Human Cancer Biology

Chemokine (C-X-C Motif) Ligand 12 Is Associated with Gallbladder Carcinoma Progression and Is a Novel Independent Poor Prognostic Factor

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Abstract

Purpose: Although recent studies have suggested that chemokine (C-X-C motif) ligand 12 (CXCL12) is important in the progression of various malignancies, its role in gallbladder carcinoma (GBC) remains unknown. We investigated CXCL12 expression in GBC and its biologic and prognostic role in GBC tumorigenesis.

Experimental Design: We examined CXCL12 expression in tumor specimens from 72 patients with GBC by immunohistochemistry and analyzed the correlation between CXCL12 expression and clinicopathologic factors or survival. The functional significance of CXCL12 expression was investigated by CXCL12 treatment and suppression of CXCR4, a major receptor of CXCL12, as well as by CXCL12 overexpression in in vitro and in vivo studies.

Results: CXCL12 was differentially expressed in GBC tissues. CXCL12 expression was significantly associated with a high histologic grade (P = 0.042) and nodal metastasis (P = 0.015). Multivariate analyses showed that CXCL12 expression (HR, 8.675; P = 0.014) was an independent risk factor for patient survival. CXCL12 significantly increased anchorage-dependent and -independent growth, migration, invasion, adhesiveness, and survival of GBC cells in vitro, and these effects were dependent on CXCR4. Consistent with these results, overexpression of CXCL12 significantly promoted GBC tumorigenicity in a xenograft model.

Conclusions: Our results indicate that GBC cells express both CXCL12 and its receptor CXCR4, and CXCL12 may have a role in GBC progression through an autocrine mechanism. In addition, CXCL12 is a novel independent poor prognostic factor in patients with GBCs. Thus, targeting CXCL12 and CXCR4 may provide a novel therapeutic strategy for GBC treatment. Clin Cancer Res; 18(12); 3270–80. ©2012 AACR.

Introduction

Gallbladder carcinoma (GBC) is the most common malignancy of the biliary tract. Although its occurrence is rare as compared with other gastrointestinal tract neoplasms, including gastric and colorectal cancers, GBC has a distinctly higher incidence in certain demographic groups and geographic areas (1, 2). The prevalence of GBC in China, Thailand, and northern India is much higher than in the United States and Europe (3). Surgical resection is currently the most effective and potentially curative treatment for GBCs. However, many patients present late in the course of the disease when surgical treatment is no longer effective, and most patients with advanced GBC experience frequent recurrence after surgery. Therefore, the overall survival rate remains poor (4). Although the most important risk factor for the development of GBC is cholelithiasis (up to 95% of GBCs are associated with gallstones; ref. 5), the molecular mechanisms involved in early carcinogenesis and the factors affecting disease progression remain unclear. Therefore, identification of factors crucial for GBC progression...
Chemokine (C-X-C Motif) Ligand 12 in Gallbladder Carcinoma

Translational Relevance
Gallbladder carcinoma (GBC) is a lethal malignancy and is hard to cure by conventional therapies. Thus, new therapeutic strategies for GBC are urgently needed. Here, we show that chemokine (C-X-C motif) ligand 12 (CXCL12) is differentially expressed in patients with GBCs. The expression of CXCL12 is significantly associated with a high histologic grade and nodal metastasis. Multivariate analyses clearly show that CXCL12 expression is an independent risk factor for patient survival. CXCL12 plays a crucial role in the progression of GBC by enhancing anchorage-dependent and -independent growth, migration, and invasion of GBC cells in vitro. Consistent with these results, overexpression of CXCL12 significantly promotes tumorigenicity of GBCs in a xenograft model. Our finding suggests that CXCL12 expression is associated with GBC progression and may be a potential prognostic marker and therapeutic target for GBCs.

Materials and Methods
Cell line and cell culture
SNL-308 cells, established from a well-differentiated gallbladder adenocarcinoma, were grown in RPMI-1640 media (Invitrogen) supplemented with 10% FBS. All cells were maintained at 37°C under 5% CO2 and 95% relative humidity.

Patients and samples
We investigated 72 consecutive patients (33 men and 39 women) with GBCs who underwent surgical resection between January 1998 and March 2009 at Chungnam National University Hospital (Daejeon, Republic of Korea). The median age of the patients was 68 years (range, 35–87 years). All specimens were routinely fixed in 10% formalin and embedded in paraffin. All tumors were diagnosed as adenocarcinoma and defined as a primary tumor arising from the gallbladder. Tumor stage was classified according to the 2002 American Joint Committee on Cancer System. All protocols were approved by the Institutional Review Board.

Immunohistochemistry
Immunohistochemistry for CXCL12 was conducted using the EnVision-HRP Detection System (DakoCytomation) and a monoclonal CXCL12 antibody (MAB350; R&D Systems). Briefly, 3-µm thick sections were cut from tumor tissue blocks mounted on slides and dried for 1 hour at 56°C. The sections were deparaffinized in xylene and rehydrated in graded alcohol. After antigen retrieval in a pressure cooker with target retrieval solution (DakoCytomation s1699) at full power for 4 minutes, tissue sections were treated with 3% hydrogen peroxide for 10 minutes to block endogenous peroxidase activity. Sections were incubated with the CXCL12 antibody diluted with background reducing diluent (1:50 dilution, DakoCytomation s3022) in a humid chamber at 4°C overnight. Slides were incubated with Envision reagent for 30 minutes followed by DAB chromogen for 5 minutes. Slides were then counterstained with Mayer's hematoxylin and mounted. A mouse IgG1 control excluding the primary antibody was used as a negative control.
Scoring of immunostaining
Immunostaining was reviewed independently by 2 of the authors (J.-M. Kim and Hyun Jung Lee) who were blinded to the patient’s clinicopathologic information. Staining was scored according to the intensity and percentage of positive cells. Membranous and/or cytoplasmic staining of the tumor cells was considered as positive. Tumors were classified into 4 grades by intensity: grade 0 (negative), no staining; grade I, weak intensity (+); grade II, moderate intensity (+++); and grade III, strong intensity (++++). In the case of heterogeneous staining, the higher score was accepted if more than 50% of the cells displayed the higher intensity of staining. The percentage of positive cells was scored as follows: score 0 (no positive cells, 0%), score 0.1 (percentage of positive cells, 1%–9%), score 0.5 (percentage of positive cells, 10%–49%), and score 1.0 (percentage of positive cells, >50%). For semiquantitative analysis of immunostaining, we used an H-score. The H-score was calculated by multiplying the grade of the intensity and score of the positive staining cells. Thus, this score produces a continuous variable that ranges from 0 to 3.0. The median value of the H-score was chosen a priori as the cutoff point for separating positive from negative tumors (35).

Quantitative real-time PCR
Total RNA was isolated from GBC tissues using Ambion RecoverAll Total Nucleic Acid Isolation Kit (Ambion Inc.) according to the manufacturer’s protocol. Target RNA was converted to cDNA by treatment with 200 units of reverse transcriptase and 500 ng oligo(dT) primer in 50 mmol/L Tris-HCl (pH 8.3), 75 mmol/L KCl, 3 mmol/L MgCl₂, 10 mmol/L dithiothreitol, and 1 mmol/L deoxynucleotide triphosphates for 1 hour at 42°C. The reaction was quenched by heating for 15 minutes at 70°C. Quantitative real-time PCR analyses were conducted in a Rotor-gene 6000 Thermocycler (Corbett Research) using 1× SYBR Green Mix (Invitrogen).

Short hairpin RNA targeting CXCR4 mRNA and CXCL12 overexpression in GBC cells
Knockdown of CXCR4 in GBC cells was achieved through lentivirus-mediated transduction via CXCR4 mRNA–specific short hairpin RNA (shRNA) interference using MISSION RNAi system clones (Sigma). Overexpression of CXCL12 in GBC cells was achieved through retrovirus-mediated transduction of full-length human CXCL12 subcloned into a retrovector vector. To generate stable transfectants, lentiviral or retroviral vectors and packaging vectors were cotransfected into HEK293T cells with packaging vectors using Lipofectamine, according to the manufacturer’s instructions (Invitrogen). The next day, virus harvested from the supernatant was added to SNU-308 cells along with 5 µg/mL polybrene. After 24 hours, the media were removed and replaced with fresh media containing 1 µg/mL puromycin. Puromycin-resistant clones were selected after culture for 1 week in the presence of puromycin. CXCL12 or CXCR4 expression levels were analyzed by reverse transcriptase PCR (RT-PCR) and Western blotting.

Cell proliferation assay
Cell proliferation was measured by using the WST-1 cell proliferation assay (Roche Diagnostics) according to the manufacturer’s instructions. Briefly, the cells were seeded in triplicate in flat-bottomed 48-well plates at a density of 2×10⁵ cells per well and allowed to adhere for 24 hours in media supplemented with 10% FBS. Thereafter, the cells were treated with various concentrations of CXCL12 as indicated in reduced serum (3% FBS) media for 72 or 96 hours. After incubation with 30 µL WST-1 reagent for 4 hours, the absorbance of the samples was measured at 450 nm (with a background control as a blank) using a microplate reader.

Migration and invasion assays
Migration and invasion of GBC cells was carried out using Transwell plates (Corning Costar) with 6.5-mm diameter polycarbonate filters (8-μm pore size). Briefly, the lower surface of the filter was coated with 10 µg gelatin for the migration assay and the upper side was coated with 12 µg reconstituted basement membrane substance for the invasion assay (Matrigel; BD Biosciences). Fresh media containing 5% FBS were placed in the lower wells. GBC cells were incubated for 24 hours in media containing 1% FBS, trypsinized, and suspended at a final concentration of 1×10⁶ cells/mL in media containing 1% FBS. One hundred microliters of the cell suspension was loaded into each of the upper wells, and the chamber was incubated at 37°C for 24 hours (migration) or 48 to 72 hours (invasion). Cells were fixed and stained with hematoxylin and eosin. Nonmigrating cells on the upper surface of the filter were removed by wiping with a cotton swab. Chemotaxis was quantified by counting the cells that migrated to the lower side of the filter with an optical microscope (>×200). Eight random fields were counted for each assay.

Soft agar colony-forming assay
Anchorage-independent growth assays were conducted using the CytoSelect 96-well Cell Transformation Assay Kit (Cell Biolabs). Briefly, SNU-308 cells (1×10⁵ cells) were plated in Dulbecco's Modified Eagle's Medium containing 10% FBS in a cell suspension agar matrix between layers of base agar matrix. After 2 weeks, the agar matrix was solubilized and the cells were stained with MTT solution. Absorbance at 570 nm was measured using a microplate reader.

Cell adhesion assay
Culture plates (96-well) were coated with purified collagen, laminin, fibronectin, or vitronectin at a concentration of 2 µg/mL each and incubated at 37°C for 18 hours. Wells were washed with PBS, incubated with 2×10⁵ cells in serum-free RPMI-1640 supplemented with 1% bovine serum albumin at 37°C for 30 minutes, and washed 3 times.
to remove unbound cells. The attached cells were measured by a WST-1 assay as described above.

**Nude mice xenograft assays**

Nude mice (6-week-old) were obtained from Charles River Laboratories. Mice were housed under specific pathogen-free conditions and were used in accordance with the guidelines of the Animal Care Committee at the Korea Research Institute of Bioscience and Biotechnology (Daejeon, Republic of Korea). SNU-308 cells (1.5 x 10⁷) were inoculated s.c. into the right flank of each mouse. Tumor growth was monitored at 5-day intervals by measuring the length and width of the tumor with a caliper and calculating tumor volume based on following formula: volume = 0.523Lu².

**Western blot analyses**

Cell lysates or immunoprecipitates from cell lysates were subjected to SDS-PAGE and transferred to polyvinylidene fluoride membranes (Chemicon). The membranes were incubated with the indicated primary antibody followed by horseradish peroxidase–conjugated secondary antibody (Santa Cruz Biotechnology). The immunoreactive polypeptides were visualized using a chemiluminescent substrate (GE Life Sciences).

**Statistical analyses**

Group comparisons of categorical variables were evaluated using the χ² test or linear-by-linear association. Comparisons of average means were carried out with independent sample t test or one-way ANOVA. Cancer-specific survival was defined from the date of surgery to the date of death from GBCs. Survival curves were plotted using the Kaplan–Meier method and analyzed using the log-rank test. Cox proportional hazards model was carried out to identify prognostic factors for survival. P < 0.05 was considered statistically significant. All statistical analyses were conducted using SPSS version 17.0 statistical software program.

**Results**

**Expression of CXCL12 in GBC**

To analyze the function of CXCL12 in GBC progression, we first evaluated CXCL12 expression by immunohistochemical analyses in tumor specimens from 72 patients with GBCs. CXCL12 was located in the membrane and/or cytoplasm and the intensity of the immunohistochemical staining was variable: negative staining intensity (grade 0), 4 cases; weak staining intensity (grade I), 18 cases; moderate staining intensity (grade II), 22 cases; and strong staining intensity (grade III), 28 cases (Fig. 1A). The percentage of

![Figure 1](https://example.com/figure1.png)

**Figure 1.** Expression of CXCL12 in GBCs. A, representative photomicrographs of immunohistochemical staining for CXCL12 in human GBC tissues: isotype control, normal gallbladder tissue, negative staining intensity, weak staining intensity, intermediate staining intensity, and strong staining intensity (original magnification, ×400). B, quantitative evaluation of CXCL12 expression in GBC tissues (grade 0–III; n = 10 per group) by quantitative real-time PCR. Three independent experiments were carried out in duplicate. Data are expressed as mean ± SD. *, P < 0.05; **, P < 0.01 versus grade 0–I group. C, correlation between CXCL12 expression and survival in patients with GBC. Cancer-specific survival curve according to CXCL12 expression (P = 0.005).
The median H-score for GBC was 1.5. On the basis of these data, the patients were divided into CXCL12-positive (CXCL12 > 1.5) or CXCL12-negative (CXCL12 ≤ 1.5) expression groups. Of the 72 tumors examined, 58 (81%) were classified as CXCL12-positive and 14 (19%) were classified as CXCL12-negative (Table 1).

**Correlation between CXCL12 expression and clinicopathologic factors**

We next analyzed the correlation between CXCL12 expression and various clinicopathologic factors that can affect the prognosis of patients with GBCs. The results are summarized in Table 1. There was no significant difference in age, gender, pathologic tumor (T) stage, distant metastasis, perineural invasion, or lymphatic invasion between the CXCL12-negative group and the CXCL12-positive group. However, CXCL12 expression was significantly associated with lymph node metastasis (P = 0.015) and histologic grade (P = 0.042).

**Correlation between CXCL12 expression and survival**

To further investigate the clinical relevance of CXCL12 expression in GBCs, we compared cancer-specific survival according to CXCL12 expression (Fig. 1C). The median survival time of patients with GBC was 13.5 (range, 1–117) months. Remarkably, the 10-year survival rates in the CXCL12-positive and -negative groups were 10% and 85.7%, respectively (P = 0.005), indicating a crucial impact of CXCL12 expression on clinical outcome in patients.

Next, to estimate the clinical significance of various prognostic factors that might influence survival in the study population, univariate analyses were conducted.

### Table 1. Relationship of CXCL12 expression and clinicopathologic characteristics of GBC

<table>
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<th>Variable</th>
<th>Total (N = 72)</th>
<th>Positive (n = 58)</th>
<th>Negative (n = 14)</th>
<th>P</th>
</tr>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt; 65</td>
<td>21</td>
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<td>4 (28.6%)</td>
<td>1.000a</td>
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<tr>
<td>≥ 65</td>
<td>51</td>
<td>41 (70.7%)</td>
<td>10 (71.4%)</td>
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</tr>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
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<td>4 (28.6%)</td>
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<tr>
<td>Female</td>
<td>39</td>
<td>29 (50.0%)</td>
<td>10 (71.4%)</td>
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<td>4 (28.6%)</td>
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<td>3 (21.4%)</td>
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<td>4</td>
<td>3</td>
<td>3 (5.2%)</td>
<td>0 (0%)</td>
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<td>Nodal metastasis</td>
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<td>40 (69.0%)</td>
<td>14 (100%)</td>
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<td>Present</td>
<td>18</td>
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<td>Distant metastasis</td>
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<td>0 (0%)</td>
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<td>Differentiation</td>
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<tr>
<td>G1</td>
<td>12</td>
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<td>6 (42.9%)</td>
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<td>5 (35.7%)</td>
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<tr>
<td>G3</td>
<td>19</td>
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<td>3 (21.4%)</td>
<td></td>
</tr>
<tr>
<td>G4</td>
<td>4</td>
<td>4 (6.9%)</td>
<td>0 (0%)</td>
<td></td>
</tr>
<tr>
<td>Perineural invasion</td>
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<td>7 (50.0%)</td>
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<td>Lymphatic invasion</td>
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<td>0.228a</td>
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<tr>
<td>Present</td>
<td>46</td>
<td>39 (67.2%)</td>
<td>7 (50.0%)</td>
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</tbody>
</table>

*P values were calculated by pairwise comparisons from χ² test.

*P values were calculated by comparisons of 4 groups from linear-by-linear associations.
CXCL12 in tumor growth transfected cells (Fig. 2E). Next, to evaluate the role of enhanced cell growth compared with the control mock-ly, CXCL12-overexpressing cells showed significantly confirmed by Western blot analyses (Fig. 2E). Consistent-
of CXCL12 were selected. Elevated CXCL12 levels were

effect of CXCL12 on the growth of GBC cells, SNU-308

induced in a time-dependent manner. In addition,

components such as fibronectin, collagen, laminin, and
vitronectin (Fig. 3E).

CXCL12-overexpressing cells displayed significantly increased migration and invasion as compared with control cells (Supplementary Fig. S1A and S1B). In addition, CXCL12 increased the adhesion of GBC cells to matrix components such as fibronectin, collagen, laminin, and vitronectin (Fig. 3E).

One important feature of tumor cells is the ability to regulate their survival. Therefore, we addressed whether CXCL12 contributes to the survival of GBC cells. To test this, CXCL12-overexpressing cells or mock-transfected cells were cultured in serum-free media, and cell viability was evaluated after 96 or 120 hours using Trypan blue exclusion assays. Serum deprivation decreased cell viability to approximately 55% of control cells after 120 hours. However, the viability of CXCL12-overexpressing cells was significantly increased (up to 75%; Fig. 3F).

CXCL12-induced proliferation, migration, and invasion of GBC cells is inhibited by abrogation of CXCR4

To determine whether changes in CXCR4 expression affect GBC progression in response to CXCL12 treatment, we generated GBC cell clones with stable knockdown of CXCR4. Specific depletion of CXCR4 in these cells was

As summarized in Table 2, advanced pathologic T stage (P = 0.002), nodal metastasis (P = 0.003), distant metastasis (P = 0.045), differentiation (P = 0.023), lymphatic invasion (P = 0.001), and CXCL12 expression (P = 0.012) were statistically significant risk factors affecting overall survival of patients with GBC. To further determine the independent prognostic impacts of these various factors, multivariate analyses were conducted using the Cox proportional hazards model. These analyses showed that CXCL12 expression [HR, 8.675; 95% confidence interval (CI), 1.554–48.413; P = 0.014] was an independent risk factor predicting cancer-specific survival in patients with GBCs (Table 2). Taken together, our findings indicate that CXCL12 expression may be a useful marker to predict the survival of patients with GBCs.

CXCL12 promotes GBC cell growth and tumorigenicity

To investigate whether CXCL12 plays an important role in the progression of GBCs, we selected a GBC cell line, SNU-308, that expresses a low level of CXCL12 (Fig. 2A) and treated these cells with CXCL12 for the indicated times. As shown in Fig. 2B, phosphorylation of intracellular signals such as ERK, AKT, and FAK was significantly induced in a time-dependent manner. In addition, CXCL12 increased anchorage-dependent or -independent growth of the cells (Fig. 2C and D). To further confirm the effect of CXCL12 on the growth of GBC cells, SNU-308 cells were stably transfectected with full-length human CXCL12 and the cell lines showing high-level expression of CXCL12 were selected. Elevated CXCL12 levels were confirmed by Western blot analyses (Fig. 2E). Consistent-

ly, CXCL12-overexpressing cells showed significantly enhanced cell growth compared with the control mock-transfected cells (Fig. 2E). Next, to evaluate the role of CXCL12 in tumor growth in vivo, CXCL12-overexpressing cells were injected into the right flank of nude mice and tumor formation was monitored. As shown in Fig. 2F, an increase in tumor growth was observed in mice with CXCL12-overexpressing cell xenografts as compared with those injected with mock-transfected GBC cells. Remark-
accomplished by lentivirus-mediated transduction and expression of a CXCR4 mRNA–specific shRNA. Cell clones stably expressing low levels of CXCR4 were selected, and CXCR4 expression was confirmed by RT-PCR and Western blotting (Fig. 4A). Stable depletion of CXCR4 expression in GBC cells inhibited CXCL12-induced ERK, AKT, and FAK activation (Fig. 4B). In addition, suppression of CXCR4 in GBC cells caused significant decreases in growth, migration, and invasion with CXCL12 stimulation. Interestingly, depletion of CXCR7, a new receptor for CXCL12, did not significantly affect CXCL12-induced cellular activities (Supplementary Fig. S2A–S2C). These results suggest that the CXCR4/CXCL12 system plays an important role in the growth, migration, and invasion of GBC cells.

Discussion

In the present study, we show for the first time that CXCL12 is expressed differentially in GBCs and is associated with GBC progression. In addition, CXCL12 expression is an independent poor prognostic marker for survival in patients with GBCs who underwent surgical resection. These results may have important clinical implications for risk stratification and the planning of postsurgical
surveillance, as well as for the potential of CXCL12 as a therapeutic target.

We investigated and clarified the clinical significance of CXCL12 expression in GBCs. Recently, data showed that CXCL12 expression is upregulated and associated with tumor progression and poor prognosis in several types of cancer (30–33, 36, 37), suggesting that tumor-derived CXCL12 plays a role in tumorigenesis. Ishigami and colleagues reported that CXCL12 positivity was significantly associated with lymph node metastasis, depth of invasion, lymphatic invasion, tumor diameter, and higher stage in gastric cancer (33). In addition, CXCL12-positive patients showed significantly poorer oncologic outcomes than did the CXCL12-negative patients, suggesting that CXCL12 is an independent prognostic factor in gastric cancer. Salmaggi and colleagues also showed that CXCL12 expression was correlated with a significantly shorter time to progression in glioma as an independent predictor (30). A similar pattern has been reported for colon cancer (32), esophageal cancer (31), malignant glioma (36), and non–small cell lung cancer (37). However, CXCL12 expression and its clinical relevance in GBC have not yet been investigated. In this study, we observed overexpression of CXCL12 in GBCs. Moreover, we showed that CXCL12 expression was significantly associated with a high histologic grade and lymph node metastasis and is an independent poor risk factor for predicting survival in patients with GBCs. Our results suggest that CXCL12 could be involved in GBC tumorigenesis and be useful as a potential prognostic biomarker for patients with GBCs.

Next, we investigated and clarified the functional role of CXCL12 in GBC progression. CXCL12 directly impacts cancer cell proliferation through interactions with its cognate receptor, CXCR4 (25, 26). When GBC cells were treated with CXCL12, SNU-308 cells, which express an endogenously high level of CXCR4, showed increased anchorage-dependent and -independent growth. Furthermore, xenograft mice injected with CXCL12-overexpressing cells showed a significant increase in tumor growth as compared with controls. These observations suggest that CXCL12 promotes the growth and tumorigenicity of GBC through interaction with CXCR4. CXCL12 is involved in cell migration, invasion, and adhesiveness in several types of cancer (13, 22, 23, 27). In this study, GBC cells showed enhanced motility and invasiveness in response to CXCL12. Furthermore, CXCL12 increased the adhesiveness of GBC cells to extracellular matrix components and significantly reduced serum-deprived apoptosis, indicating that CXCL12 is deeply involved in motility, invasiveness, adhesiveness, and survival of GBC cells expressing CXCR4. Taken together,
these observations indicate that CXCL12 may affect biologic behaviors in GBC via CXCR4 activation.

Finally, we sought to confirm whether changes in CXCR4 expression influence GBC progression by CXCL12 using GBC cell clones with stable knockdown of CXCR4 because several recent reports indicate that CXCL12 also binds to another 7-transmembrane span receptor called CXCR7 (38, 39). Indeed, with CXCR7 identified as a new receptor for CXCL12, the role of the CXCL12/CXCR4 axis in regulating biologic processes in cancer development and progression has become more complex (40). In the present study, stable depletion of CXCR4 in GBC cells caused a significant decrease in growth, migration, and invasion upon CXCL12 treatment. Interestingly, depletion of CXCR7 had no significant effect on CXCL12-induced cellular activities (Supplementary Fig. S2A–S2C). These observations suggest that the CXCL12/CXCR4 axis plays a critical role in the tumorigenesis of GBCs.

Next, to evaluate the clinical significance of CXCR4 expression in GBCs, we also examined CXCR4 expression in GBCs by immunohistochemistry as in CXCL12 expression, patients were classified into CXCR4-positive and -negative groups (Supplementary Fig. S3A). Of the 72 tumors examined, 47 (65%) were classified as CXCR4-positive and 25 (35%) were classified as CXCR4-negative. However, we did not find any correlation between CXCR4 expression and various clinicopathologic factors or patient survival (Supplementary Table S1 and Supplementary Fig. S3B). These results suggest that CXCL12 expression may play an important functional role in GBC progression, whereas CXCR4 alone may not.

Several signaling molecules related to the activation of CXCR4 by CXCL12 have been identified and include AKT/PKB, ERK1/2 mitogen-activated protein kinase (MAPK), phosphoinositide 3-kinase (PI3K), Stat3, paxillin, Crk, and NF-κB. The Janus-activated kinase (JAK) and FAK system has also been involved in the CXCL12/CXCR4 signaling cascades (28, 41, 42). However, these signaling pathways are strictly regulated by cell type. We found that CXCL12 activated ERK, AKT, and FAK in GBC cells expressing a high level of CXCR4 in a time-dependent manner. In addition, stable depletion of CXCR4 in GBC cells, which express a high endogenous level of CXCR4, inhibited CXCL12-induced ERK, AKT, and FAK activation. Our findings suggest that CXCL12-induced intracellular signal activations are downstream effectors of CXCR4. These observations are
also compatible with the changes in biologic responses, such as cell growth, migration, and invasion, to CXCL12 treatment that we showed using GBC cell clones with knockdown of CXCR4.

However, the precise mechanism by which tumor-derived CXCL12 contributes to tumor development and progression is not clear. One potential explanation is that CXCL12 is engaged in tumorigenesis in an autocrine and/or paracrine manner. The concomitant expression of CXCL12 and its receptor CXCR4 in brain tumor cells has been characterized as an autocrine and/or paracrine mechanism of cancer cell stimulation, resulting in aggressive behavior (43, 44). Subsequently, autocrine/paracrine mitogenic activity of CXCL12 was reported in glioblastoma multiforme in vitro (26, 45). Barbieri and colleagues also showed that CXCL12 overexpression induced autocrine/paracrine cell proliferation in pituitary tumor cells (43). Collectively, these reports support our data. Another possible mechanism is that CXCL12 may play a role in attracting endothelial cells to the tumor microenvironment. Pathologically induced CXCL12 secretion by brain tumor cells increases the recruitment of circulating endothelial progenitors (46). Furthermore, inhibition of the CXCL12/CXCR4 axis reduced recruitment of vascular progenitors and decreased tumor growth through suppression of angiogenesis (47, 48). Finally, CXCL12 has also been shown to repel tumor-specific effector T cells and to recruit immunosuppressive cells at the tumor site, suggesting that CXCL12 is involved in immune evasion of cancer cells (49).

In conclusion, our results indicate that CXCL12 is overexpressed in patients with GBCs and is significantly associated with oncogenic properties and tumor progression. Furthermore, CXCL12 expression is a novel independent poor prognostic factor for predicting survival in patients with GBCs. In vitro and in vivo experiments using GBC cells clearly showed that CXCL12 induced cell growth, migration, invasion, adhesiveness, and tumor formation through interaction with CXCR4. Collectively, we postulate that tumor-derived CXCL12 may be involved in tumorigenesis of GBCs in an autocrine and/or paracrine manner via the CXCL12/CXCR4 axis.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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