

## DNA demethylation of *Vascular endothelial growth factor-C* is associated with gene expression and its possible involvement of lymphangiogenesis in gastric cancer

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Previous studies have indicated that lymphangiogenesis in solid tumors is associated with lymphatic metastasis. Overexpression of Vascular endothelial growth factor (VEGF)-C plays a major role in lymphangiogenesis in cancers. In the present study, DNA methylation and expression of the *VEGF-C* gene was investigated in gastric cancer (GC). Four GC cell lines (MKN-45, MKN-74, HSC-39 and HSC-43) showed no expression of *VEGF-C*, and the *VEGF-C* gene was found to be methylated in these cells. In contrast, 7 GC cell lines (MKN-1, MKN-7, MKN-28, TMK-1, KATO-III, SH101-P4 and HSC-44PE) expressed *VEGF-C*, and the *VEGF-C* gene was found to be unmethylated in these cell lines. In addition, expression of *VEGF-C* mRNA was retrieved by treatment with a demethylating agent, Aza-2'-deoxycytidine. In GC tissue samples, bisulfite DNA sequencing analysis revealed that *VEGF-C* was not methylated in 9 (29.0%) of 31 GC samples, whereas demethylation was not observed in corresponding non-neoplastic mucosa samples. Overexpression of *VEGF-C* mRNA was observed in 16 (51.6%) of 31 GC samples by quantitative reverse transcription-polymerase chain reaction. Of the 9 GC cases with *VEGF-C* demethylation, 8 (88.9%) overexpressed *VEGF-C*. In contrast, of the 22 GC cases without *VEGF-C* demethylation, 8 (36.4%) overexpressed *VEGF-C* ( $p = 0.0155$ ). Furthermore, lymphatic vessel density determined by immunostaining of podoplanin in GC tissues was associated with overexpression of *VEGF-C* ( $p < 0.0001$ ). These results suggest that demethylation and activation of the *VEGF-C* gene is likely involved in lymphangiogenesis in GC.

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**Key words:** DNA methylation; DNA demethylation; *VEGF-C*; lymphangiogenesis; gastric cancer

According to the World Health Organization, gastric cancer (GC) is the fourth most common malignancy in the world, with ~870,000 new cases every year, and mortality from GC is second only to that from lung cancer.<sup>1</sup> Despite improvements in diagnostic and therapeutic methods, the prognosis of advanced GC with extensive invasion and metastasis remains poor. Several molecules associated with invasion and metastasis have been identified<sup>2,3</sup>; however, all the mechanisms underlying metastasis remains unclear.

We previously reported that hypoacetylation of histone H4 is associated with tumor progression and lymph node metastasis.<sup>4</sup> Genes with expression regulated by histone acetylation may be involved in tumor progression or metastasis. In GC, expression of *p21<sup>WAF1/CIP1</sup>* and *PINX1*<sup>6</sup> are regulated by histone acetylation, but expression of these genes is not associated with tumor progression or metastasis. Histone deacetylation also plays an important role in CpG island methylation-associated gene inactivation.<sup>7</sup> DNA methylation of CpG islands is detected commonly in human cancers including GC.<sup>8–11</sup> Hypermethylation of CpG islands is associated with silencing of several genes,<sup>12,13</sup> especially defective tumor-related genes, and has been proposed as an alternative way to inactivate tumor-related genes in human cancers.<sup>14,15</sup>

Several genes whose expression is activated by DNA demethylation have been reported. Demethylation of both *MAGE16* and *synuclein  $\gamma$* <sup>17</sup> are correlated with tumor progression and lymph node metastasis in GC. Activation of *matrix metalloproteinase* genes by DNA demethylation has been observed in pancreatic cancer cell lines.<sup>18</sup> Taken together, the currently available data suggest that certain genes activated by DNA demethy-

lation may be involved in tumor progression and lymph node metastasis.

It has been shown a close association between vascular endothelial growth factor (VEGF) family members and tumor metastasis.<sup>19</sup> VEGF has been established as a primary angiogenic molecule involved in development, adult physiology and pathology. VEGF-C and VEGF-D are primarily lymphangiogenic factors, but they can also induce angiogenesis under some conditions. Overexpression of VEGF-C has been detected in a variety of cancers.<sup>20</sup> However, the role of demethylation of *VEGF-C* in human cancer has not been examined.

In the present study, we examined whether DNA demethylation may be associated with the overexpression of the *VEGF-C* in GC. We show that the overexpression of *VEGF-C* is associated with DNA demethylation and can be restored in GC cell lines after aza-2'-deoxycytidine (Aza-dC)-induced demethylation. We further investigated DNA demethylation of *VEGF-C* and its possible involvement in lymphangiogenesis by immunostaining of podoplanin, a marker of lymphatic endothelial cell, in GC.

### Material and methods

#### GC cell lines and drug treatment

Eleven cell lines derived from human GC were used. The TMK-1 cell line was established in our laboratory from a poorly differentiated adenocarcinoma.<sup>21</sup> Five gastric carcinoma cell lines of the MKN series (MKN-1, adenocarcinoma cell carcinoma; MKN-7; MKN-28; MKN-74, well differentiated adenocarcinoma; and MKN-45, poorly differentiated adenocarcinoma) were kindly provided by Dr. Toshimitsu Suzuki. KATO-III cell lines were kindly provided by Dr. Morimasa Sekiguchi. SH101-P4, HSC-39, HSC-43 and HSC-44PE cell lines were kindly provided by Dr. Kazuyoshi Yanagihara.<sup>22–25</sup> All cell lines were maintained in RPMI 1640 (Nissui Pharmaceutical, Tokyo, Japan) containing 10% fetal bovine serum (BioWhittaker, Walkersville, MD) in a humidified atmosphere of 5% CO<sub>2</sub> and 95% air at 37°C. To analyze transcriptional activation of *VEGF-C*, MKN-1, MKN-45 and MKN-74 cells were incubated for 5 days with 1  $\mu$ M Aza-dC (Sigma Chemical, St. Louis, MO, USA) or for 24 h with 300 nM TSA (Wako, Tokyo, Japan).

**Abbreviations:** VEGF, vascular endothelial growth factor; GC, gastric cancer; Aza-dC, aza-2'-deoxycytidine; PCR, polymerase chain reaction; RT-PCR, reverse transcription-PCR; LVD, lymphatic vessel density; T, GC tissue; N, corresponding non-neoplastic mucosa; TAM, tumor-associated macrophage.

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TABLE 1 - PRIMER SEQUENCES FOR BISULFITE DNA SEQUENCING, CONVENTIONAL RT-PCR AND QUANTITATIVE RT-PCR

Primer sequence	Annealing temperature (°C)	Size (bp)
Bisulfite DNA sequencing (Region 1)		
F: 5'-TTTTTCGGTATTGGTTGGG-3'	53	181
R: 5'-CCGCTAACGAAAACAAAAAT-3'		
Bisulfite DNA sequencing (Region 2)		
F: 5'-GCGGGGTGTTTTGGTGT-3'	54	187
R: 5'-ACGCCCTCCCAACCAATACC-3'		
Conventional RT-PCR ( <i>VEGF-C</i> )		
F: 5'-TCGCGACAAACACCTTCTTT-3'	56	610
R: 5'-CTGGGGCAGGTTCTTTTACA-3'		
Conventional RT-PCR ( <i>ACTB</i> )		
F: 5'-CTGTCTGGCGGCACCACCAT-3'	55	254
R: 5'-GCAACTAAGTCATAGTCCGC-3'		
Quantitative RT-PCR ( <i>VEGF-C</i> )		
F: 5'-TGCCGATGCATGTCTAAACT-3'	55	251
R: 5'-TGAACAGGTCTCTTCATCCAGC-3'		
Probe: 5'-FAM CAGCAACTACCACAGTGTCCAGGCA TAMRA-3'		
Quantitative RT-PCR ( <i>ACTB</i> )		
F: 5'-TCACCGAGCGCGCT-3'	55	60
R: 5'-TAATGTCACGCACGATTTCCC-3'		

### Tissue samples

Frozen tissue samples were collected from 31 patients (age range, 41–86 years; mean, 67.8 years) with GC who underwent surgery between 1998 and 2001 at the Department of Surgical Oncology, Hiroshima University Hospital (Hiroshima, Japan). All patients underwent curative resection, and all GC samples were advanced GC. These 31 GC tissue specimens and 5 corresponding non-neoplastic mucosa samples from the 5 GC patients (age range, 57–75 years; mean, 68.3 years) were analyzed for methylation of the *VEGF-C* gene. Total RNA was available for 31 pairs of tumor and corresponding non-neoplastic mucosa. GC and corresponding non-neoplastic mucosa were removed surgically, frozen immediately in liquid nitrogen and stored at  $-80^{\circ}\text{C}$  until use. We confirmed microscopically that the tumor specimens consisted mainly of carcinoma tissue (>50%, on a nuclear basis) and that specimens of non-neoplastic mucosa did not show tumor cell invasion or significant inflammatory involvement. Tumor staging was carried out according to the TNM staging system.<sup>26</sup> We also examined levels of *VEGF-C* mRNA in 10 samples of normal gastric mucosa obtained endoscopically from 10 healthy young individuals (age range, 22–35 years; mean, 26.4 years) and evaluated methylation status of the *VEGF-C* gene in 2 samples from normal healthy young individuals. These healthy volunteers were confirmed to be free of malignancy by gastrointestinal endoscopy and biopsy. Because written informed consent was not obtained, for strict privacy protection, identifying information for all samples was removed before analysis; the procedure was in accordance with the Ethical Guidelines for Human Genome/Gene Research enacted by the Japanese Government.

### Conventional and quantitative reverse transcription-polymerase chain reaction analyses

Total RNA was extracted with an RNeasy Mini Kit (Qiagen, Valencia, CA), and 1  $\mu\text{g}$  of total RNA was converted to cDNA with a First Strand cDNA Synthesis Kit (Amersham Biosciences, Piscataway, NJ). Conventional RT-PCR was performed to investigate *VEGF*, *VEGF-B*, *VEGF-C* and *VEGF-D* expression in GC cell lines. Amplification products were then separated by 1% agarose gel electrophoresis, stained with ethidium bromide, and visualized under UV light. *ACTB*-specific PCR products served as internal controls. Primer sequences and additional PCR conditions are available upon request.

Quantitation of *VEGF-C* mRNA levels in human tissue samples was done by real-time fluorescence detection as described previously.<sup>27</sup> Primer sequences and annealing temperatures are shown in Table I. PCR was performed with a TaqMan Universal PCR

Master Mix (Applied Biosystems, Foster City, CA, USA). Real-time detection of the emission intensity of fluorescent reporter dye was performed with an ABI PRISM 7700 Sequence Detection System (Applied Biosystems) as described previously.<sup>28</sup> *ACTB*-specific PCR products were amplified from the same RNA samples and served as internal controls. We calculated the ratio of *VEGF-C* mRNA levels in GC tissue (T) to those in corresponding non-neoplastic mucosa (N). T/N ratios >2-fold were considered to represent overexpression.

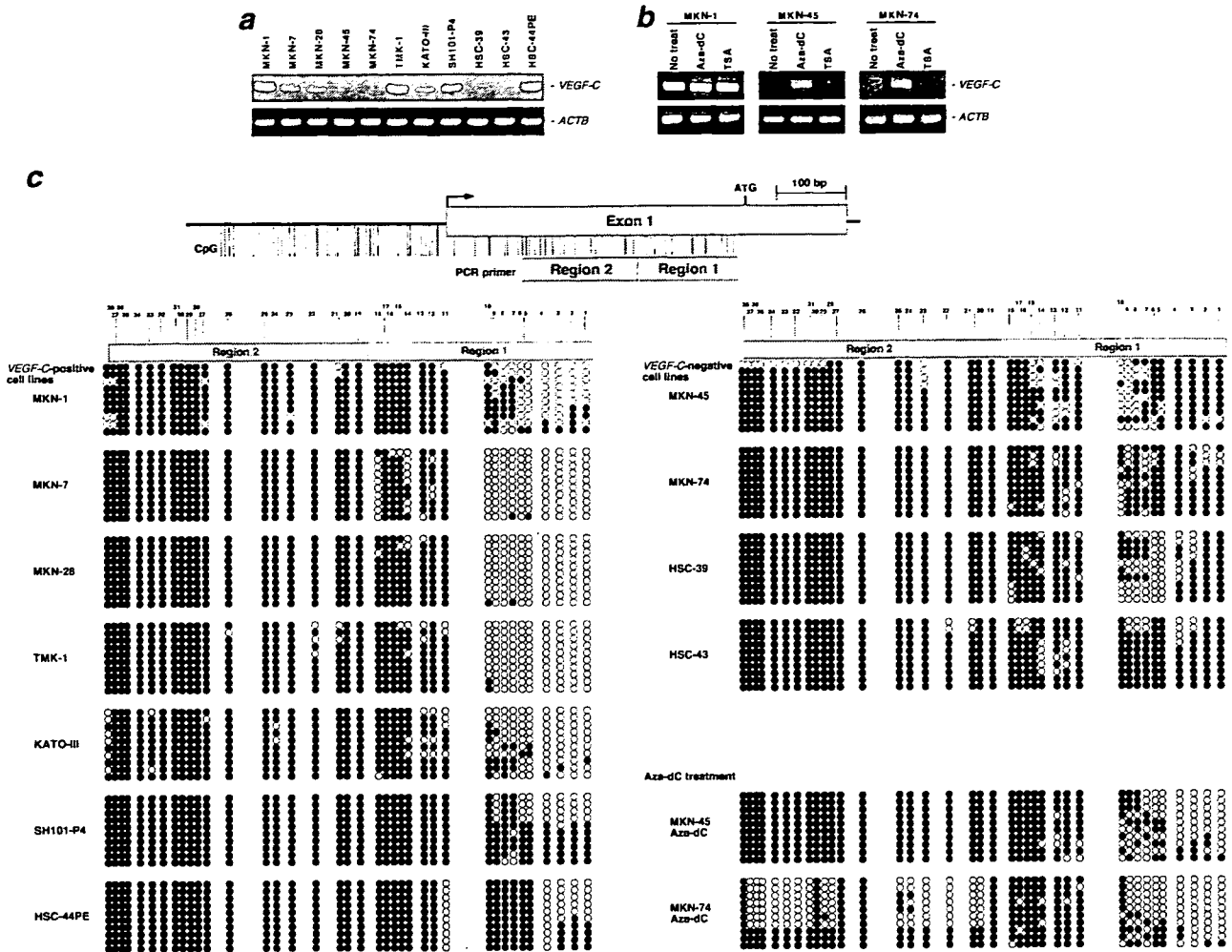
### Genomic DNA extraction and bisulfite genomic DNA sequencing

Genomic DNAs were extracted with a Genomic DNA Purification Kit (Promega, Madison, WI). To examine DNA methylation patterns, genomic DNA was treated with 3 M sodium bisulfite as described previously.<sup>29</sup> For analysis of DNA methylation of *VEGF-C*, we performed bisulfite genomic DNA sequencing analysis. Two sets of primers were used to assess the different regions (Regions 1 and 2) of the *VEGF-C* gene (Fig. 1c). Except for primer complementary sequences, Region 1 contains 18 CpG sites, and Region 2 contains 20 CpG sites. Two-microliter aliquots were used as templates for PCR reactions. Primer sequences and annealing temperatures are shown in Table I. Each target sequence was amplified in a 50- $\mu\text{l}$  reaction containing 0.2  $\mu\text{M}$  dNTPs, 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 2 mM  $\text{MgCl}_2$ , 0.3  $\mu\text{M}$  each primer and 0.75 units of AmpliTaq Gold (Applied Biosystems). PCR amplification consisted of 35 cycles after the initial AmpliTaq Gold activation step.

PCR products were purified and cloned into pCR2.1 (Invitrogen, Carlsbad, CA). The cloned PCR fragments obtained from each sample were sequenced with M13 forward primer and a PRISM AmpliTaq DNA Polymerase FS Ready Reaction Dye Terminator Sequencing Kit (Applied Biosystems). Reamplified DNA fragments were purified with Centri-Sep Columns (Applied Biosystems) and sequenced with an ABI PRISM 310 Genetic Analyzer (Applied Biosystems).

### Immunostaining of lymphatic vessels and determination of lymphatic vessel density

Consecutive 4- $\mu\text{m}$  sections of formalin-fixed, paraffin-embedded tissue were cut onto glass slides from each study block. Sections were immunostained for podoplanin. Podoplanin, a 38-kDa membrane glycoprotein originally identified on podocytes, is expressed on the endothelium of lymphatic capillaries but not in quiescent or proliferating blood vascular endothelium.<sup>30</sup> Immunostaining was done with the Histofine Simplestain MAX-PO (MULTI) (Nichirei Biosciences, Tokyo, Japan) immunoperox-



**FIGURE 1** – RT-PCR analysis and bisulfite genomic DNA sequencing analysis of *VEGF-C* in GC cell lines. (a) Conventional RT-PCR of *VEGF-C*. *VEGF-C* was not expressed in the MKN-45, MKN-74, HSC-39 and HSC-43 cell lines. (b) Treatment of MKN-45 and MKN-74 cells with Aza-dC activated *VEGF-C* expression. Treatment of these cells with TSA did not induce *VEGF-C* expression. Treatment with Aza-dC and TSA did not significantly affect *VEGF-C* expression in MKN-1 cells. (c) Bisulfite genomic DNA sequencing analysis of *VEGF-C* in GC cell lines. Vertical lines indicate CpG sites. Ten cloned bisulfite PCR products of *VEGF-C* were analyzed. Each row of circles represents a single clone, and each circle represents a single CpG site (open circle, nonmethylated cytosine; filled circle, methylated cytosine). The numbering in this scheme corresponds to the position relative to the translation initiation site.

dase technique. Primary antibody was a mouse antipodoplanin monoclonal antibody (1:200, AngioBio, Del Mar, CA) and was incubated on the sections for 3 h at room temperature. Negative controls were done with nonspecific IgG as the primary antibody. Sections were counterstained with hematoxylin. LVD was evaluated by 2 independent investigators (S.M., N.O.), who were blind to the clinical course of the patients and the *VEGF-C* expression status of the tumors. In brief, after scanning an immunostained section at low magnification ( $\times 100$ ), the area of tissue with the greatest number of distinctly highlighted lymphatic vessels (“hot spot”) at the border of invasive cancer or inside the tumor was selected. LVD was then determined by counting all antipodoplanin immunostained lymphatic vessels at  $\times 200$  in an examination area. Only vessels with typical morphology (lumen) were considered lymphatic microvessels. After the 6 areas of highest neovascularization were identified, lymphatic vessels were counted and the average count was determined.

#### Statistical methods

Differences were analyzed statistically by Fisher’s exact and Mann–Whitney *U* tests. *p* values less than 0.05 were considered statistically significant.

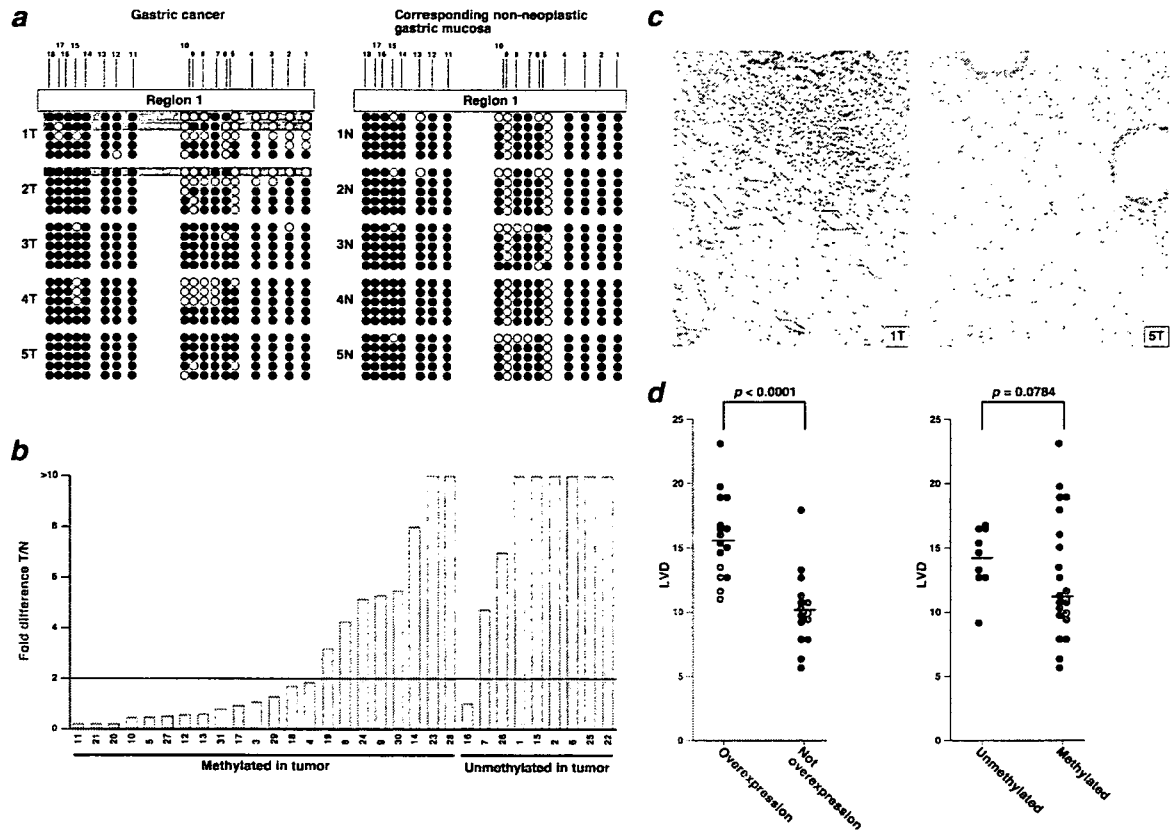
## Results

### Expression of *VEGF*, *VEGF-B*, *VEGF-C*, and *VEGF-D* mRNAs in GC cell lines

To examine expression of *VEGF* genes, we performed conventional RT-PCR analysis of 11 GC cell lines. Expression of *VEGF*, *VEGF-B* and *VEGF-D* was detected in all GC cell lines (data not shown). Four cell lines, MKN-45, MKN-74, HSC-39, and HSC-43, showed no expression of *VEGF-C* (Fig. 1a). We hypothesized that loss of *VEGF-C* expression might be caused by DNA methylation or histone hypoacetylation. To test this hypothesis, MKN-1, MKN-45 and MKN-74 cells were treated with Aza-dC or TSA and then subjected to RT-PCR analysis (Fig. 1b). Treatment with Aza-dC induced *VEGF-C* expression in MKN-45 and MKN-74 cells, whereas treatment with TSA did not. Treatment with Aza-dC or TSA did not significantly change *VEGF-C* expression in MKN-1 cells. These results suggest that DNA methylation may suppress *VEGF-C* expression.

### Analysis of *VEGF-C* methylation in GC cell lines

To evaluate the extent of *VEGF-C* methylation, we performed bisulfite DNA sequencing of genomic DNAs from 7 *VEGF-C*-



**FIGURE 2** – DNA methylation and expression of *VEGF-C* and LVD analysis in GC tissue. (a) Representative results of bisulfite genomic DNA sequencing for GC tissues. In cases 1T and 2T, the unmethylated allele (allele contains unmethylated CpG sites 1, 2, 3 and 4, red box) was detected. In corresponding non-neoplastic mucosa, the unmethylated allele was not found. (b) Quantitative RT-PCR of *VEGF-C* in GC tissues. Fold-change indicates the ratio of target gene mRNA level in GC (T) to that in corresponding non-neoplastic mucosa (N) (T/N ratio). Overexpression (T/N > 2) of *VEGF-C* was detected in 16 (51.6%) of the 31 GC samples. Of 9 GC cases showing *VEGF-C* demethylation, 8 (88.9%) cases, including Cases 1 and 2, showed overexpression of this gene. (c) Immunostaining of lymphatic vessels in GC. In case 1T, which overexpresses *VEGF-C*, podoplanin-positive lymphatic vessels are present at the tumor margin. (original magnification,  $\times 200$ ). In case 5T, in which overexpression of *VEGF-C* was not observed, LVD was low (original magnification,  $\times 200$ ). (d) Summary of LVD. Overexpression of *VEGF-C* was associated with high LVD ( $p < 0.0001$ , Mann-Whitney *U* test), whereas DNA methylation status of *VEGF-C* was not associated with LVD ( $p = 0.0784$ , Mann-Whitney *U* test).

positive (MKN-1, MKN-7, MKN-28, TMK-1, KATO-III, SH101-P4 and HSC-44PE) and 4 *VEGF-C*-negative (MKN-45, MKN-74, HSC-39 and HSC-43) cell lines. Results of bisulfite genomic DNA sequencing are shown in Figure 1c. In *VEGF-C*-positive cells, all 4 CpG sites (sites 1, 2, 3 and 4) of the 3' region of *VEGF-C* were unmethylated in 6 of 10 MKN-1 clones, all MKN-7 clones, all MKN-28 clones, all TMK-1 clones, 7 of 10 KATO-III clones, 4 of 10 SH101-P4 clones and 5 of 10 HSC-44PE clones. In contrast, no *VEGF-C*-negative cell clones showed unmethylation in all 4 CpG sites in the 3' region of *VEGF-C*. In addition, in AzadC-treated MKN-45 and MKN-74 cells, all 4 CpG sites in the 3' region were demethylated. Thus, DNA methylation of the 4 CpG sites plays an important role in transcriptional inactivation of *VEGF-C* gene, at least in the MKN-45 and MKN-74 cell lines.

#### DNA methylation status of *VEGF-C* gene in GC tissue samples

Because overexpression of *VEGF-C* has been reported in GC,<sup>31,32</sup> we examined whether DNA demethylation is involved in overexpression of *VEGF-C* in GC tissue samples. Bisulfite DNA sequencing was performed on genomic DNAs from 31 GC samples. Because bisulfite sequencing analyses of the GC cell lines revealed that DNA methylation of 4 CpG sites in the 3' region (sites 1, 2, 3 and 4) was associated with *VEGF-C* expression, we analyzed the DNA methylation status of Region 1. Five clones from each GC sample were sequenced. Representative results of bisulfite genomic DNA sequencing analysis are shown in Figure

2a. In general, many CpG sites were methylated; however, the 4 CpG sites of the 3' region of Region 1 were unmethylated in several GC samples. In most cases, the CpG sites of the 5' region of Region 1 were densely methylated. On the basis of the data obtained from the GC cell lines, it was considered "unmethylated clone" if all 4 CpG sites 1, 2, 3 and 4 were unmethylated. We regarded the *VEGF-C* methylation status of a case as "unmethylated" if that case contains at least 1 unmethylated clone. *VEGF-C* was unmethylated in 9 (29.0%) of 31 GC samples. No association was detected between methylation status of *VEGF-C* and T grade ( $p = 0.7043$ ), N grade ( $p = 1.0000$ ) or tumor stage ( $p = 0.4564$ , Table II).

We then examined DNA methylation status of *VEGF-C* in 5 samples of corresponding non-neoplastic mucosa. In contrast to the variations in DNA methylation patterns observed in the GC samples, the DNA methylation pattern in non-neoplastic gastric mucosa samples was fairly consistent. With the exception of 2 CpG sites (sites 5 and 9), 5' and 3' CpG sites were densely methylated. Importantly, in contrast to GC samples, all 4 CpG sites (sites 1, 2, 3 and 4) were methylated in non-neoplastic samples, suggesting that demethylation of these 4 CpG sites is a cancer-specific event.

#### Relation between *VEGF-C* DNA methylation status, mRNA expression and LVD

We measured levels of *VEGF-C* mRNA by quantitative RT-PCR to investigate whether methylation of *VEGF-C* was associ-

TABLE II - ASSOCIATION BETWEEN *VEGF-C* METHYLATION STATUS AND CLINICAL FEATURES

	<i>VEGF-C</i> methylation status		<i>p</i> Value <sup>1</sup>
	Unmethylated	Methylated	
T grade			
T1/2	5 (33.3%)	10	0.7043
T3/4	4 (25.0%)	12	
N grade			
N0	3 (33.3%)	6	1.0000
N1/2/3	6 (27.3%)	16	
Stage			
Stage I/II	6 (35.3%)	11	0.4564
Stage III/IV	3 (21.4%)	11	

<sup>1</sup>Fisher's exact test.TABLE III - ASSOCIATION BETWEEN DNA METHYLATION STATUS AND MRNA EXPRESSION OF *VEGF-C*

Methylation status	<i>VEGF-C</i> overexpression		<i>p</i> Value <sup>1</sup>
	Positive	Negative	
Unmethylated	8 (88.9%)	1	0.0155
Methylated	8 (36.4%)	14	

<sup>1</sup>Fisher's exact test.

ated with gene expression. Overexpression of *VEGF-C* mRNA (T/N > 2) was observed in 16 (51.6%) of 31 GC samples (Fig. 2b). Of 9 GC cases with unmethylated *VEGF-C*, 8 (88.9%) showed overexpression of *VEGF-C*. In contrast, only 8 of 22 (36.4%) GC cases with methylated *VEGF-C* showed overexpression ( $p = 0.0155$ , Fisher's exact test, Table III).

To investigate whether an association exists between LVD and methylation status or mRNA expression of *VEGF-C*, we evaluated LVD of 31 GC cases by immunostaining for podoplanin (Fig. 2c). Most podoplanin-positive lymphatic vessels were present at the tumor margin, whereas intratumoral lymphatics were rare as previously reported in other tumors.<sup>33,34</sup> LVD was significantly higher in GC cases with overexpressing *VEGF-C* than in those without overexpression ( $p < 0.0001$ , Fig. 2d). No association was noted between DNA methylation status of *VEGF-C* and LVD ( $p = 0.0784$ , Fig. 2d).

If lack of methylation of *VEGF-C* is cancer-specific and associated with gene expression, non-neoplastic tissues should not express *VEGF-C* mRNA. To investigate this hypothesis, we performed quantitative RT-PCR of 10 normal gastric mucosa samples from healthy young individuals. Expression of *VEGF-C* was not detected in 10 normal gastric mucosa samples from healthy young individuals (Fig. 3a). Bisulfite genomic DNA sequencing was performed for 2 of these 10 samples, and we confirmed that all the 4 CpG sites (sites 1, 2, 3 and 4) were methylated (Fig. 3b). In contrast, expression of *VEGF-C* was detected in several corresponding non-neoplastic gastric mucosa samples (Fig. 3a). However, the *VEGF-C* mRNA levels in corresponding non-neoplastic gastric mucosa samples were very low compared with those in GC tissues with *VEGF-C* unmethylation. As shown in Figure 2a, in samples 1N, 2N, 3N, 4N and 5N, *VEGF-C* was methylated, but expression of *VEGF-C* was detected in samples 1N, 2N, 3N and 5N.

## Discussion

*VEGF-C* is a ligand for VEGF receptor-3, which is expressed on endothelial cells of lymphatic vessels.<sup>35</sup> Expression of *VEGF-C* is associated with the development of lymphatic vessels. The prognostic value of *VEGF-C* overexpression in GC has been reported; overexpression of *VEGF-C* is associated with lymph node metastasis and poor prognosis.<sup>31,36</sup> However, the mechanism that underlies overexpression of *VEGF-C* in cancers remains unclear. In the present study, we demonstrated that demethylation

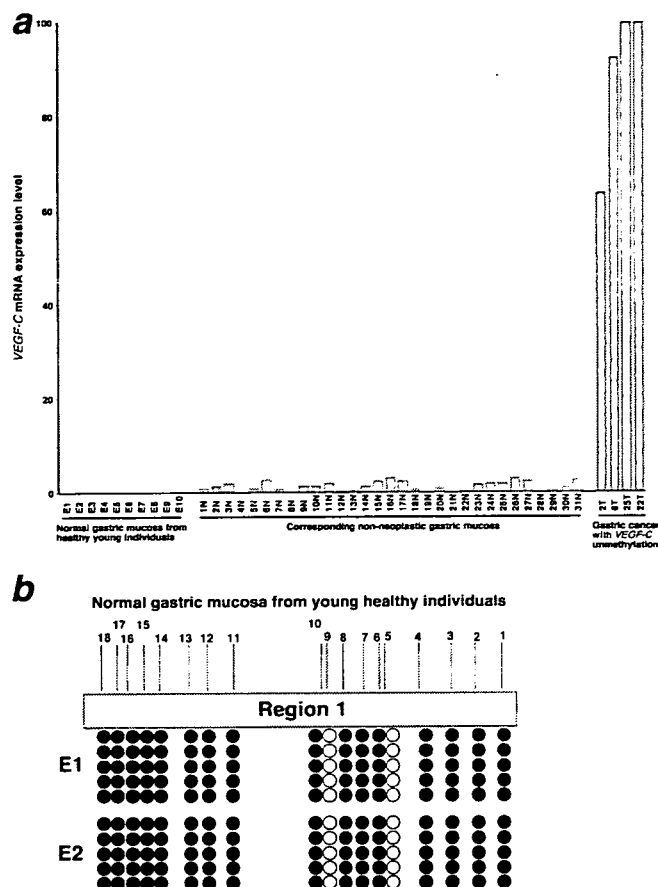


FIGURE 3 - mRNA expression and DNA methylation of *VEGF-C* in non-neoplastic tissue. (a) Quantitative RT-PCR analysis of *VEGF-C* in normal gastric mucosa, corresponding non-neoplastic mucosa, and GC. Units are arbitrary, and we calculated *VEGF-C* mRNA levels by standardization against 1  $\mu$ g total RNA from corresponding non-neoplastic gastric mucosa from Case 1, which was taken as 1.0. (b) Bisulfite genomic DNA sequence of *VEGF-C* in normal gastric mucosa samples from healthy young individuals. Unmethylated allele was not detected.

of the *VEGF-C* gene is associated with expression in GC cell lines and that demethylation of *VEGF-C* by Aza-dC can activate expression of *VEGF-C* mRNA although it has been suggested that genes activated by Aza-dC may not result from the direct inhibition of DNA methylation.<sup>37</sup> Our results suggest that demethylation of the *VEGF-C* gene plays an important role in transcriptional activation of *VEGF-C* in GC. In addition, we found that the *VEGF-C* gene is frequently unmethylated in GC tissues and that this lack of methylation is associated with overexpression of *VEGF-C*. We confirmed that *VEGF-C* is methylated in non-neoplastic gastric mucosa samples from patients with GC, indicating that the lack of *VEGF-C* methylation in GC samples is due to demethylation of the gene. It is important to note that the source of *VEGF-C* in GC tissues can be from the GC cells themselves or from stromal cells such as tumor-associated macrophages (TAMs), because in squamous carcinoma of the uterine cervix, a subfraction of TAMs are a major source of *VEGF-C*.<sup>38</sup> Our findings cannot determine in which cell population changes in demethylation occur. Our previous immunohistochemical study has indicated that *VEGF-C* is expressed in GC cells but not in stromal cells.<sup>39,40</sup> Therefore, we presume that demethylation of the *VEGF-C* gene might occur in GC cells.

In the present study, several GC samples showed overexpression of *VEGF-C* mRNA in the absence of DNA demethylation and some GC cases showed partial methylation in the 4 CpG sites

(sites 1, 2, 3 and 4). In normal gastric mucosa samples from healthy young individuals, no expression of *VEGF-C* was observed, but in some non-neoplastic gastric mucosa samples from patients with GC, slight expression of *VEGF-C* was observed without DNA demethylation. These findings indicate that DNA methylation of the region we analyzed does not completely inactivate *VEGF-C* expression in some conditions. Alternative activating pathways, such as alteration of transcription factors, may account for the overexpression of *VEGF-C* in these samples. Although demethylation of *VEGF-C* by Aza-dC treatment activated expression of *VEGF-C* mRNA, our findings cannot rule out that Aza-dC treatment indirectly affects *VEGF-C* expression, for example by demethylation of a transcription factor gene required for *VEGF-C* expression. Recent studies suggest that Foxc2 can regulate *VEGF-C* expression (reviewed in Ref. 41). It is known that only methylation of a small region within a promoter CpG islands can repress gene transcription.<sup>42</sup> Methylation of Exon 1 or a far upstream region can be associated with loss of transcription, but usually does not have a causal role in transcriptional repression. Because slight expression of *VEGF-C* was observed without DNA demethylation in non-neoplastic gastric mucosa samples from patients with GC, DNA methylation of the region we analyzed may not have a causal role in transcriptional repression. At least however, our present data indicate that DNA demethylation is important for *VEGF-C* overexpression because most GC samples (88.9%) showing DNA demethylation overexpressed *VEGF-C* mRNA.

In the present study, high LVD was associated with overexpression of *VEGF-C* but not DNA demethylation, suggesting that overexpression of *VEGF-C* caused by DNA demethylation participate partly in lymphangiogenesis in GC. In addition to DNA

demethylation, another mechanism may be involved in lymphangiogenesis. Furthermore, there was no association between DNA methylation status of *VEGF-C* and clinical features, such as lymph node metastasis. Many studies have indicated that *VEGF-C* levels in primary tumors are correlated with lymph node metastasis in thyroid, prostate, gastric, colorectal, lung and esophageal cancers.<sup>43</sup> To produce a metastasis, tumor cells must complete a multistep progression through a series of sequential and selective events,<sup>44</sup> and several molecules associated with metastasis have been reported. Therefore, other molecules may affect lymph node metastasis in the present study.

In conclusion, our data clarify one of the mechanisms involved in overexpression of *VEGF-C* in human GC. Clinical trials of DNA methylation inhibitors as cancer therapeutics are underway.<sup>45,46</sup> Although we did not investigate the potential effect of DNA methylation inhibitors on tumor lymphangiogenesis *in vivo*, DNA methylation inhibitors could stimulate the tumor cell metastasis by activation of *VEGF-C* gene expression at least in GC with DNA methylation of *VEGF-C*. Our data suggest that combinations of DNA methylation inhibitors and *VEGF-C* inhibitors<sup>47</sup> may be more effective anticancer therapeutics.

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## ORIGINAL ARTICLE

# Reg IV is a serum biomarker for gastric cancer patients and predicts response to 5-fluorouracil-based chemotherapy

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Regenerating gene family, member 4 (Reg IV), a secreted protein, is overexpressed in several cancers, including gastric cancer (GC). In the present study, we measured Reg IV levels in sera from patients with GC by enzyme-linked immunosorbent assay. We also examined the effect of forced Reg IV expression on the apoptotic susceptibility to 5-fluorouracil (5-FU). Forced expression of Reg IV inhibited 5-FU-induced apoptosis. Induction of Bcl-2 and dihydropyrimidine dehydrogenase was involved in inhibition of apoptosis. Among 36 GC patients treated with a combination chemotherapy of low-dose 5-FU and cisplatin, all 14 Reg IV-positive patients showed no change or disease progression. The serum Reg IV concentration was similar between healthy individuals (mean  $\pm$  s.e.,  $0.52 \pm 0.05$  ng/ml) and patients with chronic-active gastritis ( $0.36 \pm 0.09$  ng/ml). However, the serum Reg IV concentration in presurgical GC patients was significantly elevated ( $1.96 \pm 0.17$  ng/ml), even at stage I. The diagnostic sensitivity of serum Reg IV (36.1%) was superior to that of serum carcinoembryonic antigen (11.5%) or carbohydrate antigen 19-9 (13.1%). These results indicate that expression of Reg IV is a marker for prediction of resistance to 5-FU-based chemotherapy in patients with GC. Serum Reg IV represents a novel biomarker for GC. *Oncogene* (2007) 26, 4383–4393; doi:10.1038/sj.onc.1210215; published online 22 January 2007

**Keywords:** Reg IV; apoptosis; 5-fluorouracil; serum tumor marker; SAGE; gastric cancer

## Introduction

Gastric cancer (GC) is one of the most common human cancers. Early detection remains the most promising approach to improve long-term survival of patients with GC. Assessment of tumor markers in serum may

be useful for detection of GC. There are two available tumor markers for GC, carcinoembryonic antigen (CEA) and carbohydrate antigen 19-9 (CA19-9). However, CEA and CA19-9 are not suitable for early screening because preoperative positivity for these markers depends on the tumor stage at the time of detection (Kochi *et al.*, 2000). Therefore, there is an urgent need for new biomarkers for GC. Genes encoding transmembrane/secretory proteins expressed specifically in cancers may be ideal diagnostic biomarkers (Buckhaults *et al.*, 2001). Moreover, if the gene product functions in the neoplastic process, the gene is not just a biomarker but may also be a therapeutic target (Yasui *et al.*, 2004).

Despite improvements in cancer diagnosis and therapy, many patients are still diagnosed at the late stages of the disease, and the disease often recurs even after curative surgery. 5-fluorouracil (5-FU) is one of the most widely used chemotherapeutic agents for breast cancer, colorectal cancer (CRC), and GC (Longley *et al.*, 2003). Unfortunately, some patients showed a poor response, possibly owing to inefficiency of the chemotherapy. For effective treatment, identification of the patients who will respond well to a specific chemotherapy may be important. Therefore, it is also important to look for biomarker to predict patients' response to 5-FU in GC.

We previously performed serial analysis of gene expression (SAGE) of four primary GCs (Oue *et al.*, 2004) and identified several GC-specific genes (Aung *et al.*, 2006). Of these genes, Regenerating gene family (REG), member 4 (*REG4*, which encodes Reg IV) is a candidate gene for cancer-specific expression, at least in patients with GC. Reg IV, a member of the REG gene family, was originally identified by high-throughput sequencing of a complementary DNA (cDNA) library derived from inflammatory bowel disease patient (Hartupée *et al.*, 2001). Quantitative reverse transcription–polymerase chain reaction (PCR) analysis revealed that approximately 50% of GCs overexpress the *REG4* gene (Oue *et al.*, 2004). Although various normal tissues express *REG4* (Hartupée *et al.*, 2001), the levels of expression are much lower in normal tissues than in

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cancerous tissues (Oue *et al.*, 2005). We reported previously that Reg IV is expressed in GC cells but not stromal cells. Reg IV was expressed in 30% of GC tissues and was associated with both the intestinal mucin phenotype and neuroendocrine differentiation. In CRC, expression of Reg IV was observed in 36% of cases and was associated with tumor stage (Oue *et al.*, 2005). Furthermore, because it is a secreted protein, Reg IV may be a serum biomarker for GC; however, the concentration of Reg IV in serum has not been investigated.

The biologic function of Reg IV is poorly understood. Involvement of *REG4* in drug resistance has been suggested, but the detailed mechanism remains unclear (Violette *et al.*, 2003). A more recent study revealed that Reg IV is a potent activator of the epidermal growth factor receptor (EGFR)/Akt/activator protein-1 (AP-1) signaling pathway and those colon cancer cell lines treated with recombinant Reg IV showed increased expression of Bcl-2, Bcl-xl and survivin, which are proteins associated with inhibition of apoptosis (Bishnupuri *et al.*, 2006). EGFR activation modulates apoptotic susceptibility (reviewed by Kari *et al.*, 2003), and we have shown that EGFR is overexpressed in GC (Yasui *et al.*, 1988). Taken together, Reg IV may be a marker for prediction of resistance to 5-FU-based chemotherapy; however, modulation of apoptotic susceptibility by Reg IV has not been investigated.

In the present study, we show that forced expression of Reg IV inhibits apoptosis induced by 5-FU. Several molecules associated with resistance to 5-FU have been identified (reviewed by Longley *et al.*, 2003). We investigated expression of molecules associated with resistance to 5-FU in Reg IV-overexpressing cells. Because Reg IV activates EGFR, we also performed immunohistochemical analysis of Reg IV and EGFR expression in 161 cases of GC. We measured Reg IV levels in sera from patients with GC by enzyme-linked immunosorbent assay (ELISA) to investigate the potential utility of Reg IV measurements in the diagnosis of GC.

## Results

### *Forced expression of Reg IV inhibits the mitochondrial apoptotic pathway*

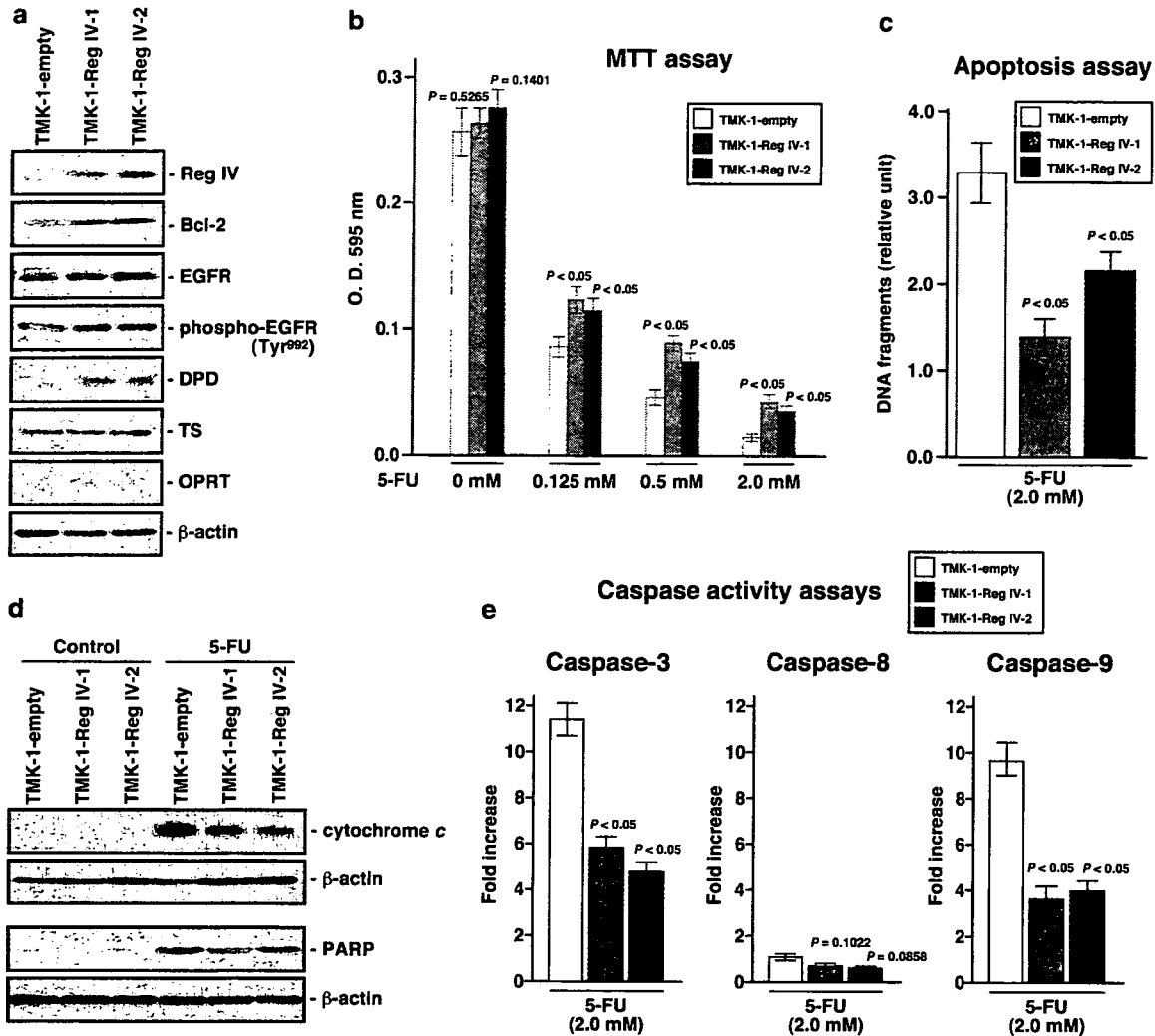
To investigate the biologic significance of Reg IV, the TMK-1 GC cell line was stably transfected with vector expressing Reg IV. TMK-1 cells were selected because they express low levels of Reg IV (Oue *et al.*, 2005). Clones were selected in G418 and examined for Reg IV expression by Western blot. Two clones, TMK-1-Reg IV-1 and TMK-1-Reg IV-2, expressed Reg IV at significantly higher levels than TMK-1 cells transfected with empty vector (Figure 1a). To determine the effect of Reg IV on 5-FU treatment, 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide (MTT) assays were performed. Cell growth of TMK-1 cells transfected with empty vector was inhibited by 5-FU in a dose-dependent manner (Figure 1b). This inhibition was

partially ameliorated in Reg IV-overexpressing cells (Figure 1b), suggesting that cell proliferation was activated or apoptosis was inhibited in Reg IV-overexpressing cells. We investigated the effect of Reg IV on cell proliferation activity. Reg IV transfectants did not show significant differences in proliferation activity compared with cells transfected with empty vector (data not shown). We next examined the effect of forced Reg IV expression on the apoptotic susceptibility of these cells to 5-FU. As shown in Figure 1c, overexpression of Reg IV in both TMK-1-Reg IV-1 and TMK-1-Reg IV-2 cells significantly inhibited 5-FU-induced apoptosis in comparison with cells transfected with empty vector.

Apoptosis is controlled by two major pathways, the mitochondrial pathway (Green and Reed, 1998) and the membrane death receptor (DR) pathway (Ashkenazi and Dixit, 1999). In the mitochondrial pathway, release of cytochrome *c* by mitochondria into the cytosol is the rate-limiting step for the activation of caspases and endonucleases (Martinou *et al.*, 2000). Cytosolic cytochrome *c* activates procaspase-9 by binding to Apaf1 in the presence of dATP, leading to caspase-9 activation and subsequent activation of downstream effector caspases, including caspase-3, with triggering of apoptosis (Li *et al.*, 1997). Caspase-8 plays an important role in the DR-mediated apoptotic pathway, which is independent of cytochrome *c* release (Ashkenazi and Dixit, 1999). In our previous study, the mitochondrial apoptotic pathway was activated in 5-FU-induced apoptosis in TMK-1 cells (Tahara *et al.*, 2005). To determine the associated pathway inhibited by Reg IV overexpression, we examined expression of cytosolic cytochrome *c* protein in cytosolic extracts of 5-FU-treated and untreated cells by Western blotting. Incubation of cells with 5-FU induced cytochrome *c* expression in empty vector-transfected cells (Figure 1d). Cytochrome *c* release was inhibited in cells overexpressing Reg IV (Figure 1d). Next, we examined the activities of caspase-3, -8 and -9. As shown in Figure 1e, treatment of cells with 5-FU significantly increased caspase-9 and -3 activities; but had no effect on caspase-8 activity. The activities of caspase-9 and -3 were significantly lower in Reg IV-overexpressing cells than in empty vector-transfected cells. The nuclear DNA repair enzyme poly(ADP-ribose)polymerase (PARP) is a target of caspase-3, and its cleavage can serve as a biochemical marker of apoptosis (Kaufmann *et al.*, 1993). We examined whether 5-FU-induced apoptosis is associated with PARP cleavage by Western blotting. Cleaved PARP was detected in 5-FU-treated empty vector-transfected cells; however, cleavage of PARP was reduced in Reg IV-overexpressing cells (Figure 1d). These results indicate that overexpression of Reg IV suppresses 5-FU-induced apoptosis by inhibiting the mitochondrial apoptotic pathway.

### *Reg IV activates phosphorylation of EGFR*

Recombinant human Reg IV has been shown to induce rapid phosphorylation of EGFR at Tyr<sup>992</sup> and Tyr<sup>1068</sup>



**Figure 1** Forced expression of Reg IV inhibits 5-FU-induced apoptosis. (a) Western blot analysis of the TMK-1 GC cell line stably transfected with vector expressing Reg IV. Two G418 resistant clones, TMK-1-Reg IV-1 and TMK-1-Reg IV-2, overexpressing Reg IV protein were isolated. (b) Effect of forced Reg IV expression on cell growth of TMK-1 cells. Cell growth was assessed by MTT assay at 48 h after 5-FU treatment. Bars and error bars represent mean and s.d., respectively, from three different experiments. *P*-values for all the assays were calculated using Student's *t*-test. (c) Forced Reg IV expression inhibits 5-FU-induced apoptosis. Cells were incubated with 2 mM 5-FU for 48 h, and both floating and attached cells were collected. Apoptosis was determined with a Cell Death Detection ELISA<sup>Plus</sup> Kit. Bars and error bars represent mean and s.d., respectively, from three different experiments. *P*-values for all the assays were calculated using Student's *t*-test. (d) Forced Reg IV expression inhibits cytochrome *c* release and PARP cleavage induced by 5-FU. Cells were incubated with 2 mM 5-FU for 36 h, and both floating and attached cells were collected for Western blot analysis. (e) Forced Reg IV expression inhibits caspase activation by 5-FU. Cells were treated with 5-FU (2 mM) for 36 h, and floating and attached cells were collected. 5-FU induced activation of caspase-9 and -3, and to a lesser extent, caspase-8. Reg IV-overexpressing cells (TMK-1-Reg IV-1 and TMK-1-Reg IV-2) showed significantly lower activation of caspase-9 and -3 in response to 5-FU than empty vector-transfected cells. Bars and error bars represent mean and s.d., respectively, from three different experiments. *P*-values for all the assays were calculated using Student's *t*-test.

and Akt at Thr<sup>308</sup> and Ser<sup>473</sup>, resulting in increased AP-1 transcription factor activity (Bishnupuri *et al.*, 2006). In addition, HCT116 and HT29 colon cancer cell lines treated with recombinant Reg IV showed increased expression of Bcl-2 (Bishnupuri *et al.*, 2006). Bcl-2 is an antiapoptotic protein located on mitochondria and expressed at high levels in some tumor cells and tissues (Vander Heiden and Thompson, 1999). In the mitochondrial pathway, antiapoptotic Bcl-2 family proteins prevent mitochondrial membrane permeabilization and thereby inhibit changes in the mitochondrial membrane potential and cytochrome *c* release (Vander Heiden and

Thompson, 1999). We examined phosphorylation of EGFR at Tyr<sup>992</sup> and Tyr<sup>1068</sup> in Reg IV-overexpressing cells. EGFR was phosphorylated at Tyr<sup>992</sup> (Figure 1a) but not Tyr<sup>1068</sup> in our Reg IV-overexpressing cells (data not shown). Expression of Bcl-2 was also examined by Western blotting, and induction of Bcl-2 in Reg IV-overexpressing cells was confirmed (Figure 1a). These results suggest that expression of Bcl-2 contributes to inhibition of the mitochondrial apoptotic pathway in Reg IV-overexpressing cells.

It was recently reported that AP-1 induces expression of dihydropyrimidine dehydrogenase (DPD) (Ukon

*et al.*, 2005). DPD, an initial and rate-limiting enzyme in 5-FU catabolism, has significance for the pharmacokinetics and toxicity of 5-FU (Harris *et al.*, 1990). Overexpression of DPD in tumor cell lines is associated with resistance to 5-FU (Takebe *et al.*, 2001). Degradation of 5-FU by induction of DPD expression may also inhibit 5-FU-induced apoptosis. We examined expression of DPD in Reg IV-overexpressing cells by Western blotting. Induction of DPD expression was observed in Reg IV-overexpressing cells (Figure 1a). We also examined expression of other enzymes involved in 5-FU metabolism. Expression of thymidylate synthase (TS) and orotate phosphoribosyl transferase (OPRT) was not changed significantly (Figure 1a). These results indicate that degradation of 5-FU by induction of DPD is also involved in inhibition of apoptosis by Reg IV.

#### *Expression and distribution of Reg IV and EGFR in GC tissues*

Because forced Reg IV expression induces phosphorylation of EGFR at Tyr<sup>992</sup> in TMK-1 cells, we examined whether expression of Reg IV activates phosphorylation of EGFR at Tyr<sup>992</sup> in human GC tissue samples. Immunostaining of Reg IV and EGFR was observed in 61 (37.9%) and 40 (24.8%) of 161 GC cases, respectively. Immunostaining of Tyr<sup>992</sup> phospho-EGFR was also performed in 40 EGFR-positive GC cases. Interestingly, some, but not all, EGFR-positive cells showed phosphorylation at Tyr<sup>992</sup>. Immunohistochemical analysis revealed that Reg IV was expressed in almost all EGFR-positive GC cases. Of 40 EGFR-positive GC cases, 37 (92.5%) were positive for Reg IV, whereas of 121 EGFR-negative GC cases, only 24 (19.8%) ( $P < 0.0001$ , Fisher's exact test) were positive for Reg IV. In 37 GC cases expressing both Reg IV and EGFR, Reg IV and EGFR were rarely expressed in the same GC cells; however, Reg IV-positive GC cells were found near EGFR-positive GC cells (Figure 2a–f). Some GC cells were positive for both Reg IV and EGFR. Triple-immunofluorescence staining revealed that GC cells positive for both Reg IV and EGFR did not show phosphorylation of EGFR at Tyr<sup>992</sup>. In addition, GC cells positive for phosphorylation at Tyr<sup>992</sup> were located near Reg IV-positive cells (Figure 2g–j). We then analysed the relation of Reg IV and EGFR expression to clinicopathologic characteristics. There was no clear association between Reg IV expression and clinical characteristics (Table 1). In contrast, expression of EGFR was associated with advanced T grade (depth of invasion,  $P = 0.0004$ , Fisher's exact test) and N grade (degree of lymph node metastasis,  $P = 0.0218$ , Fisher's exact test) (Table 1). Moreover, EGFR staining was observed more frequently in stage III/IV cases (27 of 84 cases, 32.1%) than in stage I/II cases (13 of 77 cases, 16.9%,  $P = 0.0291$ , Fisher's exact test) (Table 1). No statistically significant prognostic effect of Reg IV was found in the 101 advanced GC patients ( $P = 0.9857$ , log-rank test) (Figure 2k); however, expression of EGFR was associated with poor survival ( $P = 0.0006$ , log-rank test) (Figure 2k). These results suggest that

Reg IV-positive GC cells were different from EGFR-positive GC cells, but GC cases containing EGFR-positive GC cells also contained Reg IV-positive GC cells, resulting in phosphorylation of EGFR at Tyr<sup>992</sup> in human GC tissues.

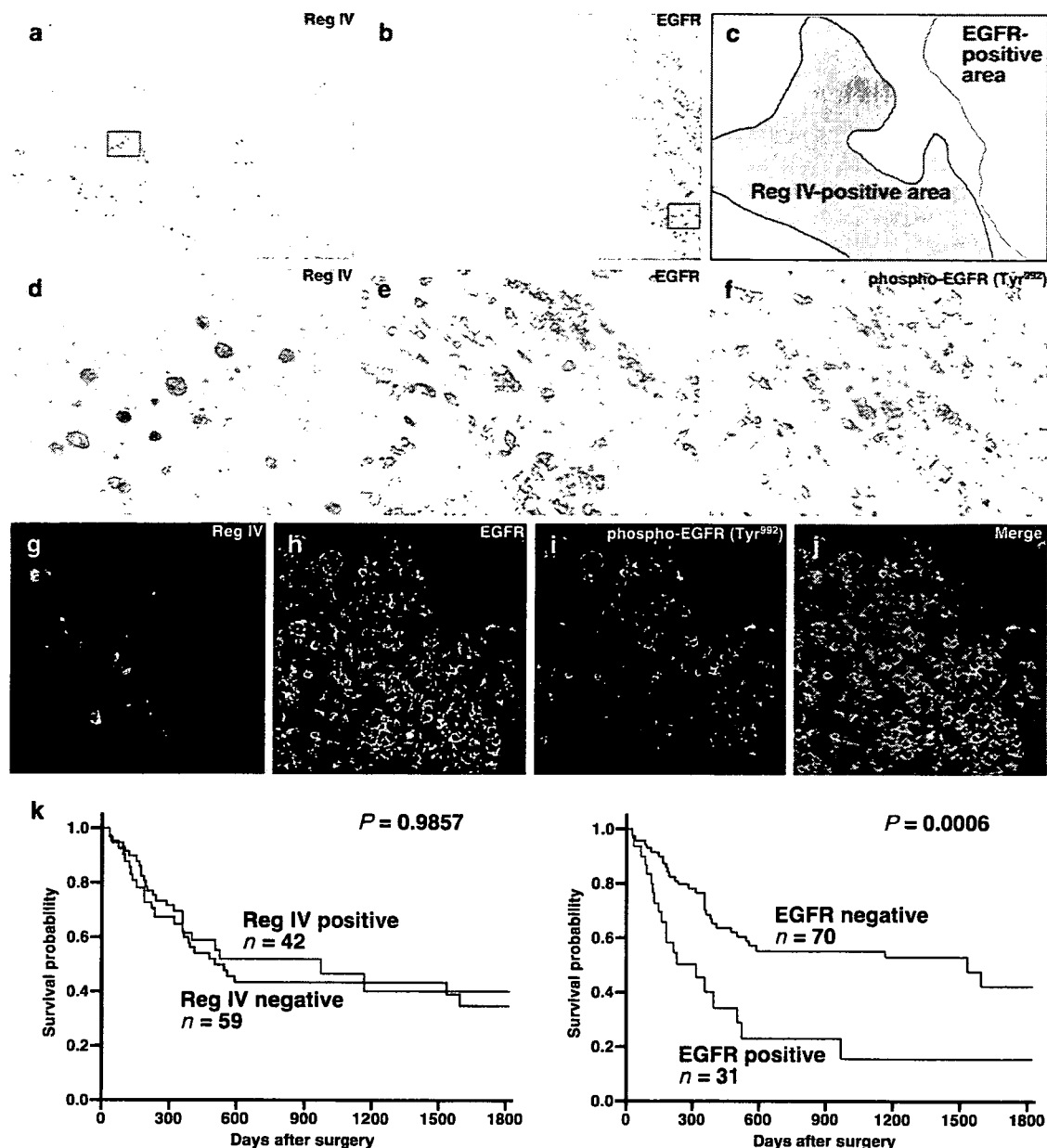
#### *Relation between Reg IV expression and response of GC to a combination chemotherapy of low-dose 5-FU and cisplatin*

We next examined the relation between Reg IV expression and response of GC to combination chemotherapy of low-dose 5-FU and cisplatin in recurrent GC tissue specimens. Reg IV expression was investigated in primary tumor samples obtained by surgical resection before the initiation of chemotherapy. We did not investigate the Reg IV expression in metastatic lesions because of lack of biopsy materials from the metastatic sites. The overall results are summarized in Table 2. Among the 36 patients treated with the combination chemotherapy, all 14 patients with Reg IV expression showed no change (NC) or a progressive disease (PD) to the combination chemotherapy, whereas eight (36.4%) of 22 patients without Reg IV expression showed a partial response (PR) ( $P = 0.0132$ , Fisher's exact test). There was no association between EGFR expression and response to combination therapy ( $P = 0.1596$ , Fisher's exact test). In these 36 GC cases, Reg IV expression was observed in all EGFR-positive GC cases.

#### *Serum Reg IV concentration in healthy subjects, non-cancer patients and GC patients*

We next examined whether Reg IV could be detected by ELISA in sera from patients with GC. Western blot analysis did not detect Reg IV protein in culture media of the MKN-1 and TMK-1 GC cell lines, whereas high levels of Reg IV protein were found in culture media of Reg IV-transfected TMK-1 cells (TMK-1-Reg IV-1 and TMK-1-Reg IV-2) and the MKN-45 GC cell line (Figure 3a). We confirmed by anti- $\beta$ -actin Western blot that contamination of cells in culture medium was minimal. We used ELISA to test culture media from these cell lines. Reg IV protein was detected in culture media from TMK-1-Reg IV-1, TMK-1-Reg IV-2 and MKN-45 cell lines (Figure 3b), and the levels of Reg IV protein detected by ELISA were similar to those obtained by Western blot analysis (Figure 3a). Reg IV protein was not detected in culture media of MKN-1 and TMK-1 cell lines by ELISA (Figure 3b). Culture media of Reg IV-transfected TMK-1 and MKN-45 cells were preabsorbed with recombinant Reg IV protein before being tested by ELISA. The specificity of Reg IV recognition was confirmed by the marked decrease in the ELISA signals after preabsorption (Figure 3b).

The levels of serum Reg IV in healthy individuals, patients with chronic-active gastritis (*Helicobacter pylori* positive) and patients with GC before surgery are shown in Figure 3c. The serum Reg IV concentration was similar between healthy individuals ( $n = 101$ , mean  $\pm$  s.e.,  $0.52 \pm 0.05$  ng/ml) and patients with



**Figure 2** Expression and distribution of Reg IV and EGFR in GC tissues. Immunostaining of Reg IV (a, brown color) and EGFR (b, brown color) in both Reg IV- and EGFR-positive GC case (original magnification,  $\times 40$ ). (c) Schematic representation of Reg IV-positive GC cells (blue) and EGFR-positive GC cells (green). In both Reg IV- and EGFR-positive GC case, Reg IV-positive GC cells were different from EGFR-positive GC cells although Reg IV-positive GC cells were found near EGFR-positive GC cells. (d and e) High magnification images of the fields indicated by boxes in panels a and b (original magnification,  $\times 400$ ). A subset of EGFR-positive GC cells was positive for Tyr<sup>992</sup> phospho-EGFR (f) (original magnification,  $\times 400$ ). (g–j) Triple-immunofluorescence staining of Reg IV (g), EGFR (h) and Tyr<sup>992</sup> phospho-EGFR (i). Cells with EGFR with phosphorylation at Tyr<sup>992</sup> were located near Reg IV-positive GC cells (j) (original magnification,  $\times 400$ ). (k) Prognostic value of Reg IV and EGFR staining.

chronic-active gastritis ( $n = 20$ ,  $0.36 \pm 0.09$  ng/ml). However, the serum Reg IV concentration in presurgical GC patients ( $n = 61$ ,  $1.96 \pm 0.17$  ng/ml) was significantly elevated (healthy individuals vs all GC patients,  $P < 0.0001$ , Mann–Whitney *U*-test), even at stage I (healthy individuals vs stage I GC patients,  $P < 0.0001$ , Mann–Whitney *U*-test) (Figure 3c). In Cases 36 and 42, which showed high serum concentrations of Reg IV, strong and extensive Reg IV staining was observed in

the primary GC samples. In contrast, in Case 18, in which the serum Reg IV concentration was very low, no Reg IV staining was observed in the primary GC sample (Figure 3d). The Reg IV concentration in serum samples from patients with GC showing Reg IV-positive immunostaining ( $n = 12$ ,  $2.51 \pm 0.40$  ng/ml) was statistically significantly higher than that with GC showing Reg IV-negative immunostaining ( $n = 49$ ,  $1.82 \pm 0.18$  ng/ml) ( $P = 0.0251$ , Mann–Whitney *U*-test). When the

cutoff level for Reg IV was set at 2.00 ng/ml, the sensitivity and specificity for detection of GC were 36.1% (22/61) and 99.0% (100/101), respectively.

CEA and CA19-9 levels were also measured in the same serum samples. The sensitivity and specificity of CEA for detection of GC were 11.5% (7/61) and 100.0% (101/101), respectively. The sensitivity and specificity of CA19-9 for detection of GC were 13.1% (8/61) and 100.0% (101/101), respectively. Spearman's rank correlation test revealed only a weak correlation between serum Reg IV and CEA ( $r=0.0173$ ,  $P=0.3123$ ) or CA19-9 ( $r=0.0107$ ,  $P=0.4279$ ) (Figure 3e and f). Of GC patients with normal serum CEA values, 31.5% were found to express Reg IV at 99.0% specificity, and 32.1% of GC patients with normal serum CA19-9 values were found to express Reg IV at 99.0% specificity. The sensitivities of serum Reg IV, CEA and CA19-9 with respect to tumor stage are shown

**Table 1** Association of Reg IV and EGFR expression with clinicopathologic features of gastric cancer

	Reg IV expression			EGFR expression		
	Positive	Negative	P-value <sup>a</sup>	Positive	Negative	P-value <sup>a</sup>
<i>T grade</i>						
T1	8 (29.6%)	19	0.3895	0 (0.0%)	27	0.0004
T2/3/4	53 (39.6%)	81		40 (29.9%)	94	
<i>N grade</i>						
N0	20 (34.5%)	38	0.6120	8 (13.8%)	50	0.0218
N1/2/3	41 (39.8%)	62		32 (31.1%)	71	
<i>Stage</i>						
I/II	27 (35.1%)	50	0.5180	13 (16.9%)	64	0.0291
III/IV	34 (50.5%)	50		27 (32.1%)	57	

Abbreviations: EGFR, epidermal growth factor receptor; Reg IV, regenerating gene IV. <sup>a</sup>Fisher's exact test.

in Table 3. In patients with stage I GC, the sensitivity of serum Reg IV (36.1%) was significantly higher than that of CEA (5.6%,  $P=0.0028$ , Fisher's exact test) or CA19-9 (8.3%,  $P=0.0093$ , Fisher's exact test).

**Discussion**

It is generally accepted that apoptosis suppresses oncogenic transformation. The ability of tumor cell populations to expand in number is determined not only by the rate of cell proliferation but also by the rate of cell attrition. Apoptosis represents a major source of this attrition (Hanahan and Weinberg, 2000). Thus, resistance to apoptosis is a hallmark of most and perhaps all types of cancer. In the present study, we showed that overexpression of Reg IV inhibits 5-FU-induced apoptosis. At least two mechanisms are involved in inhibition of apoptosis by Reg IV, induction of Bcl-2 and induction of DPD.

In 5-FU-treated TMK-1 cells, overexpression of Reg IV inhibited the mitochondrial apoptotic pathway that involves cytosolic cytochrome *c* release and subsequent activation of caspase-9 and -3. Increased Bcl-2 by forced Reg IV expression may act to inhibit the mitochondrial apoptotic pathway. Bcl-2 induction by Reg IV is blocked by AG1478, a tyrosine kinase inhibitor specific for EGFR (Bishnupuri *et al.*, 2006), indicating that phosphorylation of EGFR is required for Bcl-2 induction and that EGFR plays an important role in inhibition of apoptosis by Reg IV. In the present study, immunohistochemical analysis of GC tissues revealed that almost all EGFR-positive GC cases (92.5%) also expressed Reg IV and that EGFR was phosphorylated at Tyr<sup>992</sup> in all EGFR-positive GC cases. Although it is possible that other molecules, such as EGF, induce phosphorylation of EGFR at Tyr<sup>992</sup>, the present results

**Table 2** Association of Reg IV and EGFR expression with response to combination chemotherapy of low-dose 5-FU and cisplatin

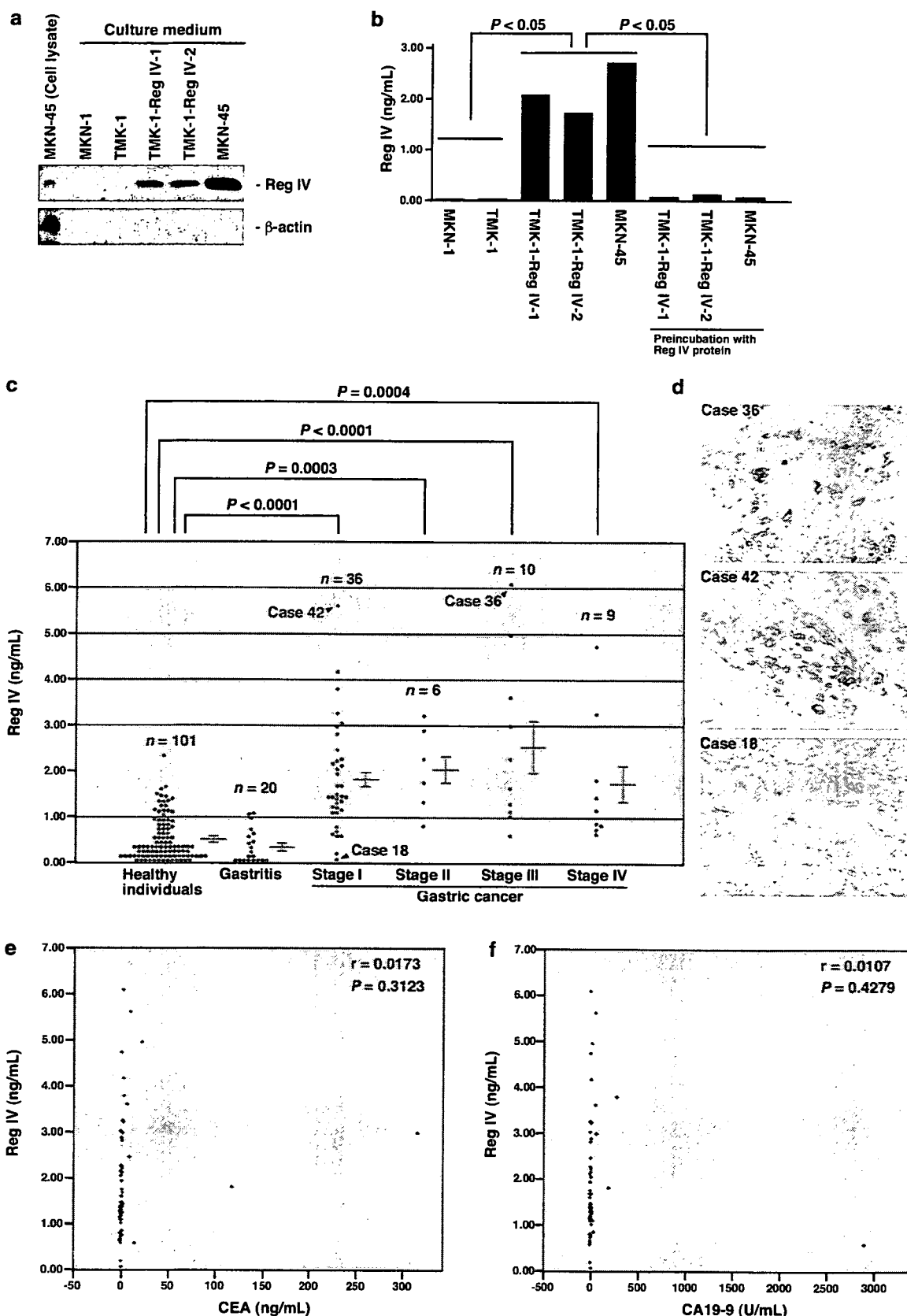
	Reg IV expression		P-value <sup>a</sup>	EGFR expression		P-value <sup>a</sup>
	Positive	Negative		Positive	Negative	
CR and PR	0 (0.0%)	8	0.0132	0 (0.0%)	8	0.1596
NC and PD	14 (50.0%)	14		9 (32.1%)	19	

Abbreviations: CR, complete response; EGFR, epidermal growth factor receptor; NC, no change; PD, progressive disease; PR, partial response; Reg IV, regenerating gene IV. <sup>a</sup>Fisher's exact test.

**Figure 3** ELISA of serum samples from patients with GC. (a) Western blot analysis of Reg IV. Culture media of Reg IV-transfected TMK-1 cells (TMK-1-Reg IV-1 and TMK-1-Reg IV-2) and MKN-45 GC cell lines contain Reg IV. Extracts of MKN-45 cells served as a positive control. Western blotting with anti-β-actin antibody confirmed that there was minimal contamination of culture medium with cells. (b) Detection of Reg IV in culture media by ELISA. Reg IV was detected in culture media of Reg IV-transfected TMK-1 and MKN-45 cells but not MKN-1 and TMK-1 cells. Culture media of Reg IV-transfected TMK-1 and MKN-45 cells were preincubated with recombinant Reg IV and then tested by ELISA. A significant reduction in the signal intensity of the ELISA was observed. P-values were calculated using Student's *t*-test. (c) Detection of Reg IV protein in serum samples by ELISA. A high concentration (2.00 ng/ml) of Reg IV was detected in 22 serum samples from patients with GC. Yellow bars indicate the cutoff levels defined in this study. Red bars indicate the means ± s.e. Differences in the serum concentration of Reg IV between two groups were tested by non-parametric Mann-Whitney *U*-test. (d) Immunostaining of Reg IV in primary GC samples. Strong and extensive Reg IV staining was observed in Cases 36 and 42, which also showed high concentrations of Reg IV in serum samples (c). In Case 18, no staining of Reg IV was observed, and the serum concentration of Reg IV was low (c). (e) Relation between serum concentrations of Reg IV and CEA. Correlation was examined using Spearman's rank correlation. (f) Relation between serum concentrations of Reg IV and CA19-9. Correlation was examined using Spearman's rank correlation.

suggest that in a subset of EGFR-positive GC, Reg IV affects phosphorylation of EGFR at Tyr<sup>992</sup> and stimulates tumor cell growth by inhibiting apoptosis. It is

important to note that in the immunohistochemical analysis, GC cells expressing both Reg IV and EGFR were rare. Triple-immunofluorescence staining revealed



**Table 3** Diagnostic sensitivity of serum Reg IV, CEA and CA19-9 with respect to tumor stage

	Reg IV (%)	CEA (%)	P-value <sup>a</sup>	CA19-9 (%)	P-value <sup>b</sup>
Stage I (n = 36)	36.1	5.6	0.0028	8.3	0.0093
Stage II (n = 6)	50.0	0.0	0.1818	0.0	0.1818
Stage III (n = 10)	50.0	40.0	1.0000	30.0	0.6499
Stage IV (n = 9)	22.2	11.1	1.0000	22.2	1.0000
Specificity	99.0	100.0		100.0	

Abbreviations: CA19-9, carbohydrate antigen; CEA, carcinoembryonic antigen; Reg IV, regenerating gene IV. <sup>a</sup>Fisher's exact test. Reg IV vs CEA. <sup>b</sup>Fisher's exact test. Reg IV vs CA19-9.

that GC cells positive for both Reg IV and EGFR did not show phosphorylation of EGFR at Tyr<sup>992</sup>. We cannot explain completely the discrepancy between GC cell line data and GC tissue data. Because GC cells positive for phosphorylation at Tyr<sup>992</sup> were located near Reg IV-positive cells, Reg IV expression may induce expression and secretion of EGFR ligands, such as EGF, which could lead to EGFR phosphorylation of the adjacent cells. EGF secretion in Reg IV-over-expressing cells should be examined. Furthermore, clinical characteristics of Reg IV-positive GC cases were quite different from those of EGFR-positive GC cases in the present study. Expression of Reg IV was found in both early- and late-stage GC, whereas expression of EGFR was detected mainly in late-stage tumors. These results led us to speculate that continuous expression of Reg IV may be a selective pressure for the development of EGFR-positive GC cells and may confer selective growth advantage to EGFR-positive GC cells. In Reg IV-positive GC, even at an early stage, EGFR-positive GC cells may develop in accordance with tumor progression.

Forced Reg IV expression induced expression of DPD. DPD is a catabolic enzyme of 5-FU (Harris *et al.*, 1990), and several studies have indicated an inverse correlation between expression or activity of DPD and sensitivity to 5-FU-based chemotherapy in GC (Inada *et al.*, 2000; Ishikawa *et al.*, 2000). Degradation of 5-FU by DPD may play an important role in inhibition of 5-FU-induced apoptosis. In the present study, Reg IV expression in primary tumors was associated with response to 5-FU/cisplatin combination chemotherapy in recurrent GC cases. Although we did not evaluate activation of AP-1 in the present study, EGFR-dependent activation of AP-1 by Reg IV has been reported (Bishnupuri *et al.*, 2006). Because DPD is a downstream target gene of AP-1 (Ukon *et al.*, 2005), phosphorylation of EGFR may be required for induction of DPD by Reg IV. As mentioned above, induction of Bcl-2 also depends on phosphorylation of EGFR. Phosphorylation of EGFR may be a crucial event in inhibition of 5-FU-induced apoptosis by Reg IV. Interestingly, EGFR expression in primary tumors was not associated with response to combination chemotherapy in the present study. We confirmed that all EGFR-positive GC cases were positive for phosphorylation of EGFR at Tyr<sup>992</sup>. We investigated both Reg IV and

EGFR expression in primary tumors, but the response to chemotherapy was evaluated in metastatic lesions. Several lines of evidence suggest that primary and metastatic lesions bear different biologic properties. DPD gene expression levels were reported to be lower in primary cancers than in liver metastases in several studies (Kuramochi *et al.*, 2006). Because expression of EGFR is a late event in GC progression, metastatic lesions may express EGFR even though EGFR is not expressed by the primary tumor. Because we investigated neither Reg IV nor EGFR expression in metastatic lesions, further studies are needed to clarify the predictive value of Reg IV and EGFR expression analysis.

It is important to note that while TMK-1-Reg IV-2 clone expresses more Reg IV than TMK-1-Reg IV-1, the intensity of the DPD band for TMK-1-Reg IV-1 looks slightly more intense than the intensity of the DPD band for TMK-1-Reg IV-2. In the present study, Western blotting was performed 1 or more months after the TMK-1 cell line had been stably transfected with vector expressing Reg IV. It has been reported that EGFR phosphorylation induced by treatment with recombinant human Reg IV occurred rapidly, with maximum effect at 5 min (Bishnupuri *et al.*, 2006), suggesting that EGFR phosphorylation levels may reach plateau in Reg IV-transfected TMK-1 cells and DPD expression may not increase further with increase in Reg IV expression.

Serum Reg IV is a novel biomarker for GC. Despite the reliability of CEA and CA19-9 as markers for detection of GC, CEA and CA19-9 are unsuitable for detection of early GC. In fact, in the present study, CEA and CA19-9 were found in serum in 5.6 and 8.3%, respectively, of patients with stage I GC. Of 36 serum samples from patients with stage I GC, 13 (36.1%) showed high levels of Reg IV, indicating that Reg IV is a good serum marker for early detection of GC. In addition, because Reg IV levels in serum samples from patients with GC expressing Reg IV were significantly higher than those of Reg IV-negative GC, Reg IV concentration in sera may be a marker for prediction of the response to 5-FU-based chemotherapy. However, all GC cases with high serum concentrations of Reg IV did not necessarily show Reg IV immunostaining of the primary tumor. This discrepancy between immunostaining and ELISA results may be due to methodologic differences. Reg IV immunohistochemistry results were evaluated as the percentage of stained cancer cells; the intensity of immunostaining was not evaluated because we had no suitable internal control for the immunohistochemistry. More detailed quantitative methods for the measurement of Reg IV protein, such as intratumor Reg IV concentration, are needed to clarify the relation between levels of Reg IV protein in sera and levels in primary GC samples.

In conclusion, our present data show that Reg IV can confer resistance to 5-FU-induced apoptosis in GC cells, suggesting that overexpression of Reg IV may represent a novel mechanism of intrinsic drug resistance in human GC. We detected Reg IV in sera from patients with GC. This indicates not only that serum Reg IV is a novel

biomarker for GC but also that serum Reg IV may have some effect on normal organs in patients with GC. Identification of a cell-surface receptor for Reg IV may further improve our understanding of the basic biology of Reg IV.

## Materials and methods

### *Cell line, expression vector, transfection and 5-FU treatment*

A human GC-derived cell line, TMK-1, was established in our laboratory (Ochiai *et al.*, 1985). TMK-1 cells were maintained in Roswell's Park Memorial Institute 1640 medium (Nissui Pharmaceutical, Tokyo, Japan) containing 10% fetal bovine serum (Whittaker, Walkersville, MD, USA) in a humidified atmosphere of 5% CO<sub>2</sub> and 95% air at 37°C. For constitutive expression of the *REG4* gene, cDNA was PCR amplified and subcloned into pcDNA 3.1 (Invitrogen, Carlsbad, CA, USA). The pcDNA-Reg IV expression vector was transfected into TMK-1 cells with FuGENE6 (Roche Diagnostics, Indianapolis, IN, USA), according to the manufacturer's instructions. Stable transfectants were selected after 2 weeks of culture with 100 µg/ml G418 (Invitrogen). The effect of 5-FU (Acros Organics, Fairlawn, NJ, USA) on apoptosis was studied. 5-FU was dissolved in 100% dimethyl sulfoxide (DMSO) and then diluted in cell culture medium for experiments. The final concentration of DMSO was maintained at 0.1%. For apoptosis assay, caspase activation assays and Western blot analysis, both floating and attached cells were collected after 5-FU treatment.

### *MTT, cell proliferation, apoptosis and caspase activation assays*

For MTT assay, the cells were seeded at a density of 2000 cells per well in 96-well plates. The cells were then treated with 5-FU for 48 h. Cell growth was monitored by MTT assay (Alley *et al.*, 1988). Cell proliferation activity was determined with a Cell Proliferation ELISA (Amersham Biosciences, Piscataway, NJ, USA), according to the manufacturer's instructions. For apoptosis assay, cultured cells were treated for 48 h with 2 mM 5-FU, and apoptosis was evaluated with a Cell Death Detection ELISA<sup>Plus</sup> Kit (Roche Diagnostics), according to the manufacturer's instructions. For caspase activation assays, cultured cells were treated for 36 h with 2 mM 5-FU and the activities of caspase-3, -8 and -9 were determined with caspase-3, -8 and -9 Colorimetric Activity Assay Kits, respectively (Chemicon, Temecula, CA, USA), according to the manufacturer's instructions. *P*-values for all the assays were calculated using Student's *t*-test.

### *Western blot analysis*

Western blot analysis was performed as described previously (Yasui *et al.*, 1993). The filter was incubated for 1 h at room temperature with an anti-Reg IV antibody (rabbit polyclonal antibody raised in our laboratory; Oue *et al.*, 2005), anti-Bcl-2 antibody (Santa Cruz Biotechnology, Santa Cruz, CA, USA), anti-EGFR antibody (Cell Signaling Technology, Beverly, MA, USA), anti-phospho-EGFR (Tyr<sup>992</sup>) antibody (Cell Signaling Technology), anti-phospho-EGFR (Tyr<sup>1068</sup>) antibody (Cell Signaling Technology), anti-DPD antibody (Taiho Pharmaceutical, Tokyo, Japan), anti-TS antibody (Taiho Pharmaceutical), anti-OPRT antibody (Taiho Pharmaceutical), anti-PARP p85 fragment antibody (Promega, Madison, MD, USA) or anti-β-actin antibody (Sigma Chemical, St Louis, MO, USA). To quantify cytochrome *c* release into the cytosol, floating and attached cells were collected after incubation with 2 mM 5-FU for 36 h, and cytochrome *c* in

cytosolic extracts was detected with an ApoAlert Cell Fractionation Kit (Takara Bio, Shiga, Japan).

### *Tissue samples*

In all, 161 primary tumors and 61 serum samples were collected from patients diagnosed with GC. Patients were treated at the Hiroshima University Hospital or an affiliated hospital.

For immunohistochemical analysis, we used archival formalin-fixed, paraffin-embedded tissues from 161 patients who had undergone surgical excision of GC. Of the 161 patients, 27 had early GC and 134 had advanced GC. Early GC is limited to the mucosa or the mucosa and submucosa regardless of nodal status. Advanced GC is a tumor that has invaded beyond the muscularis propria (Hohenberger and Gretschel, 2003). Information on patient survival was available for 101 of the 134 advanced GC cases.

Of the 161 patients, 36 had recurrent GC and were treated with a combination of low-dose 5-FU and cisplatin (Kim *et al.*, 1999). All 36 patients with recurrent GC provided a medical history and underwent physical examination, including evaluation of performance status, complete blood cell count, serum chemistry profile, chest X-ray and computed tomography (CT) and/or magnetic resonance imaging, at the time of enrollment. Tumor markers, including CEA and CA19-9, were checked monthly. The responses of metastatic lesions to treatment were assessed according to the World Health Organization criteria. Metastatic lesions were evaluated by CT, ultrasonography and other radiographic examinations. Complete response (CR) was defined as disappearance of all evidence of cancer for more than 4 weeks. PR was defined as at least 50% reduction in the sum of the products of the perpendicular diameters of all the lesions for more than 4 weeks without any evidence of new lesions or progression of existing lesions. NC was defined as less than 50% reduction or less than 25% increase in the sum of the products of the perpendicular diameters of all lesions without any evidence of new lesions. PD was defined as more than a 25% increase in more than one lesion or the appearance of new lesions.

Among the 161 GC cases used for immunohistochemical analysis, serum samples were available for ELISA from 61 cases (36 men and 25 women; age range, 35–88 years; mean, 67.5 years). Serum samples were collected before surgery and before initiation of therapy, and were stored at –80°C until analysis. Serum samples from 20 patients with chronic active gastritis with *H. pylori* infection (13 men and 7 women; age range, 57–85 years; mean, 68.8 years) were also collected. Control serum samples were obtained from 101 healthy individuals (75 men and 26 women; age range, 32–79 years; mean, 59.4 years).

Tumor staging was according to the TNM classification system (Sobin and Wittekind, 2002). Because written informed consent was not obtained, for strict privacy protection, identifying information for all samples was removed before analysis. This procedure was in accordance with the Ethical Guidelines for Human Genome/Gene Research of the Japanese Government.

### *Immunohistochemistry*

For immunostaining of EGFR and phospho-EGFR (Tyr<sup>992</sup>), a Dako LSAB Kit (Dako, Carpinteria, CA, USA) was used as described previously (Oue *et al.*, 2005). Sections were incubated with the following antibodies: goat anti-Reg IV (diluted 1:50, R&D Systems, Abingdon, UK), mouse anti-EGFR (1:20, Novocastra, Newcastle, UK) and rabbit anti-phospho-EGFR (Tyr<sup>992</sup>) antibody (1:20, Cell Signaling



Technology). For immunostaining of Reg IV, peroxidase-conjugated anti-goat IgG was used as the secondary antibody. Staining was completed with a 10-min incubation with the substrate-chromogen solution. The sections were counterstained with 0.1% hematoxylin. The percentage of stained cancer cells was evaluated for each antibody. A result was considered positive if at least 10% of cells were stained. When fewer than 10% of cancer cells were stained, the immunostaining was considered negative.

For triple-immunofluorescence staining, Alexa Fluor 405-conjugated anti-goat IgG (Molecular Probes, Eugene, OR, USA), Alexa Fluor 488-conjugated anti-mouse IgG (Molecular Probes) and Alexa Fluor 546-conjugated anti-rabbit IgG (Molecular Probes) were used as secondary antibodies.

### ELISA

For measurement of the serum concentration of Reg IV, a sandwich ELISA was developed. First, polystyrene microtiter plates were coated with mouse monoclonal anti-Reg IV antibody (R&D Systems) by overnight incubation of 50  $\mu$ l/125 ng/well antibody diluted in Tris buffer (pH 7.4). The plates were then washed three times with washing buffer. After the plates were blocked with 1% milk in phosphate-buffered saline, 50  $\mu$ l of recombinant Reg IV standard or sample was added to each well and incubated overnight at 4°C. After three washes, 50  $\mu$ l of biotinylated goat polyclonal anti-Reg IV antibody (R&D Systems) in assay buffer (1% bovine serum albumin (BSA), Tris buffer (pH 7.4), 0.05% normal goat serum) was added to each well (75 ng antibody/well). The mixture was then incubated for 1 h with shaking at 37°C and washed three times with washing buffer. The plates were incubated with 50  $\mu$ l/well alkaline phosphatase-conjugated streptavidin (Dako) diluted 2000-fold in diluent containing 1% BSA and Tris buffer (pH 7.4) for 1 h at 37°C and washed three times. Color development was performed with the addition of pNPP chromogenic substrate (Sigma) followed by incubation at 37°C for 1 h. Absorbance at 405 nm was measured with an ELISA plate reader. As a reference

standard, known concentrations of human recombinant Reg IV (Oue *et al.*, 2005) from 0 to 30 ng/ml were tested in triplicate.

### Measurement of CEA and CA19-9

CEA and CA19-9 were measured with a commercially available automated immunoassay method (Modular Analytics, Roche Diagnostics). The upper limits of normal for this method are 5.0 ng/ml for CEA and 37 U/ml for CA19-9.

### Statistical methods

Associations between clinicopathologic parameters and Reg IV or EGFR expression were analysed by Fisher's exact test. Kaplan–Meier survival curves were constructed for Reg IV- or EGFR-positive and Reg IV- or EGFR-negative patients. Survival rates were compared between Reg IV- or EGFR-positive and Reg IV- or EGFR-negative groups. Differences between survival curves were tested for statistical significance by log-rank test (Mantel, 1966). Differences in the serum concentration of Reg IV between two groups were tested by non-parametric Mann–Whitney *U*-test. Correlation between the serum concentration of Reg IV and that of CEA or CA19-9 was assessed by Spearman's rank correlation. A *P*-value of less than 0.05 was considered statistically significant.

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## ORIGINAL ARTICLE

**Dynamic transcriptional regulatory complexes including BORIS, CTCF and Sp1 modulate NY-ESO-1 expression in lung cancer cells**

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Previously, we reported that the paralogous zinc-finger proteins – CTCF and brother of the regulator of imprinted sites (BORIS), directly contribute to transcriptional regulation of *NY-ESO-1* in lung cancer cells. To further examine mechanisms that mediate expression of this cancer-testis gene, we performed software-guided analysis of the *NY-ESO-1* promoter region, which revealed several potential Sp1-binding motifs. Sequential 5-aza-2'-deoxycytidine/depisepptide FK228 treatment markedly induced BORIS expression and enhanced nuclear translocation of Sp1 in lung cancer cells. Transient transfection assays using promoter-reporter constructs, as well as gel-shift and chromatin immunoprecipitation experiments revealed that *NY-ESO-1* promoter activity coincided with occupancy of the proximal Sp1-binding site in lung cancer cells. Mutations within the Sp1 recognition sequence specifically eliminated binding of Sp1 to this motif *in vitro*, and markedly diminished *NY-ESO-1* promoter activity *in vivo*. siRNA-mediated inhibition of Sp1 expression decreased *NY-ESO-1* promoter activity, whereas knock down of CTCF expression augmented *NY-ESO-1* transcription in lung cancer cells. Co-immunoprecipitation experiments indicated that Sp1 physically interacts with BORIS but not with CTCF *in vivo*. Collectively, these findings suggest that BORIS recruits Sp1 to mediate de-repression of *NY-ESO-1* during pulmonary carcinogenesis.

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**Keywords:** lung cancer; epigenetics; NY-ESO-1; BORIS; CTCF; Sp1

**Introduction**

Cancer-testis antigens (CTA) constitute a unique and growing class of germ cell-related proteins that are aberrantly expressed in a variety of human malignancies, and are recognized by cytolytic T lymphocytes

(CTL) from cancer patients (Simpson *et al.*, 2005). During recent years, the CTAs have emerged as attractive targets for cancer immunotherapy. Of particular interest in this regard, are CTAs encoded on the X chromosome (CT-X), such as NY-ESO-1, which elicits cellular, as well as humoral immunity in approximately 50% of patients whose tumors express this cytoplasmic protein (Gnjatic *et al.*, 2006).

Recent studies indicate that the nuclear proteins CTCF and BORIS (Brother of the Regulator of Imprinted Sites) may contribute to regulation of *NY-ESO-1* expression during pulmonary carcinogenesis (Hong *et al.*, 2005). CTCF is a ubiquitous DNA-binding protein bearing a central 11 zinc (Zn)-finger region that contributes to formation of chromatin insulator/boundaries, X chromosome inactivation, reading of gene-imprinting marks, and regulation of a variety of genes mediating cell cycle progression and apoptosis (reviewed by Ohlsson *et al.* (2001); Klenova *et al.* (2002)). BORIS exhibits considerable homology to CTCF in the central 11 Zn-finger DNA-binding domain, but not in the NH<sub>2</sub>- and COOH-terminal regions that constitute approximately two-thirds of the full-length amino-acid sequences of these proteins (Loukinov *et al.*, 2002). Thus, whereas CTCF and BORIS apparently recognize the same DNA-binding sequences, these transcription factors may exhibit significant differences regarding recruitment of functional partners (reviewed in Klenova *et al.* (2002)). Unlike CTCF, BORIS is not expressed in normal somatic cells (Klenova *et al.*, 2002; Loukinov *et al.*, 2002). In male germ cells, transient expression of BORIS coincides with a marked decrease in CTCF expression, erasure of global DNA methylation patterns, and upregulation of CT genes (Loukinov *et al.*, 2002).

Recently, we reported that BORIS is activated during pulmonary carcinogenesis, and that BORIS expression coincides with de-repression of *NY-ESO-1* (Hong *et al.*, 2005). In addition, we have demonstrated that BORIS as well as *NY-ESO-1* expression can be induced in cultured lung cancer cells (but not normal human bronchial epithelial (NHBE) cells) following exposure to the DNA-demethylating agent 5-aza-2' deoxycytidine (DAC), the histone deacetylase (HDAC) inhibitor Depisepptide FK228 (DP), or sequential DAC/DP. Furthermore, we have shown that a CTCF-to-BORIS-shift in occupancy of the *NY-ESO-1* promoter coincides with de-repression of this CT gene in lung cancer cells

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## The association between RAD18 Arg302Gln polymorphism and the risk of human non-small-cell lung cancer

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### Abstract

**Purpose** The repair enzyme RAD18 plays a key role in the post-replication repair process in various organisms from yeast to human, and the molecular function of the RAD18 protein has been elucidated. Single nucleotide polymorphism (SNP) of arginine (Arg, CGA) or glutamine (Gln, CAA) at codon 302 is known on RAD18; however, the association between the SNP and the risk of any human cancers including non-small-cell lung cancer (NSCLC) has not been reported. We therefore investigated the relationship between the polymorphism and the development and progression of human NSCLC.

**Methods** The study population included 159 patients with NSCLC and 200 healthy controls. The SNP was genotyped by polymerase chain reaction with the confronting two-pair primer (PCR-CTPP) assay. Genotype frequencies were compared between patients and controls, and the association of genotypes with clinicopathological parameters was also studied.

**Results** The Gln/Gln genotype was significantly more frequent in NSCLC patients (20.7%) than in healthy controls (11.5%) ( $P = 0.003$ ). The increased risk was detected in NSCLC patients with the Gln/Gln genotype [Odds ratio (OR) = 2.63, 95% confidence interval (CI) = 1.38–4.98]. As to the relationship of the SNP with clinicopathological parameters of NSCLC, significantly higher risks were detected in lung squamous cell carcinoma (LSC) (OR = 4.40, 95% CI = 1.60–12.1).

**Conclusions** Our results suggested that Gln/Gln genotype of the RAD18 SNP has the increased risk of NSCLC, especially of LSC. This is the first report to provide evidence for an association between the RAD18 Arg302Gln polymorphism and human NSCLC risk.

**Keywords** SNPs · RAD18 · Non-small-cell lung cancer (NSCLC) · Cancer predisposition

### Abbreviations

LAD	Lung adenocarcinoma
LSC	Lung squamous cell carcinoma
NSCLC	Non-small-cell lung cancer
OR	Odds ratio
PCNA	Proliferating cell nuclear antigen
PCR-CTPP	Polymerase chain reaction with the confronting two-pair primers
PRR	Postreplication repair
SNP	Single nucleotide polymorphism

### Introduction

DNA in living cells is damaged by environmental damaging agents and mutagens, such as UV light and mutagenic chemicals (Hoeijmakers 2001). DNA damage must be repaired by

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