

Connective tissue growth factor (CTGF) and cancer progression

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Abstract Connective tissue growth factor (CTGF) is a member of the CCN family of secreted, matrix-associated proteins encoded by immediate early genes that play various roles in angiogenesis and tumor growth. CCN family proteins share uniform modular structure which mediates various cellular functions such as regulation of cell division, chemotaxis, apoptosis, adhesion, motility, angiogenesis, neoplastic transformation, and ion transport. Recently, CTGF expression has been shown to be associated with tumor development and progression. There is growing body of evidence that CTGF may regulate cancer cell migration, invasion, angiogenesis, and anoikis. In this review, we will highlight the influence of CTGF expression on the biological behavior and progression of various cancer cells, as well as its regulation on various types of protein signals and their mechanisms.

Keywords Angiogenesis · Anoikis · Cancer · Connective tissue growth factor · CTGF · Invasion · Migration

Introduction

Connective tissue growth factor (CTGF) was initially discovered in 1991 as a secreted protein in the conditioned media of cultured human umbilical vascular endothelial cells [1]. CTGF is a member of the CCN family of secreted, matrix-associated proteins encoded by immediate early genes that play various roles in angiogenesis and tumor growth [2–9]. The name CCN stands for Cyr61 (cysteine-rich 61), Ctgf (connective tissue growth factor), and Nov (nephroblastoma overexpressed) [6]. The CCN family now comprises six members including Cyr61 (CCN1), CTGF (CCN2), Nov (CCN3), Wisp-1/elm1 (CCN4), Wisp-2/rCop1 (CCN5), and Wisp-3 (CCN6). These proteins share uniform modular structure which mediates various cellular functions such as regulation of cell division, chemotaxis, apoptosis, adhesion, motility, angiogenesis, neoplastic transformation, and ion transport [2–9]. Recently, CTGF expression has been shown to be associated with tumor development and progression [10–17]. For example, the level of CTGF expression is positively correlated with bone metastasis in breast cancer [10], glioblastoma growth [11], poor prognosis in esophageal adenocarcinoma [12], aggressive behavior of pancreatic cancer cells [13], and invasive melanoma [14]. In contrast, CTGF expression was negatively correlated with proliferation activity and tumor grade of chondrosarcomas [15], and overexpression of CTGF has been shown to suppress the tumor growth of oral squamous cell carcinoma (SCC) cells transplanted into mice [16]. Accordingly, there is growing body of evidence that CTGF may regulate cancer cell migration, invasion, angiogenesis, and anoikis. In this review, we will highlight the influence of CTGF expression on the biological behavior and progression of various cancer cells, as well as its regulation on various types of protein signals and their mechanisms.

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The biological functions of CTGF

The basic structure of CTGF, as in other CCN family proteins, consists of up to four modules that resemble the functional domains previously identified in major regulatory proteins (Fig. 1). These four modules share identity with insulin-like growth factor binding proteins (IGFBP), the von Willebrand factor (VW), thrombospondin-1 (TSP1), and a cysteine knot motif [3]. There are also a few biologically active isoforms, generated by either post-translational processing or alternate splicing. A carboxy-truncated CTGF protein, lacking the CT module, was also isolated in high concentration from the primary human osteoblasts [5]. The absence of CT module does not necessarily abrogate its ability to promote adhesion of osteoblasts. Nevertheless, this module is responsible for determining the ability of CTGF to induce dose-dependent adhesion to various other cell types [18, 19]. The existence of two biologically active truncated isoforms of CTGF in normal uterine secretory fluids provided the functional clue for the importance of post-translational processing of CTGF [2].

CTGF, a 36–38 kD cysteine-rich peptide containing 349 amino acids, is predominantly identified in endothelial cells, fibroblasts, cartilaginous cells, smooth muscle cells, and some cancer cell lines [20]. After synthesis, CTGF is secreted through the Golgi apparatus [21], which requires its N-terminal 37 amino acid signal sequence. Given that CTGF is secreted, most of the studies regarding CTGF function have focused on the effect of exogenously added recombinant CTGF in cell cultures [22]. Although CTGF is glycosylated, the glycosylational modification is neither a

prerequisite for secretion [21] nor it has yet been attributed to any of the reported functions of CTGF.

One of the main functions of CTGF is to promote cell adhesion through a unique integrin and heparin sulfate proteoglycan dependent mechanism [23]. The carboxyl-terminal 10 kDa of CTGF, which binds heparin, has been shown to be sufficient to promote cell adhesion [18]. This fragment also promotes fibroblast proliferation [24]. The integrins through which CTGF promotes adhesion vary depending on the cell type; for example, CTGF promotes adhesion to human foreskin fibroblasts through integrin $\alpha 6 \beta 1$, to human platelets through integrin $\alpha II \beta 3$, to endothelial cells through integrin $\alpha v \beta 3$, and to blood monocytes through integrin $\alpha M \beta 2$ [22].

High levels of CTGF expression has been detected in many fibrotic lesions, indicating its role in promoting fibrosis. CTGF exhibits mitogenic and chemotactic effects on fibroblasts [1] and is also reported to enhance the mRNA expression of $\alpha 1(I)$ collagen, fibronectin, and $\alpha 5$ integrin in fibroblasts [25]. The finding that TGF- β increases CTGF synthesis and that TGF- β and CTGF share many functions in common, is consistent with the hypothesis that CTGF is a downstream mediator of TGF- β [20]. In endothelial cells, CTGF mediates several functions such as proliferation, migration, differentiation, and survival, leading to enhanced angiogenesis [26, 27]. It also induces chondrocyte proliferation and differentiation [28, 29].

Expression of CTGF in different cancers

CTGF is believed to be a multifunctional signaling modulator involved in a wide variety of biologic or pathologic processes, such as angiogenesis, osteogenesis, renal disease, skin disorders, and tumor development [2–6, 17]. There are at least 21 different human tumors or cancers that have been found to have CTGF expression (Table 1), signifying its influence on the biology and progression of cancer [10–16, 30–62]. Of particular interest is the fact that CTGF is found to be expressed in human tumor cells or surrounding stromal cells, including acute lymphoblastic leukemia (ALL) [30, 31], breast cancer cells [32, 34–39], cervical cancer [41], chondrosarcoma [15], cutaneous fibrohistiocytic and vascular tumors [42], esophageal cancer [12], gastric cancer [43], glioblastoma and gliomas [11, 44], hepatocellular carcinomas [45], laryngeal squamous cell carcinoma (SCC) [46], non-small-cell lung cancer [47–49], melanoma [14, 62], myofibroblastic tumors [51], oral SCC [16], ovarian cancer [52], pancreatic cancer [13, 53–56], prostate cancer [57], rhabdomyosarcoma [58], and Wilms tumor [59–61]. In glioblastoma, CTGF is strongly stained in tumor cells and proliferating endothelial cells, strongly emphasizing a role for CTGF in angiogenesis [11]. Furthermore, the level of CTGF

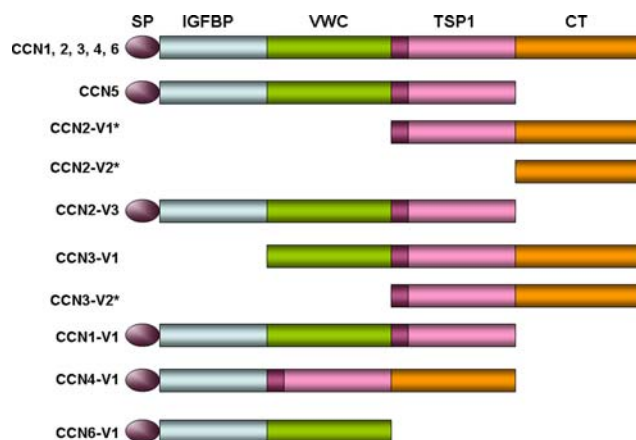


Fig. 1 Structure of full-length and truncated CTGF, in comparison with other members of CCN family proteins. IGFBP: insulin-like growth factor-binding protein; VWC: von Willebrand type C motif; TSP1: thrombospondin type 1 motif; CT: carboxyl-terminal cysteine knots module. *: These isoforms are believed to originate from post-translational processing. They are present in biological fluids and cell-culture medium

Table 1 Summary of the expression of CTGF in cancer cells

Cancers	Cells expressing CTGF	Effects of CTGF expression	References
1. Acute lymphoblastic leukemia (ALL)	1. Leukemic cells	1. Worsening of overall survival	[30, 31]
	2. B cell lineage of ALL		
2. Breast cancer	1. Breast cancer cell	1. Promote osteolytic bone metastasis	[10, 32–40]
	2. Fibrous stroma cells	2. Promote angiogenesis	
		3. Induce apoptosis (MCF-7 cells)	
		4. Enhance breast cancer cell motility	
3. Cervical cancer	NM	Cancer progression	[41]
4. Chondrosarcoma	Chondrosarcoma cells	Negative correlation with proliferation, tumor grade and prognosis	[15]
5. Cutaneous fibrohistiocytic tumors (dermatofibroma, dermatofibrosarcoma protuberans, malignant fibrous histiocytoma)	Tumor cells	Loss of CTGF expression when benign fibrohistiocytic tumors achieve malignant potency	[42]
6. Cutaneous vascular tumors (angioliipoma, angioleiomyoma)	Tumor cells	Loss of CTGF expression when benign vascular tumors achieve malignant potency	[42]
7. Esophageal cancer	1. Adenocarcinoma cells	1. Tumor progression and poor survival in adenocarcinoma cells	[12]
	2. Surrounding stroma cells	2. Longer survival in SCC	
8. Fibrosarcoma	Fibrosarcoma cell	Enhanced angiogenesis	[36]
9. Gastric cancer	Cancer cells	1. Increased lymph node metastasis	[43]
		2. Poor survival	
10. Glioblastoma and glioma	1. Glioblastoma and glioma tumor cells	1. Stimulate angiogenesis	[11, 44]
	2. Proliferating endothelial cells in glioblastoma	2. Positive correlation between CTGF mRNA levels and tumor grade, gender and pathology	
11. Hepatocellular carcinoma (HCC)	NM	1. CTGF expression was higher in HCC tissue compared to those of control	[45]
		2. Positively correlated with venous invasion and tumor grade	
12. Laryngeal squamous cell carcinoma (SCC)	Tumor cells	1. Negatively correlated with metastasis and clinical staging	[46]
13. Lung adenocarcinoma	Tumor cells	1. Inhibit invasion and metastasis	[47–50]
		2. Suppression of cell proliferation and signaling transduction	
		3. Negatively correlated with patient survival and metastasis	
		4. Inhibit angiogenesis	
14. Melanoma	Tumor stroma	Correlated with invasive histological type	[14]
15. Myofibroblastic tumors ^a	1. Tumor cells	Involved in the pathogenesis of myofibroblastic tumors	[51]
	2. Endothelial cells		
16. Oral SCC	Tumor cells	1. Attenuated cell growth	[16]
		2. Less potent tumorigenicity	
17. Ovarian cancer	Tumor cells	Inhibit growth of ovarian cancer cells	[52]
18. Pancreatic cancer	1. Pancreatic stellate cells	1. Increased proliferation and invasiveness of PANC-1 cells	[13, 53–56]
	2. Cultured pancreatic cancer cells	2. Enhanced pancreatic tumor growth	
	3. Cancer-associated fibroblasts		
19. Prostate cancer	Stromal cells	CTGF-expressing stroma induced significant increases in microvessel density and xenograft growth	[57]

Table 1 continued

Cancers	Cells expressing CTGF	Effects of CTGF expression	References
20. Rhabdomyosarcoma	Tumor cells	CTGF emerges as a survival and differentiation factor	[58]
21. Wilms tumor	Tumor cells	1. The expression of CTGF was suppressed by WT1 2. May be related to tumor progression	[59–61]

^a Including angiofibroma, malignant fibrous histiocytoma, infantile myofibromatosis, and malignant hemangiopericytoma; NM: not mentioned

expression is positively correlated with bone metastasis in breast cancer [10, 39], progression of cervical cancer [41], poor prognosis in esophageal adenocarcinoma [12], aggressive behavior of pancreatic cancer cells [13], invasiveness of melanoma [14], lymph node metastasis and poor survival of gastric cancer [43], progression of gliomas [44], recurrence and metastasis of hepatocellular carcinoma [45], increased proliferation, anchorage-independent growth and invasiveness of pancreatic cancer cells [54, 55] (Fig. 2). Based on these studies, CTGF seems to be a positive regulator of tumor development and progression.

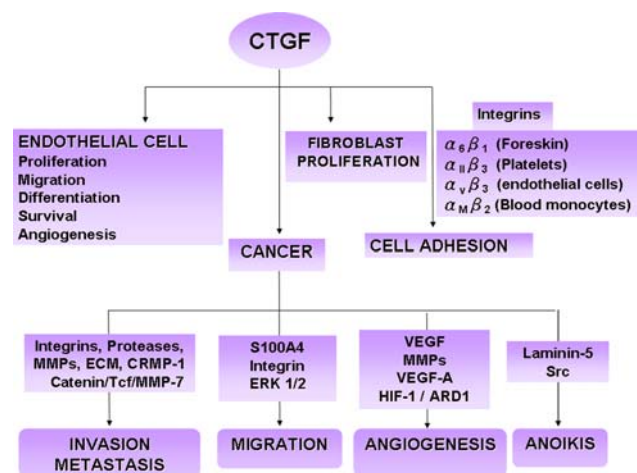
In contrast to the above reports on CTGF as tumor inducer, ectopic overexpression of CTGF in oral squamous cell carcinoma cells induces attenuated cell growth and decreases tumorigenicity in an animal model [16]. CTGF has also been found to induce apoptosis in the human breast cancer cell line MCF-7 [33] while the expression of CTGF was negatively correlated with proliferation activity and tumor grade of chondrosarcomas [15], and also negatively correlated with lymph node metastasis and clinical staging of laryngeal SCC [46]. CTGF has been found to suppress cell proliferation and behave as a tumor suppressor in non-small-cell lung cancer [47–49]. In ovarian cancers, epigenetic silencing by hypermethylation of the CTGF promoter leads to a loss of CTGF function, which may be a causative factor in the carcinogenesis of ovarian cancer [52]. In addition, exogenous

restoration of CTGF expression or treatment with recombinant CTGF inhibited the growth of ovarian cancer cells lacking its expression, whereas knockdown of endogenous CTGF accelerated growth of ovarian cancer cells expressing *CTGF* gene [52]. Collectively, these results suggest that the role of CTGF in different types of cancer may vary considerably, depending on the tissue involved. The question as how the action of CTGF protein is determined in a cell or tissue context, is interesting and deserves further investigation [63].

Roles of CTGF on cancer cell invasion and metastasis

Cancer cell invasion is the most intricate step in the cascade of events leading to metastasis, which occurs through biological activities and interaction of cancer cells with the surrounding environment. The invasion process is categorized into three steps: binding of extracellular matrix (ECM) with tumor cell; protease production; tumor cell motility via matrix degradation, and after completing these steps tumor cells enter into the blood stream and lymph system to initiate distant metastasis [64–68]. Several factors including integrins, protease, metalloproteinases (MMPs) and ECM components have been correlated with cancer cell invasion and metastasis [69]. The MMPs degrade basement membrane and stroma, facilitating the invasion of the cancer cells into the adjacent tissues [70].

Metastasis is the dissemination of cancer cells from primary tumor to distant site, which is a major prognostic factor governing cancer patient mortality. The metastatic process involves detachment of tumor cells from primary tumor mass, micro-invasion of tumor cells into stromal tissue, intravasation of tumor cells into blood vessels and extravasation of tumor cell growth in secondary site [71, 72]. Metastatic competence requires a complex set of cellular functions that are associated with a cadre of molecular and cellular changes [73, 74]. To enable metastasis, tumor cells must coordinate the expression of metastasis promoter genes and/or decrease the expression of metastasis suppressor genes. Metastasis suppressor genes are operationally defined as genes that encode proteins which could suppress the formation of overt metastases but exert no measurable effect on in vitro or

**Fig. 2** The roles of CTGF in various aspects of cancer progression

in vivo proliferation [73, 74]. As a dynamic process, metastasis requires cells to sequentially invade local tissues and disseminate from the primary tumor, lodge in and extravasate from the microvasculature at a secondary site, and finally form microscopic colonies giving rise to clinical metastases [75]. Proteins encoded by metastasis suppressor genes can block any of the steps in this process, the net result being suppression of overt metastases [76].

Recently, we found that CTGF appears to be a suppressor of lung tumor invasion and metastasis [47]. Our studies directly demonstrated that overexpression of CTGF not only suppressed the ability of lung adenocarcinoma cells to invade Matrigel in vitro, but also strongly inhibited tumor metastasis in an animal model. Decreased CTGF expression in tumor tissues was associated with advanced tumor stage, lymph node metastasis, early postoperative relapse, and reduced patient survival rates. We have also demonstrated that the level of CTGF protein was significantly higher in normal lung type I and II epithelial cells than in the majority of metastatic adenocarcinoma specimens, suggesting that the level of CTGF protein decreases during metastasis. Furthermore, we showed that a metastasis suppressor gene, collapsin response mediator protein 1 (CRMP-1), was functionally involved in the CTGF-mediated invasion and metastasis inhibition of human lung adenocarcinoma. CTGF-mediated increase in CRMP-1 expression was abolished by treatment with antibodies that specifically block the function of integrins $\alpha v \beta 3$ and $\alpha v \beta 5$. In addition, antisense CRMP-1 oligonucleotides essentially abolished the CTGF-mediated inhibition of cell invasion. These data indicate that CRMP-1 acts downstream of CTGF and is regulated by an integrin-related signaling pathway.

Integrins are important receptors for CCN proteins, and receptor activation may produce a variety of effects. CTGF protein can bind directly to integrins $\alpha v \beta 3$ and $\alpha I I b \beta 3$ [27]. Interaction of CTGF with integrin $\alpha v \beta 3$ promotes endothelial cell adhesion, migration, and survival and also induces angiogenesis in vivo [27]. CTGF also stimulates human skin fibroblast migration and proliferation through integrin $\alpha 6 \beta 1$. In contrast, we show that both $\alpha v \beta 3$ and $\alpha v \beta 5$ integrins were required for the inhibition of CTGF-mediated invasion [47].

In addition, we also found that colorectal cancer patients with decreased CTGF expression pronounced strong lymph node metastasis, with low recurrence time, and a short survival period [63]. Particularly, CTGF seemed to be an independent prognostic factor that will allow the successful differentiation of a high-risk population from the group of patients with stage II and stage III disease. At a mechanistic level, overexpression of CTGF in human colorectal cancer cells results in a decrease in the invasive ability. Consistent with these reports, reduced CTGF expression significantly enhanced hepatic metastasis of colorectal

cancer cells in a mouse model. Interestingly, CTGF transfection strongly reduced β -catenin/Tcf signaling and the level of its downstream gene target MMP-7 in human colorectal cancer cells [63]. The accumulating evidence indicates that the signaling/oncogenic activity of β -catenin/Tcf can be trans-repressed by the activation of nuclear receptors such as the retinoic acid receptor, the vitamin D receptor, and the androgen receptor. Our preliminary data from microarray analysis show that retinoic acid receptor mRNA was up-regulated in CTGF transfectants. It is therefore possible that CTGF expression up-regulates nuclear receptor genes and inhibits β -catenin/Tcf activity by interacting with them [63]. We suggest that CTGF inhibits colorectal cancer invasion and metastasis perhaps through inhibition of the β -catenin/Tcf/MMP-7 pathway. Furthermore, the ability of CTGF to inhibit metastasis and invasion suggests that this growth factor may be a potential candidate of therapeutic importance for patients with colorectal cancer [63].

Roles of CTGF on cancer cell migration

Migratory ability of a cancer cell is a major prerequisite for the successful execution of metastatic process, including movement within the connective tissue of primary site, entry of cancer cells into circulation by intravasation, and invasion of the target organ by extravasation; therefore the migration ability is positively correlated with tumor metastasis [40]. In order to invade, a tumor cell must undergo major changes in shape. Cellular motility depends on localized actin polymerization at the leading edge of the cells [77], and the polymerization and depolymerization of actin filaments must be under dynamic control. Simultaneously, paxillin and vinculin interact at focal contacts of the actin stress fibers, providing a link to the extracellular matrix (e.g. fibronectin and vitronectin). These cytoskeletal changes enable the invading cell to pass through the stromal cells, extracellular matrix and endothelial cell layer. Integrins, paxillin, selectins, transmembrane receptor tyrosine kinases, phospholipids, focal adhesion kinases (FAKs), GTPases and the S100 calcium binding protein A4 (S100A4) calcium binding protein have been described as being involved in regulating the organization of the actin cytoskeleton [78–80].

Previous large scale microarray analysis revealed that CTGF is crucial for the formation of osteolytic bone metastasis in breast cancer [10, 81]. Recently, we further demonstrated that the molecular mechanism by which CTGF confers cellular metastatic ability of breast cancer is mediated by S100A4 upregulation by integrin $\alpha v \beta 3$ and/or ERK1/2 [40]. This is based on the following evidence. First, overexpression of CTGF appreciably increases the

migratory ability of MCF-7 cells. Conversely, knockdown of CTGF abolishes the migratory ability of MDA231 cells. Second, CTGF expression leads to morphological alterations and formation of F-actin and focal adhesions. Third, ERK1/2 activation is essential for the CTGF-mediated migratory effects. Fourth, blockade of the CTGF–integrin- $\alpha v \beta 3$ axis attenuates CTGF-induced ERK1/2 activation and subsequent cellular migration. Fifth, the prometastatic *S100A4* gene is regulated by the signaling cascades of CTGF–integrin- $\alpha v \beta 3$ –ERK1/2 and contributes to the metastatic ability. Finally, CTGF expression levels are correlated with *S100A4* expression levels in primary human breast tumors [40].

Roles of CTGF on cancer cell angiogenesis

Angiogenesis, the formation of new blood vessels, is a highly coordinated process involving several molecules and is vital for tumor growth and metastasis [82–85]. Proteins mediating angiogenesis are widely known as angiogenic factors, including vascular endothelial growth factor (VEGF), basic fibroblast growth factor (bFGF), and other growth factors. Among them, VEGF is the major regulator of tumor-associated angiogenesis [86]. It has previously been reported that VEGF-A protein expression is strongly associated with many types of cancer progression and with clinical manifestation [87, 88]. Inhibition of VEGF reduces angiogenesis and tumor growth in vivo [88]. Conversely, VEGF overexpression is associated with increased microvessel density, tumor metastasis, and poor prognosis [89–95].

Hypoxia-inducible factor (HIF)-1 α is a transcription factor that regulates the supply of blood to tissues through its effects on VEGF expression [96]. HIF-1 α activity is induced by hypoxia in almost all cell types; however, under normoxic conditions, the protein is quite sensitive to ubiquitin-dependent degradation. HIF-1 α protein degradation is reduced under hypoxic conditions by posttranslational modification and binding to the von Hippel-Lindau (pVHL) tumor suppressor protein [97]. HIF-1 α binds to pVHL only after it is hydroxylated by HIF-prolyl hydroxylase (PHD1) and acetylated by arrest-defective 1 protein (ARD1) acetyltransferase [98–101]. HIF-1 α protein levels also increase in response to growth factor stimulation by mechanisms that differ from those that occur under hypoxic conditions. These oxygen-independent mechanisms are not clearly understood, but they are thought to involve growth factors, cytokines, and other signaling molecules that stimulate synthesis of HIF-1 α or decrease its degradation [102–107].

One possible mechanism involves the activity of connective tissue growth factor (CTGF), an extracellular matrix-associated signaling molecule that binds directly

with moieties in the pericellular environment. CTGF has recently been identified as a regulator of angiogenesis and has many functions in normal and pathologic processes [1, 6, 11, 17, 26, 27, 35–37, 57, 108–110]. Although CTGF was originally purified from medium conditioned by human umbilical vein endothelial cells [111], it can be produced by and acts on many cell types, including fibroblasts, smooth muscle, endothelial, neural, and cancer cells [28, 29, 47, 112–115]. CTGF can influence several functions of endothelial cells, including in vitro proliferation and tube formation [26], cell adhesion and migration [27], and induction of angiogenesis in vivo [26, 27, 108]. However, it has also been reported that CTGF inhibits angiogenesis in vitro through an interaction with VEGF [111]. Angiogenic activity of VEGF was restored after the CTGF–VEGF complex was digested by matrix metalloproteinase 3 or –7 [112]. Therefore, CTGF may play an inhibitory role through VEGF-induced angiogenesis during embryonic development, tissue maintenance, and the pathological processes of various diseases. Although CTGF itself is an angiogenesis factor, its interaction with other molecules may alter its function.

One previous study revealed that stromal expression of CTGF promotes angiogenesis of prostate cancer cells [57]. To evaluate the role of stromal-expressed CTGF in tumor progression, either engineered mouse prostate stromal fibroblasts expressing CTGF or 3T3 fibroblasts engineered with mifepristone-regulated CTGF were combined with LNCaP human prostate cancer cells in the “differential reactive stroma (DRS)” xenograft tumor model. The results showed that the expression of CTGF in tumor-reactive stroma induced significant increases in microvessel density and xenograft tumor growth [57].

In breast cancer cells, CTGF has been found to be abundantly present in MDA-MB-231 cells, and its gene expression and protein secretion are up-regulated by hypoxia [35]. In vivo experiments also confirmed that the xenograft formation and neovascularization activity of this breast cancer cell line could be suppressed by neutralizing CTGF-specific polyclonal antibody [36]. In addition, hypoxia-induced release of CTGF has been found to initiate the invasive angiogenesis cascade by modulating the balance of extracellular matrix synthesis and degradation via matrix metalloproteinases (MMPs) secreted by endothelial cells in response to CTGF [37].

In contrast, CTGF may inhibit tumor angiogenesis by regulating the expression of VEGF-A. Recently, we have demonstrated that CTGF expression can inhibit tumor growth in primary or metastatic sites by reducing VEGF-A gene expression and its subsequent angiogenic effects in tumor cells [50]. We also observed that the effect of CTGF on VEGF-A gene expression was mediated by accelerating HIF-1 α protein degradation through ARD1-dependent

acetylation. Most importantly, we have provided functional evidence that CTGF acts as an angiogenesis suppressor, inhibiting tumor growth and metastasis in mouse models of human lung adenocarcinoma [50].

Roles of CTGF on cancer cell anoikis

Anoikis is a form of apoptosis induced by loss of cell anchorage [116], a remarkably complex process involving several adhesion molecules that interact with an array of different structural components referred to as the extracellular matrix (cell–matrix anchorage) and neighboring homotypic or heterotypic cells (cell–cell anchorage). The process of ‘loss of cell anchorage’ therefore embraces the dissolution of potentially many different kinds of cell–cell/cell–matrix interactions. Several means of cell anchorage provide survival signals to the cell and therefore the term ‘anoikis’ describes rather the final outcome of what results once these different means of cell adhesion are disturbed than standing for a distinct and single molecular mechanism leading to apoptosis [116].

Anoikis resistance or anchorage-independent survival and growth are certain hallmarks of tumor cells. This property of tumor cells suggests altered activities in tumor cells that compensates for the cell survival signals lost by disrupting cell–matrix interactions. However, the exact mechanisms that are responsible for anoikis resistance of naturally occurring human cancer cells have not been clearly understood [117]. Recently, several studies found that the anoikis resistance of lung adenocarcinoma may be related to the expression of laminin-5 or Src [117–119]. However, we also found CTGF expression in lung adenocarcinoma cell lines may induce their sensitivity to anoikis and may lead to inhibited metastasis potential (unpublished results), indicating that CTGF may also play a role in regulating anoikis of cancer cells.

Conclusion

CTGF is a multifunctional signaling modulator involved in a wide variety of biologic or pathologic processes, such as angiogenesis, osteogenesis, renal disease, skin disorders, and tumor development. Although it was originally isolated from the conditioned media of cultured human umbilical vascular endothelial cells, it could also be detected in endothelial cells, fibroblasts, cartilaginous cells, smooth muscle cells, and some cancer cells. Recently, CTGF expression has been found to regulate cancer cell migration, invasion, angiogenesis, and anoikis. Although CTGF expression seems to be associated with progression of many kinds of cancers, its expression may have tumor

suppressive effects in lung adenocarcinoma cells, colorectal cancer cells and oral squamous cell carcinoma cells. Therefore, the role of CTGF in different types of cancer may vary considerably, depending on the tissue involved. Furthermore, the expression of some important cancer progression-related molecules, such as CRMP-1, HIF-1 α , β -catenin/Tcf/MMP-7, and S100A4, has been found to be regulated by CTGF. Understanding the detailed mechanisms involved in CTGF-mediated regulation will extend us further insight on the progression and metastasis of human cancers. Moreover, deciphering tumor suppressive effects of CTGF may have future important therapeutic applications.

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