of the 27 informative cases (52%) (table 2).

The presence of LOH on at least 1 locus on chromosome 9 significantly correlated with histological grade (chi-square test p = 0.0313, table 3). LOH on at least 1 locus was detected in all 6 nodular carcinomas and its incidence (100%) was significantly higher than in papillary carcinomas (chi-square test p = 0.0074, table 3).

Correlation between DNA methylation status on pericentromeric satellite regions and allelic status of chromosome 9. DNA