

Expression of placenta growth factor is regulated by both VEGF and hyperglycaemia via VEGFR-2

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Abstract

Placenta growth factor (PlGF) has been implicated in both physiological and pathological angiogenesis; however, little is known about what regulates its expression. In this study, retinal microvascular endothelial cells and pericytes were exposed to varying concentrations of VEGF and glucose and PlGF expression measured by RT-PCR and Western blotting. Both PlGF mRNA and protein were observed in unstimulated microvascular endothelial cells with only weak expression in pericytes. In endothelial cells, VEGF (100 ng/ml) and glucose (15 mM) induced an increase in expression of PlGF at both the mRNA and protein level while no effect was observed for pericytes. The increase in PlGF expression could be totally abolished by blocking VEGFR-2, and in the case of glucose by neutralising VEGF. VEGF-stimulated PlGF expression was largely inhibited by PD 98059, an inhibitor of mitogen-activated protein kinase (MAPK) and partially by GF 109203X, an inhibitor of protein kinase C (PKC), indicating that VEGF up-regulates PlGF expression via the MAPK signalling pathway and partially through PKC. Taken together, our findings suggest that VEGF orchestrates the contribution of PlGF in angiogenesis via more than one intracellular pathway and that hyperglycaemia, as occurs in diabetes, is an important regulator of PlGF expression via VEGF up-regulation. © 2004 Elsevier Inc. All rights reserved.

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Introduction

Aberrant capillary formation is a devastating complication of microvascular diseases (Boulton et al., 1988; Cai and Boulton, 2002). A number of growth factors have been implicated in these diseases of which the VEGF family is considered of major importance (Neufeld et al., 1999).

Abbreviations: PlGF, placenta growth factor; VEGF, vascular endothelial growth factor; VEGFR-1 (Flt-1), vascular endothelial growth factor receptor-1 (fms-like tyrosine kinase); VEGFR-2 (KDR/Flk-1), vascular endothelial growth factor receptor-2 (human kinase-insert-domain-containing receptor/fetal liver kinase-1 of mouse); MAPK, mitogen-activated protein kinase; PKC, protein kinase C; PI3K, phosphatidylinositol 3-kinase; PLC- γ , Phospholipase C- γ ; ERK, extracellular signal regulated kinase.

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There is now increasing evidence that placenta growth factor (PlGF), in addition to VEGF, plays a critical role in eliciting and sustaining a newly forming vasculature (Cai et al., 2003; Khaliq et al., 1998; Luttun et al., 2002a).

Placenta growth factor (PlGF) is a polypeptide growth factor that shares 53% amino acid sequence homology with the platelet-derived growth factor domain of VEGF (Maglione et al., 1991). This member of the VEGF family occurs at least as three isoforms PlGF-1, PlGF-2 and PlGF-3, which are derived from the same gene via alternate splicing (Cao et al., 1997; Maglione et al., 1993). PlGF-2 differs from PlGF-1 in that it has an additional 21 basic amino acid domain that confers a strong heparin binding site similar to that of VEGF₁₆₅ (Cao et al., 1997). Little is known about the structure and function of PlGF-3. Unlike VEGF, which acts by binding both to VEGFR-1 (flt-1) and VEGFR-2 (KDR/flk-1), PlGF is believed to bind only to VEGFR-1 (Park et al., 1994). VEGFR-1 is a high-affinity

tyrosine kinase receptor, which regulates metabolic activity and more recently has been shown to be implicated in angiogenesis (Bussolati et al., 2001; Lutun et al., 2002b; Weng and Usman, 2001). However, its role in intracellular signalling is not fully understood. Although PIGF alone has been previously reported to have a weak mitogenic effect on cultured microvascular endothelial cells, it is now evident that PIGF plays a crucial role either by potentiating the angiogenic effects of VEGF by displacing VEGF from the 'VEGFR-1 decoy' (Park et al., 1994) and/or by forming heterodimers with VEGF that can activate the VEGFR-2 (DiSalvo et al., 1995). Furthermore, we recently demonstrated that PIGF via VEGFR-1 contributes to pathological angiogenesis by prolonging cell survival signals and maintaining vascular networks (Cai et al., 2003). Additionally, in mPIGF null mice, the lack of PIGF induced regression of neovascular complexes (Carmeliet et al., 2001).

PIGF expression was originally thought to be restricted to the primary cytotrophoblasts of the placenta (Shore et al., 1997), but is now known to be widely distributed in many nonplacental cells including cells of the microvasculature during pathological angiogenesis. PIGF is highly expressed in the capillaries associated with tumors, wound healing, proliferative diabetic retinopathy and rheumatoid arthritis (Bottomley et al., 2000; Carmeliet et al., 2001; Failla et al., 2000; Nomura et al., 1998; Yamashita et al., 1999). However, it is unclear which microvascular cells produce PIGF nor what regulates its expression. PIGF, unlike VEGF, is considered not to be strongly hypoxia-inducible, suggesting that other factors must be important in its regulation.

In this study, we examined the expression of PIGF at both the gene and protein level in retinal microvascular endothelial cells and pericytes in response to VEGF and hyperglycaemia (a predictor of ocular angiogenesis associated with diabetes). We further investigated the role of VEGFR and the intracellular signalling pathways involved in the regulation of PIGF expression.

Materials and methods

Reagents

Recombinant VEGF₁₆₅ and neutralising antibodies raised against the extracellular domains of VEGFR-1, VEGFR-2 and VEGFR-3 were obtained from R&D Systems (R&D Systems Europe Ltd., Abingdon, UK). Anti-phospho-MAP kinase/Erk1/2 polyclonal antibody was purchased from Upstate (Upstate, UK). Glucose was from BDH (BDH, UK). The antibody against PIGF was from Santa Cruz (UK). PD 98059 and GF 109203X were bought from LC Laboratory (Boston, MA). TRIzol Reagent was from Invitrogen (Glasgow, UK), Reverse-iT™ and PCR ReddyMix™ were purchased from Abgene

(UK). All other materials were from Sigma unless otherwise stated.

Cell culture

Primary cultures of bovine retinal microvascular endothelial cells and pericytes were isolated from freshly isolated bovine eyes by homogenisation and a series of filtration steps, as described previously (Wong et al., 1987). Endothelial cells were maintained in endothelial cell basal medium with growth supplement (TCS Works Ltd., Buckingham, UK). Endothelial cells were characterised by their cobblestone appearance and expression of factor VIII antigen (Wong et al., 1987). Pericytes were cultured in Eagle's Minimal Essential Medium (GibcoBRL, UK) containing 10% fetal calf serum (FCS) and identified and distinguished from endothelial cells by their size and irregular morphology (Wong et al., 1987). Both types of cells were used between passages 1 and 3 for all experiments. Upon reaching near confluence, the medium was replaced with medium containing either VEGF at 10 and 100 ng/ml or glucose at 15 and 25 mM for 24 and 48 h (these time points were identified as optimal from preliminary experiments). Medium alone (containing 5.6 mM glucose) served as the control for all experiments.

RT-PCR

Total RNA was isolated from cells that had been cultured under various concentrations of VEGF or glucose, using TRIzol Reagent (Invitrogen), and then analysed by RT-PCR using Reverse-iT™ and PCR ReddyMix™ (ABgene) according to the manufacturer's protocol. The RNA concentration was determined by the spectrophotometer from GeneQuant II (Pharmacia Biotech, England) and equal quantity of total RNA was used from different samples. The primers for PIGF were designed according to the sequences of PIGF-1 and -2 mRNA from the GenBank™. The oligonucleotide primers used for the amplification of bovine PIGF cDNA were 5'-GTG CCC TTC CAG CAA GTG T-3' and 5'-TCT TCC GAG GGA CTG GTT AC-3'. The resultant PCR products were 347 and 410 bp for PIGF-1 and PIGF-2, respectively. The cDNA was amplified using the PCR ReddyMix™, each cycle consisting of 20 s at 94°C, 30 s at 55°C and 60 s at 72°C. All the samples were amplified in a linear amplification range established using a serial cDNA dilution and varying the number of cycles. PCR products were electrophoresed onto a 1.2% agarose gel containing ethidium bromide and visualised under UV light. The relative intensities of the bands were quantified by densitometric analysis.

Immunoprecipitation and Western blotting

For detection of PIGF, conditioned medium was centrifuged at 200 × g for 5 min to remove any debris.

The protein concentration in the medium was determined by the BCA protein assay (Pierce, UK) using bovine serum albumin as standard according to the manufacturer's instructions. The medium was immunoprecipitated by incubation with an anti-PIGF antibody with reactivity against both PIGF-1 and -2 and then protein A/G-agarose (Santa Cruz Biotechnology, USA). The immunoprecipitates were subjected to SDS-PAGE and the resolved proteins transferred onto nitrocellulose membranes. The membranes were probed with an anti-PIGF antibody followed by incubation with a secondary antibody conjugated with HRP. The ECL system (Santa Cruz) was used to visualise the bands. For detection of phosphorylation of ERK1/2, endothelial cells were pretreated with or without 25 μ M PD98059 for 20 min before administration of VEGF100 ng/ml. Vehicle only was as a control. After incubation for 24 h, endothelial cells were harvested and lysed with RIPA buffer (50 mM Tris-HCl, 1% NP-40, 0.25% Na-deoxycholate, 150 mM NaCl, 1 mM of EDTA, PMSF, Na₃VO₄, NaF each) containing protease inhibitors (1 μ g/ml each of aprotinin, leupeptin, pepstatin). Western blotting were performed and the phosphorylation of ERK1/2 was detected with an anti-phospho-MAP kinase/Erk1/2 polyclonal antibody.

Inhibition studies

To identify which VEGFR is involved in the regulation of PIGF expression, total RNA was isolated from cultures treated with 60 ng neutralising antibody to VEGFR-1, -2, or -3 per milliliter of culture medium for 1 h before incubation with 100 ng/ml VEGF for 24 h. PIGF mRNA expression was determined using RT-PCR. To determine if glucose regulates PIGF expression via the production of VEGF, total RNA was isolated at 24 h after stimulation of cells by 15 mM glucose with or without 200 ng/ml anti-VEGF antibody.

Intracellular signalling studies

To investigate the intracellular signalling pathways involved in the regulation of PIGF expression, endothelial cells were incubated with either PD 98059 (an inhibitor of MAPK) at 25 μ M, or GF 109203X (an inhibitor of PKC) at 5 μ M, or Wortmannin (an inhibitor of PI3 kinase) at 100 ng/ml, or medium containing the DMSO carrier alone for 20 min before the addition of 100 ng/ml VEGF. To rule out the inhibitors having an effect on the RT-PCR data, they were included in the positive control of the First-Strand Synthesis Kit. Neither inhibitor had an effect on the PCR results (data not shown).

Statistical analysis

The results represent the mean of at least three separate experiments. Statistical analysis was carried out by unpaired

Student's *t* test. Values were measured by laser densitometry and expressed as mean \pm SEM. Statistical significance was defined as $P < 0.05$.

Results

Expression of PIGF mRNA in microvascular cells

PIGF-1 and PIGF-2 mRNA expression was observed in both retinal microvascular endothelial cells and pericytes under normal culture conditions (Fig. 1). The bovine primers gave an intense band for PIGF-2 at the expected 410 bp and a very weak signal for PIGF-1 at 347 bp. The signal intensity for PIGF-2 mRNA from the microvascular endothelial cells was 3.5 times stronger than that of the pericytes.

The effect of VEGF and glucose on PIGF expression in endothelial cells

Exposure of microvascular endothelial cells to 10 and 100 ng/ml VEGF or 15 mM glucose for 24 h resulted in a significant increase in PIGF-2 mRNA expression compared to untreated control (Fig. 2A). This increase was greatest at 100 ng/ml VEGF and 15 mM glucose. Exposure to 25 mM glucose did not affect PIGF-2 mRNA expression compared to control. Ten-millimolar glucose was similar to control while 20 mM glucose was similar to that with 15 mM glucose on the expression of PIGF. A similar result was observed following immunoprecipitation and immunoblotting of the conditioned

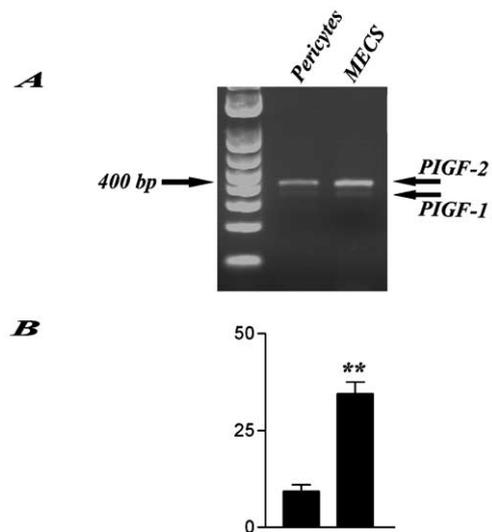


Fig. 1. RT-PCR analysis of PIGF mRNA expression in microvascular endothelial cells and pericytes. Total RNA was isolated from cultured bovine retinal microvascular endothelial cells and pericytes. After reverse transcription, cDNA was amplified using bovine-specific primers. (A) The RT-PCR products were analyzed by agarose gel electrophoresis. The PIGF-1 and PIGF-2 bands ran at 347 and 410 bp, respectively. (B) Band intensity (arbitrary units) for PIGF-2 was quantified by laser densitometry from at least three separate experiments. The vertical bar represent SEM; ** $P < 0.01$.

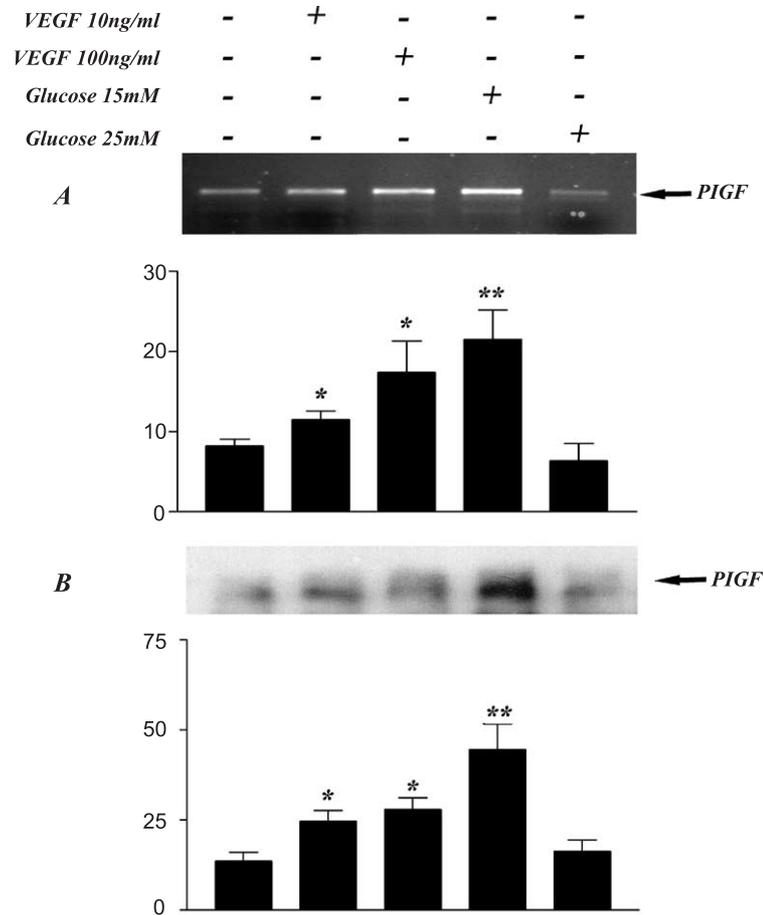


Fig. 2. The expression of PIGF mRNA and protein in microvascular endothelial cells under different conditions. Microvascular endothelial cells were treated with VEGF 10 and 100 ng/ml, glucose 15 mM or glucose 25 mM, or exposed to medium alone (5.6 mM glucose) for 24 h. (A) Total RNA was extracted and RT-PCR performed to determine changes in PIGF mRNA expression. PCR products were analyzed by agarose gel electrophoresis and intensity of the PIGF-2 bands was quantified by laser densitometry from at least three separate experiments. (B) Conditioned media were immunoprecipitated using a polyclonal antibody raised against PIGF and the immunoprecipitates electrophoresed on a 12% SDS-PAGE followed by blotting on a nitrocellulose membrane. Positive bands were visualized by an ECL detection system. Band intensity (arbitrary units) for PIGF was quantified by laser densitometry from at least three separate experiments. Vertical bars represent \pm SEM; P values ($*P < 0.05$, $**P < 0.01$) indicate the significant difference between VEGF/glucose stimulation and untreated control.

medium for PIGF peptide (Fig. 2B). The secreted peptide was present at higher amounts in the medium of cells exposed to 10 and 100 ng/ml VEGF or 15 mM glucose compared to either control cultures or cells exposed to 25 mM glucose. A faint PCR band could be observed at 347 bp (PIGF-1), which appeared to be more intense at 100 ng/ml VEGF and 15 mM glucose than any of the other conditions tested. There was little difference between PIGF expression at 24 and 48 h post exposure apart from a slight increase at 10 ng/ml VEGF at the later time point (data not shown). Neither VEGF nor glucose appeared to have any effect on the regulation of PIGF expression in pericytes at either 24 or 48 h post exposure (data not shown).

Identification of the receptor mediating VEGF-induced PIGF expression

To identify the receptor(s) responsible for the VEGF-induced expression of PIGF, VEGFR-1, -2 and -3 were

blocked by neutralising antibodies before addition of VEGF. The stimulatory effect of VEGF on PIGF expression was completely inhibited by blocking VEGFR-2 (Fig. 3B) while blockade of either VEGFR-1 or -3 had no effect on the expression of PIGF mRNA (Figs. 3A,C). Blocking VEGFR-2 also blocked PIGF peptide release into the conditioned medium (Fig. 3D).

We also investigated the mechanism by which 15 mM glucose can up-regulate the expression of PIGF-2 mRNA. PIGF expression induced by 15 mM glucose was decreased by greater than 85% in microvascular endothelial cells treated with an anti-VEGF₁₆₅ antibody compared to cells exposed to glucose alone (Fig. 4).

The intracellular signalling pathways involved in PIGF expression

Because previous reports have shown that MAPK, PKC and PI3K have significant roles in VEGF-induced intra-

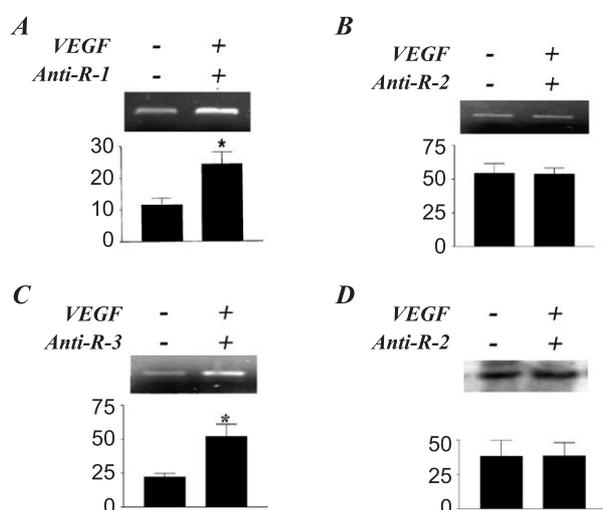


Fig. 3. The effects of blocking VEGF receptors on the expression of PIGF mRNA and protein. Microvascular endothelial cells were treated with neutralizing antibodies for VEGFR-1 (A), VEGFR-2 (B, D) and VEGFR-3 (C) for 1 h before incubation with 100 ng/ml VEGF. Medium alone acted as the control. After incubation for 24 h, the cells were harvested for RT-PCR (A–C) and the culture medium for PIGF peptide analysis (D). The PCR product for PIGF-2 and the PIGF peptide were analyzed electrophoretically and the band intensity (arbitrary units) quantified by laser densitometry from at least three separate experiments. The vertical bars represent the SEM; * $P < 0.05$.

cellular signalling pathways, we determined which of these kinases was involved in the regulation of PIGF expression. Addition of the MAPK inhibitor PD 98059 completely abolished VEGF-induced up-regulation of PIGF expression while addition of the PI3K inhibitor Wortmannin had no effect. The PKC inhibitor GF 109203X only partially abolished the VEGF-induced expression of PIGF (Fig. 5A). We further demonstrated that VEGF 100 ng/ml

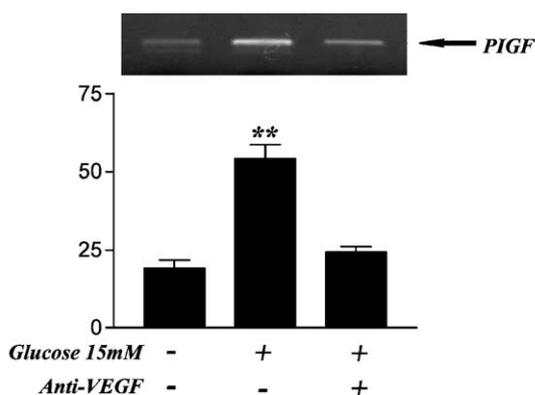


Fig. 4. Effect of VEGF₁₆₅ neutralizing antibody on glucose-induced PIGF mRNA expression. Microvascular endothelial cells were exposed to 15 mM glucose for 24 h in the presence or absence of 200 ng/ml neutralizing antibody for VEGF₁₆₅. Medium alone acted as the control. Total RNA was isolated and RT-PCR performed as described above. Band intensity for PIGF-2 was quantified by laser densitometry from at least three separate experiments. Vertical bars represent \pm SEM. The expression of PIGF-2 mRNA in cells exposed to 15 mM glucose was significantly reduced (** $P < 0.01$) in the presence of a neutralizing antibody for VEGF₁₆₅.

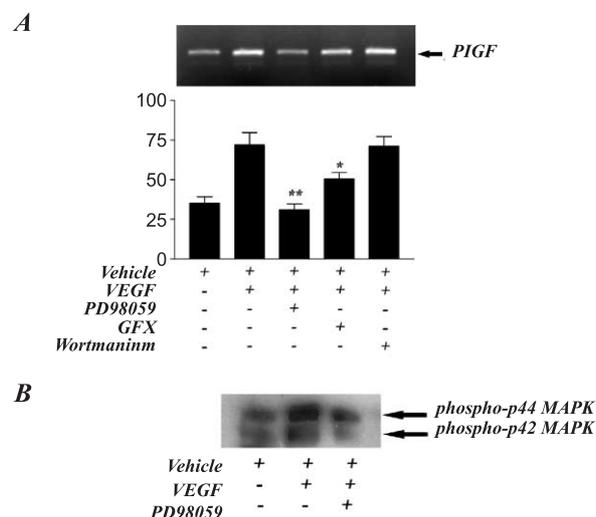


Fig. 5. VEGF up-regulates the expression of PIGF mRNA mainly via the MAPK pathway. (A) Microvascular endothelial cells were pretreated with either MAPK inhibitor, PD 98059; PKC inhibitor, GF 109203X; or a PI3K inhibitor, Wortmannin or the DMSO vehicle for 1 h before stimulation with 100 ng/ml VEGF for 24 h. Total RNA was isolated and RT-PCR was conducted. Band intensity (arbitrary units) for PIGF-2 was quantified by laser densitometry from at least three separate experiments. Vertical bars represent \pm SEM; P values (* $P < 0.05$, ** $P < 0.01$) indicate the significant difference between VEGF stimulation with and without inhibitor. (B) Microvascular endothelial cells were treated with either 100 ng/ml VEGF or 100 ng/ml VEGF plus PD 98059 for 24 h, after which the cells were lysed by RIPA buffer. The phosphorylation of ERK was detected with anti-phospho-Erk1/2 polyclonal antibody. Positive bands were visualized by an ECL detection system. A representative from three separate experiments is shown.

significantly increased the phosphorylation of ERK 1/2 and that PD 98059 abrogated this phosphorylation induced by VEGF (Fig. 5B).

Discussion

There is increasing evidence that PIGF plays a major role in pathological angiogenesis (Carmeliet et al., 2001; Luttmann et al., 2002a) and that its function differs between different vascular beds. Furthermore, while PIGF has been shown to exert a weak angiogenic effect via binding to VEGFR-1 there is increasing evidence that it acts synergistically with VEGF-A, enhancing the latter's activity (Carmeliet et al., 2001). Activation of VEGFR-1 by elevating PIGF not only results in intermolecular transphosphorylation of VEGFR-2 but also produces a distinct biological effect (Autiero et al., 2003). Studies in PIGF-deficient mice have demonstrated that loss of PIGF reduces vascular leakage induced by skin wounding, allergens and neurogenic inflammation (Carmeliet et al., 2001; Luttmann et al., 2002a). PIGF appears to exert its effect by enhancing the permeability-inducing activity of VEGF as application of endogenous PIGF does not increase vascular permeability in a mouse model (Luttmann et al.,

2002a). Up-regulation of PIGF mRNA and peptide have been demonstrated during angiogenesis (Bottomley et al., 2000; Carmeliet et al., 2001; Khaliq et al., 1998; Nomura et al., 1998; Yamashita et al., 1999); however, temporal expression appears to be dependent on tissue type and the type of pathology. In tissues such as skin (Luttun et al., 2002a) and placenta (Achen et al., 1997), PIGF expression is observed early in the angiogenic process presumably associated with increasing vascular permeability while in the retina and certain tumors its expression is only observed during the later stages of angiogenesis (Carmeliet et al., 2001; Khaliq et al., 1998), suggesting it plays a role in sustaining VEGF-induced angiogenesis. Evidence is provided that PIGF also acts as a survival factor for microvascular endothelial cells (Adini et al., 2002; Cai et al., 2003) by preventing apoptosis.

Little is known about what regulates the expression of PIGF during pathologic neovascularisation. It is considered that, unlike VEGF-A, PIGF is not hypoxia-inducible (Cao et al., 1996; Khaliq et al., 1999; Simpson et al., 1999; Yonekura et al., 1999), although some studies have reported that both hypoxia and hyperoxia can up-regulate PIGF expression during angiogenesis in certain tissues (Khaliq et al., 1999; Nomura et al., 1998). To further investigate the regulation of PIGF expression, we have focussed on VEGF and hyperglycaemia; VEGF because of its prominent role in angiogenesis and its synergism with PIGF; hyperglycaemia because of its association with retinal neovascularisation in diabetes (Boulton et al., 1988; Cai and Boulton, 2002). We show in this study that both endothelial cells and pericytes, the principal cell types of the microvasculature, express PIGF-1 and -2. While PIGF-2 was the major transcript for both endothelial cells and pericytes, its expression was more than 3.5 times greater in endothelial cells compared to pericytes. This is in agreement with the observations of Yonekura et al. (1999) who studied human dermal microvascular endothelial cells and bovine retinal pericytes. The constitutive expression of PIGF-2 in untreated cells may play a role in tissue maintenance as PIGF is known to be expressed at low levels in a variety of tissues. However, the basal levels in cell culture may also reflect, at least in part, “activation” of the cells during the culture process. That VEGF is up-regulated by hypoxia may at least in part explain the reports that hypoxia can up-regulate PIGF. Interpretation from such studies will be highly dependent on the methodology used and the degree of hypoxia obtained (Boulton et al., 1994).

Both VEGF and hyperglycaemia (15 mM glucose) were able to up-regulate PIGF expression at the gene and protein level. Microvascular endothelial cells abundantly express VEGFR-1 and VEGFR-2 (de Vries et al., 1992; Terman et al., 1992) while pericytes express VEGFR-1 only (Takagi et al., 1996). Our observation that VEGF-induced up-regulation of PIGF occurs via VEGFR-2 has several important implications for angiogenesis. First, VEGF up-regulates PIGF via VEGFR-2; in turn, PIGF enhances VEGF-driven

angiogenesis through the unique cross-talking between VEGFR-1 and VEGFR-2. Second, VEGFR-2 is up-regulated in the endothelial cells of new vessels, making them more susceptible to VEGF stimulation. Third, regulation of PIGF via VEGFR-2 will ensure availability of VEGFR-1 for ligand binding. Fourth, this effect is relatively endothelial specific since cells without VEGFR-2, e.g., pericytes, do not up-regulate PIGF in response to exogenous VEGF. However, PIGF may also regulate hematopoietic stem cells (Katoh et al., 1995), retinal progenitor cells (Yang and Cepko, 1996), neurons (Jin et al., 2002) and osteoblasts (Deckers et al., 2002), which all express VEGFR-2. Fifth, PIGF has both an autocrine and paracrine role although the importance of the latter is unclear. Elevated glucose is known to modify endothelial cell and pericyte behavior (Asakawa et al., 1996; Beltramo et al., 2002; Okuda et al., 1996; Romeo et al., 2002; Sato et al., 2001; Williams et al., 1997) including attachment, proliferation, metabolic activity, apoptosis, nitric oxide synthesis and growth factor production. One such growth factor to be up-regulated by elevated glucose is VEGF (De Vriese et al., 2001; Tilton et al., 1997; Williams et al., 1997). Our observation that neutralisation of VEGF inhibits the glucose-induced up-regulation of PIGF supports the observations that (i) glucose up-regulates VEGF in microvascular endothelial cells and (ii) glucose up-regulates PIGF via VEGF and VEGFR-2. Clinically, one of the criteria to diagnose diabetes is if plasma glucose reaches or exceeds 11.1 mM (Edwards et al., 1995). Fifteen millimolars of glucose is therefore within the hyperglycaemic range associated with diabetes while 25 mM glucose is towards the highest levels associate with diabetes and can cause cell cytotoxicity and make cells lose their compensation ability. We conclude that 25 mM glucose has no effect on VEGF production and therefore does not up-regulate PIGF in our test system. This is in general agreement with studies on other cell types that report that glucose levels up to 20 mM up-regulate VEGF with little or no effect at higher concentrations (De Vriese et al., 2001; Sone et al., 1996; Tilton et al., 1997; Williams et al., 1997).

Activation of VEGFR-2 can initiate several intracellular pathways involving PLC- γ , PKC, MAPK and PI3K (Ortega et al., 1999; Zachary and Glick, 2001). In our study, we were able to demonstrate that VEGF greatly increased the phosphorylation of ERK1/2 and PD98059, an inhibitor of MAPK, abrogated this effect and abolished the expression of PIGF induced by VEGF. However, blocking PKC also resulted in a slight reduction in VEGF-induced PIGF expression, suggesting that there is cross-talk between intracellular signaling pathways. Furthermore, the reported PIGF-specific activation of the ERK pathway in porcine aortic endothelial cells suggests that interactions between the VEGFR-1 and VEGFR-2 may serve to regulate both PIGF expression and VEGF action (Landgren et al., 1998).

This study clearly demonstrates that VEGF may play a critical role in the up-regulation of PIGF, which can promote pathological angiogenesis in the following ways: (i)

activated by PIGF, VEGFR-1 transactivates VEGFR-2 and thereby enhances the response to VEGF-A (Autiero et al., 2003); (ii) increasing levels of PIGF will compete for VEGF-A binding to the high-affinity receptor VEGFR-1, which will, in turn, allow VEGF-A to access the lower affinity VEGFR-2. Thus, PIGF can make and keep endothelial cells more sensitive to lower concentrations of VEGF-A that could be supplied by surrounding cells and/or endothelial cells themselves; (iii) PIGF:VEGF heterodimers may supplement low levels of VEGF, thereby contributing to the stimulation of endothelial cell growth (DiSalvo et al., 1995); (iv) the production of the heparin-binding form of PIGF may cause retrieval of sequestered heparin-binding angiogenic factors such as VEGF-A₁₆₅ in a soluble form (Park et al., 1994); (v) PIGF could recruit VEGFR-1-positive bone marrow-derived cells, which have been recently shown to contribute to pathological angiogenesis (Luttun et al., 2002b); (vi) PIGF induces VEGFR-1 signaling independently of cross talk with VEGFR-2 (Autiero et al., 2003; Cai et al., 2003).

Acknowledgments

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