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ORIGINAL RESEARCH

RETRACTED ARTICLE: The roles of serum CXCL16 in circulating Tregs and gastrointestinal stromal tumor cells

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Abstract: Gastrointestinal stromal tumors (GIST) are the most common sarcomas of the digestive system. Abnormal expression of CXCL16 and its sole receptor, CXCR6, has been demonstrated in many cancers. However, no studies have shown the relationship between CXCL16 or CXCR6 expression and GIST. In this study, we detected CXCL16 and CXCR6 expression in GIST patient samples by using immunohistochemistry analysis and Western blot analysis. Serum CXCL16 level was determined by using enzyme-linked immunosorbent assay. Circulating Tregs were isolated by using flow cytometry. MTT assay, cell cycle assay, and transwell assay were used to test the effects of recombinant CXCL16 on Tregs and GIST cells in vitro. The levels of CXCL16 and CXCR6 protein were higher in cancer tissues than in normal tissues. Serum CXCL16 level and circulating Tregs were higher in GIST patients than that in the healthy volunteers. CXCL16, CXCR6, serum CXCL16, and circulating Tregs were significantly associated with increased survival time of patients. Relative to control cells, high concentration recombinant CXCL16-treated Tregs and GIST cells exhibited lower proliferation and mobility rates as assessed by MTT assay and transwell assay, respectively. Taken together, CXCL16 was observed to mediate the inhibitory effects in Tregs and GIST cells, and these involved suppression of the MEK/ERK signaling pathway.

Keywords: CXCL16, CXCR6, Treg, GIST, MEK/ERK signaling pathway

Introduction

Gastrointestinal stromal tumors (GIST) are the most common sarcomas of the digestive system.[1] Although tumor recurrence or metastasis is common, the main treatment of primary GIST is still surgical resection.[2] Mitotic index and tumor size were regarded as important prognostic predictors for GIST patients.[3] Apparently, alternative therapeutic strategies and novel markers are urgently needed for these patients.

The immune system is integral to almost every aspect of tumorigenesis, such as tumor initiation,[4] prevention,[5] and progression.[6] More and more evidence showed that $CD4^+$ $CD25^+$ $Foxp3^+$ Tregs are the critical factor affecting the progression and prognosis of many cancers, including gastric cancer,[7] lung cancer,[8] and colorectal cancer.[9] Tregs play a critical role in the control of anti-tumor immune responses.[10] It has been found that increased numbers of Tregs are detected in peripheral blood of cancer patients and accumulate in tumor regions.[11,12]

CXCL16 exists both in a transmembrane and a soluble form, is not only expressed in immune cells, but also expressed constitutively in fibroblasts, keratinocytes, and cancer cells.[13] CXCL16 and its sole receptor, CXCR6, are involved in multiple biological activities, including cell adhesion, cell survival, chronic inflammation, and anti-tumor immunity.[14–16] However, to our knowledge, there have been no previous studies showing the roles of CXCL16 and CXCR6 in GIST.

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In the present study, we analyzed CXCL16 and CXCR6 expression in GIST cancer tissues and the circulating CXCL16 and Tregs in the peripheral blood to determine the clinical significance of CXCL16, CXCR6, serum CXCL16 (sCXCL16), and Tregs in GIST patients. Subsequently, the mechanisms responsible for sCXCL16 mediated inhibitory effects on Tregs and GIST cells were determined.

Materials and methods

Ethics statement

For the use of clinical materials for research purposes, approval from the China Medical University Ethical Committee was obtained. Written informed consent was obtained from all participants. The clinical investigation was conducted according to the principles expressed in the Helsinki Declaration of 1975.

GIST patient specimens

Tissue specimens (cancer tissues and their matched normal tissues) and blood samples were obtained from 43 patients (no chemotherapy or radiotherapy prior to resection) at the Department of Surgical Oncology, First Affiliated Hospital of China Medical University between January 2006 and December 2010. Blood samples from 24 healthy individuals were used as control.

Immunohistochemistry analysis

Sections were deparaffinized in xylene prior to rehydration using gradient alcohol. Endogenous peroxidase activity was then blocked with methanol containing 3% H_2O_2 for 20 minutes. For antigen retrieval, sections were treated with citrate buffer saline (pH=6.0) for 15 minutes at 95°C in a microwave oven. After blocking with 7% normal horse serum for 30 minutes at room temperature, sections were incubated with goat polyclonal anti-CXCL16 (R&D Systems, Inc., Minneapolis, MN, USA; dilution 1:20), or rabbit monoclonal anti-CXCR6 (R&D Systems, Inc.; dilution 1:40) for 15 minutes and then anti-goat or anti-rabbit antibody conjugated to horseradish peroxidase (1:100) for 15 minutes. Omission of the primary antibody was used as a negative control.

Circulating Tregs determination

$CD4^+$ $CD25^+$ $CD127^-$ Tregs were enriched by Human Regulatory T cell isolation kit (Miltenyi Biotec, Inc., Auburn, CA, USA). In brief, non-$CD4^+$ and $CD127^{high}$ cells were first depleted with microbeads and then the pre-enriched $CD4^+$ $CD127^{dim}$ cells went through positive selection for $CD25^+$ T cells. The purity of Tregs was monitored via fluorescence-activated cell sorting (BD Biosciences, San Jose, CA, USA). Freshly isolated Tregs were grown in Roswell Park Memorial Institute medium 1640 (Hyclone, Logan, UT, USA) supplemented with 10% fetal bovine serum (Invitrogen, Thermo Fisher Scientific, Waltham, MA, USA) and antibiotics (100 U/mL penicillin and 100 µg/mL streptomycin) and maintained in a humidified cell incubator with 5% CO_2 at 37°C.

Serum CXCL16 level determination

Blood samples were collected from the subjects following overnight fasting. Serum samples were obtained by centrifugation at 4°C and stored at −80°C for future use. sCXCL16 levels were determined using the enzyme-linked immunosorbent assay (ELISA) method (Human CXCL16 ELISA kit; R&D Systems, Inc.).

GIST cell lines

The human GIST cell line GIST-T1 was established and characterized in detail by Taguchi et al.[17] The GIST882 cell line with an activating KIT mutation (exon 13, K642E) was a generous gift from Dr Zheng Yan (China Medical University, Shenyang, People's Republic of China). The GIST-T1 cell line was grown in Dulbecco's Modified Eagle's Medium (Hyclone) and the GIST882 cell line was grown in Roswell Park Memorial Institute medium 1640 (Hyclone) supplemented with 10% fetal bovine serum (Invitrogen) and antibiotics (100 U/mL penicillin and 100 µg/mL streptomycin) and maintained in a humidified cell incubator with 5% CO_2 at 37°C.

Proliferation assay

Cell counting Kit-8 (Dojindo Molecular Technologies, Inc., Rockville, MD, USA) was employed to determine the number of viable cells. In brief, 1,000 cells/well were seeded in 96-well plates and allowed to adhere. Thereafter, recombinant CXCL16 (0, 3, 6, 9, 12 ng/mL; R&D Systems, Inc.) was added to the culture system for 48 hours at 37°C. Next, 10 µL of Cell counting Kit-8 solution was added into each well of the plate, and the plates were incubated for 4 hours in the incubator and absorbance rates were measured at 450 nm using a microplate reader (Bio-Rad Laboratories Inc., Hercules, CA, USA). The half maximal inhibitory concentration (IC_{50}) values of recombinant CXCL16 for Tregs, GIST-T1 cells, and GIST882 cells were determined and used in the following studies.

Gene transfection

CXCR6 siRNA (sc-39895) was obtained from Santa Cruz Biotechnology Inc. (Dallas, TX, USA). For gene transfection, Tregs, GIST-T1 cells, and GIST882 cells with CXCL16

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treatment were grown overnight and transfected with *CXCR6* siRNA using Lipofectamine 2000 (Invitrogen) according to the manufacturer's instructions.

Cell cycle assays

Cells were washed twice with ice cold phosphate-buffered saline and fixed in 70% ethanol at 4°C overnight, followed by incubation with 10 mg/mL RNase A (Sigma-Aldrich Co., St Louis, MO, USA) at 37°C for 30 minutes. The cells were then incubated with 50 mg/mL propidium iodide (KeyGEN BioTECH, Nanjing, People's Republic of China). Flow cytometry analysis of DNA content was performed on a flow cytometer (BD Biosciences).

Migration and invasion assay

Migration and invasion assays were performed using a transwell chamber (8 μm pore size; EMD Millipore, Billerica, MA, USA) according to the manufacturer's instructions. Cell culture inserts for the invasion assay were precoated with Matrigel (BD Biosciences) for 4 hours at 37°C. Cells (1×10^4) were seeded into the upper chamber, while 1 mL complete medium was added into the lower chamber as a chemotaxin. After 24 hours' culture, non-invading cells were removed with a cotton bud. Cells that migrated to the lower surface were fixed in 4% paraformaldehyde for 20 minutes and underwent Giemsa staining (Beyotime, Beijing, People's Republic of China). Five random fields were selected for cell counting under a light microscope (×200; Olympus Corporation, Tokyo, Japan). The migration assay procedure was similar except that Matrigel was not utilized.

Western blot analysis

Tissues and cells were lysed in lysis buffer (20 mM Tris-HCl, 150 mM NaCl, 2 mM ethylenediaminetetraacetic acid, 1% Triton X100, containing protease inhibitor cocktail (Sigma-Aldrich). Cell extract protein amounts were quantified using the bicinchoninic acid protein assay kit (Beyotime). Equivalent amounts of protein (30 μg) were separated using 12% sodium dodecyl sulfate polyacrylamide gel electrophoresis and transferred to polyvinylidene difluoride membrane (EMD Millipore). Immunoblotting was performed using anti-ERK, anti-phospho-ERK, anti-MEK, anti-phospho-MEK, anti-MMP2, anti-MMP9, anti-E-cadherin, anti-N-cadherin, and anti-β-actin (Santa Cruz Biotechnology Inc.). Each specific antibody binding was detected with horseradish peroxidase-conjugated respective secondary antibodies (Amersham Biosciences, Amersham, UK) and enhanced chemiluminescence solutions (Amersham Biosciences).

Statistical analysis

All experiments were performed in triplicate, and the results were expressed as the mean ± standard deviation. Data were analyzed using GraphPad Prism 5 software (GraphPad Software Inc., La Jolla, CA, USA). Statistical analysis was performed using a one-tailed Student's *t*-test (unilateral and unpaired). The Cox's proportional hazards model was employed for multivariate analysis. Pearson correlations were computed to determine the relationships between sCXCL16 and Treg cells. Kaplan–Meier survival plots were generated and comparisons between survival curves were made using log-rank statistical analysis. *P*-values <0.05 were considered to indicate statistically significant difference.

Results

CXCL16 and CXCR6 expression in GIST specimens

The results of Western blot showed that CXCL16 and CXCR6 protein expression in cancer tissue was significantly higher than in matched normal tissue ($P<0.05$, Figure 1A). Immunohistochemistry was performed to determine the protein expression of CXCL16 and CXCR6. Specific brown-colored staining for CXCL16 and CXCR6 in the cytoplasm and membrane could be clearly observed in cancer cells (Figure 1B). The cleavage of the extracellular domain of CXCL16 into serum has been previously reported for various types of cancer.[18] Therefore, serum levels of CXCL16 were determined by using ELISA in our study. The sCXCL16 concentration and circulating Tregs were higher in patients with GIST than that in healthy individuals ($P<0.05$, Figure 1C and D). The sCXCL16 and the number of Tregs were significantly positively correlated within a certain range (<3 ng/mL) ($P<0.01$, Figure 1E). However, a concentration of sCXCL16 higher than 3 ng/mL exhibited inhibitory effects on Tregs (Figure 1E).

Association of CXCL16, CXCR6, sCXCL16, and Tregs with clinicopathological parameters in patients with GIST

The association of CXCL16, CXCR6, sCXCL16, and Tregs with the clinicopathological characteristics of the sampled patients was analyzed. The results are summarized in Tables 1 and 2. CXCR6 expression was significantly associated with tumor bleeding ($P=0.004$) and tumor invasion ($P=0.042$). sCXCL16 was also associated with tumor bleeding ($P=0.024$) and tumor invasion ($P=0.046$). Circulating Tregs were associated with tumor size ($P=0.004$). Cox's proportional hazard analysis indicated that invasion was an independent

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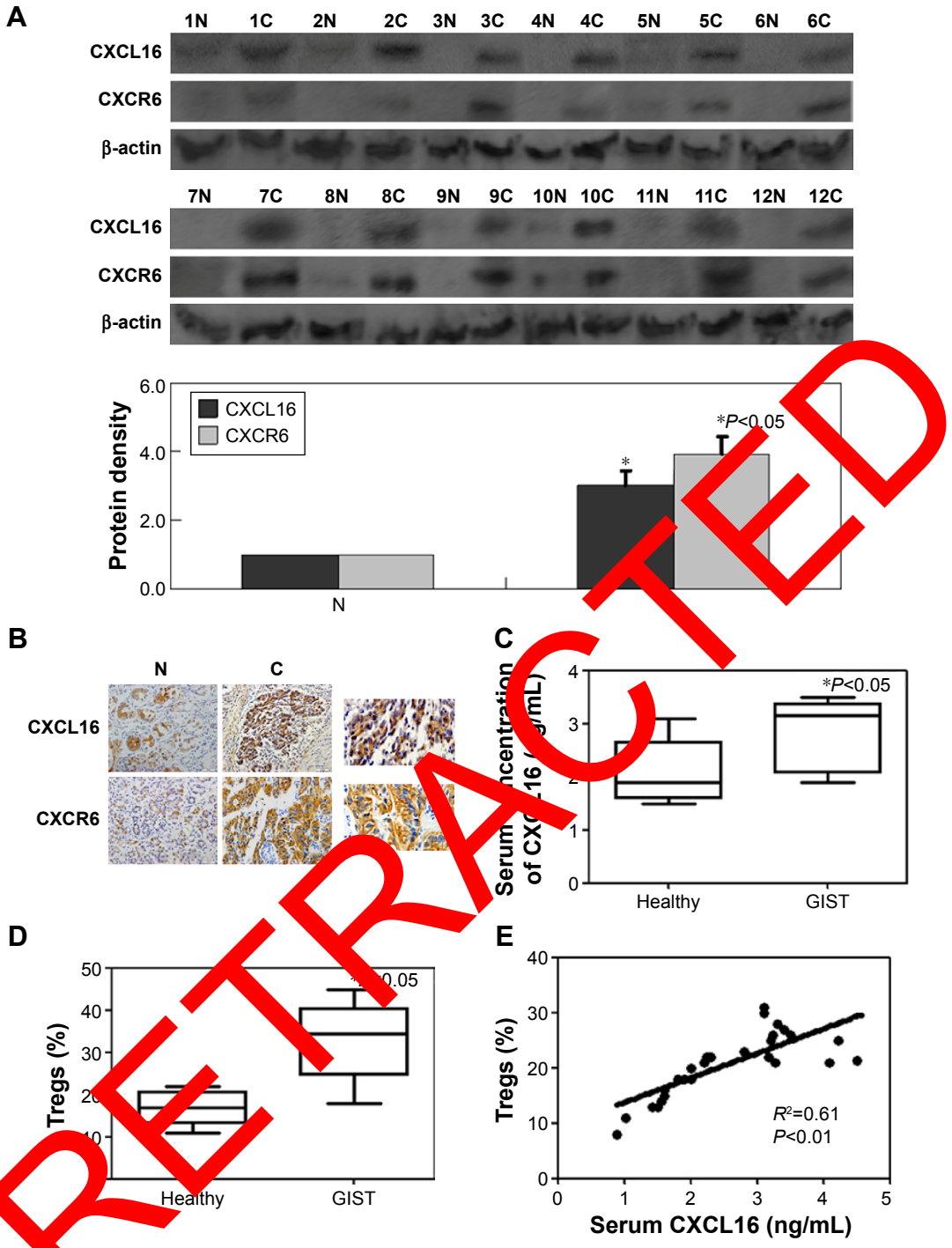

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Figure 1 CXCL16, CXC sCXCL16, and circulating Tregs in GIST specimens.
Notes: (**A**) Western blot a sis for CXCL16 and CXCR6 expression in specimens. β-actin was used as an internal loading control. (**B**) Representative results of GIST cancer tissues and corresponding noncancerous tissue by immunohistochemical staining. The nuclei were counterstained with hematoxylin. (**C**) sCXCL16 level in serum of the GIST patients was detected by using ELISA. (**D**) Circulating Tregs were determined by using fluorescence-activated cell sorting. (**E**) Positive correlation between sCXCL16 and Tregs in serum of the GIST patients.
Abbreviations: GIST, gastrointestinal stromal tumors; ELISA, enzyme-linked immunosorbent assay; N, normal; C, cancer; sCXCL16, serum CXCL16.

prognostic factor for GIST with CXCL16 protein expression, tumor bleeding and invasion were independent prognostic factors for GIST with CXCR6 protein expression, mitotic index and invasion were independent prognostic factors for GIST with sCXCL16 protein expression, tumor size and tumor number were independent prognostic factors for GIST with Tregs (Table 3, $P<0.05$). Follow-up information was available for 43 patients for periods ranging from 1 month to 5 years (median =26 months). CXCL16, CXCR6, sCXCL16, and Tregs were correlated with the poor prognosis of

Table 1 Relationship between CXCL16 and CXCR6 expression in situ and clinicopathological parameters of patients with GIST

Clinicopathological features	CXCL16					CXCR6			
	n	Low	High	χ^2	*P*-value	Low	High	χ^2	*P*-value
Sex				0.17	0.674			0.18	0.673
Female	14	6	8			7	7		
Male	29	9	20			11	18		
Age (years)				0.89	0.344			0.00	0.937
<55	20	5	15			8	12		
≥55	23	10	13			10	13		
Tumor size				0.14	0.709			2.74	0.245
<10 cm	17	7	10			4	13		
≥10 cm	26	8	18			14	12		
Tumor number				0.08	0.776			1.73	0.189
Single	9	3	6			6			
Multiple	34	12	22			12	22		
Histology				0.06	0.972			0.2	0.634
Spindle	9	3	6			5	4		
Epithelioid	15	5	10			6	9		
Mixed	19	7	12			7	12		
Mitotic index (per 50 HPFs)				2.32	0.128			0.63	0.428
<5	15	8	7			8			
≥5	28	7	21			10	18		
Tumor necrosis				0.00	0.957			1.33	0.249
–	27	10	17			9	18		
+	16	5	11			9	7		
Tumor bleeding				0.2	0.597			8.48	**0.004**
–	22	9	13			4	18		
+	21	6	15			14	7		
Surrounding tissue invasion				3.7	0.071			4.14	**0.042**
–	21	4	17			5	16		
+	22	11	11			13	9		

Note: Data in bold indicates statistical significance.
Abbreviations: GIST, gastrointestinal stromal tumor; HPFs, high power fields.

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patients with GIST as determined by Kaplan–Meier analysis ($P<0.05$, Figure 2).

The effects of recombinant CXCL16 on Tregs and GIST cells in vitro

MTT assays were performed to detect the cytotoxicity of recombinant CXCL16 in Tregs and GIST cells. The growth curves demonstrated that low concentration recombinant CXCL16 (<3 ng/mL) promoted the growth of Tregs, while high concentration (>3 ng/mL) inhibited the growth of the cells ($P<0.05$, Figure 3A). Regardless of the concentration, recombinant CXCL16 inhibited the growth of GIST-T1 cells and GIST882 cells ($P<0.05$, Figure 3A). The IC_{50} values of recombinant CXCL16 for Tregs, GIST-T1 cells, and GIST882 cells were 6.57±0.81 ng/mL, 6.49±0.73 ng/mL, and 7.24±0.89 ng/mL, respectively. Next, the effects of recombinant CXCL16 (IC_{50} value) on cell cycle progression were examined. As shown in Figure 3B, the ratio of cells in the G_2 phase increased in recombinant CXCL16 treated Tregs, GIST-T1 cells, and GIST882 cells compared with untreated ones. Migration and invasion were significantly decreased in recombinant CXCL16 treated cells compared with untreated ones ($P<0.05$, Figure 3C). Furthermore, we found MMP2 and MMP9 were inhibited in Tregs, GIST-T1 cells, and GIST882 cells by recombinant CXCL16 (Figure 4).

Recombinant CXCL16 suppressed the MEK/ERK signaling pathway via CXCR6 receptor

Western blot assays were performed to identify the mechanism of recombinant CXCL16 in Tregs, GIST-T1 cells, and GIST882 cells. In our studies, we found total levels of MEK and ERK showed no changes, while the levels of phospho-MEK and phospho-ERK were observed to be significantly lower in cells treated with recombinant CXCL16 (Figure 4). Recombinant CXCL16 treated cells showed a higher expression level of epithelial marker E-cadherin, and lower expression levels of mesenchymal markers N-cadherin (Figure 4). CXCR6 knockdown blocked the effects of recombinant CXCL16 on Tregs, GIST-T1 cells,

Table 2 Relationship between sCXCL16 and circulating Tregs and clinicopathological parameters of patients with GIST

Clinicopathological features	sCXCL16					Tregs			
	n	Low	High	χ^2	*P*-value	Low	High	χ^2	*P*-value
Sex				0.00	0.994			0.00	0.994
Female	14	7	7			6	8		
Male	29	13	16			14	15		
Age (years)				0.24	0.623			0.02	0.904
<55	20	8	12			9	11		
≥55	23	12	11			11	12		
Tumor size				0.99	0.319			8.25	**0.004**
<10 cm	17	10	7			13	4		
≥10 cm	26	10	16			7	19		
Tumor number				0.06	0.814				0.082
Single	9	5	4			7	2		
Multiple	34	15	19			13	21		
Histology				1.87	0.392			0.02	0.989
Spindle	9	6	3			4	5		
Epithelioid	15	6	9			7	8		
Mixed	19	8	11			9			
Mitotic index (per 50 HPFs)				5.11	**0.024**			0.11	0.737
<5	15	11	4			8	7		
≥5	28	9	19			12			
Tumor necrosis				0.00	0.971			1.51	0.219
–	27	12	15			15	12		
+	16	8	8			5	11		
Tumor bleeding				0.20	0.654			0.60	0.438
–	22	9	13			12	10		
+	21	11	10			8	13		
Surrounding tissue invasion					**0.048**			0.20	0.654
–	21	6	15			11	10		
+	22	14	8			9	13		

Note: Data in bold indicates statistical significance.
Abbreviations: GIST, gastrointestinal stromal tumors; HPFs, high power fields; sCXCL16, serum CXCL16.

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and GIST882 cells (Figure 4). In combination, these results suggest that recombinant CXCL16 inhibited the proliferation and the mobility of cells by suppressing the MEK/ERK signaling pathway in a CXCR6-dependent manner.

Discussion

CXCL16 is a membrane-bound chemokine that exists in a transmembrane form (TM-CXCL16) and a soluble form (sCXCL16).[15] CXCL16 is the only known ligand for CXCR6.[16] The chemokine receptor CXCR6, also known as Bonzo, STRL3 or TYMSTR, was originally described as a coreceptor for simian immunodeficiency virus and HIV.[19] In this study, we found that TM-CXCL16 and CXCR6 content were increased in GIST cancer tissue. Previous studies have verified the overexpression of CXCL16 and/or CXCR6 in several types of human cancers, including hepatocellular

Table 3 Multivariate analysis of clinical variables for patients with GIST

Clinicopathological parameters	CXCL16		CXCR6		sCXCL16		Tregs	
	Relative risk (95% CI)	*P*-value	Relative risk (95% CI)	*P*-value	Relative risk (95% CI)	*P*-value	Relative risk (95% CI)	*P*-value
Sex (male)	0.60 (0.16–2.24)	0.075	0.61 (0.17–2.22)	0.223	0.81 (0.23–2.92)	0.335	0.80 (0.22–2.90)	0.265
Age (>55 years)	2.31 (0.63–8.51)	0.067	1.15 (0.34–3.89)	0.325	1.64 (0.49–5.50)	0.421	1.12 (0.34–3.73)	0.215
Tumor size (≥10 cm)	0.63 (0.18–2.27)	0.124	3.79 (0.97–14.78)	0.053	0.44 (0.13–1.52)	0.246	0.11 (0.03–0.47)	**0.025**
Tumor number	1.09 (0.23–5.16)	0.225	0.27 (0.06–1.29)	0.084	0.63 (0.14–2.77)	0.365	0.18 (0.03–0.98)	**0.042**
Mitotic index	0.29 (0.08–1.10)	0.062	0.49 (0.14–1.74)	0.135	0.17 (0.04–0.69)	**0.034**	0.66 (0.19–2.32)	0.367
Tumor necrosis	0.77 (0.21–2.88)	0.321	2.57 (0.72–9.17)	0.086	1.25 (0.36–4.32)	0.402	0.36 (0.10–1.34)	0.435
Tumor bleeding	0.58 (0.16–2.06)	0.164	9.00 (2.19–36.9)	**0.016**	1.59 (0.48–5.31)	0.207	0.51 (0.15–1.73)	0.258
Surrounding tissue invasion	5.25 (1.35–20.4)	**0.024**	5.78 (1.58–21.1)	**0.025**	4.38 (1.21–15.8)	**0.033**	0.63 (0.19–2.10)	0.267

Note: Data in bold indicates statistical significance.
Abbreviations: GIST, gastrointestinal stromal tumors; CI, confidence interval; sCXCL16, serum CXCL16.

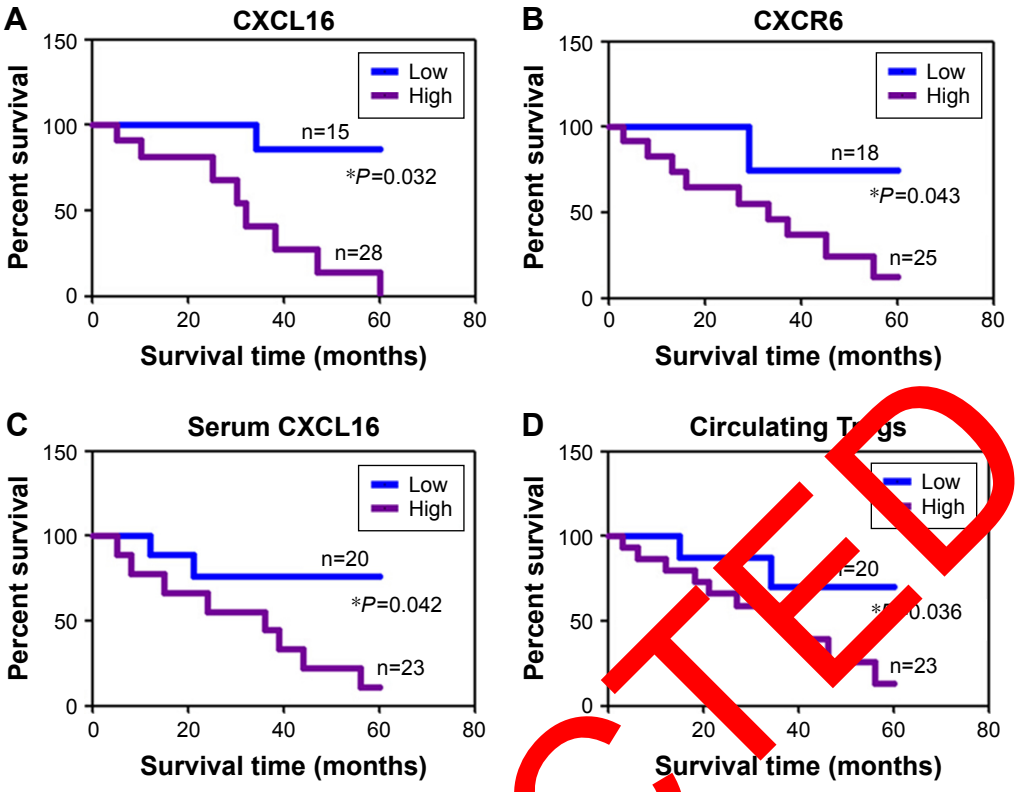

Figure 2 Kaplan–Meier curves of the cumulative survival rate of patients with GIST.
Notes: Based on patients' CXCL16 (**A**), CXCR6 (**B**), sCXCL16 (**C**) expression or circulating Tregs number (**D**).
Abbreviations: GIST, gastrointestinal stromal tumors; sCXCL16, serum CXCL16.

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carcinoma, prostate cancer, and ovarian carcinoma.[20–22] Furthermore, our study showed that TM-CXCL16 and CXCR6 protein expression had a significant association with a poor prognosis in patients with GIST. Gao et al also found that CXCL16 was associated with decreased survival of patients with ovarian carcinoma. On the other hand, Gutwein et al[23] found that high CXCL16 expression correlates with better survival of patients with renal carcinoma. These results suggest that the effect of CXCL16 and CXCR6 on clinical outcome differ between tumor types and study design. Wente et al[24] have shown that pancreatic ductal adenocarcinoma patients had higher sCXCL16 levels than that in healthy donors. Matsushita et al[25] found overexpression of sCXCL16 in the serum of colorectal patients compared with healthy volunteers. In the current study, we also demonstrated higher sCXCL16 levels in the patients with GIST compared with healthy donors. Furthermore, we confirmed the level of sCXCL16 was associated with the number of Tregs. The presence of Tregs is considered to be a key component in tumor immune suppression.[26] Tregs have been reported to be increased in the peripheral blood of various cancers.[7–9] However, no differences in the Treg numbers were observed between head and neck cancer patients and healthy controls.[27] In this study, we observed a significant increase in the Treg cell populations in GIST patients compared to healthy donors, which is correlated with a poor prognosis.

Interestingly, we found that a high level of sCXCL16 exhibited inhibitory effects on Tregs. However, regardless of the concentration, sCXCL16 inhibited the proliferation of GIST cells. Fang et al[28] also found that CXCL16 expression suppresses migration and invasion and induces apoptosis in breast cancer cells. However, Matsushita et al[25] found that CXCL16 enhanced the proliferation, migration, and invasiveness of colorectal cells. We used two GIST cell lines, GIST-T1 and GIST882, to provide results with relative credibility in this study. To determine the mechanism responsible for this decreased proliferation of Tregs and GIST cells, we speculated differential expression of CXCR6 in these cells. We confirmed that CXCR6 was expressed in the three cell lines and the inhibitory effects of CXCL16 were offset on these three cell lines after CXCR6 knockdown. Since CXCL16 and CXCR6 are co-expressed in cancer cells, it is difficult to discriminate between their individual roles in cancer formation and metastasis. We observed decreased MMP2/MMP9 protein in Tregs, GIST-T1 cells, and GIST882 cells after CXCL16 treatment. Furthermore, CXCL16 inhibited epithelial-mesenchymal-like transitions (EMT) by the up-regulation of E-cadherin and decreased the expression

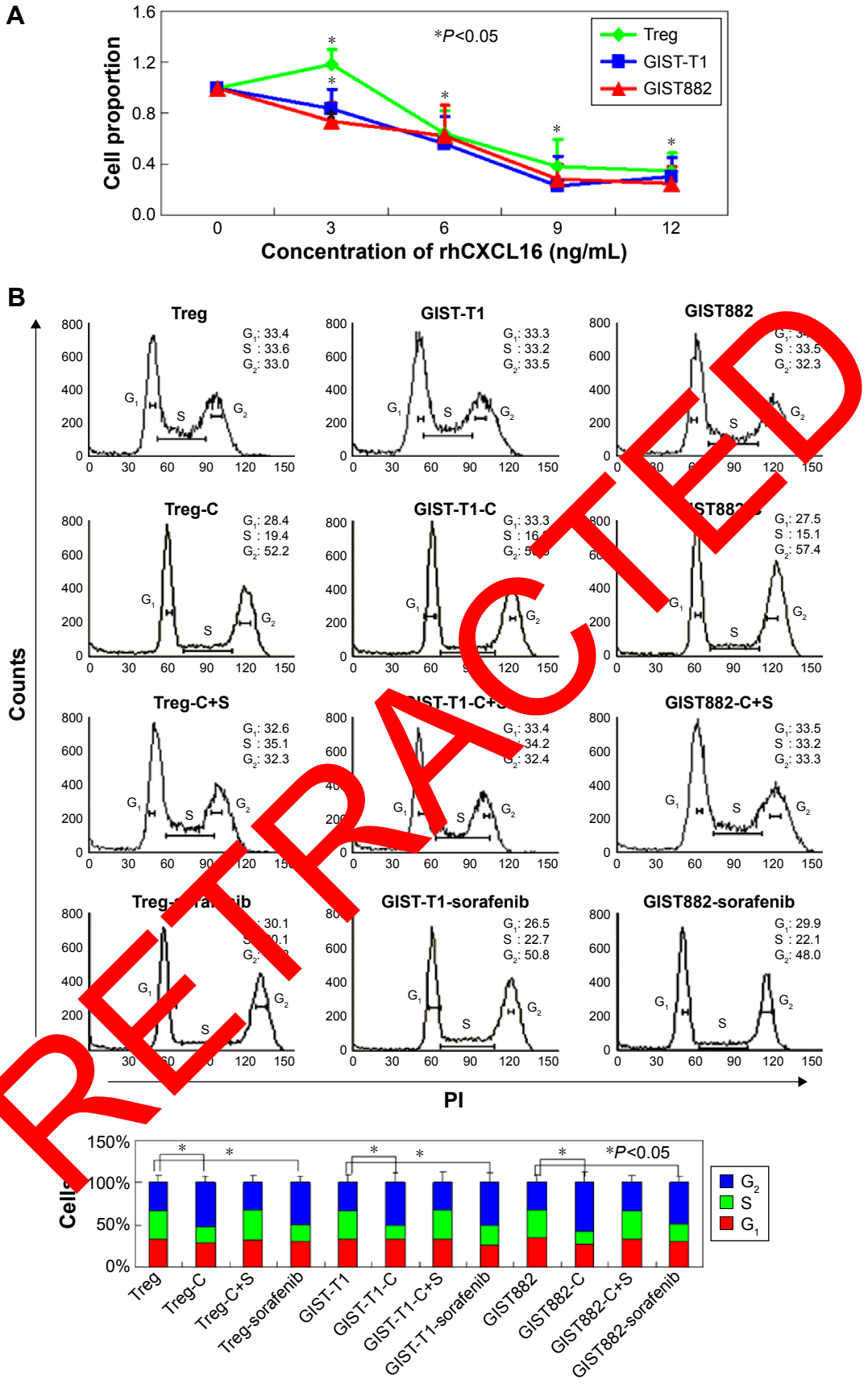

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Figure 3 (*Continued*)

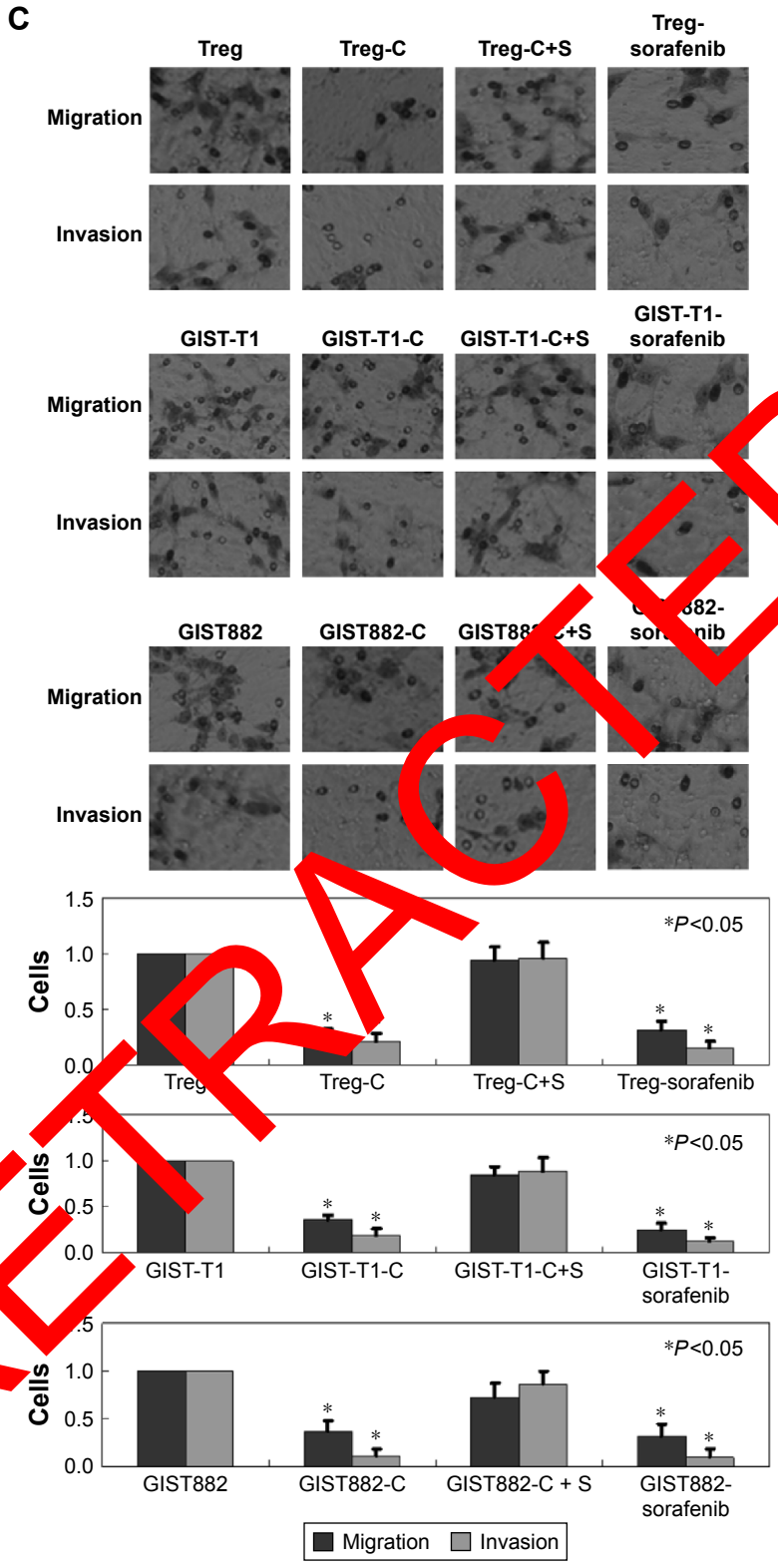

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Figure 3 Recombinant CXCL16 (IC_{50} value) displays inhibitory effects on Tregs and GIST cells in vitro.
Notes: (**A**) The proliferation ratio was determined by MTT assays. (**B**) Cells were stained with propidium iodide and fluorescence-activated cell sorting analysis was performed. (**C**) Transwell assays were performed to detect migration and invasion of cells. Cells that migrated to the bottom of the membrane were stained and counted. Treg: untreated Tregs; Treg-C: Tregs treated with recombinant CXCL16; Treg-C+S: Tregs treated with recombinant CXCL16 and CXCR6 siRNA; GIST-T1: untreated GIST-T1 cells; GIST-T1-C: GIST-T1 cells treated with recombinant CXCL16; GIST-T1-C+S: GIST-T1 cells treated with recombinant CXCL16 and CXCR6 siRNA; GIST882: untreated GIST882 cells; GIST882-C: GIST882 cells treated with recombinant CXCL16; GIST882-C+S: GIST882 cells treated with recombinant CXCL16 and CXCR6 siRNA.
Abbreviations: GIST, gastrointestinal stromal tumors; PI, propidium iodide; IC_{50}, half maximal inhibitory concentration; rhCXCL16, recombinant human CXCL16.

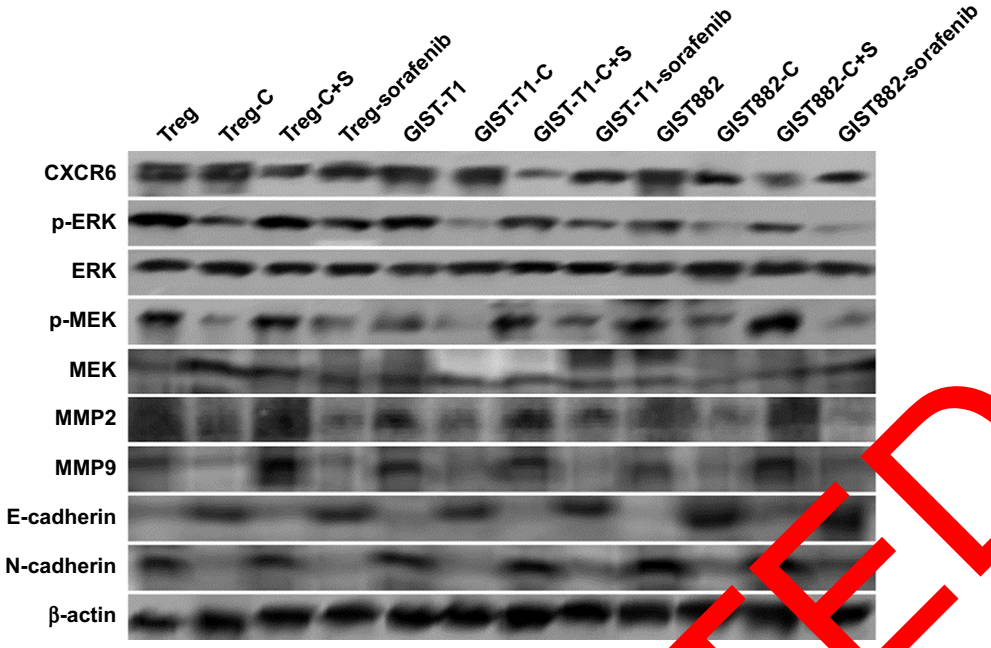

Figure 4 Western blot analysis of the ERK/MEK signaling pathway.
Notes: Recombinant CXCL16 could induce increased E-cadherin, and decreased p-ERK, p-MEK, MMP2/9, and N-cadherin. However, ERK and MEK showed no changes. β-actin was used as an internal loading control. Treg: untreated Tregs; Treg-C: Tregs treated with recombinant CXCL16; Treg-C+S: Tregs treated with recombinant CXCL16 and CXCR6 siRNA; GIST-T1: untreated GIST-T1 cells; GIST-T1-C: GIST-T1 cells treated with recombinant CXCL16; GIST-T1-C+S: GIST-T1 cells treated with recombinant CXCL16 and CXCR6 siRNA; GIST882: untreated GIST882 cells; GIST882-C: GIST882 cells treated with recombinant CXCL16; GIST882-C+S: GIST882 cells treated with recombinant CXCL16 and CXCR6 siRNA.
Abbreviation: GIST, gastrointestinal stromal tumors.

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of N-cadherin in Tregs, GIST-T1 cells, and GIST882 cells. EMT is a process by which the epithelial cells change to a mesenchymal phenotype and is a crucial step in the initiation of the metastatic spread of many tumor cells to distal organs.[29] Therefore, we can conclude CXCL16 inhibited cell mobility via suppressing EMT and MMP2/9.

In the present study, CXCL16 was found to downregulate levels of phospho-MEK and phospho-ERK. These results suggest that CXCL16 may inhibit the proliferation of Tregs and GIST cells via the MEK/ERK signaling pathway. Activation of the MEK/ERK signaling pathway has been associated with many human tumors. Han et al found that PDCD5 inhibited proliferation in osteosarcoma cells, MG-63, via the MEK/ERK signaling pathway. Niu et al[31] also found that Cyr61 inhibited the proliferation and colony formation of acute myelocytic leukemia cells through the MEK/ERK pathway.

Taken together, we showed for the first time that CXCL16, CXCR6, sCXCL16, and Tregs' expression in cancer tissue was significantly higher than in normal tissue and was correlated with the poor prognosis of patients with GIST. Recombinant CXCL16 was observed to mediate the inhibitory effects in Tregs and GIST cells though the MEK/ERK signaling pathway. Moreover, following the inhibition of this signaling pathway, mobility was inhibited by decreased MMP2/9 and N-cadherin, and increased E-cadherin. However, the major limitation of this study is that only the roles of high concentration sCXCL16 in Tregs and GIST cells were examined. Further investigation is urgently required to assess the mechanism(s) of low concentration sCXCL16-induced proliferation in Tregs.

Disclosure

The authors have no conflicts of interest to disclose.

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