Expression of connective tissue growth factor as a prognostic indicator and its possible involvement in the aggressive properties of epithelial ovarian carcinoma

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Abstract. Recently, connective tissue growth factor (CTGF) was demonstrated to be associated with aggressive characteristics, including proliferation, invasion and metastasis, in a number of malignancies. Here, we investigated the expression and function of CTGF in epithelial ovarian carcinoma (EOC) to clarify its molecular mechanism and clinical significance. Paraffin sections from clinical samples of EOC (N=104) were immunostained with the CTGF antibody, and then the staining positivity was semiquantitatively examined. Moreover, we explored the role of CTGF expression in the migration-promoting effect on and chemoresistance of EOC cells. The results revealed that of the 104 EOC patients, the low and high CTGF staining expression rates were 65 (62.5%) and 39 (37.5%), respectively. Patients belonging to the higher-level CTGF group showed poorer progression-free (PFS) and overall survival (OS) rates than those in the lower-level group [PFS (log-rank: P=0.0076) and OS (log-rank: P=0.0078), respectively]. Multivariable analysis showed that CTGF expression was a significant predictor of poorer PFS and OS [PFS: HR (high vs. low): 1.837, 95% CI: 1.023-3.289 (P=0.0418); OS: HR: 2.141, 95% CI: 1.077-4.296 (P=0.0300)]. In in vitro studies, in acquired paclitaxel (PTX)-resistant EOC cells, the silencing of CTGF expression led to the restoration of PTX sensitivity. Furthermore, we confirmed that the TGF-β-dependent migration-promoting effect on these CTGF-depleted cells was completely inhibited. In conclusion, the results of the present study suggest the possible involvement of CTGF in the migration-promoting effect and chemoresistance of EOC, suggesting that it may be a target for overcoming the malignant properties of EOC.

Introduction

Based on recent global cancer statistics, 295,414 patients were newly diagnosed with epithelial ovarian carcinoma (EOC) and 184,799 patients died of this tumor worldwide in 2018 (1). Thus, EOC is a leading cause of mortality in women among all gynecologic cancers (2). Since EOC commonly remains asymptomatic, in clinical practice it is known as a ‘silent killer’, and the majority of patients present with widespread peritoneal metastases at initial diagnosis. The oncologic outcome of EOC patients is likely to be associated with the extent of peritoneal dissemination (3-5). Although complete clinical remission is achieved in about 80% of patients who undergo aggressive surgery and systematic chemotherapy, most of these clinical responders show recurrence (6). Consequently, the oncologic outcome of recurrent patients remains extremely poor (7,8).

Connective tissue growth factor (CTGF/CCN2) belongs to a member of the CCN family (9). CTGF has been reported to be involved in various aggressive tumor properties, such as cell growth, migration, angiogenesis and metastasis (10-13). Furthermore, according to prior studies, CTGF expression is closely related to the acquisition of chemoresistance to antineoplastic agents, including paclitaxel in breast cancer (14), 5-FU in colorectal cancer (15) and cisplatin in osteosarcoma (16). Regarding EOC, Wang et al revealed that the expression level of CTGF is negatively correlated with the expression of miR-143 in tissue samples, and that miR-143 exerts tumor-suppressing functions, including, migration, invasion and cell proliferation by targeting CTGF in vitro (17). However, to the best of our knowledge, studies concerning the expression and biological behavior of CTGF in relapsed EOC are limited.
We hypothesized that CTGF plays a central role in both the chemoresistance and metastatic ability of EOC, and that CTGF positivity may be a valuable predictor of a poor clinical outcome in EOC patients. Here, we investigated the prognostic impact of CTGF expression, and analyzed the functions of CTGF in EOC cell progression.

Materials and methods

Cell culture. The EOC cell lines, ES-2, SKOV3, A2780, and OVCA3, were maintained in RPMI-1640 medium with 10% FBS and penicillin/streptomycin. These cell lines were obtained from the American Type Culture Collection (ATCC; Manassas, VA, USA) in 2012-2013. NOS2 and NOS3 cells, derived from serous EOC, were established in our institute (18,19). These cell lines were maintained in RPMI-1640 (Sigma-Aldrich; Merck KGaA) supplemented with 10% fetal bovine serum (FBS) and penicillin-streptomycin at 37°C in a humidified atmosphere of 5% CO₂. The NOS2TR and NOS3TR cells, established from parental NOS2 and NOS3 cells, acquired chronic resistance to paclitaxel (PTX) as previously described (20-22).

Inhibition of CTGF by small interfering RNA (siRNA). To generate CTGF-silenced cells, EOC cells were transfected with either a pool of small interfering RNA (siRNA) oligonucleotide-specific to human CTGF (final concentration, 30 pmol/l; assay ID s3709, cat. no. 4427038; Thermo Fisher Scientific, Inc.) or control siRNA (Sigma-Aldrich; Merck KGaA) using Invitrogen™ Lipofectamine™ RNAiMAX Transfection Regent (Thermo Fisher Scientific, Inc.). The sequences for CTGF siRNA were as follows: Sense, 5'-CCU AUC AAG UUU GAG CUU UTT-3' and antisense, 5'-AAA GCU CAA ACU UGA ACC GAG CT-3'. After overnight incubation at 37°C, the culture medium was replaced with fresh complete medium containing 10% FBS. Cells were harvested after 72 h and solubilized for western blot analysis of CTGF silencing.

PTX chemosensitivity assay. The PTX chemosensitivity assay was performed as described previously (23). Briefly, cells were seeded in triplicate in 96-well plates at a density of 5,000 cells in a volume of 200 µl of culture media containing 10% FBS. After incubation for 24 h at 37°C, the medium was replaced with fresh medium with or without various concentrations of PTX (Bristol Myers Squib, Tokyo, Japan). After an additional 72 h, cell viability was assayed using the Cell Titer 96 Aqueous One Solution Cell Proliferation Assay kit (Promega Corp., Tokyo, Japan).

In vitro migration assay. Cell migration was assayed in 24-well Transwell cell culture chambers (Costar, Corning Inc., Corning, NY, USA). Cells were suspended in the upper chamber at a final concentration of 1.0x10⁵/ml in 200 µl of RPMI-1640 medium. In addition, we examined the effect of siRNA transfection on the migration of parental and PTX-resistant EOC cells. Cells transfected with siRNAs were seeded in the upper chamber and allowed to migrate to the fibronectin-coated lower surface for 20 h. The number of cells that had migrated to the lower surface was counted to evaluate the migration ability. Cells were seeded in 6-cm dishes in RPMI-1640 containing 10% FBS. After reaching 50% confluency, the medium was replaced by fresh RPMI-1640 containing 10% FCS, and transfection with siRNA (si-Ctrl and si-CTGF) was performed using Lipofectamine RNAiMAX Transfection Regent. Forty-eight hours after transfection, the cells were trypsinized and pelleted. Subsequently, the cells were re-plated in the upper chambers of Transwell plates at a density of 1.0x10⁶/ml in 200 µl of RPMI-1640. The lower chamber contained 700 µl of RPMI-1640 supplemented with 10% FBS. The subsequent procedure was the same as described above. We performed four individual experiments, and each assay was performed in triplicate.

Western blot analysis. The western blot experimental procedure was described previously (24). The following primary antibodies were used: Anti-E-cadherin (cat. no. 3195, at a 1:1,000 dilution; Cell Signaling Technology), anti-fibronectin (cat. no. sc-18825, at a 1:1,000 dilution; Santa Cruz Biotechnology, Inc.), anti-vimentin (cat. no. 5741, at a 1:1,000 dilution; Cell Signaling Technology), and anti-CTGF (cat. no. sc-365970, at a 1:1,000 dilution; Santa Cruz Biotechnology, Inc.). The primary antibodies were washed in 0.05% Tween-20/PBS and then incubated with horseradish peroxidase-conjugated secondary antibody. Proteins were visualized using Amersham ECL Western Blotting Detection Reagent (GE Healthcare Life Sciences). Bands were visualized using ImageQuant LAS 4000 mini (GE Healthcare Life Sciences).

RNA extraction and quantitative real-time PCR. RNA extraction was performed as described previously (25,26). Total RNA was isolated using RNeasy Mini (Qiagen, Hilden, Germany). The concentration of RNA was measured according to absorbance at 260 nm, and 0.5 mg of total RNA was reverse-transcribed using M-MLV reverse transcriptase and a random primer using ReverTra Ace qPCR RT Master Mix (Toyobo, Osaka, Japan) at 42°C for 60 min. Then, 1 µl of the final cDNA solution was subjected to PCR using KOD DNA polymerase (Toyobo). Amplification conditions were as follows: Denaturation at 98°C for 2 min; 40 cycles at 98°C for 10 sec, 55°C for 10 sec, and 68°C for 30 sec using LightCycler Nano (Roche Diagnostics, Basel, Switzerland). GAPDH was used as an endogenous control, relative expression was estimated using the comparative Cq (2^ΔΔCq) method. The sequences of primers used for the experiments were as follows: CTGF forward, 5'-TTCCAGAGCAGCTGC AAAGTA and reverse, 5'-GCTGAGGCTTTCCAGTC.

Cytokine stimulation. EOC cell lines were stimulated with recombinant human TGF-β1 (10 ng/ml) (PeproTech, Inc., Rocky Hill, NJ, USA), hepatocyte growth factor (HGF) (40 ng/ml) (PeproTech, Inc.) and tumor necrosis factor α (TNF-α) (100 ng/ml) (R&D System, Minneapolis, MN, USA) in RPMI-1640 medium supplemented with 10% FBS for each incubation time.

Patients and immunohistochemical staining. A total of 104 human EOC tissues were obtained from patients who underwent surgical treatment at Nagoya University Hospital between January 1994 and December 2010 after providing informed consent. In regards to the histological types, we
adopted the World Health Organization (WHO) classification criteria (27). The clinical stage was assigned according to the International Federation of Gynecology and Obstetrics (FIGO) staging system (28,29). This study was approved by the Ethics Committee of Nagoya University (Approval No. 2011-1234-2).

Formalin-fixed, paraffin-embedded tissue sections were cut at a thickness of 4 µm. For heat-induced epitope retrieval, deparaffinized sections in 0.01 M citrate buffer were heated three times at 90°C for 5 min using a microwave oven. Sections were incubated at 4°C for 12 h with primary antibody (anti-goat-CTGF polyclonal, sc-14939, at a 1:100 dilution; Santa Cruz Biotechnology, Inc.). The sections were rinsed and incubated for 30 min with biotinylated anti-goat IgG antibody (Histofine SAB-PO (goat) kit, cat. no. 414012; Nichirei Corp., Tokyo, Japan). The immunoreactive staining was processed using the peroxidase-anti-peroxidase method according to the manufacturer’s instructions (Dako, Hamburg, Germany). To detect the reaction, 3,3’-diaminobenzidine tetrachloride (DAB) chromogen solution was used. After rinsing in water for 30 min, the sections were counterstained with hematoxylin and then dehydrated. Finally, they were mounted in mounting medium for examination.

**Evaluation of immunohistochemical staining.** For evaluation of the results of immunohistochemical staining, 10 fields for each specimen were selected and evaluated with both low- (x100) and high- (x400) power microscopy (Axio Imager A1, Carl Zeiss). Two investigators assessed the slides without knowledge of the clinicopathologic features and were blinded to each other's evaluation. The two investigators were in agreement on all the slides examined. Based on the immunostaining activity, a semiquantitative score was assigned according to the intensity and area of the stained cells, as described previously (30). For the evaluation of CTGF expression, the staining intensity was scored as 0 (negative-weak), 1 (medium), 2 (strong), or 3 (very strong). The percentage of the staining area was scored as 0 (0-10%), 1 (11-50%), and 2 (51-100%) relative to the total tumor area. The sum of the staining intensity and area scores was calculated as the final score (0-5) for CTGF. Tumors with final scores of 0-1 and 2-5 were classified as showing low and high expression, respectively.

**Survival analyses.** The distributions of the clinicopathologic factors were assessed using the Chi-square test. The progression-free survival (PFS) was defined as the time interval between the date of surgery and the date of the last follow-up or recurrence/progression. The overall survival (OS) was defined as the time interval between the date of surgery and the date of the last follow-up or death from any cause. The survival curves were compared employing the Log-rank test. Survival analysis was conducted using the Kaplan-Meier method. The prognostic significance of CTGF expression concerning other clinicopathologic variables was assessed using univariable and multivariable Cox's proportional hazard's analyses. All statistical analyses were performed with JMP Pro version 10.0 (SAS Institute, Japan). A P-value of <0.05 was considered indicative of statistical significance.

**Statistical analysis.** All data are expressed as the mean ± SD. Data were calculated from at least three independent experiments. The significance of differences was analyzed by Student’s t-test or one-way analysis of variance (ANOVA) followed by Tukey's post-hoc test. A P-value of <0.05 was considered indicative of statistical significance.

**Results**

**Patient characteristics.** We initially examined CTGF expression and its possible association with the prognostic outcome of EOC patients employing an immunohistochemical experiment. Patient characteristics are presented in Table I. The median age was 54, ranging from 24-78 years. The distributions of the FIGO stages were: 42.3% (44/104) stage I, 19.2% (20/104) stage II, 34.6% (36/104) stage III and 3.8% (4/104) stage IV. Among all patients, pathological types were as follows: 34 (32.7%) with serous, 42 (40.4%) with clear-cell, 18 (17.3%) with endometrioid, and 8 (7.7%) with mucinous carcinoma. One hundred and one (97.1%) patients underwent postoperative chemotherapy. Three patients did not receive postoperative chemotherapy due to their severe complications or strong wishes. Among the 104 patients, lower- and higher-level CTGF staining expressions were noted in 65 (62.5%) and 39 (37.5%) patients, respectively. Representative images of various immunohistochemical intensities are presented in Fig. 1. The distributions of the age, stage, histological type, chemotherapy, and period of initial treatment did not differ between the two groups Table I.

**Clinical outcome based on CTGF expression.** The median (range) follow-up duration was 93.6 (3.8-284.4) months in all patients. During the observation period, 48 (46.1%) patients experienced recurrence and 34 (32.7%) succumbed to the disease. The median times to recurrence and death were 17.2 and 26.0 months, respectively. The five-year PFS and OS rates of all patients were 57.4 and 75.1%, respectively. Patients in the higher-level CTGF group showed poorer PFS and OS rates than those in the lower-level group [PFS (log-rank: P=0.0076, and OS (log-rank: P=0.0078), respectively (Fig. 2A and B). Analysis of those with clear-cell carcinoma (CCC) revealed no significant difference in PFS or OS between the two groups (Fig. 3A and B). In contrast, analysis of those with a non-clear-cell (non-CCC) histology revealed that CTGF expression was significantly correlated with poorer long-term survival (PFS: P=0.0036, OS: P=0.0070) (Fig. 3C and D).

**Univariate and multivariate analyses.** We next conducted univariate and multivariate Cox proportional analyses regarding PFS/OS. FIGO stage (1 vs. II-IV), age (≤50 vs. >50 years), histological type (non-clear-cell vs. clear-cell), chemotherapy (taxane plus platinum vs. other chemotherapy or none), period of initial treatment (before 2005 vs. after 2006), and CTGF immunoreactivity (low vs. high) (Table SI). Based on univariate analysis, the FIGO stage, histological type, and CTGF expression were significant prognostic indicators of a poorer PFS. We evaluated the age, stage, histological type and CTGF expressions in multivariate analysis. This analysis demonstrated that the CTGF expression was a significantly independent predictor of a poorer OS and PFS (OS: Hazard ratio (HR): 2.141, 95% confidence interval (CI): 1.077-4.296 (P=0.0300); PFS: HR (high vs. low): 1.837,95% CI: 1.023-3.289 (P=0.0418)].
Involvement of CTGF expression in the tumor-promoting effect. Subsequently, we examined the role of CTGF in the malignant properties of EOC in vitro. Previously, we generated PTX-resistant cell lines using parental EOC cells (NOS2). We treated these cells for months with stepwisely increasing concentrations of PTX and finally generated highly PTX-resistant NOS2TR cells (Fig. 4A). The NOS2TR cells displayed a spindle-shaped morphology with looser cell-cell adhesion. Transforming growth factor (TGF) -β as well as hepatocyte growth factor (HGF) and tumor necrosis factor (TNF)-α play an important role in the dissemination of ovarian cancer, stimulating tumor invasion and metastasis of tumor cells (31-33). When in the presence of TGF-β, the morphology of NOS2TR cells showed a more mesenchymal cell shape with decreased E-cadherin and increased vimentin expressions, compared with the parental NOS2 cells (Fig. 4B and C). Furthermore, the addition of TGF-β to NOS2TR cells significantly increased the migratory potential compared with that noted in the parental NOS2 cells (Fig. 4D and E) (P<0.05).

We further explored the role of CTGF in the malignant properties of EOC using several in vitro experiments. We first investigated the expression of CTGF in various EOC cell

Table I. Association between the expression of CTGF and clinicopathologic parameters of the EOC cases.

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Total</th>
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<tr>
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<td>%</td>
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<tr>
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<td>3</td>
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<tr>
<td>Clear-cell</td>
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<td>41.5</td>
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<td>87.5</td>
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<td>Platinum-based</td>
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<td>71.4</td>
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<tr>
<td>After 2006</td>
<td>71</td>
<td>43</td>
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EOC, epithelial ovarian carcinoma; CTGF, connective tissue growth factor; FIGO, International Federation of Gynecology and Obstetrics.
lines. CTGF was expressed in ES-2 cells; however, a lower level of expression of CTGF was observed in the SKOV3, A2780, OVCAR, NOS2, and NOS2TR cells. The addition of TGF-β induced the upregulation of CTGF expression in both the NOS2 and NOS2TR cell lines (Fig. 5A). However, the expression of CTGF following the addition of TGF-β was more markedly increased in the NOS2TR than in the NOS2 cells. These results suggest that TGF-β generated in the microenvironment through cell-to-cell communication may contribute to the enhancement of CTGF, leading to the acquisition of the chronic chemoresistance/metastatic potential of EOC. Thus, we next examined whether the acquired PTX-resistance of NOS2TR depended on the upregulation of TGF-β. Using specific si-RNA of CTGF, we confirmed that the enhanced expression of CTGF in both cell lines was completely blocked at the protein and transcriptional levels (Fig. 5B and C). As shown in Fig. 5D, the enhanced migratory potential induced by the addition of TGF-β was completely inhibited in the CTGF-depleted NOS2TR cells. In contrast, in control siRNA-transfected NOS2TR cells, we did not observe such an inhibitory effect (Fig. 5E). We subsequently investigated whether CTGF is associated with

Figure 2. Kaplan-Meier progression-free survival (PFS) and overall survival (OS) curves of EOC patients according to the immunoreactivity of CTGF. (A) PFS. Green line indicates low CTGF expression (N=65). Blue line represents high CTGF immunoexpression (N=39). Patients with positive CTGF expression showed a significantly poorer PFS (P=0.0076). (B) OS. Green line indicates low CTGF expression (N=65). Blue line represents high CTGF immunoexpression (N=39). Patients positive for CTGF expression showed a significantly poorer OS (P=0.0078). EOC, epithelial ovarian carcinoma; CTGF, connective tissue growth factor.

Figure 3. Kaplan-Meier progression-free survival (PFS) and overall survival (OS) curves of EOC patients with clear-cell carcinoma (CCC) or non-clear-cell carcinoma (Non-CCC) according to the immunoreactivity of CTGF. (A and B) CCC. Green line indicates low CTGF expression (N=27). Blue line represents high CTGF immunoexpression (N=15). (C and D) Non-CCC. Green line indicates low CTGF expression (N=38). Blue line represents high CTGF immunoexpression (N=24) [C (PFS): P=0.0036 and D (OS): P=0.0070]. EOC, epithelial ovarian carcinoma; CTGF, connective tissue growth factor.
the chemoresistance-promoting effect in vitro. The NOS3TR cells, another type of chronic PTX-resistant EOC cell line, transfected with siRNAs (si-CTGF) were assessed by the PTX-sensitivity assay as described above. In NOS3TR cells, the silencing of CTGF expression led to restoration of the PTX sensitivity (Fig. 6A and B). Furthermore, we confirmed
that the TGF-β-dependent migration-promoting effect was completely inhibited in CTGF-depleted NOS3TR cells, as observed in NOS3 cells (Fig. 6C and D) (P=0.05).

Discussion

In the present study, we initially revealed that connective tissue growth factor (CTGF) expression was significantly correlated with a poorer prognostic outcome in epithelial ovarian carcinoma (EOC) patients. Indeed, those with higher-level CTGF expression demonstrated poorer OS and PFS rates than those with lower-level expression. Moreover, multivariate analyses showed that higher-level CTGF expression was an independent prognostic indicator of poorer survival in those cases. Various studies have revealed positive associations among CTGF expression, aggressive features, and a poor oncologic outcome in patients with a number of solid and hematological malignancies, including pre-B acute lymphoblastic leukemia, gallbladder cancer, pancreatic carcinoma and esophageal squamous cell carcinoma (34-37). Wang et al demonstrated that CTGF expression was negatively associated with the response to chemotherapy in breast cancer patients who received neoadjuvant chemotherapy, and its cellular overexpression resulted in resistance to doxorubicin- and paclitaxel-induced apoptosis by the upregulation of Bcl-XL and cellular inhibitor of apoptosis protein 1 (cIAP1) (38). Mao et al reported that the expression of CTGF was significantly upregulated in clinical tissues of gastric carcinoma patients, and the overexpression of CTGF in gastric carcinoma cells promoted their migratory capability in vitro and significantly increased tumor metastasis in nude mice (39). Furthermore, the downregulation of pancreatic tumor cells was found to lead to markedly reduced growth on soft agar and in a murine subcutaneous implantation model, and CTGF expression and secretion were found to be increased in hypoxic pancreatic tumors (35). The current findings are consistent with these results. However, in the present study, although patients with a non-clear-cell histology and similar prognostic tendencies were observed, analysis of those with clear-cell carcinoma (CCC) revealed no significant difference between the low and high CTGF expression groups. Indeed, EOC consists of heterogeneous histological types with a different tumor biology. CCC patients in general display a lower response rate to platinum-based compounds, leading to intrinsic chemoresistance (40,41). Thus, it is likely that chemoresistance of this tumor is based on a CTGF-independent mechanism. Indeed, earlier studies did not refer to the effect of CTGF expression on a variety of histological types of EOC tumors. In a future study, this observation should be verified.

A possible explanation of the poor survival in patients with higher-level CTGF expression may be the enhanced metastatic potential and chronic chemoresistance of this tumor. Our previous study revealed that chronic PTX resistance induced more marked mesenchymal hallmarks, including the switch of an epithelial to a fibroblast-like morphology, upregulation of epithelial-mesenchymal-transition-related biomarkers, and the enhancement of motile capabilities (20). In the present study, the silencing of CTGF significantly restored PTX susceptibility and reduced invasiveness/motility in cells.
chronically resistant to PTX. This suggests that the development/maintenance of both the PTX-resistance and metastatic ability of these cells were attributable to CTGF expression. A previous study showed that the expression of CTGF was upregulated in human osteosarcoma cells after treatment with cisplatin, and CTGF overexpression induced enhanced resistance to cisplatin-mediated cell apoptosis through upregulation of Bcl-xl and surviving (16). Yang et al demonstrated that the overexpression of CTGF enhanced resistance to 5-FU-induced cell apoptosis. They also reported that downregulation of the expression of CTGF promoted the curative effect of chemotherapy and blocked the cell cycle in the G1 phase (15). Moreover, the expression of CTGF was found to be associated with increased resistance to PTX-mediated cell apoptosis through the upregulation of survivin and the AMP-activated protein kinase (AMPK)-dependent nuclear factor κB pathway (42). In the treatment of EOC patients, acquired or intrinsic chemoresistance is a major clinical cause of a poor prognosis. The present study demonstrated that CTGF plays a central role in the chemoresistance of EOC cells.

As well as tumor cells, stromal-cell derived CTGF expression can exert tumor-promoting effects, such as proliferation and invasion in glioma as well as pancreatic and prostate cancer (43-45). Yang et al demonstrated that stromal expression of CTGF induced significant increases in microvessel density and xenograft tumor growth, suggesting that this molecule is one of the key regulators of angiogenesis in the tumor-reactive stromal microenvironment as a downstream mediator of TGF-β1 (45). Similarly, according to a recent study by Kim et al, immunohistochemical analyses of high-grade serous ovarian tumors revealed that the highest level of tumor stromal CTGF expression was correlated with the poorest prognosis (46). Based on the molecular signature in a subset of high-grade serous ovarian cancer (HGSOC) samples that was primarily driven by a high stromal response, CTGF was overexpressed in the stroma of these tumors in association with a poor oncologic outcome (47). In our current analyses, we assessed the CTGF immunoreactivity in normal tissues. Indeed, CTGF may function in the stromal cells as a metastasis-promoting factor through tumor-stromal interaction. Considering the CTGF expression as a molecular target of epithelial ovarian cancer (EOC) with aggressive behavior, this substance plays an important role in not only stromal-cancer communication but also the multidisciplinary functions of tumor cells, including the development of chemoresistance and metastatic potential.

The TGF-β signaling pathways are crucial regulators of the multiple steps of the tumor microenvironment associated with EMT (48-50). TGF-β was found to lead to a long-lasting upregulation of CTGF mRNA and protein expression in mouse and human proximal tubular epithelial cell lines (51). Tsai et al reported that CTGF is an essential downstream mediator of TGF-β1-induced extracellular matrix production and myofibroblast transdifferentiation in Graves’ orbital fibroblasts (52). Our previous study demonstrated that TGF-β is generated by EOC cells, which was synergistically upregulated under co-culture conditions with human mesothelial cells (23). In the present study, it was demonstrated that TGF-β stimulation led to an increase in CTGF expression. Furthermore, it was revealed that TGF-β-induced migratory potential and restoration of PTX sensitivity were completely inhibited in CTGF-silenced PTX-chemoresistant cells. Thus, there may be a close link between the enhanced metastatic potential and PTX resistance of EOC via the TGF-β/CTGF axis. However, in the present study, we did not conduct relevant experiments regarding CTGF overexpression. We consider that this was one of the critical limitations of the present investigation. We hope to verify the significance of CTGF overexpression in a future investigation. Overall, we consider CTGF to be a valuable biomarker and effective therapeutic target for EOC. Therefore, CTGF may be a therapeutic candidate for modulating the PTX sensitivity of EOC.

In summary, we identified CTGF as a prognostic indicator of and therapeutic target for EOC, particularly in non-clear-cell carcinoma. An unfavorable outcome in patients with higher-level CTGF expression may be due to the increased metastatic capability and chemoresistance of EOC. However, the detailed functions of CTGF remain unclear. We hope that the further mechanistic elucidation of CTGF will contribute to improving treatment for EOC patients by adding criteria for the administration of systematic therapy in the future.

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Availability of data and materials

The datasets used during the present study are available from the corresponding author upon reasonable request.

Authors' contributions

AS and HK carried out the data analysis and interpretation and writing of the manuscript. ST, SS, YI, KN, JS, KN and NY carried out the data collection. FK supervised the research and was responsible for the funding. All authors read and approved the manuscript and agree to be accountable for all aspects of the research in ensuring that the accuracy or integrity of any part of the work are appropriately investigated and resolved.

Ethics approval and consent to participate

The present study was approved by the Ethics Committee of Nagoya University (Approval No. 2011-1234-2).

Patient consent for publication

Not applicable.
Competing interests

All authors declare that there are no competing interests, and no financial or personal relationships with other people or organizations that could inappropriately influence this work.

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