Role of placenta growth factor in cancer and inflammation

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Abbreviations: FGF2, fibroblast growth factor 2; MMPs, matrix metalloproteinases; oxLDL, oxidized low-density lipoprotein; PDGFB, platelet-derived growth factor- β ; PIGF, placenta growth factor; RA, rheumatoid arthritis; SRs, scavenger receptors; TAMs, tumor-associated macrophages; TLRs, toll-like receptors; VCAM-1, vascular cell adhesion molecule-1; VEGFR, vascular endothelial growth factor receptor

Abstract

Accumulating evidences have documented that angiogenesis is closely linked to inflammation and regulators of angiogenesis play key roles in various inflammatory conditions. PIGF is an angiogenic protein belonging to the VEGF family and is upregulated mainly in pathologic conditions. Recently, PIGF was discovered having a proinflammatory role in inflammatory arthritis and its serum level drew attention not only as a useful surrogate biomarker but also a potential therapeutic target in atherosclerosis and various cancers. Particularly, PIGF has attractive clinical values because endogenous PIGF is redundant for vascular development and physiological vessel maintenance in healthy adults. However, there have been conflicting results about the efficacy of PIGF inhibition depending on the experimental and clinical settings. Further close investigations for resolving the puzzle of PIGF biology are required.

Keywords: angiogenesis inducing agents; inflammation; neoplasms; neovascularization, pathologic; placenta growth factor

Introduction

Inflammation is a complex set of interaction between soluble factors and cells that can arise in any tissue in response to traumatic, infectious, postischemic, toxic or autoimmune injuries. If targeted destruction and assisted repair are not properly phased, inflammation can lead to persistent tissue damage (Nathan, 2002). Angiogenesis is closely coupled with inflammation in many chronic inflammatory conditions with distinct etiopathogeneses, such as atherosclerosis, rheumatoid arthritis, and cancer. Regulators of angiogenesis can modulate inflammatory response and inflammatory response can modulate regulators of angiogenesis, which indicates that angiogenesis and inflammation are components of a common signaling pathway (Imhof and Aurrand-Lions, 2006). In this review, we discuss the distinctive role of PIGF in the mediation of angiogenic and inflammatory signaling in cancer and atherosclerosis. in which inflammation plays a key role as a positive or negative regulator, and rheumatoid arthritis, a representative of chronic inflammatory diseases.

Role of PIGF in cancer

Angiogenesis is a hallmark of tumor pathogenesis and contributes to the progression of cancer from a dormant in situ lesion to a life-threatening metastatic disease (Carmeliet, 2005; Kerbel, 2008). The major mediators of tumor angiogenesis are VEGF family and its receptors, and targeted therapies against mediators of tumor angiogenesis are currently under clinical trial (Kerbel, 2008). Angiogenesis inhibitors that target VEGF signaling pathways have proven to be successful clinical treatments in part for various types of cancer. However, a substantial fraction of tumors are resistant to current anti-angiogenic therapies and relapses are not even uncommon after a progression-free period (Hurwitz et al., 2004; Bergers and Hanahan, 2008; Burris and Rocha-Lima, 2008). Moreover, VEGF-A is a trophic factor or survival signal that maintains the quiescent endothelial cells of healthy vessels, and therefore anti-angiogenic therapies cause grave side effects that can lead to life-threatening conditions in a subset of cancer patients (Verheul and Pinedo, 2007). Hypothyroidism and leukopenia as well as vascular complications such as bleeding, disturbed wound healing and thrombotic

events are included in this wide spectrum, which emphasizes the importance of VEGF signaling during physiologic homeostasis of many organ systems (Verheul and Pinedo, 2007). The recently considered attractive alternative for overcoming these problems is the modulation of PIGF-VEGFR1 (also known as Flt1) signaling (Verheul and Pinedo, 2007; Fischer *et al.*, 2008; Loges *et al.*, 2009). The nub of the reason is that PIGF expression, unlike that of VEGF, is undetectable in most organs in healthy conditions, but is highly upregulated in tumor conditions, contributing to the angiogenic and inflammatory switch (Marrony *et al.*, 2003; Fischer *et al.*, 2008).

The first investigation conducted on PIGF expression in tumors was undertaken by Takahashi et al. (1994), who demonstrated that PIGF is expressed in hypervascular renal cell carcinoma. Since then, clinical and experimental research on the significance and role of PIGF in tumor progression has been pursued extensively. Accumulating reports have suggested that PIGF might be a useful prognostic marker of cancer progression. Plasma PIGF levels are upregulated and correlate with tumor grade and survival in patients with renal-cell carcinoma (Matsumoto et al., 2003b), and a preoperative high PIGF serum level is a useful prognostic indicator of recurrence and survival in colorectal cancer (Wei et al., 2009). In addition, PIGF mRNA and protein in tumor tissues have been found to be correlated with tumor stage in lung cancer (Zhang et al., 2005), with disease progression and patient survival in colorectal cancer (Wei et al., 2005), with tumor stage and patient survival in gastric cancer (Chen et al., 2004), with recurrence, metastasis and mortality in breast cancer (Parr et al., 2005), and even with post-operative early recurrence in hepatocellular carcinoma (Ho et al., 2007). In tumors, PIGF is not only produced by malignant cells, but also by endothelial cells, smooth-muscle cells, pericytes, cancer-associated fibroblasts, tumor-associated macrophages, and various other inflammatory cells in tumor stroma (Yonekura et al., 1999; Carmeliet et al., 2001; Fischer et al., 2007). However, conflicting data have documented that PIGF expression differs in lung, colorectal, prostate, and thyroid cancers, as it appears to be lower than in matched normal tissues (Viglietto et al., 1995; Matsumoto et al., 2003a; Xu et al., 2006). Thus, it remains to be determined whether PIGF acts as a positive regulator of cancer growth and metastasis in man.

When highly upregulated PIGF transmits its signal through Flt1 by stimulating the phosphorylations of specific Flt1 tyrosine residues, and thus induces

the expression of distinct downstream target genes. PIGF also amplifies VEGF-mediated signal transduction through VEGFR2 (also known as FIk1) by inducing the transphosphorylations of the tyrosine residues of FIk1 (Autiero *et al.*, 2003b). Furthermore, PIGF displaces VEGF-A from FIt1, which releases VEGF-A and allows it to activate FIk1 and enhance VEGF-driven angiogenesis (Park *et al.*, 1994). PIGF has also been reported to form heterodimer formation could deplete VEGF-A intracellular pool, and thus, reduce the formation of angiogenic VEGF-A-VEGF-A homodimers (Cao *et al.*, 1996; Eriksson *et al.*, 2002).

PIGF induces various biological effects by affecting a wide range of different cell types. PIGF can stimulate vessel growth and maturation directly by affecting endothelial and mural cells, and indirectly by recruiting pro-angiogenic cell types. For example, PIGF stimulates the growth, migration and survival of endothelial cells (Ziche et al., 1997; Carmeliet et al., 2001; Adini et al., 2002; Fischer et al., 2007), increases the proliferations of fibroblasts and smooth-muscle cells, induces vasodilatation, and stimulates collateral vessel growth (Yonekura et al., 1999; Bellik et al., 2005). It also promotes the recruitment and maturation of angiogenesis-competent myeloid progenitors to growing sprouts and collateral vessels (Hattori et al., 2002; Luttun et al., 2002b; Pipp et al., 2003; Rafii et al., 2003; Scholz et al., 2003). In addition, PIGF activates and attracts macrophages that release angiogenic and lymphangiogenic molecules (Selvaraj et al., 2003), and inhibits the differentiation of dendritic cells. Malignant tumors take advantage of these pleiotropic functions of PIGF to promote growth, angiogenesis, and resistance toward antiangiogenic treatments. PIGF signaling participates directly in the tumoral angiogenic switch by stimulating the proliferation of endothelial cells and acting on mural cells, including pericytes and smooth muscle cells, and indirectly by upregulating the expressions of VEGF-A, FGF2, PDGFB, MMPs, and other angiogenic factors (Roy et al., 2005; Marcellini et al., 2006). PIGF also recruits Flt1-positive hematopoietic progenitor cells and macrophages to growing tumor sites, and thus, contributes to neovascularization and lymphangiogenesis (Hattori et al., 2002; Luttun et al., 2002b; Schoppmann et al., 2002; Pipp et al., 2003; Rafii et al., 2003; Cursiefen et al., 2004; Murakami et al., 2008). In particular, tumor- associated macrophages (TAMs), representing up to 50% of tumor mass, play a major role in cancerrelated inflammation and angiogenesis (Solinas et al., 2009). TAMs preferentially localizes in hypoxic regions of tumor mass and secretes several angiogenic factors and angiogenesis-modulating enzymes, that sustain angiogenesis and reorganizes tumor vasculature. Moreover, TAMs promotes lymphangiogenesis by secreting VEGF-C and possibly, by promoting the transdifferentiation of peritumoral stroma cells to lymphatic endothelial cells in lymph vessels (Schoppmann *et al.*, 2002; Cursiefen *et al.*, 2004). Indeed, anti-PIGF therapy suppressed lymphangiogenesis, which might be dependent on macrophage inhibition because lymphatic endothelial cells do not express detectable levels of FIt1 (Carmeliet *et al.*, 2001; Fischer *et al.*, 2007). Furthermore, PIGF play a direct role in the control of tumor cell motility and invasiveness (Taylor and Goldenberg, 2007).

As mentioned above, current anti-angiogenic strategies mainly focus on inhibiting the signaling of VEGF-A and Flk1, which pose some challenging problems. One is that a substantial proportion of cancer patients are resistant to VEGF-based therapy. Various mechanisms contribute to this resistance, and allow escape from anti-VEGF therapy. One is angiogenic rescue, a process involving the increased expressions of other pro-angiogenic factors (Bergers and Hanahan, 2008). In particular, after anti-VEGF therapy, PIGF-Flt1 signaling provides a major route for angiogenic rescue (Willett *et al.*, 2005; Kerbel, 2008). Therefore, the inhibition of PIGF could provide an attractive means of supplementing the deficient

anti-VEGF therapy. In fact, Fisher et al. have demonstrated that anti-PIGF blocking antibody inhibits the growth and metastasis of various tumors in mice, including those resistant to VEGFR inhibitors, and that it enhances the efficacy of chemotherapy and of VEGFR inhibitors (Fischer et al., 2007). Remarkably, anti-PIGF antibody has also been reported to inhibit angiogenesis, lymphangiogenesis, and tumor cell motility without switching on the angiogenic rescue program and affecting healthy vessels (Fischer et al., 2007). Additional and supportive evidences for the efficacy of PIGF inhibition in cancer were adduced by Van De Viere et al. (2010). However, Bais et al. (2010) took issue with these results and showed that neutralization of PIGF, genetic ablation of host PIGF receptor signaling, or combined anti-PIGF treatment and loss of host Flt1 tyrosine kinase signaling do not inhibit angiogenesis during primary tumor growth. Xu et al. (2006) even found that blocking PIGF could aggravate tumor progression by demonstrating that PIGF overexpression impairs tumor growth and angiogenesis in xenograft models. Although it has been recently suggested that expression of a functional FIt1 in tumor cells is a major determinant of anti-PIGF antibodies efficacy (Yao et al., 2011), no clear reason for result discrepancies has been provided to date. Experimental observations regarding the in vivo role of PIGF in mouse models of tumors

Model	Tumor subtype	PIGF manipulation	Tumor growth	Angiogenesis	Metastasis	Reference
Pro-promoting evidence	S					
C57Bl/6 mice	B16 melanoma / Pancreatic Panc02 adenocarcinoma / CT26 colon carcinoma	Anti-PIGF blocking antibody	Ļ	Ļ	Ļ	Glaser <i>et</i> <i>al</i> ., 2011
Balb/c nude mice	B16F10 melanoma	Anti-PIGF blocking antibody	\leftrightarrow	n.d.	\downarrow	Pipp <i>et al</i> ., 2003
C57BI/6 PIGF-/- mice	Skin papilloma	PIGF knockout	\downarrow	\downarrow	n.d.	Pope, 2002
C57BI6/ASV-B mice	Hepatocellular carcinoma	PIGF silencing	\downarrow	\downarrow	n.d.	Pope, 2002
C57Bl/6 Rip1Tag2 $ imes$ PIGF-/- mice	Pancreatic β cell carcinoma	PIGF knockout	\leftrightarrow	\leftrightarrow	n.d.	Pope, 2002
Pro-inhibitory evidences						
C57BL/6 mice	Murine fibrosarcoma	PIGF overexpression	\downarrow	\downarrow	n.d.	Kerbel, 2008
C57BI/6 mice	Murine Lewis lung carcinoma	PIGF overexpression	\downarrow	\downarrow	n.d.	Zhang <i>et</i> <i>al</i> ., 2005
C57BI/6 Rip1 PIGF-1 transgenic mice	Pancreatic β cell carcinoma	PIGF overexpression	\downarrow	\downarrow	n.d.	Ziche <i>et al</i> ., 1997
SCID mice	Human tumor cell lines (HCT116, A549, and U87-MG)	PIGF overexpression	\downarrow	\downarrow	n.d.	Hattori et al., 2002

Table 1. Summary of controversial evidence regarding the effect of PIGF on tumor biology

n.d., not determined; \downarrow , inhibition; \leftrightarrow , not inhibition.

are summarized in Table 1. Further meticulous investigations are required to clarify the efficacies of anti-PIGF therapies in cancer patients.

Role of PIGF in chronic inflammatory conditions

Atherosclerosis

Atherosclerosis is a chronic inflammatory disease characterized by lipid-containing inflammatory lesions in large and medium-sized arteries (Hansson and Libby, 2006). Accumulating evidence shows that angiogenesis plays a key role in atherogenesis and acute lesion instability of progressive atherosclerosis, and is intimately associated with inflammation (Luttun *et al.*, 2002b; Herrmann *et al.*, 2006) and a variety of pro- and anti-angiogenic factors are involved in the angiogenesis of athero-

genesis (Herrmann et al., 2006).

PIGF is upregulated in early and advanced atherosclerotic lesions and is detectable in adventitial cells and in the shoulders and caps of plaque (Luttun et al., 2002a). In particular, PIGF is mainly located at the shoulders of atherosclerotic plaque (Roncal et al., 2010), where high density microvessels exist with marked macrophage infiltration. PIGF promotes atherosclerotic intimal thickening and macrophage accumulation and induces neovascularization and endothelial activation (Khurana et al., 2005). PIGF seems to act more effectively during the early phase of atherogenesis, because anti-PIGF antibody treatment significantly inhibits early lesions, but is ineffective during the more advanced stages of plaque development (Roncal et al., 2010). Inhibition of Flt1 failed to affect angiogenesis in plaque (Luttun et al., 2002b). Plaque microvessels were not found in the early lesions of ApoE knockout mice regardless of the presence of

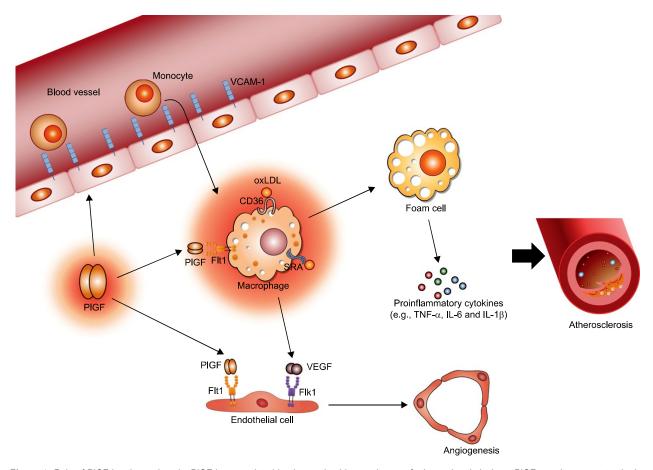


Figure 1. Role of PIGF in atherosclerosis. PIGF is upregulated in plaque shoulders and caps of atherosclerotic lesions. PIGF recruits monocytes by increasing the expression of VCAM-1, a key molecule in the processes of monocyte/macrophage adhesion and rolling at the luminal side of arteries *via* the activation of FIt1 in endothelial cells. Inflowing monocytes differentiate into macrophages, accumulate oxidized LDL (oxLDL) *via* scavenger receptors (SRA) and are further activated by PIGF, and form foam cells. Activated macrophages and foam cells produce proinflammatory and angiogenic mediators, which promote inflammatory response, stimulate lesion progression, and increase the risk of plaque rupture.

PIGF, and PIGF deficiency caused a significant reduction in size and macrophage content of early atherosclerotic plaques in ApoE knockout mice compared with mice deficient only in ApoE (Khurana *et al.*, 2005). Thus, the suppressive effect of anti-PIGF on plague growth and vulnerability might be dependent on inhibition of macrophage infiltration and activation rather than on the direct inhibition of angiogenesis. PIGF recruits macrophages by augmenting the expression of VCAM-1, a key molecule in the monocyte/macrophage adhesion and rolling processes on activated endothelial cells in the luminal side of arteries (Selvaraj *et al.*, 2003; Roncal *et al.*, 2010).

Regulation of monocyte/macrophage recruitment by PIGF is important because monocyte/macrophage is the predominant cell type present within atherosclerotic vessels and is involved in all stages of atherosclerosis development (initiation, progression, and rupture) (Saha *et al.*, 2009). Recruited monocytes differentiate into macrophages with upregulated expression of scavenger receptors (SRs) and innate immune recognition receptors such as Toll-like receptors (TLRs) under the influence of locally produced factors like monocyte colony-stimulating factor and other stimuli. SRs mediate the

macrophage uptake of oxidized LDL (oxLDL) particles, which leads to intracellular cholesterol accumulation and the formation of foam cells. Innate immune recognition receptors like TLRs interact with oxLDL and microbial components, such as LPS, Hsp60, and other ligands, and results in macrophage activation and the productions of proinflammatory mediators. Macrophages also activate T cells by presenting specific antigens and modulate T-cell responses by producing cytokines, such as IL-18 and IL-12. These inflammatory mediators, in concert with T-cell-produced cytokines, promote inflammatory responses, stimulate lesion progression, and increase the risk of plaque rupture (Figure 1) (Yan and Hansson, 2007). Furthermore, activated macrophages also stimulate angiogenesis, which can recruit more inflammatory cells and increases angiogenesis (Moulton et al., 2003).

Circulating levels of PIGF are undetectable in normal individuals, but are elevated in patients with atherosclerotic or ischemic heart disease. In patients with acute coronary syndrome, a high plasma PIGF level within 12 h of symptom onset has been shown to predict a poor prognosis in the short and long-term (Heeschen *et al.*, 2004; Lenderink *et al.*, 2006;

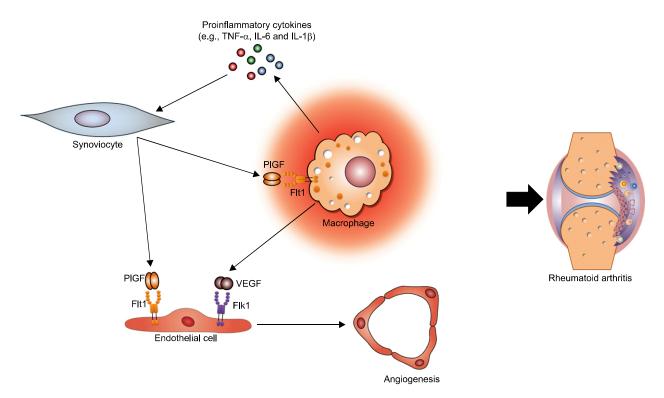


Figure 2. Role of PIGF in rheumatoid arthritis. PIGF, predominantly produced by rheumatoid synoviocytes, promotes angiogenesis and stimulates vascular endothelial cell permeability. Newly employed macrophages produce TNF- α and IL-6 when stimulated by PIGF/FIt-1 binding or by contact with activated endothelial cells. TNF- α and IL-6, in turn, further enhance PIGF secretion by macrophages and synoviocytes, and thus create a vicious cycle of inflammation.

Markovic *et al.*, 2010; Glaser *et al.*, 2011). Furthermore, a single initial measurement of plasma PIGF appears to enhance the predictive and prognostic abilities of traditional markers, such as, B type-natriuretic peptide and troponin I (Glaser *et al.*, 2011).

However, the pathophysiologic role of PIGF during the late symptomatic phase of acute coronary syndrome could differ from that during early disease. Thickened atherosclerotic plaque results in hypoxia of vessel walls and myocardium, and hypoxia is one of the most potent angiogenic stimuli (Bjornheden et al., 1999). Under hypoxic conditions, PIGF is upregulated in cardiomyocytes and fibroblasts, and contributes to myocardial angiogenesis and tissue healing (Green et al., 2001; Torry et al., 2009). PIGF is also known to promote the mobilization, chemotaxis, and recruitment of bone marrow-derived endothelial progenitor cells to ischemic tissues to facilitate the healing of injured vessels (Li et al., 2006). Thus, depending on the stage of atherosclerosis progression, PIGF may be beneficial or deleterious. In this regard, the timely controlled properties of PIGF should be taken into account when considering PIGF a potential therapeutic target in atherosclerotic heart disease.

Rheumatoid arthritis

Rheumatoid arthritis (RA) is a chronic inflammatory synovitis that is dominated by the presence of macrophages, lymphocytes and synovial fibroblasts, which cause bone and cartilage destruction (Pope, 2002). The deformed synovial architecture of RA, called pannus, is characterized by high density of sub-lining blood vessels. These new blood vessels can maintain the chronic inflammatory state by transporting inflammatory cells to sites of inflammation and by supplying nutrients and oxygen to proliferating inflamed tissues (Marrelli et al., 2011). Indeed, increases in blood vessel numbers has been shown to be correlated with synovial cells hyperplasia and mononuclear cell infiltration and with the indices of joint tenderness (Rooney et al., 1988; Rosu et al., 2008), which suggests that a close association exists between angiogenesis and inflammation in the synovium of RA.

Angiogenesis is finely tuned by balances between pro-angiogenic and anti-angiogenic mediators such as growth factors, cytokines, chemokines, cellular adhesion molecules and others (Szekanecz *et al.*, 2010). Of these, VEGF and its receptors are key regulators of the angiogenic process also in inflammatory synovium of RA. Recently, we found that PIGF, a member of the VEGF family, is also highly expressed in the layer that lines the hyperplastic synovium of RA joints and that it is also increased in the synovial fluid of patients (Bottomley et al., 2000; Yoo et al., 2009). As a specific ligand for FIt1, PIGF has potent angiogenic properties and also induces growth and migration of endothelial cells (Luttun et al., 2002a; Autiero et al., 2003a). PIGF is copiously highly produced by fibroblast-like synoviocytes exposed to proinflammatory cytokines such as IL-1 β and TNF- α , and it, in turn, increases the productions of TNF- α , IL-1, IL-6, and VEGF by mononuclear cells in RA (Bottomley et al., 2000; Selvaraj et al., 2003; Yoo et al., 2009). Furthermore, monocytes from patients with active RA exhibit an exaggerated response to PIGF because Flt1 expression is elevated in the monocytes from these patients (Yoo et al., 2009). Finally, a chain of these processes creates a vicious cycle that encourages the perpetuation of chronic joint inflammation (Figure 2) (Yoo et al., 2008). Therefore, synovial inflammation and angiogenesis would seem to be controllable if the action of PIGF were interrupted. In fact, arthritis seldom develops in response to anti-collagen II antibodies in PIGF knockout mice, which suggests that PIGF is a critical mediator of the inflammation of RA (Yoo et al., 2009). Furthermore, PIGF induces VEGF release from mononuclear cells, and the binding of PIGF to Flt1 leads to intermolecular crosstalk between Flt-1 and Flk1, which amplifies Flk1 signaling and consequently enhances VEGF-driven response (Bottomley et al., 2000; Autiero et al., 2003b). Therefore, the inhibition of PIGF could suppress both VEGF-driven inflammation and angiogenesis. Another possible mechanism responsible for the effects of anti-PIGF treatment is that more VEGF would be trapped by Flt1 due to loss of competition from PIGF, which would reduce binding opportunity between VEGF and Flk1 (Park et al., 1994), a more potent pro-angiogenic receptor than Flt1, and reduce angiogenesis.

Taken together, enhanced expression and signaling by PIGF-FIt1 system potentiates rheumatoid inflammation both directly and indirectly by encouraging inflammation and angiogenesis. Since PIGF is redundant in terms of vascular development and physiological vessel maintenance in healthy adults (Carmeliet *et al.*, 2001), it represents a promising novel target for the control of RA with negligible side effects.

Concluding remarks

PIGF lies dormant in the normal healthy state and becomes active in the presence of pathologic conditions, such as, those associated with chronic inflammatory diseases. PIGF induces angiogenesis directly by activating endothelial cells but it also promotes inflammation by recruiting and activating macrophages via Flt1 signaling. Macrophages, stimulated by PIGF, secrete proinflammatory cytokines like TNF- α and IL-6 and angiogenic factors like VEGF and perpetuate inflammation and angiogenesis, which are critical for tumour progression, plague vulnerability, and pannus formation in rheumatoid arthritis. Although blocking or inhibiting the PIGF-FIt1 system has successfully controlled inflammation and angiogenesis in many animal studies of disease models, observed effects should be interpreted with caution for two reasons. First, PIGF can have beneficial or harmful effects that depend on the stage of disease progression in some diseases such as atherosclerosis. Second, modulation of PIGF-FIt1system can have an influence on expression and action of VEGF family system or other angiogenesis-modulating factors, which might give rise to unexpected responses in in vivo system. The dimerization pattern of PIGF and VEGF-A varies, and PIGF may antagonize or enhance VEGF-A function (Xu et al., 2006; Cao, 2009). And the possibility cannot be excluded that anti-PIGF therapy could induce angiogenic rescue programme through stimulating expression of various pro-angiogenic factors as in anti-VEGF therapy. Indeed, anti-PIGF induces a small but angiogenic escape effect (Fischer et al., 2007), and which could be another reason for failure of PIGF blockade to inhibit angiogenesis in primary tumor growth in different experimental systems (Bais et al., 2010). Therefore, further investigation on the temporal expression pattern and functional property of PIGF in relation to VEGF family members and their receptors or other angiogenic factors is warranted in disease models, before the efficacy of PIGF-FIt1 system inhibition is confirmed clinically in patients with chronic inflammatory diseases or conditions.

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