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# **Signaling Regulation of Fetoplacental Angiogenesis**

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# Abstract

During normal pregnancy, dramatically increased placental blood flow is critical for fetal growth and survival as well as neonatal birth weights and survivability. This increased blood flow results from angiogenesis, vasodilatation, and vascular remodeling. Locally produced growth factors including fibroblast growth factor2 (FGF2) and vascular endothelial growth factor (VEGFA) are key regulators of placental endothelial functions including cell proliferation, migration, and vasodilatation. However, the precise signaling mechanisms underlying such regulation in fetoplacental endothelium are less well defined, specifically with regard to the interactions amongst protein kinases, protein phosphatase, and nitric oxide (NO). Recently we and others researchers have obtained solid evidence showing that different signaling mechanisms participate in FGF2- and VEGFA-regulated fetoplacental endothelial cell proliferation and migration as well as NO production. This review will briefly summarize currently available data on signaling mediating fetoplacental angiogenesis with a specific emphasis on protein kinases, ERK1/2, AKT1, and p38 MAPK and protein phosphatases, PPP2 and PPP3.

# INTRODUCTION

During normal pregnancy, dramatically increased feto- and uteo-placental blood flows are highly correlated with fetal growth and survival as well as neonatal birth weights and survivability (Alexander 1974, Rosenfeld *et al.* 1974, Reynolds & Redmer 1995, Reynolds *et al.* 2005). These increased blood flows are primarily caused by angiogenesis, vasodilatation, and vascular remodeling (Barcroft & Barron 1946, Magness & Zheng 1996, Osol & Mandala 2009). Two potent angiogenic factors, fibroblast growth factor 2 (FGF2) and vascular endothelial growth factor (VEGFA), are key factors regulating placental vascular growth, vasodilatation, and vascular remodeling (Brigstock 1991, Klagsbrun & D'Amore 1991, Ferrara *et al.* 2003, Osol & Mandala 2009). Local endothelial production of vasodilators such as nitric oxide (NO) is increased during pregnancy in temporal association with increases in the production of placental angiogenesis and vasodilatation (Myatt 1992, Magness & Zheng 1996, Sladek *et al.* 1997, Magness, 1998, Szukiewicz *et al.* 2005, Brownbill *et al.* 2007, Sprague *et al.* 2010).

FGF2 is one of the most extensively studied members in FGF family, which consists of at least nine structurally related polypeptides (Klein *et al.* 1997, Powers *et al.* 2000). Not only

#### Declaration of interest

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FGF2 is expressed in endothelial cells but it is thought to act as an autocrine factor. However, it is still not fully understood how FGF2 is released from the cells. The cellular response to FGF2 is mediated by binding and activating its high affinity receptors that have cytoplasmic tyrosine kinase domains. Similar to FGF2, VEGFA is also a member of a family of structurally homologous growth factors with a potent angiogenic activity for vascular endothelial cells (Ferrara *et al.* 2003). Biological actions of VEGFA are initiated upon binding to its high affinity receptors including VEGFR1 (Flt1) and VEGFR2 (Flk1/ KDR) (Gille *et al.* 2000, Ferrara *et al.* 2003). VEGFR2 is the major signal transducer of VEGFA, responsible for mediating VEGFA-stimulated major steps of angiogenesis (endothelial cell proliferation and migration) and vasodilatation, whereas VEGFR1 may inhibit VEGFR2-mediated endothelial functions (Gille *et al.* 2000, Ferrara *et al.* 2003). However, knocking down either of these receptors in the mouse impairs vascular growth and development growth during the early embryonic stage, ultimately leading to embryonic death, indicating that both VEGFR1 and VEGFR2 are important for vascular formation and growth during early embryonic stage (Fong *et al.* 1995, Shalaby *et al.* 1995).

Over the past decade, it has become clear that in addition to its vasodilatory activity, NO, serves as a downstream signaling mediates FGF2- and VEGFA-stimulated angiogenesis (Ziche *et al.* 1993, 1994, 1997, Arnal *et al.* 1996, Noiri *et al.* 1997, Babaei *et al.* 1998, Murohara *et al.* 1998, Fulton *et al.* 1999, Morales-Ruiz *et al.* 2000). However, it is still not well defined what the signaling pathways are participating in FGF2- and VEGFA-promoted placental angiogenesis and how NO modulates placental angiogenesis.

#### In Vitro Cell Models

As significant improvements in methodology have occurred over the past two decades (Manjunath *et al.* 2009, Morris 2009), it has become possible to analyze the roles of individual signaling molecule *in vivo*. For example, it is now possible to specifically knock down an individual signaling component in a selected tissue or cell type beyond the embryonic stage using lentivirus-mediated RNA interference in vivo. However, owing to the complexity of signaling networks and technical difficulties, it is still extremely challenging to dissect individual signaling induced by a single factor in tissues and cells *in vivo*, specifically since the same signaling pathway could be activated simultaneously by a number of humoral (i.e., steroid hormone and peptide growth factors) (Klein *et al.* 1997, Powers *et al.* 2000) and physical factors (i.e., shear stress and circumferential stress) (Li *et al.* 2003, 2004, Osol & Mandala 2009, Sprague *et al.* 2009, 2010). Hence, most of our current knowledge on signaling mechanisms governing placental endothelial cell functions has been built on *in vitro* cell models.

It is well established that under normal physiological states, angiogenesis *in vivo* primarily occurs in microvasculature consisting of arterioles, capillaries, and venules, suggesting that endothelial cells isolated from these microvascular beds are the best cell models for studying placental angiogenesis. Indeed, over the last two decades, great efforts have been made to obtain microvascular endothelial cells from human placentas (Challier *et al.* 1995, Kacemi *et al.* 1997, Ugele & Lange 2001, Lang *et al.* 2003, Wang *et al.* 2003, Dye *et al.* 2004). These placental microvascular and macrovascular (i.e., human umbilical and chorionic plate arteries and veins) endothelial cells differ in their embryological origins. For example, the villous capillary endothelia are *de novo* generated from mesodermally-derived haemangioblastic cells in early placental villi and the chorionic plate artery endothelia are derived from allantoic vessels in the connecting stack during early embryonic stage (Benirschke *et al.* 2006a, b, Wang & Zhao 2010). Additionally, these placental microvascular endothelial cells could significantly differ from those generated from macrovessels (i.e., human umbilical veins) in their morphologies and in their responses to certain growth factors such as placental growth factor, but not to others such as FGF2 and

VEGFA (Lang et al. 2003). These placental microvascular endothelial cells reportedly were enriched either from digesting enzyme effluents perfused through placentas via a chorionic artery (Lang et al. 2003) or from enzyme solutions applied to digest placental tissues or terminal villous vessels (Challier et al. 1995, Kacemi et al. 1997, Ugele & Lange 2001, Wang et al. 2003, Dye et al. 2004). These cell preparations, however, were inevitably composed of mixed populations of endothelial cells from both macro- and microvaculatures, possibly including all three types of microvasculatures (arterioles, capillaries, and venules). Specifically, the exact origin of these endothelial cells was hard to confirm due to the lack of specific markers for identifying or separating macro- or micro-vascular endothelium or each individual microvascular endothelium. Given the fact that different origins of endothelia are highly heterogeneous in global gene expression profiles, possibly leading to different cell phenotypes including morphologies, growth rates, and responses to stimuli (Chi et al. 2003, Lang et al. 2003, 2008, Aitsebaomo et al. 2008, Rocha & Adams 2009, dela Paz NG & D'Amore PA 2009), it is still questionable whether these mixed populations of cells can closely represent overall phenotypes of placental endothelial cells in vivo, especially after extensive expansion *in vitro*, during which cells derived from a specific locus are likely to become dominant.

On the other hand, endothelial cells isolated from relatively larger vessels, particularly placental arteries and veins (Zheng et al. 2005, Lang *et al.* 2008, Wang *et al.* 2009) as well as umbilical cord vessels (Chi *et al.* 2003) have been widely used for studying human endothelial functions because of their technical feasibility for obtaining a large number of cells with a high purity from a single type of vessel (Baudin *et al.* 2007). Since the cell proliferative responses to FGF2 and VEGFA were similar between endothelial cells isolated from the placental microvasculature and human umbilical veins (Lang *et al.* 2003), endothelial cells from those large vessels could be used as cell models for studying placental endothelial functions at least in regard with actions of FGF2 and VEGFA. Indeed, much of our current knowledge on regulation of human endothelial functions and signaling mechanisms has been obtained from these endothelial cell models.

### **Protein Kinases**

The cellular responses to FGF2 and VEGFA are mediated by activating their specific receptors that have cytoplasmic tyrosine kinase domains. Upon activation, these receptortyrosine kinases initiate a cascade of cellular protein phosphorylation by protein kinases, including ERK1/2, AKT1, and p38 MAPK (Cobb 1999, Powers et al. 2000, Gille et al. 2000, Boilly et al. 2000, Cross et al. 2003). ERK1/2, a threonine and tyrosine kinase is phosphorylated and activated predominantly by MEK1/2 in the cytosol, translocates to the nucleus, and subsequently stimulates transcription of early response genes (Davis 1993, Blenis 1993, Blumer & Johnson 1994). AKT1 (also referred to as protein kinase B [PKB]) is a serine and threonine kinase, which is one major downstream target of PI3K. The MEK1/2/ ERK1/2 and the PI3K/AKT1 signaling pathway are heavily involved in regulation of cell survival, proliferation, and migration (Rousseau et al. 1997, Cobb 1999, Powers et al. 2000, Gille et al. 2000, Boilly et al. 2000, Matsumoto & Claesson-Welsh 2001, Vivanco & Sawyers 2002,). p38 MAPK is also a serine and threonine kinase comprising at least four isoforms,  $\alpha$ ,  $\beta$ ,  $\gamma$ , and  $\delta$ , and is activated predominantly by MEK3/6. p38 MAPK $\alpha$ ,  $\beta$ , and  $\delta$ isoforms are ubiquitously expressed, whereas  $p38\gamma$  appears to be specially expressed in skeletal muscle. Activation of p38 MAPK was initially considered to be induced by environmental stress and inflammatory cytokines (Kyriakis et al. 1996); however, increasing evidence has shown that p38 MAPK also participates in growth factor-regulated cell functions including growth and migration (Boilly et al. 2000, Cross et al. 2003).

Activation of the ERK1/2, AKT1, and p38 MAPK is well known to play a critical role in FGF2- and VEGFA-stimulated endothelial cell proliferation and differentiation (Sa *et al.* 

1995, D'Angelo *et al.* 1995, Matsumoto *et al.* 2002). However, the integration of these different kinases is extremely complicated in endothelium. It has been shown that activation of both ERK1/2 and PI3K is required for inducing a complete cell proliferation in response to FGF2, but not VEGFA in bovine choroidal endothelial cells (Zubilewicz *et al.* 2001). Similarly, activation of both ERK1/2 and p38 MAPK was also needed to induce FGF2-stimulated cell proliferation and migration in mouse spleen endothelial cells (Tanaka *et al.* 1999). These data suggest important mediation of parallel activation of both ERK1/2/PI3K and ERK1/2/p38 MAPK in growth factor-induced angiogenesis. On the other hand, inhibition of p38 MAPK has been show to enhance VEGFA-induced angiogenesis, accompanied by prolonged ERK1/2 activation in human lung-derived microvascular endothelial (HLDME) cells (Issbrucker *et al.* 2003). Inhibition of p38 MAPK also promoted VEGFA-promoted endothelial cell survival, partially via enhancing activation of the PI3K/ AKT1 pathway in bovine aortic endothelial (BAE) and human umbilical cord vein (HUVE) cells (Gratton *et al.* 2001). Thus, an antagonistic regulation between p38 MAPK and ERK1/2 or AKT1 may also be important for endothelial functions including angiogenesis.

In ovine fetal placental artery endothelial (OFPAE) cells which were derived from secondary and tertiary branches of umbilical cords of late pregnant ewes (Zheng et al. 2005), both FGF2 and VEGFA robustly induced activation of the ERK1/2, AKT1, and p38 MAPK pathways, which at least partially mediated FGF2- and VEGFA-stimulated cell proliferation and migration (Zheng et al. 1999, 2008, Wang et al. 2008, 2009, Song et al. 2009, Liao et al. 2009, 2010, Figs. 1 and 2). Intriguingly, the MEK1/2/ERK1/2 and/or PI3K/ AKT1 pathways differentially mediated the FGF2- and VEGFA-stimulated OFPAE cell proliferation and migration (Zheng et al. 2008, Figs. 1 and 2). For example, inhibition of either of the MEK1/2/ERK1/2 or PI3K/AKT1 pathways alone only partially attenuated the FGF2-stimulated cell proliferation, whereas it completely blocked the VEGFA-stimulated cell proliferation as well as the VEGFA- and FGF2-stimulated cell migration (Zheng et al. 2008, Fig. 1). Similarly, inhibition of p38 MAPK moderately suppressed the FGF2stimulated cell proliferation and migration (Fig. 2), whereas it did not alter VEGFAstimulated cell proliferation (Fig. 2) and migration (Liao et al. 2009, 2010). Additionally, inhibition of MEK1/2 by PD98059 (a selective MEK inhibitor) significantly decreased FGF2- and VEGFA-induced p38 MAPK, but not AKT1 phosphorylation, whereas LY294002 (a selective PI3K inhibitor) and SB203580 (a selective p38 MAPK inhibitor) did not appear to alter ERK1/2 phosphorylation (Fig. 3). These observations suggest that activation of either MEK/1/2/ERK1/2 or PI3K/AKT1 pathway only partially mediates FGF2-stimulated cell proliferation, but is sufficient to mediate the VEGFA-stimulated complete cell proliferation as well as FGF2- and VEGFA-stimulated complete cell migration in OFPAE cells (Zheng et al. 2008). Moreover, activation of the p38 MAPK pathway critically mediated FGF2-stimulated cell proliferation and migration, whereas was not sufficient for mediating VEGFA-induced cell proliferation and migration in OFPAE cells (Zheng et al. 2006, Liao et al 2010). These data imply that unlike the antagonistic roles of p38 MAPK in HLDME, BAE, and HUVE cells (Gratton et al. 2001, Issbrucker et al. 2003), p38 MAPK plays a positive role in regulating FGF2-, but not VEGFA-stimulated angiogenic activities of OFPAE cells. It is noteworthy that distinct signaling pathways might differentially mediate endothelial cell responses to FGF2 and VEGFA in different origins of placental endothelial cells. For example, we have reported that the PI3K/AKT1, but not MEK/ERK1/2 pathway mediates FGF2-stimulated cell proliferation, whereas the MEK1/2/ ERK1/2, but not the PI3K/AKT1 pathway mediates VEGFA-stimulated cell proliferation in human placental artery endothelial cells (Wang et al. 2009). Thus, a complex signaling network may mediate placental angiogenesis via a parallel, synergistic and/or antagonistic manner (Yashima et al. 2001), possibly depending on signaling pathways and other vascular beds.

#### Protein Phosphatases: PPP2 and PPP3

After activation, protein kinases must undergo inactivation, returning to a status ready for the next stimulus. One of such mechanisms to inactivate protein kinases is to dephosphorylate these kinases by protein phosphatases. Reflecting the huge diversity and breadth of functions regulated by protein dephosphorylation, higher eukaryotes encode ~1000 protein phosphatase genes which can be classified into at least three families (Barford *et al.* 1998). Within each family, the catalytic domains are highly conserved, with functional diversity endowed by regulatory subunits. These protein phosphatases can also be cataloged into two major classes: tyrosine phosphatases and serine/threonine phosphatases, depending on their substrates (Liu *et al.* 2007). Serine/threonine phospho-protein phosphatases (PPP), which specifically dephosphorylate phosphoserine and phosphothreonine residues, include PPP1, PPP2 (formally termed as PP2A), PPP3 (PP2B or calcineurin), and PPM1B (PP2C) (Aramburu *et al.* 2004, Wilkins & Molkentin 2004).

PPP2, one of the most extensively studied members of PPP, is believed to make up most of total serine/threonine phosphatase activity in cells (Lechward et al. 2001, Sontag 2001). PPP2 consists of catalytic (C) and scaffolding (A) subunits, which can bind to at least another eighteen regulatory (B) subunits to form a trimeric holoenzyme (see Lechward et al. 2001, Sontag 2001, Cho et al. 2007, Shi 2009 for detail PPP2 structures). In mammals, the C subunit of PPP2 has two major isoforms,  $\alpha$  (PPP2CA) and  $\beta$  (PPP2CB), between which PPP2CA is the most abundant isoform with the mRNA level ~ 10-fold more than PPP2CB in most tissues (Lechward et al. 2001, Sontag 2001). It is still unclear if these two catalytic subunits have distinct functions. However, PPP2CB cannot completely compensate for the absence of PPP2CA in early embryonic development, as knockdown of PPP2CA alone in the mouse lead to early embryonic death, mostly owing to impaired mesoderm formation (Gotz et al. 1998). PPP2 mediates a variety of essential cellular processes such as cell growth, protein synthesis, and metabolism (Lechward et al. 2001, Sontag 2001), which could be partially a result of dephosphorylating and inactivating protein kinases ERK1/2, AKT1, and p38 MAPK (Alessi et al. 1995, Camps et al. 2000, Janssens & Goris 2001, Silverstein et al. 2002, Lee et al. 2003, Liao & Hung 2004, Van Kanegan et al. 2005).

Similar to PPP2, PPP3 is also composed of catalytic and regulatory subunits, including three catalytic ( $\alpha$ ,  $\beta$ , and  $\lambda$ ) and two regulatory (B1 and B2) subunits (Perrino *et al.* 2002, Aramburu *et al.* 2004, Wilkins & Molkentin 2004), among which  $\alpha$ ,  $\beta$ , and B1 subunits are widely expressed in mammalian tissues, whereas  $\lambda$  and B2 subunits are primarily found in the testis and brain (Perrino *et al.* 2004). The PPP3 catalytic subunit  $\alpha$  (PPP3CA) appears to account for the majority (70–80%) of total phosphatase activity of PPP3, while the catalytic  $\beta$  subunit (PPP3CB) constitutes ~ 20–30% (Im & Rao 2004). Like PPP2, PPP3 also participates in many cellular functions (e.g., immune responses, and cardiac hypertrophy), partially via directly dephosphorylating members of nuclear factor of activated T cell (NFAT) transcriptional factors, which in turn could be modulated by ERK1/2 (Aramburu et al. 2004, Wilkins & Molkentin 2004). A positive role of PPP3 in mediating vascular development has been proposed as disruption of *Ppp3r1*, *Nfatc3*, and *Nfatc4* genes in the mouse is embryonic lethal, due to impaired vascular development (Graef et al. 2001). This premise is further supported by the reports that suppression of PPP3 activity by its pharmacological inhibitor cyclosporin A (CsA) attenuated VEGFA-induced angiogenesis in HUVE cells (Hernandez et al. 2001) and intestinal microvascular endothelial cells (Rafiee et al. 2004). This inhibition by CsA was partially mediated via suppressing ERK1/2 and p38 MAPK activation (Rafiee et al. 2004, Farivar et al. 2005). Similar reciprocal relationships between PPP3 and ERK1/2 also have been reported in cardiomyocytes (Molkentin 2004) and in B cells (Gary-Gouy et al. 2006). However, in other types of cells, suppression of PPP3 activity could lead to completely opposite effects. For example, CsA has been shown to enhance ERK1/2 activation in human trophoblast cells (Du et al. 2007) and canine kidney

epithelial cells (Kiely *et al.* 2003). Little is known about the mediation of PPP3 in activation of the PI3K/AKT1 cascade although it has been shown that PPP3 inhibition does not alter activation of the PI3K/AKT cascade in A549 cells (Wen *et al.* 2003).

The involvement of protein phosphatases in regulating endothelial functions has received much less attention as compared to the protein kinases, particularly regarding the roles of PPP2/PPP3 in placental angiogenesis. Recently, we have identified the expression of PPP2CA and PPP3CA in OFPAE cells (Wang *et al.* 2008, Song *et al.* 2009). Nonetheless, suppression of PPP2CA protein expression by its specific siRNA did not significantly affect VEGFA- and FGF2-stimulated OFPAE cell proliferation (Song *et al.* 2009). On the other hand, knockdown of PPP3CA protein by its specific siRNA only moderately enhanced VEGFA-stimulated (~20% increase), but not FGF2-stimulated cell proliferation. Thus, PPP3CA alone has a critical role in modulating VEGFA-stimulated cell proliferation, whereas PPP2CA alone does not have such a role in modulating both VEGFA- and FGF2-stimulated cell proliferation in OFPAE cells.

Failure of PPP2CA suppression to alter VEGFA- and FGF2-stimulated OFPAE cell proliferation is in disagreement with the previous reports showing that inhibition of PPP2 activity promoted cell motility in bovine aortic endothelial cells and primary human mouth endothelial cells (Gabel et al. 1999, Young et al. 2002) and cell proliferation in bovine aortic endothelial cells (Murata et al. 1996). Additionally, although participation of PPP3 in VEGFA-, but not FGF2-stimulated OFPAE cell proliferation was consistent with the previous reports using other endothelial cell types (Hernandez et al. 2001, Rafiee et al. 2004), the PPP3CA knockdown-enhanced VEGFA-stimulated OFPAE cell proliferation also contrasted with these previous reports (Hernandez et al. 2001, Rafiee et al. 2004). It is currently unknown whether different origins of endothelial cells cause these different or complete opposite actions of PPP3CA in modulating cell proliferation. Nonetheless, in those previous studies (Murata et al. 1996, Gabel et al. 1999, Hernandez et al. 2001, Young et al. 2002, Rafiee et al. 2004), inhibition of PPP2 and PPP3 activity was carried out by their pharmacological inhibitors (okadiac acid or cantharidin for PPP2 or CsA for PPP3). Given the specificity of these pharmacological inhibitors is highly dependent on the doses and relatively high doses of pharmacological PPP2 inhibitors were used in these studies, the effects of PPP2 and PPP3 inhibition on endothelial responses by their pharmacological inhibitors might result from suppression of multiple protein phosphatases. Moreover, unlike these pharmacological inhibitors which attenuate/block all catalytic subunits of PPP2 and PPP3, the siRNA used in OFPAE cells targeted only on catalytic subunit  $\alpha$  of PPP2 and PPP3. This specific knockdown of a single catalytic subunit by the siRNA might cause upregulation of PPP2CB and PPP3CB to compensate the loss of phosphatase activity after PPP2CA and PPP3CA suppression, leading to differential modulation of different cell responses. Conversely, the different duration of PPP2 and PPP3 inhibition before growth factor stimulation can also contribute to such different cell responses caused by these pharmacological inhibitors (30 min to 1 hr) and siRNA (at least 16 hr). This supposition is supported by a recent observation that chronic and acute inhibition of PPP2 induced the opposite regulation of ERK1/2 and AKT1 activation since the PPP2 siRNA induced chronic ERK1/2 and AKT1 hyperphosphorylation, downregulating signaling molecules upstream of Ras in response to growth factors including FGF2 (Van Kanegan et al. 2005). In OFPAE cells, suppression of PPP2CA and PPP3CA by their special siRNA did attenuate FGF2induced ERK1/2 and AKT1 activation (Wang et al. 2008, Song et al. 2009). Thus, a negative feedback mechanism might be involved in PPP2CA and PPP3CA modulation of ERK1/2 and AKT1 activation induced by FGF2 in OFPAE cells.

The roles of protein phosphatases in the modulation of placental angiogenesis and underlying signaling are much more complicated than originally thought, as PPP2 and PPP3

differentially modulated the VEGFA- and FGF2-stimulated cell proliferation and signaling cascades in OFPAE cells (Wang *et al.* 2008, Song *et al.* 2009, Fig. 4). Moreover, protein phosphatases other than PPP2 and PPP3 such as MAPK phosphatase and Phosphatase and TENsin (PTEN) homolog could play a more important role in differential modulation of ERK1/2, AKT1, and p38 MAPK activation in placental endothelial cells, ultimately regulating placental angiogenesis.

#### Angiogenesis and Nitric Oxide

Over the past two decades, it has become clear that apart from being a potent vasodilator (Dulak & Jozkowicz 2003), NO is also a key mediator of angiogenesis (Pipili-Synetos et al. 1993, Ziche et al. 1993, 1994, 1997a, b, Noiri et al. 1997, Parenti et al. 1998, Babaei et al. 1998, Murohara et al. 1998, Bussolati et al. 2001, Hida et al. 2004). The participation of NO in mediating angiogenesis was first reported by Pipili-Synetos et al. (1993) using the chick embryo chorioallantoic membrane (CAM) model, in which NO was believed to act as an anti-angiogenic mediator. However, Ziche and colleagues have subsequently provided several lines of evidence showing that NO functions as a positive mediator of angiogenesis (Ziche et al. 1993, 1994, 1997a,b, Parenti et al. 1998). They reported that both exogenous and endogenous NO stimulated cellular DNA synthesis, proliferation and migration in bovine post capillary venule endothelial cells in vitro (Ziche et al. 1993, 1994) and that exogenous NO potentiated angiogenesis in the rabbit "cornea pocket assay", in which VEGFA-induced angiogenesis was also completely inhibited by the NOS inhibitor, L-NAME (Ziche et al. 1997a). Using the same in vivo assay, they further proposed that VEGFA-, but not FGF2-induced angiogenesis was mediated by NOS via the NO/cyclic guanylate monophosphate pathway (Ziche et al. 1997a). Positive involvement of endogenous NO as a downstream signal of VEGFA-induced angiogenesis was confirmed by in vivo observations showing significantly improved angiogenesis in response to dietary supplementation L-arginine in the rabbit (Murohara et al. 1998) and in the rat (eNOS overexpression, Namba et al. 2003) ischemia models, as well as the considerably limited angiogenesis in eNOS knockout mice (Fukumura et al. 2001). Bussolati and colleagues et al. (2001) have also proposed that VEGFR-1 promoted formation of capillary networks in HUVE cells via NO, while inhibiting VEGFR-2-mediated cell proliferation. Exogenous NO can also act as a crucial signal in the angiogenic response, in which NO promotes FGF2induced endothelial cell differentiation into capillary tubes, while terminating the proliferative actions in both HUVE and calf pulmonary artery endothelial cells (Babaei et al. 1998). Thus, NO differentially regulate FGF2- and VEGFA-induced angiogenesis at different steps (i.e., proliferation/migration vs. capillary tube formation).

Expression of eNOS and iNOS has been identified in the placenta of human, rhesus monkey, rat, and sheep (Myatt *et al.* 1993, Conrad *et al.* 1993, Zarlingo *et al.* 1997). In association with robust fetoplacental angiogenesis (Reynolds LP & Redmer DA 1995, Magness RR & Zheng 1996), the NO level was increased in maternal circulation as pregnancy progresses in sheep (Vonnahme *et al.* 2005) and in late human pregnancy (Williams et al., 1997). In ovine cotyledons (fetal side of the placentome) during late pregnancy, eNOS, but not iNOS was present in the fetal component of the placentome, primarily in microvascular endothelial cells in the villous core (Zheng *et al.* 2000), similar to the findings reported in the term placentae of rhesus monkeys, baboon, guinea-pig, rat and sheep (Zarlingo *et al.* 1997). Together with the observation that increased expression of eNOS, but not iNOS protein run parallel to increased total NO (nitrate and nitrite) production (Zheng *et al.* 2000), eNOS seems to be a predominant isoform of NOS responsible for the NO production in the fetal component of the placentome pregnancy. Additionally, these increases in eNOS protein expression and NO production in the fetal component of the placental and nitrite) associated with increased placental vascular density and expression of FGF2

(Magness & Zheng 1996, Zheng *et al.* 1997), supporting a critical role NO in modulate fetoplacental angiogenesis.

Indeed, similar to the NO-mediated angiogenic responses in those endothelial cells reported (Ziche et al. 1993, 1994, 1997a,b, Parenti et al. 1998), exogenous NO (sodium nitroprusside [SNP], a potent NO donor) alone promoted OFPAE and human placental artery endothelial (HPAE) cell proliferation (Zheng et al. 2006) and OFPAE migration (Liao et al. 2010). Of note, NO mediation of angiogenesis is highly dependent on NO levels. At relatively lower levels, NO might be pro-angiogenic as shown in OFPAE cells (Zheng et al. 2006, Liao et al. 2010) and in other endothelial cells (Fukuo et al. 1995, Hida et al. 2004), while at relatively high levels NO could act as a pro-apoptotic or anti-angiogenic factor (Kimura & Esumi 2003, Zheng et al. 2006). These seemingly contradictory observations are likely due to the reaction of NO with super-oxidants, which in turn forms peroxynitrite, causing cytostasis and apoptosis (Pacher et al. 2007, Frey et al. 2009). Interestingly, the stimulatory actions of exogenous NO on OFPAE cell proliferation and migration (Zheng et al. 2006, Liao et al. 2010) were not associated with increased mRNA expression of FGF2, VEGFA, or their major receptors (VEGFR1, VEGFR2, NP1, NP2, and FGFR1) (Zheng et al. 2006). This is contradictory to previous reports demonstrating existence of the VEGFA/FGF2-NO reciprocal regulation between endothelial cells and the surrounding non-endothelial cells, including vascular smooth muscle cells, macrophages, keratinocytes, and tumor cells as described (Tuder et al. 1995, Tsurumi et al. 1997, Dembinska-Kiec et al. 1997, Ziche et al. 1997b, Frank et al. 1999, Namba et al. 2003, Zhang et al. 2003, Dulak J & Jozkowicz A 2003). In these studies, NO either promoted angiogenesis via increasing VEGFA expression in the rat ischemic hindlimb (Namba et al. 2003) and brain (Zhang et al. 2003) or FGF2 expression in bovine coronary venular endothelium (Ziche et al. 1997b) or suppressing mRNA expression of VEGFA and/or its receptors (VEGFR1 and VEGFR2) in rat vascular smooth muscle (Tsurumi et al. 1997), in rat lung tissue (Tuder et al. 1995), and in rat renal mesangial cells (Frank et al. 1999). Thus, the observation that SNP-derived NO failed to alter expression of FGF2, VEGFA, and their major receptors in OFPAE cells cultured under standard cell culture conditions (37° C, 5% CO2, 95% air) (Zheng et al. 2006) implicates that the VEGF/FGF2-NO reciprocal regulation may not occur within placental endothelia, although such regulation may exist between placental vascular endothelia and smooth muscle cells. It is noteworthy that this discrepancy in such NO regulation could also be attributed to different NO donors used since they are known to differentially mediate the cellular responses, possibly due to differences in the amount and duration of NO generation (Dulak & Jozkowicz 2003). Moreover, in our studies, even after stimulated with VEGFA and FGF2 at physiological concentrations, OFPAE and HUVE cells under standard culture conditions produced much lower levels of NO (unpublished data) as compared to those released from SNP at doses  $(1-10 \,\mu\text{M})$  which stimulated OFPAE cell proliferation (Zheng et al. 2006). This suggests that under physiological conditions, NO generated by these endothelial cells might never reach to a dangerous level, even when one assumes the existence of a positive feedback loop for VEGFA/FGF2 and NO between placental vascular endothelial and smooth muscle cells. This phenomenon could also be attributed to the fact that NO itself can negatively regulate eNOS dimerization, expression and/or activity in endothelial cells, possibly via S-nitrosylation, thereby decreasing NO production (Sheehy et al. 1998, Black et al. 1999, Ravi et al. 2004, Kopincova et al. 2011) and potentially preventing apoptosis.

What the downstream signaling is for exogenous NO-mediated angiogenesis is still poorly defined. We have found that an NO donor might activate different signaling pathways, depending on the origin of the cells utilized. For example, SNP induced activation of ERK1/2, but not AKT1 in OFPAE cells, whereas activated both kinases in HPAE cells (Zheng *et al.* 2006). Additionally, a previous report has also shown NO donors (S-nitosol-L-

glutathion and S-nitroso-N-penicillamine) promote migration and angiogenesis of human and bovine endothelial cells via activation of the soluble GC (sGC)/cGMP/PI3K/AKT1 pathway (Kawasaki *et al.* 2003). However, OFPAE cells used (Zheng *et al.* 2006, Liao *et al.* 2010) did not have detectable sGC activity and did not produce cGMP in response to SNP (Itoh *et al.* 1999). Thus, exogenous NO-stimulated angiogenic responses and NO-induced ERK1/2 activation (Zheng *et al.* 2006, Liao *et al.* 2010) are unlikely coupled to the sGC/ cGMP pathway in OFPAE cells.

It is well recognized that FGF2 and VEGFA promote NO production by endothelial cells isolated from either placental (Zheng et al. 2008, Liao et al. 2010) or other non-placental tissues (Cuevas et al. 1991, Kadota et al. 1995, Kostyk et al. 1995, Rousseau et al. 1997, 2000, Babaei et al. 1998, Murohara et al. 1998, Dimmeler et al. 1999, Fulton et al. 1999, 2001, Michell et al. 1999, Morales-Ruiz et al. 2000, Zubilewicz et al. 2001, Fukumura et al. 2001, Namba et al. 2003). In OFPAE cells, FGF2 and VEGFA stimulated NO production via increasing eNOS protein expression (FGF2) or directly enhancing enzymatic activity of eNOS (FGF2/VEGFA) (Zheng et al. 2008, Mata-Greenwood et al. 2008, 2010, Liao et al. 2010), in which FGF2-increased eNOS expression and NO production was mediated primarily by AP-1-dependent transcription involving JunB and Fra1 up-regulation (Mata-Greenwood et al. 2010). After generation, endogenous NO positively mediated both FGF2and VEGFA-stimulated cell proliferation and VEGFA-stimulated migration in OFPAE cells, primarily via an intracellular mechanism (Zheng et al. 2008, Liao et al 2010). However, in contrast to the previous studies showing that NO acted as an upstream signaling of ERK1/2 in VEGFA-stimulated cell proliferation and migration in non-placental endothelial cells (Ziche et al. 1997, Parenti et al. 1998), we found that NO lay downstream of ERK1/2 and AKT1 in OFPAE cells (Li et al. 2004, Zheng et al. 2008), consistent with the observations made in some other types of endothelial cells (Fulton 1999, Dimmeler et al. 1999, Souttou et al. 2001).

Activation of eNOS can be tightly regulated by multiple processes including phosphorylation and nitrosylation (Fulton et al. 2001, Boo & Jo 2003, Kopincova et al. 2011), the former of which has been recognized as critical for eNOS activation (Fulton et al. 2001, Boo & Jo 2003). Human eNOS can be phosphorylated on at least three residues: serine 116 (Ser116) and 1177 (Ser1177; Ser1179 in ovine and bovine) and threonine 495 (Thr495; Thr497 in ovine and bovine). Upon phosphorylation of these residues by the kinases, eNOS activity could be either enhanced (at Ser1177) or attenuated (at Thr495 and Ser116) (Boo & Jo 2003). To date, one of the best-studied signaling pathways which mediate eNOS phosphorylation is PI3K/AKT1. It has been reported that VEGFA-activated PI3K/AKT directly phosphorylates eNOS Ser1179, leading to stimulating NO production, and endothelial migration, proliferation, and capillary-like structure formation (Dimmeler et al. 1999, Fulton et al. 1999, Michell et al. 1999 Morales-Ruiz et al. 2000, Souttou et al. 2001). In OFPAE cells, shear stress-elevated NO production was associated with an increased NOS Ser1179 phosphorylation, which was blocked by PI3K inhibitors Wortmannin and LY294002, but not the MEK inhibitor UO126, suggesting that PI3K/AkteNOS Ser1179 is also major signaling pathways for activating eNOS activity in OFPAE cells (Li et al. 2003, 2004). In contrast to Ser1177, the VEGFA-induced eNOS Ser116 phosphorylation was completely blocked by the protein kinase C inhibitor calphostin, but not by either Wortmannin or U0126 (Kou et al. 2002). Thus, these data indicate that eNOS phosphorylation at different sites is controlled by a variety of protein kinases, coordinating eNOS activity and NO production.

Little is known about signaling pathways modulating eNOS dephosphorylation by protein phosphatases. It has been shown that PPP2 preferentially dephosphorylates eNOS at Thr497 and Ser1177, but not at Ser116, leading to deactivation of eNOS and impaired angiogenesis

(Michell *et al.* 2001, Greif *et al.* 2002, Urbich *et al.* 2002, Leidi *et al.* 2010). Intriguingly, NO was also able to activate PPP2 to modulate chromatin folding in HUVE cells (Illi *et al.* 2008). Thus, the reciprocal interactions between protein phosphatases and NO might play a critical role in mediating placental angiogenesis.

#### **Conclusions and Perspectives**

In conclusion, an increasing body of evidence either from our laboratories or other investigators has shown that FGF2 and VEGFA regulate fetoplacental angiogenesis via an extremely complex signaling network involving multiple of protein kinases and phosphatases as well as NO (Fig. 4). While much progress has been made, many difficult challenges still remain for dissecting signaling mechanisms underlying fetoplacental angiogenesis. For example, how can we isolate, establish, and maintain fetoplacental microvascular endothelial cell models with highly homogenous cellular purity? What and how are protein phosphatases activated and how do they modulate activation of protein kinases in fetoplacental angiogenesis? Moreover, to date, almost all endothelial cell models used to study placental angiogenesis have been cultured and expanded under an ambient  $O_2$ level (~ 21% or pO<sub>2</sub> ~ 160 mmHg), which obviously does not closely reflect in vivo physiological O2 levels under which placental endothelial cells constantly reside (~ 1.5-8.0%  $O_2$  or  $pO_2 < 12-60$  mmHg) (Meschia 2004, Bertout *et al.* 2008). These endothelial cells cultured under such a condition might represent a subpopulation of endothelial cells which have adapted to hyperoxia. Therefore, culturing and investigating placental endothelial cells under chronic physiological O2 levels are critical to provide information on fetoplacental angiogenesis and underlying signaling mechanisms, more closely mimicking in vivo states.

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A. Represent Images of OFPAE Cell Migration



B. Quantitative Analysis for OFPAE Cell Migration



#### Figure 1.

Effects of PD98059 and LY294002 on FGF2- and VEGFA-Stimulated OFPAE Cell Migration. Cell migration was measured using a Multiwell BD Falcon FluoroBlok Insert System (8.0-um pores, BD Biosciences). Cells were treated with 10 ng/ml of FGF2 or VEGFA in the absence or presence of PD98059 or LY294002 (1 hr of pretreatment). Cells were counted after 16 hr of treatment. A) Representative images are shown, in which concentrations of PD98059 and LY294002 were at 40 and 6  $\mu$ M, respectively. *Bar* = 100  $\mu$ m. B) Data are expressed as means  $\pm$  SEM % of the controls. All data were analyzed using one-way ANOVA. When an F test was significant, data were compared to the control by Bonferroni's multiple comparisons or Student's t test. \*differ from the control (n = 5; *p* ≤ 0.05).



#### Figure 2.

Effects of SB203580 on FGF2- and VEGFA-Stimulated Cell Proliferation and FGF2-Stimulated Cell Migration in OFPAE Cells. A) A time course for FGF2- and VEGFAinduced phosphorylation of p38 MAPK. *Note*: 1) Both FGF2 and VEGFA (10 ng/ml) rapidly (~ 10 min) induced ( $p \le 0.05$ ) overall p38 MAPK phosphorylation; 2) FGF2 appeared to be much more potent in inducing p38 MAPK phosphorylation as compared to VEGFA; and 3) FGF2 and VEGFA did not significantly alter protein levels of total p38 MAPK (p38). Data shown were collected after 10 min of FGF2 and VEGFA stimulation, pooled from all three p38 MAPK isoforms, and analyzed as described above. Data normalized to total p38 are expressed as means ± SEM fold of the controls. \*differ from the

control (n = 5;  $p \le 0.05$ ). B) Effects of SB203580 on OFPAE cell proliferation and migration. Cell proliferation assay was carried out using a crystal violet method. Cells were treated with 10 ng/ml of FGF2 or VEGFA in the absence or presence of SB203580 (1 hr pretreatment). Cells were counted after 72 or 16 hr of treatments, respectively for cell proliferation and migration assays.



#### Figure 3.

Effects of PD98059, LY294002, and SB203580 on Phosphorylation of ERK1/2, AKT1 and p38 MAPK Induced by FGF2 and VEGFA in OFPAE Cells. After 16 hr of serum starvation, cells were treated with 10 ng/ml of FGF2 or VEGFA for 10 min in the absence or presence of PD 98059 (20  $\mu$ M), LY294002 (5  $\mu$ M), or SB203580 (10  $\mu$ M) (1 hr pretreatment). Proteins (20 $\mu$ g/lane) were subjected to Western blotting using antibody against phosphospecific ERK1/2 (pERK1/2; 1:2000), AKT1 (pAKT1; 1:1000) or p38 MAPK (pp38; 1:1000).



#### Figure 4.

A Proposed Model of the Signal Transduction Pathways for FGF2- and VEGFA-Stimulated Proliferation and Migration in OFPAE Cells. In this working model, we propose that FGF2 and VEGFA activate ERK1/2, AKT1, and p38 MAPK, which in turn increase eNOS protein expression and/or eNOS activity, increasing NO production. This increased NO as an intracellular signaling modulates FGF2- and VEGFA-stimulated cell proliferation and migration. Inhibition of PPP3CA, but not PPP2CA enhances VEGFA-, but not FGF2- stimulated cell proliferation, while failing to affect FGF2- and VEGFA-induced activation of ERK1/2 and AKT1, suggesting that yet to be identified signaling molecules play an important role in FGF2- and VEGFA-stimulated cell proliferation after knockdown of PPP3CA in OFPAE cells.