Loss of Heterozygosity on Chromosome 18q in Cohesive-type Gastric Cancer Is Associated with Tumor Progression and Poor Prognosis

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ABSTRACT
Although loss of heterozygosity (LOH) on chromosome 18q is frequently found in gastric cancer, the clinical significance of this abnormality has not been well documented. We examined LOH on chromosome 18q22-23 in DNA extracted from the tissues of gastric cancer patients using the PCR-based dinucleotide repeat assay with two microsatellite markers, D18S61 and D18S58. We investigated LOH in 100 samples of DNA extracted from formalin-fixed, paraffin-embedded tissues of cohesive-type gastric cancer patients operated on between 1984 and 1993. Thirty-two of 83 informative cases (39%) showed LOH on chromosome 18q22-23 at one or two loci. The LOH correlated significantly with serosal invasion of the tumor (P = 0.004) and hematogenous recurrence (P = 0.035). In 60 cases who were cured, the 5-year survival rate in patients with LOH (54%) was lower than that in patients without LOH (81%; P = 0.019). These results suggest that 18q22-23 LOH in cohesive gastric cancer is associated with tumor progression and a patient's poor prognosis.

INTRODUCTION
Recent studies have helped to increase our understanding of the genetic alterations in the alleles of oncogenes (1) and tumor suppressor genes (2) involved in the carcinogenesis or progression of cancers in various organs. Gastric cancer is one of the most common cancers in the world, and the prognosis of patients with tumor invading the serosa or neighboring structures is extremely poor. However, in contrast to colorectal cancer, oncogenes and tumor suppressor genes in gastric cancer are poorly understood (3–6).

LOH on the long arm of chromosome 18 is frequently found in tissues of colorectal cancer (3–8). The DCC gene was isolated from the commonly deleted region of chromosome 18q21 (9). This gene is thought to be one of the tumor suppressor genes and encodes a deduced protein with an immunoglobulin-like C2 domain and a fibronectin type III domain. The predicted amino acid sequence shows homology to the IgG superfamily of cell adhesion molecules, including the neural cell adhesion molecule (9). The expression of mRNA was extremely decreased in colorectal cancer tissues with the deletion of the DCC gene. Furthermore, LOH at the DCC locus was found in all metastatic liver tissues of colorectal cancer, although the incidence of 18q LOH in the primary site was about 70% (8). Additionally, LOH on chromosome 18q or reduced expression of the DCC protein in colorectal cancer is reported to be a prognostic marker in patients with stage II or III colorectal cancer (7, 10). This evidence suggests that the loss of DCC protein may be associated with tumor invasion or metastasis. Moreover, DPC4, a candidate tumor suppressor gene, has recently been identified at 18q21.1 (11).

We previously reported that the long arm of chromosome 18, which includes the DCC locus, was also frequently deleted in gastric cancer (12). The implication of LOH on chromosome 18q in the development or progression of gastric cancer has not yet been elucidated. To investigate the relationship between LOH on chromosome 18q and the clinicopathological features of gastric cancer, we examined LOH on chromosome 18q22–23 with special reference to tumor histological type using the PCR-based dinucleotide repeat assay.

MATERIALS AND METHODS
Patients. Histopathological classification was based on the General Rules for the Gastric Cancer Study outlined by the Japanese Research Society for Gastric Cancer (13). In addition to these criteria, we subdivided gastric cancers into two types as described previously (12, 14–18). One was cohesive type (papillary adenocarcinoma, well and moderately differentiated tubular adenocarcinoma, and poorly differentiated adenocarcinoma with solid nests or focal tubular structures) and the other was scattered type (signet ring cell carcinoma and poorly differentiated adenocarcinoma growing in a scattered manner). First, fresh frozen tumor tissues and corresponding normal gastric mucosae were randomly collected from 16 patients with solitary gastric cancer who underwent gastrectomy at Oita Medical University between 1992 and 1993. Five cases were diagnosed...
as well to moderately differentiated tubular adenocarcinoma, six as poorly differentiated adenocarcinoma of solid type, three as poorly differentiated adenocarcinoma of diffuse type, and two as signet ring cell carcinoma. In the alternative classification, 11 cases were diagnosed as cohesive type and 5 as scattered type.

To investigate the correlation between LOH on chromosome 18q22–23 and the clinicopathological parameters of the cohesive type of gastric cancer, we also examined formalin-fixed, paraffin-embedded tumor tissues and corresponding normal gastric mucosae from patients who underwent gastrectomy for solitary gastric cancer at Department of Surgery I, Oita Medical University, between January 1984 and December 1993. All cases underwent surgery during this period, and the cases that had a cancer cell-rich portion were selected. Twenty-five cases were diagnosed as papillary adenocarcinoma, 46 as well to moderately differentiated tubular adenocarcinoma, and 29 as poorly differentiated adenocarcinoma. The total number of cases was 100. Curative operation was performed in 76 patients and palliative operation in 24. The reasons of palliative operation were hepatic metastasis in 10 cases, peritoneal dissemination in 2, both hepatic metastasis and peritoneal dissemination in 3, and residual primary tumor with nonresectable para-aortic lymph node metastasis in 9. Clinicopathological evaluations were made according to the General Rules for the Gastric Cancer Study (13).

**DNA Extraction and the PCR-based Dinucleotide Repeat Assay.** Because gastric cancer tissue often has numerous nonneoplastic cells, we used a microscopic dissection method as described previously (12). Briefly, to ascertain the area where the cancer cells were relatively dominant, 5-μm sections of fresh frozen materials immersed in OCT compound (Miles Scientific) or formalin-fixed, paraffin-embedded materials were stained with H&E. Carcinomas that contained 40% more cancer cells than nonneoplastic cells were judged to be cancer cell rich, and only these cases were selected in this study. The cancer cell-rich portion was then cut with a scalpel from successive 50-μm sections. These sections, including the predominant cancer cells, were subjected to DNA extraction. DNAs were extracted from primary gastric tumor tissues and corresponding normal gastric mucosae from patients who underwent gastrectomy for solitary gastric cancer at Department of Surgery I, Oita Medical University, between January 1984 and December 1993.

RESULTS

Among 16 randomly selected cases of DNAs extracted from fresh frozen samples of gastric cancer, 10 cases (63%) were informative at the D18S61 locus, and of these, 5 (50%) showed LOH. In addition, 11 cases (69%) were informative at the D18S58 locus, and of these, 4 (36%) showed LOH. With the combined results of the two loci, LOH was specifically found in 5 of 10 informative cases of the cohesive type (50%) but was not found in 2 informative cases of the scattered type (0%). From this result and our previous investigation, there is a possibility that 18q LOH may occur selectively in gastric cancer of cohesive type, so we investigated an additional 100 cases of cohesive type of gastric cancer.

PCR products of some tumors (1 of the 16 fresh frozen samples and 5 of the 100 (5%) formalin-fixed, paraffin-embedded samples) showed a ladder band in addition to the standard band, and these were considered to be cases of replication error (19–21). The replication error cases were excluded from this LOH analysis, because they may have a different genetic mechanism from that of the LOH cases.

Fifty eight cases (58%) were informative at the D18S61 locus, and 19 of 58 (33%) showed LOH. Seventy cases (70%) were informative at the D18S58 locus, and 24 of 70 (34%) showed LOH (Fig. 1). With the combined results of the two loci, 83 cases (83%) were informative at least at one loci, and 32 of 83 (39%) had LOH on chromosome 18q22–23 (Table 1). Two cases showed LOH at the D18S58 locus but not at the D18S61 locus.

The relationship between LOH on chromosome 18q22–23 and the clinicopathological parameters are shown in Table 2. LOH was significantly correlated with serosal invasion of the tumor (P = 0.004). However, there was no significant difference between LOH-positive and LOH-negative cases in tumor size, lymphatic invasion, vascular invasion, lymph node metastasis, or postoperative chemotherapy. Of 83 informative cases, 60 underwent curative surgery. LOH was also significantly correlated with serosal invasion of the tumor in cases who were cured (P = 0.031; Table 3). Among these, three died of postoperative complication and were excluded from the follow-up analysis. As for recurrence, liver metastasis occurred in 10 (18%), peritoneal dissemination in 4 (7%), lymph node recurrence in 4 (7%), and local recurrence in 1 (2%). Liver metastasis was significantly higher in patients with LOH (33%) than in those without LOH (10%; P = 0.035; Table 4). In the 57 cases who were cured, the five-year survival rate of LOH-positive group (54%) was significantly lower than that of the LOH-negative group (81%; P = 0.019; Fig. 2).
Fig. 1 Examples of LOH on chromosome 18q22–23 at the two markers of cognate in primary gastric tumor tissue and corresponding normal gastric mucosa. Case numbers are shown at the top of each lane. N, normal DNA; T, tumor DNA. The tumors in panels 39, 45, 52, 54, and 82 showed LOH (arrowheads), whereas those in panels 2, 13, and 68 did not.

**Table 1** Chromosome 18q LOH in cohesive-type gastric cancer

<table>
<thead>
<tr>
<th>Locus</th>
<th>Localization</th>
<th>No. of cases tested</th>
<th>No. of Informative cases</th>
<th>No. of LOH-positive cases (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>D18S61</td>
<td>18q22.3</td>
<td>100</td>
<td>58</td>
<td>19 (33)</td>
</tr>
<tr>
<td>D18S58</td>
<td>18q22.3-23</td>
<td>100</td>
<td>70</td>
<td>24 (34)</td>
</tr>
<tr>
<td>Combined</td>
<td></td>
<td>100</td>
<td>83</td>
<td>32 (39)</td>
</tr>
</tbody>
</table>

**DISCUSSION**

A high incidence of LOH on chromosome 18q22–23 occurred selectively in gastric cancers of the cohesive type but not in those of the scattered type. Our previous study also revealed histopathological specificity concerning genetic alterations (12, 14–18). Histologically, the two main types of gastric carcinoma, cohesive and scattered, display a different spectra of genetic alterations. Point mutations in the c-Ki-ras (22) and p53 genes (14, 15, 23) and amplification of c-erbB-2 gene (16, 24, 25) are associated with the cohesive type. On the other hand, K-sam amplification (26, 27) and abnormalities of E-cadherin and catenins (17, 28) are associated with the scattered type. These two types of cancer are considered to develop through independent genetic pathways, and the difference of genetic abnormalities is directly reflected in the different histological features.

We also previously reported that LOH on chromosome 18q was frequently detected in gastric cancers of the cohesive type using RFLP analysis, and a putative common region showing LOH was 18q21.3-qter, which includes the DCC locus (12). Gastric cancers were examined for LOH on chromosome 18q by another several researchers (29, 30); however, a significantly high incidence of LOH was not demonstrated. Numerous non-neoplastic cells are often intermingled with the cancer stroma, and tissues with predominantly cancer cells are difficult to collect, even in the cohesive type. Therefore, the selection of patients and collection of cancer cells from the gastric cancers with consideration of histological type are very important in studying the molecular biology of gastric cancer. Jen et al. (7) recommended the use of two dinucleotide repeat markers, D18S58 and D18S61, because these markers from chromosome 18q22–23 were sufficient to determine the status of its chromosome. We confirmed a high informative rate on chromosome 18q22–23 using these two markers.

**Table 2** Clinicopathological characteristics with regard to chromosome 18q status

<table>
<thead>
<tr>
<th></th>
<th>18q LOH-negative (n = 51)</th>
<th>18q LOH-positive (n = 32)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex ratio (M:F)</td>
<td>2:6:1</td>
<td>2:6:1</td>
<td>NS</td>
</tr>
<tr>
<td>Mean age (yr)</td>
<td>67.4 ± 10.2</td>
<td>69.9 ± 10.6</td>
<td>NS</td>
</tr>
<tr>
<td>Mean tumor size (cm)</td>
<td>6.4 ± 2.7</td>
<td>7.4 ± 2.7</td>
<td>NS</td>
</tr>
<tr>
<td>Serosal invasion</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Absent</td>
<td>41 (80)*</td>
<td>16 (50)</td>
<td></td>
</tr>
<tr>
<td>Present</td>
<td>10 (20)</td>
<td>16 (50)</td>
<td>0.004</td>
</tr>
<tr>
<td>Lymphatic invasion</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Absent</td>
<td>6 (12)</td>
<td>4 (13)</td>
<td></td>
</tr>
<tr>
<td>Present</td>
<td>45 (88)</td>
<td>28 (87)</td>
<td>NS</td>
</tr>
<tr>
<td>Vascular invasion</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Absent</td>
<td>21 (41)</td>
<td>17 (53)</td>
<td>NS</td>
</tr>
<tr>
<td>Present</td>
<td>30 (59)</td>
<td>15 (47)</td>
<td></td>
</tr>
<tr>
<td>Lymph node metastasis</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Absent</td>
<td>14 (27)</td>
<td>5 (16)</td>
<td>NS</td>
</tr>
<tr>
<td>Present</td>
<td>37 (73)</td>
<td>27 (84)</td>
<td></td>
</tr>
<tr>
<td>Operation</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Curative</td>
<td>40 (78)</td>
<td>20 (62)</td>
<td></td>
</tr>
<tr>
<td>Noncurative</td>
<td>11 (22)</td>
<td>12 (38)</td>
<td>NS</td>
</tr>
<tr>
<td>Postoperative chemotherapy</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Absent</td>
<td>18 (35)</td>
<td>7 (22)</td>
<td>NS</td>
</tr>
<tr>
<td>Present</td>
<td>33 (65)</td>
<td>25 (78)</td>
<td></td>
</tr>
<tr>
<td>Median follow-up time (months)</td>
<td>38.8</td>
<td>27.4</td>
<td>NS</td>
</tr>
</tbody>
</table>

* NS, not significant.
* Numbers in parentheses are percentages.
Certain specific genetic alterations have been studied as potential prognostic markers in gastric cancer. The c-Ki-ras point mutation has an important role in the development from adenoma to carcinomas in the stomach, but it has no prognostic importance (22). We reported that overexpression of c-erbB-2 protein was found selectively in the cohesive type of gastric tumors suppressor gene, which is one of the most commonly affected genes in various human cancers, is also frequently inactivated in gastric cancer (14, 15). Our data from an examination of the p53 mutation and immunohistochemical analysis suggest that it is useless for determining patient’s prognosis (14, 15). In gastric cancer of the cohesive type, a significant association was found between LOH on chromosome 18q22-23 and the serosal tumor invasion, and in addition, the survival rate for patients with LOH on chromosome 18q22-23 who underwent curative surgery was significantly poorer than those of patients without LOH. Moreover, hematogenous recurrence was found significantly more frequently in the group of patients with LOH on chromosome 18q22-23 than in those without LOH. Therefore, LOH on chromosome 18q22-23 may be associated with the grade of malignancy, tumor progression, and high metastatic potential through the vessel.

In colorectal cancer, Jen et al. (7) reported that LOH on chromosome 18q was an important prognostic factor in stage II disease, and O’Connell et al. (31) reported from analysis of disease-free survival after surgical resection in colorectal carcinoma patients that a poorer prognosis was associated with LOH on chromosome 18q. In the studies of Vogelstein and co-workers (5, 7), distant metastasis in colorectal cancer was significantly associated with LOH on chromosome 18q. In addition, Ookawa et al. (8) reported that 18q LOH was found in almost all of the liver metastases from colorectal carcinoma. The association of LOH on chromosome 18q22-23 with patient’s prognosis, serosal tumor invasion, and metastasis in gastric cancer suggests the possibility that the abnormalities of the gene present on chromosome 18q22-23 or nearby may lead to a decrease in the ability of cell to cell contacts, thereby contributing to tumor growth, invasion, and metastasis.

Although the specific gene(s) on chromosome 18q22-23 in gastric and colorectal cancer has not yet been identified, the DCC and DPC4 genes are candidates. Using RFLP analysis with several DCC probes, we noted allele loss at the DCC locus in 61% of cohesive type gastric cancers (12). Barletta et al. (29) also reported DCC allele loss in 4 of 4 gastric carcinomas, whereas Kataoka et al. (32) reported that DCC mRNA was decreased in 40% of gastric cancers. Recently, DPC4, a candidate tumor suppressor gene, has been identified at 18q21.1 (11). This gene is inactivated in nearly one-half of pancreatic carcinoma cases. However, Powell et al. (33) reported that only one case of apparent biallelic inactivation of DPC4 was found in the study of 35 gastric carcinoma cases, and Nishizuka et al. (34) reported that no DPC4 mutations were found in 30 primary
gastrointestinal cancer cases and 5 gastric carcinoma cell line. Therefore, there is a possibility that an additional gene(s) on chromosome 18q may be the gene responsible for the progression of gastric cancer, and further genetic and biological testing is necessary to resolve this question. In the near future, tests for the status of chromosome 18q may be combined with other genetic and biochemical assays to improve the prognostic evaluation of patients with gastric cancer.

REFERENCES

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