Aberrant Methylation in Gastric Cancer Associated with the CpG Island
Methylator Phenotype

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Abstract

Aberrant methylation of 5′ CpG islands is thought to play an important role in the inactivation of tumor suppressor genes in cancer. In colorectal cancer, a group of tumors is characterized by a hypermethylation phenotype termed CpG island methylator phenotype (CIMP), which includes methylation of such genes as p16 and hMLH1. To study whether CIMP is present in gastric cancer, the methylation status of five newly cloned CpG islands was examined in 56 gastric cancers using bisulfite-PCR. Simultaneous methylation of three loci or more was observed in 23 (41%) of 56 cancers, which suggests that these tumors have the hypermethylator phenotype. There was a significant concordance between CIMP cancers, which suggests that these tumors have the hypermethylator phenotype. CIMP in colorectal cancers seems to be related to a new phenotype termed CIMP (21). CIMP was identified by studying seven newly cloned CpG islands that are methylated exclusively in cancer. In colorectal cancer, CIMP tumors include most cases with hypermethylation of known genes such as p16, hMLH1, and THBS1. We now report that CIMP is also present in gastric cancers, in which it is an early event. CIMP in gastric cancer also affects inactivation of known tumor suppressor genes such as p16 and hMLH1. These results indicate that CIMP is one of the major pathways of tumorigenesis in gastric cancers, in which genetic alterations described to date are relatively infrequent.

Materials and Methods

Samples. Tumor specimens were obtained from 56 patients. All of the patients had given informed consent before collection of the samples according to institutional guidelines. For most of these tumors, paired normal tissues were also obtained. These tissues were frozen and stored at −80°C until DNA was extracted. MSI analysis was performed as described previously (22). Briefly, five markers, including dinucleotide and mononucleotide markers (BAT26, BAT40, D5S346, D17S250, and MYCL1), were amplified by PCR followed by electrophoresis. When only one marker was altered, the cases were defined as MSI-L, when 2 or more markers were altered those were defined as MSI-H and when no marker was altered those were defined as microsatellite stable. Genomic DNA was extracted using standard methods.

MSP and Bisulfite-PCR. Both MSP and bisulfite-PCR take advantage of the fact that unmethylated cytosines are efficiently converted to uracil after 16 h of Na-bisulfite treatment, whereas methylated cytosines remain unchanged. Thus, after treatment, methylated alleles have a different sequence than unmethylated alleles, which can be used to design allele-specific PCR primers (for MSP; Ref. 23). Alternatively, the primers can be designed to amplify both methylated and unmethylated alleles, with the discrimination obtained by digesting amplified fragments with restriction enzymes specific for the methylated alleles (24).

Genomic DNA was treated with Na-bisulfite as described previously (23). Briefly, 2 µg of genomic DNA were denatured by 0.2 M NaOH for 10 min at 37°C. Thirty µl of 10 mM hydroquinone (Sigma) and 520 µl of 3 M Na-bisulfite (Sigma) at pH 5.0 were added and incubated at 50°C for 16 h. Treated DNA was subsequently purified using a PCR-purification system (Promega) and precipitated with ethanol. Two µl of treated DNA were used for each PCR reaction.

The methylation status of p16 was determined as described previously (23). Briefly, 2 µl of genomic DNA treated with Na-bisulfite was amplified using primers that specifically amplify methylated or unmethylated alleles. PCR was performed in 50-µl reaction volumes containing 1× PCR buffer [67 mM Tris-HCl (pH 8.8), 6.6 mM MgCl2, 16.6 mM NH4SO4, and 10 mM 2-mercaptoethanol], 1.25 mM dNTP mixture, 1 µM of each primer, and 1 unit of Taq DNA polymerase (Sigma). Ten µl of PCR products were electrophoresed in 6% acrylamide gels and visualized by ethidium bromide staining.

Received 6/8/99; accepted 9/20/99.

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This work was supported by NIH Colon Cancer Spore Grant CA62924 and National Cancer Institute Grant CA7045 and by American Cancer Society Grant RGP0909801 MGO. M. T. is a postdoctoral fellow of the Japan Society for Promotion of Science. N. A. is supported by NIH Training Grant 1-T32-DK07713. J.-P. J. I. is a Kimmel Foundation Scholar.

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The abbreviations used are: MSI, microsatellite instability; CIMP, CpG island methylator phenotype; MSP, methylation-specific PCR; MINT, methylated in tumors.
The methylation status of hMLH1 and MINT1, 2, 4, 6, 12, 23, 25, 31, and 32 were determined by bisulfite-PCR followed by restriction digestion. Briefly, PCR primers were designed to amplify methylated alleles and unmethylated alleles equally. Two μl DNA treated with Na-bisulfite were amplified as described previously (21). Twenty to 50% of the PCR products were then digested with restriction enzymes specific to the methylated alleles by virtue of having CpG sites in their recognition sequence. After digestion, DNA was precipitated with ethanol, electrophoresed in a 6% polyacrylamide gel, and stained with ethidium bromide. The methylated alleles were evaluated by densitometry (Image Quant, Molecular Dynamics) as described previously (24).^4

Results

To examine the methylation status of multiple loci in gastric cancer, nine sequences that fulfill the criteria for CpG islands (25) were selected for analysis. These MINT loci were originally recovered from a colorectal cancer cell line using methylated CpG island amplification, a PCR-based technique developed to clone differentially methylated DNA sequences (26). The methylation status of these nine loci was first examined for 27 gastric cancers and adjacent normal stomach mucosa (examples in Fig. 1, summarized in Table 1). These results indicate that hypermethylation of these loci is a common event in gastric cancer. This pattern of methylation (termed Type A for aging) is identical to that observed in colorectal cancer, in which genes affected by age-related methylation in normal colon are almost always methylated in cancers as well (21, 27). By contrast to these loci, methylation of MINT1, 2, 12, 25, and 31 was exclusively detected in gastric cancers and was absent in most normal gastric mucosa samples (examples in Fig. 1, summarized in Table 1 and Fig. 2). This pattern of methylation was also observed in colorectal cancer and was termed Type C for cancer-specific (21). The CIMP phenotype in colorectal cancer was identified using such cancer-specific clones (21). Therefore, to study CIMP in gastric cancer, the methylation status of these five cancer-specific loci was further examined in a total of 56 cases.

The frequency of methylation of the cancer-specific MINT clones varied between 34 and 71% of the 56 cases examined (examples in Fig. 1, summarized in Table 1). Of these cancer-specific clones, MINT25 stands out as the most frequently affected. This CpG island maps to chromosome 22q11–13, but the associated gene is unknown at this point. Despite its high frequency of methylation in tumors, no methylation of MINT25 was observed in either normal stomach or normal colon (21, 27). Interestingly, MINT25 is hypermethylated in less than 10% of colorectal tumors (21), which suggests that it may play a special role in stomach neoplasia.

To establish whether there was an unusual clustering of methylation (or lack thereof), we determined the expected rates of concordance of methylation based on the measured rates of methylation at each of these five loci. If methylation was random in the 56 cases studied, we would have expected to see 2 cases with zero of five positive loci, 11 cases with one of five positive loci, 19 cases with two of five positive loci, 6 cases with three of five positive loci, and only 1 case in which all of the loci are methylated. The observed numbers were 9 cases with zero of five loci, 13 cases

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^4 Primer sequences and detailed cycling parameters are available at http://www.med.jhu.edu/methylation/primers.html.

^5 Detailed protocols can also be found at http://www.med.jhu.edu/methylation.
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Table 1  Frequency of methylation of multiple loci in gastric cancer

<table>
<thead>
<tr>
<th>Cases</th>
<th>Type C (%)</th>
<th>Type A (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>MINT1</td>
<td>MINT2</td>
</tr>
<tr>
<td>CIMP* (n = 23)</td>
<td>87</td>
<td>71</td>
</tr>
<tr>
<td>CIMP* (n = 12)</td>
<td>42</td>
<td>40</td>
</tr>
<tr>
<td>CIMP* (n = 21)</td>
<td>0</td>
<td>5</td>
</tr>
<tr>
<td>Total (n = 56)</td>
<td>45</td>
<td>38</td>
</tr>
</tbody>
</table>

* n = 27 for Type A loci.

Fig. 2. CIMP in gastric cancer. The methylation status of 7 CpG islands in 56 gastric cancers is shown. Each column represents a separate gene locus indicated on the top. Each row represents a primary gastric cancer. White squares, unmethylated alleles in the tumor. N.D., and n.d. not done. The top group is CIMP* (= three MINT loci methylated); the bottom group is CIMP* (< two MINT loci methylated); and the middle group is CIMP-I (intermediate, 2 MINT loci methylated).

with one of five loci, 11 cases with two of five loci, 7 cases with three of five loci, 10 cases with four of five loci, and 6 cases with five of five loci methylated, respectively, which was significantly different from what was expected (P = 0.004 by \( \chi^2 \) analysis performed by dividing the cases into three groups with zero of one, two of three, and four of five loci methylated). As shown in Fig. 2, this difference is due to an excess of cases with high levels of methylation, as well as cases with no methylation at all. This indicates the presence of a hypermethylator phenotype in gastric cancer similar to that seen in colorectal cancer and referred to as CIMP (21). The cases showing methylation at more than three loci were defined as CIMP*, those methylated at two loci called CIMP-I (intermediate), and the cases where less than two loci were methylated were defined as CIMP-. The above analyses and classification remain largely unchanged if we exclude MINT25. In fact, in the absence of MINT25, the distinction between the three CIMP groups becomes more pronounced.

To investigate whether CIMP affects the methylation of known genes in gastric cancers, the cyclin-dependent kinase inhibitor \( p16 \) on chromosome 9p21 (12–14) and the mismatch repair gene \( hMLH1 \) on chromosome 3p21 (7, 16–19), which are known to be methylated in various cancers, were examined. Of 56 cases, 18 (32%) showed methylation of \( p16 \), and 3 (5%) showed methylation of \( hMLH1 \). Just like the MINT loci examined, methylation of \( p16 \) and \( hMLH1 \) clustered in CIMP* cases (Fig. 2), \( p16 \) was methylated in 16 (70%) of 23 CIMP* tumors, 1 (8%) of 12 CIMP-I tumors, and 1 (5%) of 21 CIMP- tumors (\( P < 0.0001 \) by Fisher’s exact test). All three of the gastric cancers that showed \( hMLH1 \) methylation were CIMP*. Next, we examined the relation between MSI status and CIMP. In total, 5 tumors were MSI-H, 4 tumors were MSI-L, and 47 tumors were microsatellite stable. Three (60%) of five MSI-H tumors were methylated at \( hMLH1 \), and all three of the cases were CIMP*. None of the other tumors had \( hMLH1 \) methylation. The other two MSI-H tumors were CIMP-.

Gastric cancer often arises from a background of dysplasia (28). To determine whether CIMP could precede cancer formation, we next examined the methylation status of multiple CpG islands in normal stomach mucosa adjacent to cancer. Although the methylation of cancer-specific loci was rarely detected in normal stomach mucosa, in five cases (Cases 17, 44, 60, 28, and 1151), the normal mucosa adjacent to CIMP* tumors showed methylation of multiple loci, including \( p16 \) (examples in Fig. 3). These data suggested the possibility that some CIMP* gastric cancers arise from CIMP* dysplasia. Interestingly, in one case (No. 44), the apparently normal CIMP* tissue was unmethylated at \( hMLH1 \), whereas the adjacent cancer was in fact methylated at this locus (data not shown).

Finally, the clinicopathological features of these tumors were studied in reference to the CIMP phenotype. There was no statistical difference between CIMP* and CIMP- cases in age (64 ± 2.6 versus 64.7 ± 2.4), tumor size, gender, or presence of lymph node metastasis. However, there seemed to be a significant difference in the stages of the tumors. Six of 23 CIMP* tumors were early stage (Stage I),
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In gastric cancer, CIMP tumors have a hypermethylator phenotype (CIMP), which leads to the de novo methylation of known genes, including p16 and hMLH1. In colorectal cancer, which are often CIMP, methylation may explain many cases of tumor suppressor gene expression in sporadic gastric cancers. This gene is rarely methylated in colorectal, lung, prostate, and brain tumors (data not shown). This Cpg island may then be useful as a specific diagnostic marker in gastric cancer in which there is no perfect marker for noninvasive diagnosis. It may also be useful to combine some of these markers to detect circulating tumor cells in blood or predict the prognosis of patients. Moreover, methylation profiling may be useful to establish the epigenotype of each tumor to detect potential differences in sensitivity to chemotherapy, occurrence of metastasis, and overall prognosis.

Acknowledgments

We thank Drs. Masanobu Kusano and Hiroaki Mita for helpful assistance in collecting gastric cancer specimens.

References


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