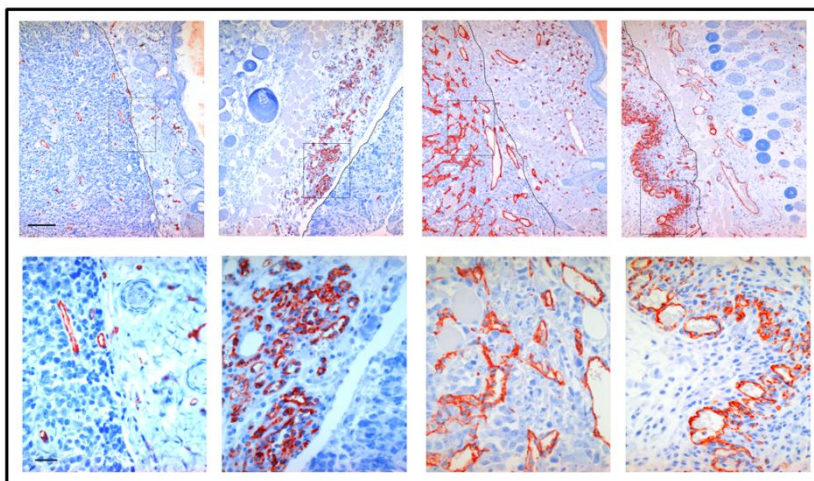


LABORATORY OF CONNECTIVE TISSUES BIOLOGY

Professor A. Colige

Doctor C. Lambert

**Cooperation between carboxy-terminal domains of VEGF-A dictates
its biological properties *in vitro* and *in vivo***



DELCOMBEL Romain

**Thesis presented to obtain the degree of
PhD in Pharmaceutical and Biomedical Sciences**

Academic year 2012-2013

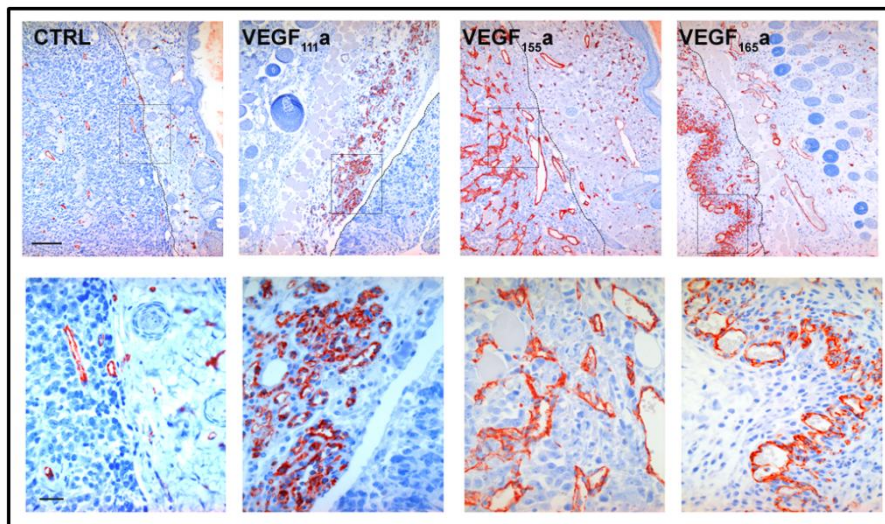
UNIVERSITY OF LIEGE
FACULTY OF MEDICINE

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Blood vessels staining (anti-CD31 antibody) in tumours formed by HEK293 cells (either control or expressing VEGF_{111a}, VEGF_{155a} and VEGF_{165a}) and in adjacent healthy tissues (upper panel: 10x magnification, lower panel: 40x magnification).

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ABBREVIATIONS LIST

Ala:	Alanine
ALT:	Alanine Transaminase
AMD:	Age-related Macular Degeneration
Ang:	Angiopoietin
Arg:	Arginine
Asn:	Asparagine
Asp:	Aspartic acid
AST:	Aspartate Transaminase
BSA :	Bovine Serum Albumin
CNV:	Choroidal Neovascularization
Cys:	Cysteine
Dll:	Delta-like ligand
dpf:	day post fertilization
DSS:	Distal Splice Site
DV:	Draining Veins
E:	Exon
EC:	Endothelial Cells
ECM:	Extra-Cellular Matix
EGF:	Epidermal Growth Factor
EPC:	Endothelial Progenitors Cells
ERK:	Extracellular signal-regulated kinases phosphorylation
ESM:	Endothelial-cell Specific Molecule
FA:	Feeder Arteries
FAK:	Focal Adhesion Kinase
FBS:	Fœtal Bovine Serum
FGF:	Fibroblast Growth Factor
GAG:	GlycosAminoGlycan
Gln:	Glutamic acid
Glu:	Glutamine
GMP:	Glomeroid Microvascular Proliferation
H:	Heparin
h:	hour (s)
HIF:	Hypoxia-Inductible Factor
His:	Histidine
HRP:	HorseRadish Peroxydase
HSPG:	Heparan Sulfate ProteoGlycans
HUVEC:	Human Umbilical Vein Endothelial Cells
Ig:	Immunoglobulin
IGF:	Insulin-like Growth Factor
IP:	Intraperitoneal
IU:	International Unit

IV:	Intravenous
Ka:	Constant of association
Kd:	Constant of dissociation
kD:	kiloDalton
LDH:	Lactate DeHydrogenase
Leu:	Leucine
Lys:	Lysine
M:	Molar
MAPK:	Mitogen-Activated Protein Kinase
min:	minute (s)
MMP:	Matrix MetalloProteinase
MV:	Mother Vessels
NO:	Nitric Oxide
NRP:	Neuropilin
OD:	Optical Density
OIR:	Oxygen Induced Retinopathy
PAEC:	Porcine Aortic Endothelial Cells
PBS:	Phosphate Buffered Saline
PBT:	PBS-BSA 0,5%-tween-80
PC:	Pericytes
PDGF:	Platelet-Derived Growth Factor
Phe:	Phylalanine
PIGF:	Placental Growth Factor
Pro:	Proline
PSS:	Proximal Splice Site
ROP:	Retinopathy of Prematurity
RPE:	Retinal Pigment Epithelial cells
RU:	Response Unit
s:	second
SC:	Subcutaneous
SDS-PAGE:	Sodium Dodecyl Sulfate-PolyAcrylamide Gel Electrophoresis
Ser:	Serine
SF:	Splicing Factor
sNRP:	soluble Neuropilin
SPR:	Surface Plasmon Resonance
SR-proteins:	Serine and Arginine rich proteins
TGF:	Transforming Growth Factor
Thr:	Threonine
Tie:	Tyrosine kinase with immunoglobulin-like and EGF-like domains
TKI:	Tyrosine Kinase Inhibitor
TNF:	Tumor Necrosis Factor
Trp:	Tryptophan
Tyr:	Tyrosine
uPA:	urokinase-type Plasminogen Activator
VEGF:	Vascular Endothelial Growth Factor
VEGF-R:	Vascular Endothelial Growth Factor Receptor

VM:	Vascular Malformation
VPF:	Vascular Permeability Factor
VSMC:	Vascular Smooth Muscle Cell
WT1:	Wilms Tumour protein 1
α -SMA:	Alpha Smooth Muscle Actin

GENERAL INTRODUCTION

I- Processes of novel vessels formation

I-1 Generalities

I-1-1 Blood vessels types

Nearly 100.000 kilometers of blood vessels and capillaries cover the entire volume of the human body. In a highly organized circuit, blood oxygenated in the lungs is pulsed from the heart to the organs by aorta, arteries, arterioles and finally capillaries that allow exchanges with the extra-vascular compartment. Blood flows then into veinules and veins up to the lung to enable its reoxygenation.

The inner lining of all types of blood vessels is the endothelium formed by vascular endothelial cells (Mehta and Malik, 2006). Capillaries are the simplest vessels. They can be considered as immature or mature depending on the presence of a continuous basement membrane and of mural cells, referred to as pericytes (Gerhardt and Betsholtz, 2003; Sims, 1991) (Fig 1A) that play critical functions in the stabilization of the vessels (Benjamin et al., 1998; Dor et al., 2002). The intermediate (arterioles and veinules) and large (arteries and veins) vessels are surrounded by one or many layers of vascular smooth muscle cells (VSMC) (Gerhardt and Betsholtz, 2003) located at the interface between the endothelium and the surrounding tissue. This localization close to endothelial cells gives VSMC a crucial role in angiogenesis, notably by secreting growth factors (Allt and Lawrenson, 2001; Sims, 1986).

I-1-2 Blood vessels origin

The development of the blood vascular system is one of the earliest events in embryogenesis, all other organs depending on vascular supply for delivery of nutrients and oxygen and for clearance of wastes. During embryonic development, the nascent vascular network is formed through two processes (Fig 1B). In the first one, identified as vasculogenesis, new vessels form *de novo* via the assembly of mesoderm-derived precursors (hemangioblasts differentiating in angioblasts) that evolve into a primitive vascular labyrinth (Eichmann et al., 1997; Isner and Asahara, 1999). In the second process, referred to as angiogenesis, the pre-existing vasculature progressively spreads through a mechanism of vessel sprouting (also called capillary branching) (Karamysheva, 2008). These two processes, together with progressive remodelling mechanisms will finally end up into a highly organized and stereotyped vascular network of large vessels ramifying into smaller ones (Carmeliet, 2000; Potente et al., 2011) (Fig 1B).

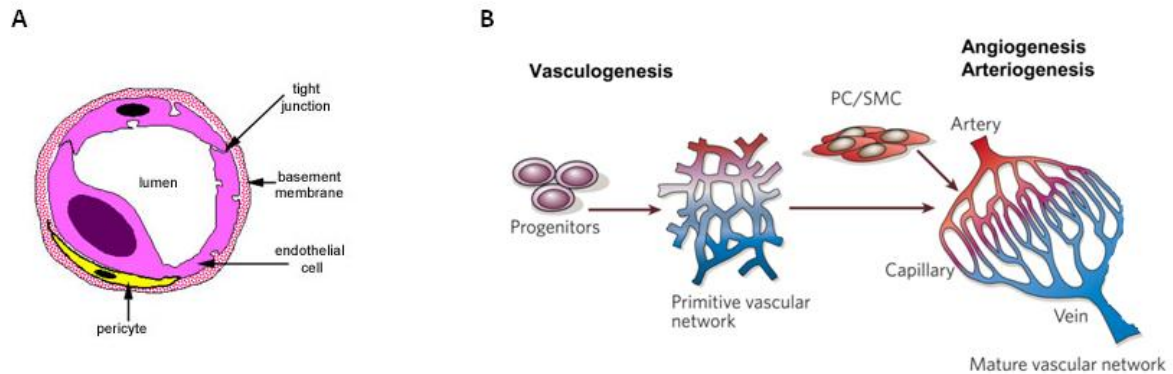


Figure 1 : Development of the vascular system

(A) Mature capillaries are formed by endothelial cells surrounded by a basement membrane and partly covered by pericytes. (B) Vessels development during embryogenesis. By vasculogenesis, endothelial progenitors (hemangioblasts) give rise to a primitive vascular labyrinth of arteries and veins. During the subsequent step of angiogenesis, the network extends and pericytes (PCs) and smooth muscle cells (SMCs) cover nascent endothelial channels. *From (Carmeliet, 2005)*

1-1-3 Blood vessel formation in adulthood

In adulthood in physiological conditions, the formation of new blood vessels is highly regulated and restricted to some defined situations such as embryonic implantation, wound healing and menstrual cycles for example. Excessive or abnormal angiogenesis is a key process in cancer, ocular or inflammatory diseases but is also implicated in pathological conditions such as asthma, diabetes, cirrhosis, multiple sclerosis, endometriosis, obesity and autoimmune diseases (Carmeliet, 2005). By contrast, insufficient angiogenesis is observed in ischemic disorders, pre-eclampsia and chronic ulcers.

Angiogenic sprouting (Fig 2A) is the main, but not the unique, mechanism of blood vessel formation in the adult (Adams and Alitalo, 2007; Carmeliet and Jain, 2011). Indeed, endothelial precursors cells (EPC) can be mobilized from bone marrow or from tissue niches and incorporated into the walls of growing blood vessels where they differentiate into endothelial cells. This process corresponds to the previously mentioned vasculogenesis (Fig 2B) (Kirton and Xu, 2010). Intussusception is another process allowing the spreading of the vascular network. It involves transluminal tissue pillars development and fusion within a mother blood vessel, thus delineating two new daughter vessels (Burri et al., 2004; Kurz et al., 2003) (Fig 2 C).

1-1-4 Blood vessel development in cancer

Interactions between cancer cells and their microenvironment are crucial for promoting tumour growth and invasiveness. Together with degradation and remodelling of the peritumoural extracellular matrix, development of blood vessels is a key factor regulating

cancer progression (Ferrara and Kerbel, 2005) by allowing the supply of sufficient amounts of oxygen and nutrients (Folkman, 1995). It is usually considered that the growth of tumours beyond 2-3 mm³ and the formation of metastases are largely dependent on angiogenesis (Folkman, 1972). Recently, additional mechanisms of vascularization have been identified in tumour environment (Carmeliet and Jain, 2011) (Fig 2D-F). For vessel co-option, appearing usually in well-vascularized tissues, cancer cells initially associate with and grow preferentially along pre-existing normal vessels. This favours tumour growth without any actual angiogenic response. By contrast, in vascular mimicry and cancer stem cell differentiation, cancer cells directly participate in blood vessel formation by differentiating and functioning as endothelial cells. These different processes may exist concomitantly in the same tumour or may be selectively involved in a specific tumour type or host environment.

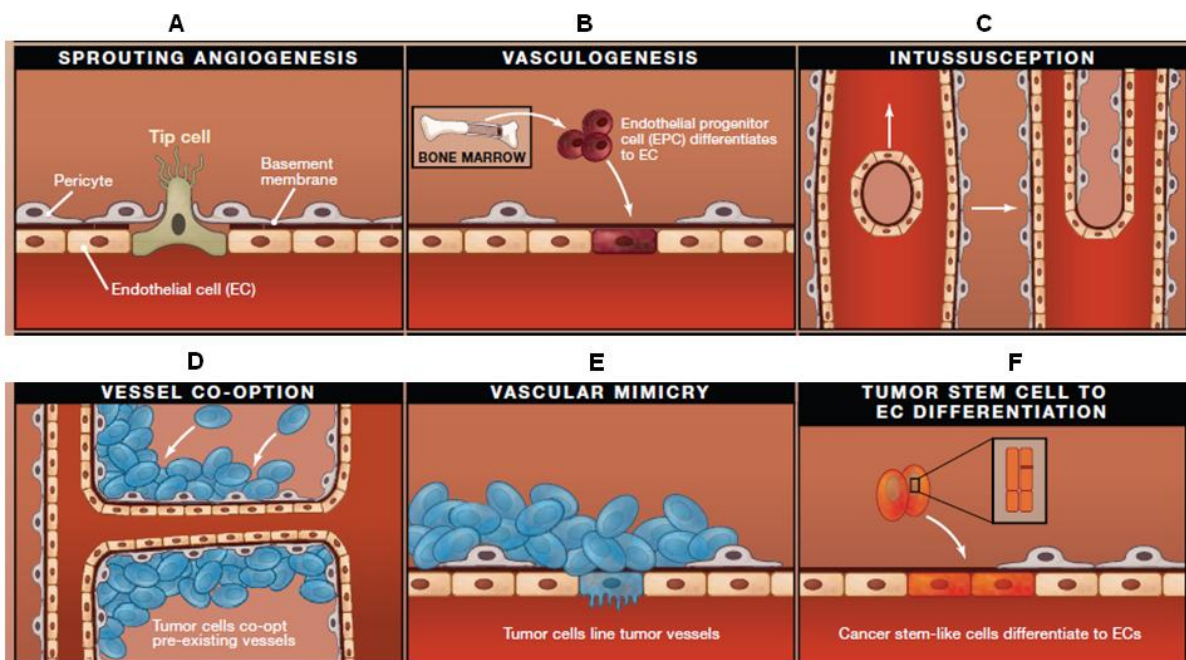


Figure 2 : Blood vessels formation in normal tissues and tumours.

Blood vessels can be formed by sprouting angiogenesis (A) and by vasculogenesis (B), a process involving the recruitment of bone-marrow-derived endothelial progenitor cells (EPCs) that differentiate into endothelial cells (ECs). Intussusception refers to a mechanism where a vessel is split in two vessels of smaller diameter (C). Tumours cells can grow along the pre-existing vessels by a mechanism referred to as vessel co-option (D) or can participate to tumour vessel formation together with endothelial cells (vascular mimicry, E). Endothelial cells with cytogenetic abnormalities and probably deriving from putative cancer stem cells have also been described in the literature (F). Unlike normal tissues, which use only angiogenesis, vasculogenesis and intussusception (A-C), blood supply in tumours can rely on any of the six modes of vessel formation (A-F). *From (Jain and Carmeliet, 2012)*

I-2 Cellular and molecular mechanisms of angiogenesis

Angiogenesis is initiated by various types of stimuli, including hypoxia, inflammation and mechanical solicitation such as shear stress (Milkiewicz et al., 2006). In hypoxic conditions, the cellular level of HIF1 α (Hypoxia-Inducible Factor 1 α) is increased, resulting in vascular endothelial growth factor-A (VEGF-A or VEGF) synthesis and secretion, which, in turn, participates to the recruitment of blood vessels towards hypoxic tissues (Kelly et al., 2003).

The process of sprouting angiogenesis involves several sequential steps, each requiring the coordinated action of mechanisms involving the activation of a large set of ligands and receptors (Karamysheva, 2008). The overall process is depicted in Figure 3.

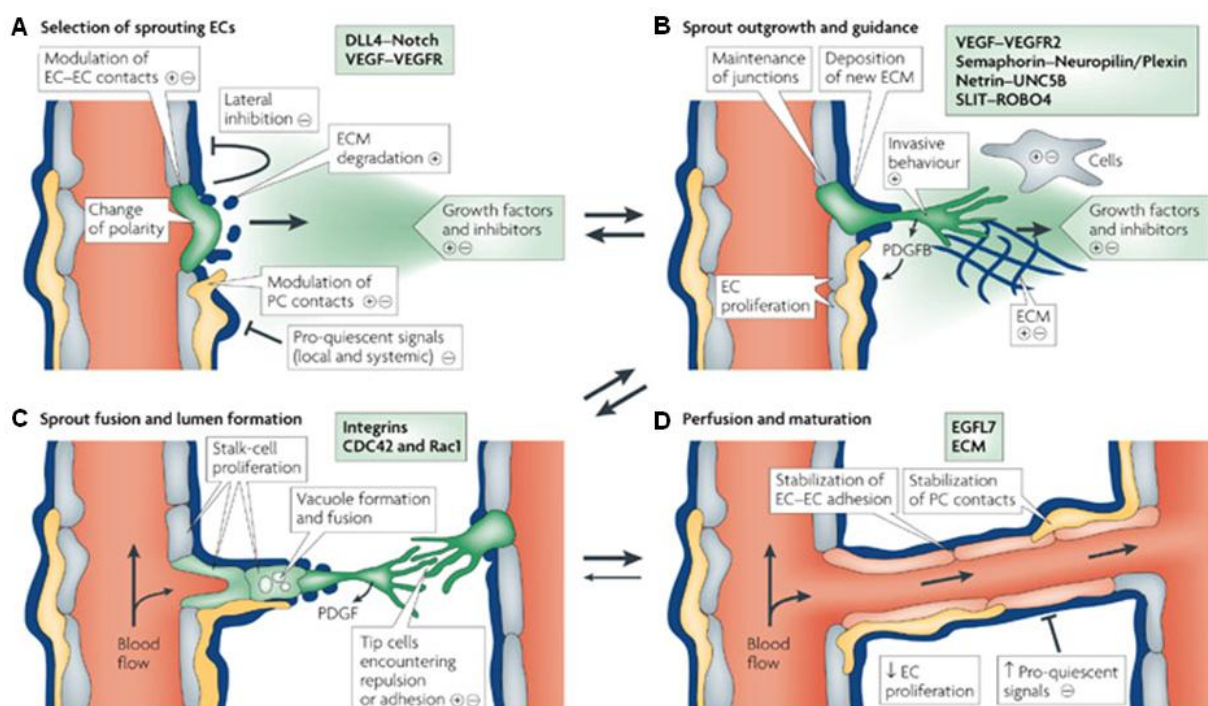


Figure 3 : Angiogenic sprouting

(A) Sprouting angiogenesis is promoted when pro-angiogenic processes (+) overwhelm anti-angiogenic (-) ones. In these conditions, some endothelial cells (EC) (green) are selected among others (grey) to become “tip cells” able to sprout. Sprouting is composed of several crucial steps: the adoption of an apico-basal polarity, the induction of motility and invasiveness, the modulation of the contacts with adjacent cells (other EC and pericytes, PC) and the degradation of the surrounding matrix (ECM). **(B)** The growing EC sprout is guided by a gradient of growth factors, such as VEGF. Other cues may include attractive (+) or repulsive (-) signals from matrix and cells found in the tissue environment. Then, the “tip cells” secrete PDGF to induce the recruitment of PC to the newly formed vessel. These cells allow to maintain EC-EC junctions and to prevent excessive vessel permeability. **(C)** Adhesive and repulsive interactions occur when “tip cells” meet each other. This controls the fusion of adjacent sprouts and the formation of the new vessel. **(D)** Fusion processes at the EC-EC interfaces establish a continuous lumen. As blood flow improves oxygen delivery the hypoxia-induced pro-angiogenic signals are reduced. Blood circulation also promotes the final maturation processes consisting in stabilization of cell junctions, matrix deposition and tight PC attachment. **From (Adams and Alitalo, 2007)**

I-2-1 Increase of vascular permeability

VEGF secretion controls the initial step of angiogenesis by inducing dilatation and increased permeability of the vessels. These two processes involve nitric oxide pathway (NO, see paragraph VI-2) and the remodelling and destabilization of the junctions between adjacent endothelial cells (Dejana et al., 2009). This results in the release of plasma proteins in the ECM to form a provisional scaffold permissive for the migration of endothelial cells (Potente et al., 2011). Prior to endothelial cells migration, mature vessels need to be destabilized. This process is induced by Angiopoietin 2 (Ang 2) and includes VSMC detachment and degradation of the surrounding matrix by several proteolytic enzymes, such as MMP (Matrix Metalloproteinases). These proteases further release and/or activate growth factors sequestered within the extracellular matrix (Thomas and Augustin, 2009).

I-2-2 Endothelial cell proliferation and migration

Some endothelial cells within the vessel wall are elected to initiate the newly formed vessel formation. These cells are named “tip cells” because they migrate and lead the growing sprout. The neighbouring endothelial cells form the “stalk” of the vascular sprout, proliferating and staying behind to maintain the integrity and perfusion of the growing vascular bed (Gerhardt et al., 2003).

The “tip” or “stalk” phenotype is mainly regulated by the VEGF-VEGFR2 and Notch-Dll4 pathways. First, VEGF-A signalling via VEGF-R2 (VEGF-Receptor 2) induces the chemotactism and the invasiveness of the “tip cell”. It also stimulates Dll4 (Delta-like ligand 4) expression in “tip cells” which activates Notch receptors in adjacent cells, which is responsible for the induction of the “stalk cell” phenotype (Liu et al., 2003; Sainson et al., 2005; Uyttendaele et al., 2001). As Notch activation also induces Dll4, this mechanism propagates the Dll4-Notch-mediated lateral inhibition along the developing vessels, limiting therefore the number of “tip cells” and precluding anarchic vascular development (Hellstrom et al., 2007; Suchting et al., 2007).

In addition to motility features, “tip cells” are also characterized by a proteolytic phenotype responsible for invasiveness. Indeed, they secrete MMPs that are able to breakdown the basement membrane and the surrounding matrix. “Tip cells” also possess numerous filipodial protrusions sensing in their environment the gradients of different attractive (eg. VEGF) and repulsive cues allowing tightly regulated guidance of the sprout (Gerhardt et al., 2003). When a “tip cell” moves forward up to a “tip cell” of another sprout or to existing capillaries, it loses its motile phenotype and establishes strong EC-EC adhesive interactions (Karamysheva, 2008). During all these processes, “stalk cells”, controlled by the VEGF-

VEGFR2 axis, maintain vessel integrity by proliferating and maintaining contacts together and with the leading tip cell (Adams and Alitalo, 2007; Adams and Eichmann, 2010; Chung et al., 2010; Eilken and Adams, 2010; Herbert and Stainier, 2011; Potente et al., 2011).

I-2-3 Lumen formation

The establishment of blood flow requires the formation of a lumen, which may occur within the sprout before or after they have joined with other vessels. Initially, forming blood vessels consist of multicellular rods of endothelial cells that are interconnected by uniform junctions. Thus, the formation of the lumen needs a lateral redistribution of adhesion molecules and the acquisition of an apico-basal polarity. This process is further expanded by several mechanisms that may be cell or situation dependent. For instance, we can mention modifications of cell shape or the formation and the coalescence of intracellular vacuoles that fuse with the apical surface of the cells delimitating the lumen (Herbert and Stainier, 2011).

I-2-4 Vessels stabilization and maturation

The generation of a lumen and the onset of blood circulation improve oxygen delivery which consequently decreases the local VEGF production (Karamysheva, 2008). This resolution phase is associated with the interruption of endothelial cells proliferation. Endothelial cells secrete platelet-derived growth factor-B (PDGF-B), which promotes recruitment of pericytes to nascent vessels (Hellstrom et al., 1999; Lindahl et al., 1997). Pericytes establish then direct contacts with endothelial cells in the immature vessels (Gerhardt and Betsholtz, 2003). Vessel maturation relies also partly on transforming growth factor β (TGF β) signalling which stimulates mural cell formation (Gerhardt and Betsholtz, 2003) and also promotes the production of extracellular matrix molecules.

Several other signalling pathways are further implicated in these maturation processes, such as Ang1 ligand/Tie2 receptor (Tyrosine kinase with Immunoglobulin-like and EGF-like domains 2) signalling (Holash et al., 1999; Ramsauer and D'Amore, 2002; Suri et al., 1996). Finally, secretion of specific extracellular matrix molecules by endothelial cells and surrounding cells results in the formation of a subendothelial basement membrane and the transition to a quiescent state (Adams and Alitalo, 2007; Chung et al., 2010; Potente et al., 2011).

I-3 Specific aspects of cancer blood vessels

Pathological angiogenesis relies on many similar inducers, regulators and mechanisms as those involved in physiological neo-vessels formation. A striking difference is however

observed at the end of the process. In physiological conditions, perfusion of the new vessel initiates cascades that will contribute to its final maturation and terminate angiogenesis. By contrast, during pathological conditions, such as tumour angiogenesis, the angiogenic cascade is persistent and generates an anarchic formation of blood vessels (Sitohy et al., 2012). This specific aspect is driven by VEGF over-expression and gives rise to 6 different types of vessels by angiogenesis and arterio-venogenesis (Fig 4) (Nagy et al., 2010; Nagy et al., 2007). In the first process, small capillaries and veinules are transformed in “*mother vessels*”, enlarged vessels devoid of pericyte and basement membrane. This structure can then evolve into three types of “*daughter vessels*”:

- “*Glomeroid Microvascular Proliferation*” units, which are poorly ordered structures composed of proliferative endothelial cells, pericytes and macrophages;
- “*capillaries*”, obtained by a process of intussusception
- “*vascular malformation*”, a mother vessel which acquired a dense coat of VSMC.

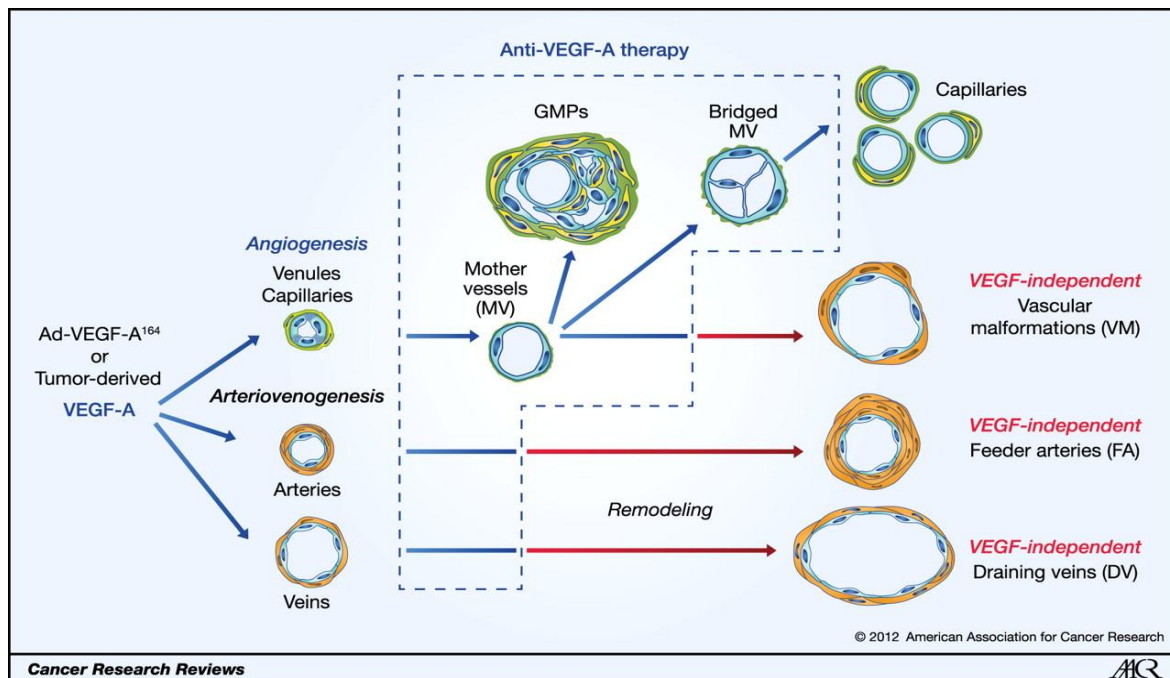


Figure 4 : Blood vessel types observed in tumours or after implantation of adenovirus expressing VEGF₁₆₄

VEGF expressed by tumour cells is responsible for the formation of typical cancer blood vessels. “Mother vessels” (MV), derived from capillaries and veinules, give rise to “Glomeroid Microvascular Proliferation” (GMPs) units, “Vessel Malformations” (VM) and, by a process of splitting, new “Capillaries”. Remodelling of arteries and veins generates respectively “Feeder arteries” (FA) and “Draining Veins” (DV). These latter vessel types, as well as “Vessel Malformation” and Capillaries, are surrounded by VSMCs (orange) and/or pericytes (yellow), a sign of maturation conferring resistance to anti-VEGF therapy. By contrast, “Mother vessels” and “Glomeroid Microvascular Proliferation” units have been described to be sensitive to anti-VEGF therapy (Dashed line box). *From (Sitohy et al., 2012).*

Arteries and veins are also affected during tumour angiogenesis. They undergo an enlargement resulting from proliferation of endothelial cells and VSMC to give birth to *feeder arteries* and *draining veins*. These vascular patterns determine resistance or sensitivity to anti-VEGF therapy (see chapter VII).

II- Alternative splicing

In Eukaryotes, most of the genes are transcribed as pre-mRNA composed by an alternation of coding (exons) and non-coding (introns) sequences (Berget et al., 1977; Chow et al., 1977). During a maturation step, introns are then spliced out while exons are joined together to form mature mRNA. This process is referred to as constitutive splicing when it remains unchanged in any condition. For more than 90 % of the genes, however, such as VEGF-A for example (Munaut et al., 2010), the pre-mRNA can give rise to several mRNA and proteins through a process of alternative splicing of defined sequences (Hilmi et al., 2012; Wang et al., 2008). This highly regulated mechanism can lead to a variety of combinations such as exclusion of one, several or part of exons or retention of sequences that are intronic in other transcripts (Fig 5). The different mRNA variants can then encode different proteins that may possess distinct or, sometimes, opposite functions.

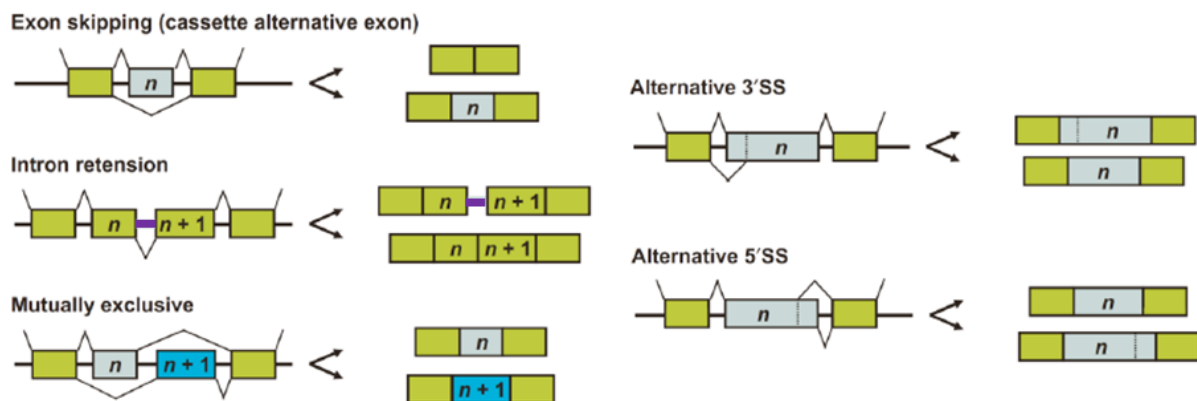


Figure: 5 Mechanisms of alternative splicing

Constitutive splicing refers to a mechanism leading always to an identical process of intron excision and exon joining. Introns are represented by black or violet lines and exons by green, grey or blue boxes, respectively. Alternative splicing of pre-mRNA can generate several isoforms (variants) of mRNA and proteins. Several mechanisms of alternative splicing can affect pre-mRNA such as “cassette exon” splicing (skipping of one or several complete exons), “intron retention” (a situation where the newly included sequence (violet line) can be formally considered as an intron for other variants), “mutually exclusive exons” (one exon (grey) or the other (blue) is present, but never both together) and “alternative 3’ or 5’ splice site (SS)” selection. **From (Miura et al., 2012)**

Several regulatory cascades and factors control the alternative splicing process. For instance, Akt (Blaustein et al., 2005) or SR-proteins kinases, SRPK1 and SRPK 2 (Nowak et al., 2010), can act as potent regulators by phosphorylating the SR-proteins (Serine and Arginine rich proteins) which induces their translocation to the nucleus where they can affect splicing decisions (Stamm, 2008).

During cancer formation and progression, pre-mRNA of many genes undergo alternative splicing to give rise to novel variants conferring specific advantages to tumour cells (Miura et al., 2012; Skotheim and Nees, 2007). Furthermore, many chemotherapeutic agents can alter alternative splicing (Sumanasekera et al., 2008). An interesting example is the generation of a novel VEGF variant, VEGF₁₁₁, by treating various tumour cells with cytotoxic drugs (Mineur et al., 2007). This example has a direct link with our work and will be therefore detailed below (see paragraph IV-8).

III- Vascular Endothelial Growth Factor-A

III-1 Discovery and generalities

VEGF-A, usually referred to as VEGF, is a glycoprotein described by N. Ferrara (Ferrara and Henzel, 1989) in the conditioned culture medium of pituitary gland cells as a factor able to trigger endothelial cells proliferation. It was also previously identified as VPF (Vascular Permeability Factor), a factor secreted by numerous tumour cells lines (Senger et al., 1983) or as FSdGF (Follicular Stellate-derived Growth Factor) (Gospodarowicz et al., 1989) and Vasotropin (Plouet and Moukadiri, 1990b; Plouet et al., 1989).

VEGF-A is now considered as the main growth factor regulating both physiological and pathological angiogenesis (Ferrara, 2004; Ferrara and Alitalo, 1999). Its expression is crucial for development as inactivation of a single VEGF allele in mice causes early embryonic mortality due to deficient endothelial cell proliferation, defective blood vessels formation and consequently numerous vascular abnormalities (Carmeliet et al., 1996; Ferrara et al., 1996; Gerber et al., 1999).

VEGF-A is a member of the VEGF family which also includes VEGF-B, -C, -D and PlGF (Placental Growth Factor). VEGF-E and -F are also considered as being members of this family although they are not of mammalian origin but produced from the pox virus genome or present in some snake venom, respectively (Ogawa et al., 1998; Pieren et al., 2006; Yamazaki et al., 2005). The specific functions of each of these VEGF are largely, but not

only, dictated by their affinity for three receptors and two co-receptors (Fig 6). For example, most of the activities of VEGF-A rely on its capacity to interact with VEGF-R1, VEGF-R2 and, according to the isoform, to neuropilins 1 and 2. VEGF-B and PlGF bind to VEGF-R1 and NRP1 but not VEGF-R2 (de Vries et al., 1992; Neufeld et al., 2002; Soker et al., 1998). VEGF-C and VEGF-D acts through VEGF-R2 and VEGF-R3 to drive lymphangiogenesis (Koch et al., 2011).

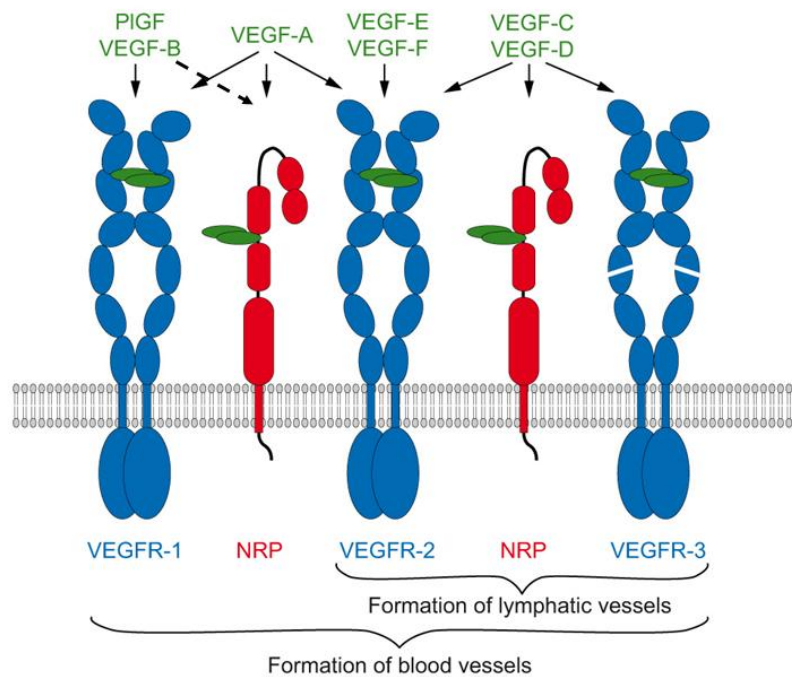


Figure 6 : VEGF family members and their receptors

VEGF-A, -B, -C, -D, -E and -F and PlGF are soluble growth factors regulating cell phenotype through binding to different receptors (VEGF-R1, VEGF-R2, VEGF-R3) and co-receptors (NRP and proteoglycans (not shown here)). A short summary of what is known about the (co-)receptors is provided elsewhere (paragraph VI-3, VI-4 and VI-5). Although a single VEGF member can bind to several (co-)receptors, redundancy between their roles is limited. VEGF: Vascular Endothelial Growth Factor, VEGF-R: VEGF-Receptors, NRP: Neuropilins 1 or 2, PlGF: Placental Growth Factor. **From (Berger and Ballmer-Hofer, 2011)**

III-2 General structure of VEGF

VEGF-A gene contains 8 exons (Ferrara et al., 2003). After transcription, the pre-mRNA gives rise to several mRNA coding for VEGF-A variants possessing some specific properties. The first 4 exons (E1-E4) are present in all mRNA variants while the terminal exons (E5-E8) can be alternatively spliced by mechanisms of cassette exon skipping, partial exon retention and alternative 3' splice sites (Fig 5, Fig 8). The nature of the regulations influencing the alternative splicing of the VEGF-A pre-mRNA remains poorly understood (Gout et al., 2012). The resulting proteins are identified by a code corresponding to the

number of amino acid present in the molecule after cleavage of the signal peptide and a letter, “a” or “b”, indicating the nature of the terminal exon, either E8a or E8b, encoding the last six amino acids (Fig 8).

As the most critical domains required for the correct folding of the VEGF molecules are located in the sequence encoded by exons 1 to 4, it is generally accepted that all these variants possess a similar general organization. VEGF is active only as a dimer formed by two monomers positioned in a head-to-tail manner (Muller et al., 1997; Pieren et al., 2006) (Fig 7). Disulfide bridges between Cys residues encoded by exons 3 and 4 are crucial for the proper folding of individual monomers (intra-chain bridges involving Cys⁵⁷ and Cys¹⁰², Cys⁶¹ and Cys¹⁰⁴, Cys²⁶ and Cys⁶⁸) but are also required for stabilizing the dimer (inter-chain bridges, Cys⁵¹ and Cys⁶⁰). Formation of dimers by two monomers of different size has been demonstrated (Keyt et al., 1996a) but their properties have not been thoroughly studied (Kurz et al., 1998; Morbidelli et al., 1997). In the same context, VEGF-A/PlGF (DiSalvo et al., 1995) and VEGF-A/VEGF-B (Olofsson et al., 1996) heterodimers have been also identified, adding an additional level of complexity in the study of the functions of the individual family members.

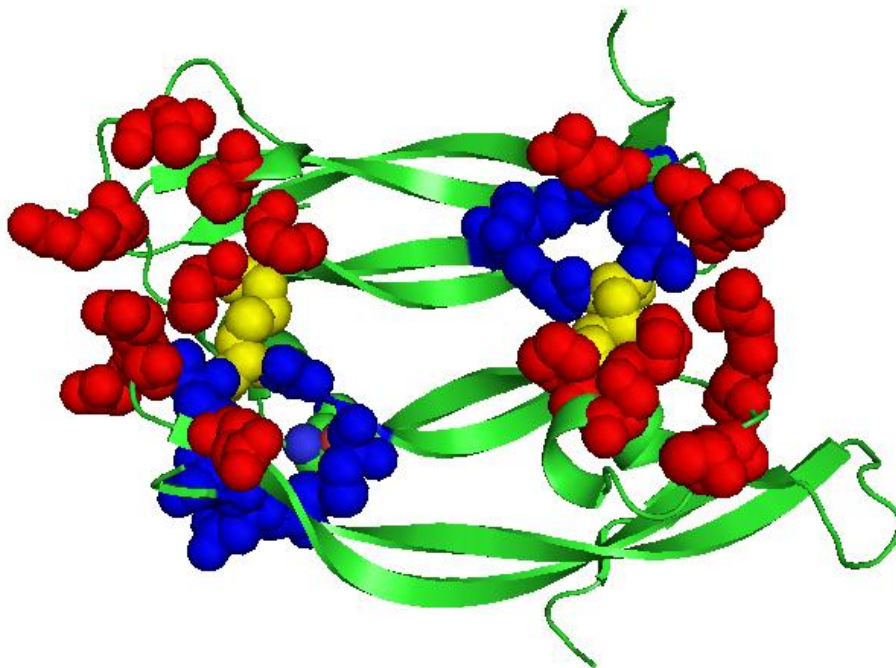


Figure 7 : 3D-Structure of VEGF dimer

VEGF, in this case VEGF-E used as a model, are composed of 2 monomers linked by 2 disulfides bonds (yellow) in head-to-tail manner. In VEGF-A, Cys⁵¹ and Cys⁶⁰ are the two critical residues involved in the formation of these disulfide bonds. Each monomer contains a “Cystin-Knot” structure (blue) where Cys⁵⁷ and Cys¹⁰², Cys⁶¹ and Cys¹⁰⁴, Cys²⁶ and Cys⁶⁸ form intra-chain bonds. The binding sites to VEGF-R2 are drawn here in red.

III-3 Regulation of VEGF-A expression

VEGF-A is expressed in almost all healthy tissues where it plays a crucial role for blood vessels homeostasis (Berse et al., 1992; Ferrara et al., 1992; Ferrara et al., 1991b). Besides alternative splicing, its expression is also controlled at the levels of transcription and mRNA stability (Neufeld et al., 1999).

VEGF is up regulated in tumours and many other pathological situations such as diabetes, rheumatoid arthritis and cardiovascular diseases (Ferrara and Davis-Smyth, 1997). It is also overexpressed in several eye diseases characterized by abnormal blood vessel formation, as, for example, age-related macular degeneration (AMD) (Kvanta et al., 1996), retinopathy of prematurity (ROP) and diabetic proliferative retinopathy (Aiello et al., 1994). High levels of VEGF are detected in vitreous and aqueous humors in patients with retinal and anterior segment pathologies (Aiello et al., 1994). The concentration is even more severely increased in patients presenting neovascular symptoms.

The VEGF expression is driven by hypoxia during development (Levy et al., 1995; Shweiki et al., 1992; Stone et al., 1995) but also during post-natal neovascularization and in ischemic conditions (Damert et al., 1997; Dor et al., 2001; Forsythe et al., 1996; Ikeda et al., 1995; Iyer et al., 1998; Shweiki et al., 1992). HIF-1 is the main factor implicated in this process (Kelly et al., 2003). The molecule is formed as a heterodimer composed of two subunits HIF-1 α and HIF-1 β (Chung and Ferrara, 2011). In normoxic conditions, HIF-1 α is maintained at low level by a constant degradation driven by von Hippel-Lindau tumor suppressor protein. On the contrary, a decrease of the oxygen concentration or the activation of the oncogene v-src promotes its expression and association with HIF-1 β (Strieter, 2005). The complete heterodimer translocates then in the nucleus and binds to a hypoxia response element hosted in the promoter of the VEGF-A gene which induces its mRNA transcription and production of VEGF protein (Tanimoto et al., 2003). Alternatively, VEGF upregulation can also be induced by several growth factors, including EGF, TGF, IGF-1, FGF and PDGF as well as by oncogenes, including activated ras (Neufeld et al., 1999; Okada et al., 1998; Rak et al., 1995).

IV- VEGF variants

Alternative splicing of the pre-mRNA gives rise to several isoforms of VEGF proteins (Fig 8) that possess specific characteristics regarding diffusibility (Ferrara, 2010), receptor activation (Soker et al., 2002), vessels maturation (Mineur et al., 2007) and pro- or anti-angiogenic functions (Bates et al., 2002).

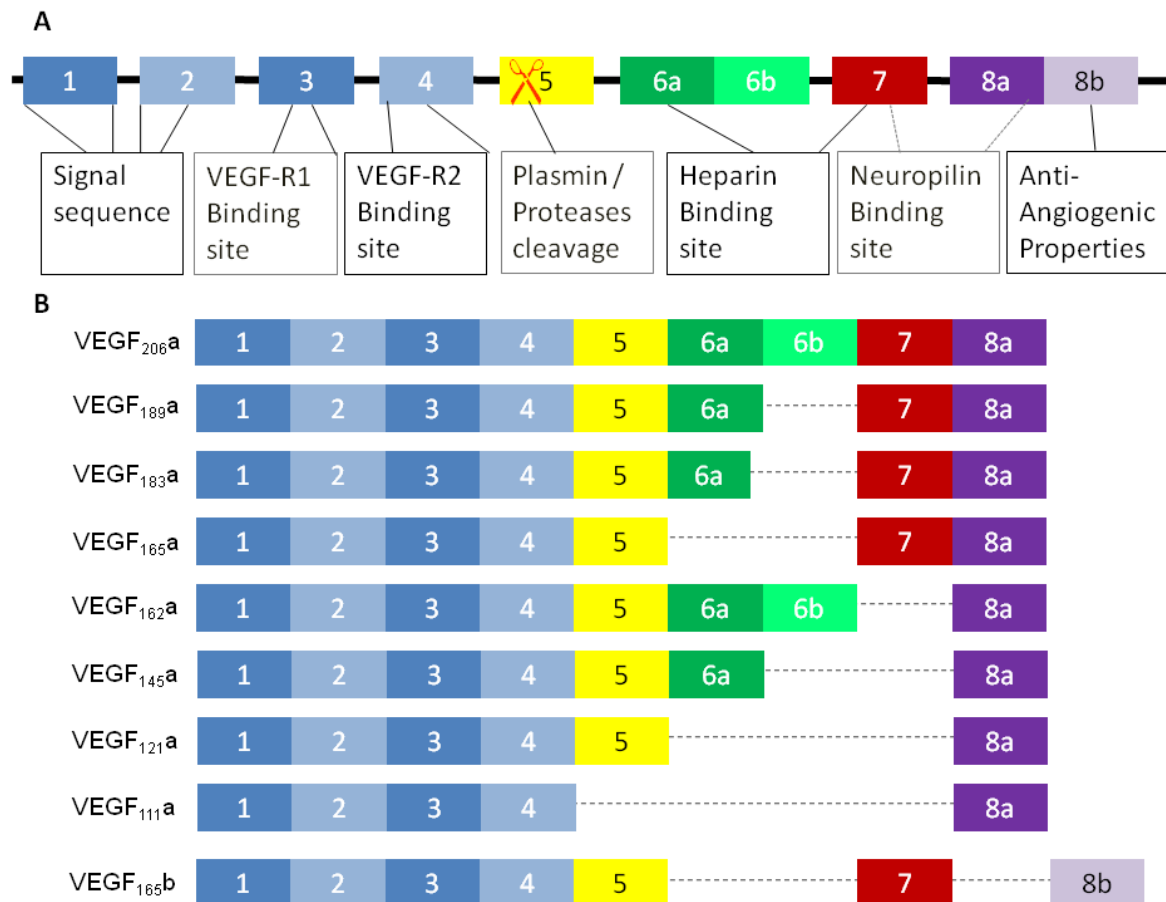


Figure 8 : Schematic representation of the different VEGF isoforms

Alternative splicing of the VEGF-A pre-mRNA gives rise to several isoforms of mRNA and proteins. **(A)** Exons (numbered from 1 to 8b) and introns are represented by boxes and lines, respectively. The biological functions associated with the protein domains encoded by different exons are provided. **(B)** Drawing of the main isoforms of VEGF. The amino-terminal portion (encoded by exons 1 to 4) is found in all known variants while the carboxy-terminal composition is highly variable. VEGF_{165b} is a particular variant where the six amino acids encoded by exon 8a are replaced by six amino acids encoded by the alternative exon 8b. VEGF_{111a} is the only variant which does not possess the exon 5 encoded domain where main sites of proteolytic cleavages are located.

VEGF variants are differentially expressed depending on tissue and life stages (Bacic et al., 1995; Ng et al., 2001). VEGF_{121a} and VEGF_{165a} are usually the most abundant variants (Ferrara et al., 1991a). In some circumstances, however, the proportion of other variants can be significantly increased. As an example, VEGF_{189a} is the dominant isoform in the uterus when progesterone is highly expressed (Ancelin et al., 2002).

It has been suggested that the combine expression of VEGF_{121a}, VEGF_{165a} and VEGF_{189a} is crucial to induce a VEGF gradient favouring a correct sprouting angiogenesis and vessel maturation (Grunstein et al., 2000). This hypothesis has been later nuanced. Even though it has been confirmed that the expression of only VEGF_{120a} or VEGF_{188a} (the murine analogous of VEGF_{121a} and VEGF_{189a}, respectively) is not sufficient to allow a good

vascular development (Carmeliet et al., 1999), the combination of both variants (Ruhrberg et al., 2002) or the solely expression of VEGF_{165a} seems to be sufficient during embryogenesis (Stalmans et al., 2002).

IV-1 VEGF_{165a} (E1-E5 ; E7; E8a)

VEGF_{165a} was the first identified VEGF molecule and is still the most investigated VEGF variant (Ferrara and Henzel, 1989; Harper and Bates, 2008). As a result the characterizations of the VEGF properties described in the literature mostly concern VEGF_{165a}. Its mRNA is formed by exons 1 to 5 (E1-E5), E7 and E8a. It binds to VEGF-R1, VEGF-R2, NRP1 (see chapter VI) and NRP2 but also to HSPG. It displays intermediate affinities for components of the extracellular matrix conferring it with an optimal “diffusibility” and availability for endothelial cell (Ferrara, 2010). This is illustrated by the fact that mice expressing exclusively the VEGF₁₆₄ variant (analogous to human VEGF_{165a}) display a normal development (Carmeliet et al., 1999; Maes et al., 2004; Stalmans et al., 2002).

IV-2 VEGF_{121a} (E1-E5 ; E8a)

As VEGF_{165a}, VEGF_{121a} is an abundant isoform. It binds with high affinity to VEGF-R1 and VEGF-R2 (Gitay-Goren et al., 1992; Kaplan et al., 1997; Leung et al., 1989). It differs from VEGF_{165a} by the absence of E7-encoded domain, which strongly reduces its affinity for heparin, proteoglycans and several components of the ECM (Cohen et al., 1995; Houck et al., 1992). As a consequence VEGF_{121a} is able to stimulate endothelial cells and to be active at distance from its site of secretion (Ferrara, 2010; Grunstein et al., 2000). Interestingly, its binding properties to NRP1 remain controversial being described as binder and non binder (Cebe Suarez et al., 2006; Herve et al., 2008; Pan et al., 2007b; Parker et al., 2012; Soker et al., 1996). This latter point has been investigated in this work.

The exclusive expression of VEGF_{120a} (the murine analogous of VEGF_{121a}) during the embryonic life is not sufficient to allow a correct foetus development (Carmeliet et al., 1999), with about 50 % of pups dying perinatally because of impaired myocardial angiogenesis and ischemic cardiomyopathy. In the retina, it has been also noticed that VEGF_{120/120} mice have a reduced number and shorter filopodia at the surface of “tips cells” (Gerhardt et al., 2003), larger capillaries, reduced vessels branching and delays in recruitment of mural cells (Ruhrberg et al., 2002; Stalmans et al., 2002). Similarly, overexpression of VEGF_{120a} during development decreases branching and increases the number of endothelial cells per capillary (Ruhrberg et al., 2002).

IV-3 VEGF_{189a} (E1-E5 ; E6a ; E7; E8a)

In addition to the sequences present in VEGF_{165a}, VEGF_{189a} contains also the 24 amino acids encoded by exon 6a (Keck et al., 1989). As this domain is highly enriched in Arg and Lys basic residues, it largely explains why VEGF_{189a} binds strongly to heparin and heparan sulphate proteoglycans and is almost only found either trapped at the cell surface or immobilized in the ECM (Houck et al., 1992; Tischer et al., 1991). This variant is therefore considered as a reservoir of VEGF becoming active and available for endothelial cells only after cleavage (Ferrara, 2010; Houck et al., 1992), treatment by heparin (Plouet et al., 1997) and/or degradation of the ECM (Park et al., 1993). As expected from these properties, expression of VEGF_{189a} by tumour cells seems to induce angiogenesis only locally (Grunstein et al., 2000). Although VEGF_{189a} was initially reported to be active only after cleavage within the exon6-encoded sequence, by plasmin or urokinase for example (Plouet et al., 1997), more recent studies describe however its effect as an uncleaved molecule on the induction of endothelial cell proliferation and migration, on the formation of dilated blood vessels *in vivo* (Herve et al., 2005; Herve et al., 2008) and as an inducer of vascular permeability (Ancelin et al., 2002). Interestingly, VEGF_{189a} binds to NRP1 with a higher affinity and a slower dissociation rate than VEGF_{165a}, probably leading to the formation of more stable tri-molecular complexes (VEGF-R2, VEGF_{189a}, NRP1) and to an increased VEGF-R2 signalling that could be related to the formation of large vessels (Herve et al., 2008; Miao et al., 2000). Finally, VEGF_{189a} presents the remarkable property of binding to fibronectin and vitronectin (via $\alpha_v\beta_5$ and $\alpha_5\beta_1$) and stimulating the recruitment of pericytes (Tozer et al., 2008), which plays a crucial role during tumour implantation and growth (Oshika et al., 2000).

In a mouse model, overexpression of VEGF_{188a} (the murine analogous of VEGF_{189a}) induces an excess of endothelial cells filopodia favouring hyperbranching of blood vessels during development and a reduction of the number of cells per capillary (Ruhrberg et al., 2002). These latter data are in contrast with those observed in tumour model expressing VEGF_{189a} where the blood vessels are dilated. Finally, in a model of mice expressing only VEGF_{188a}, cartilage and bone developments are impaired (Maes et al., 2004).

IV-4 VEGF_{206a} (E1-E5 ; E6a ; E6b ; E7; E8a)

VEGF_{206a} is considered as the full length variant as its mRNA contains all the exons (E1 to E8a). Similarly to VEGF_{189a}, from which it differs only by the presence of the 17 amino acids encoded by E6b (Lange et al., 2003), it remains largely cell and matrix associated (Park et al., 1993) and can induce vascular permeability. Furthermore, when attached to the ECM, it

is also able to stimulate endothelial cells proliferation (Houck et al., 1991; Park et al., 1993). Its expression is mainly restricted to the pre-natal period (Houck et al., 1991; Jakeman et al., 1993).

IV-5 VEGF_{145a} (E1-E5; E6a ; E8a)

VEGF_{145a} has been identified in tumourigenic cell lines established from the female reproductive system but also in ovine placenta and foetal membranes, penis, kidney and skin (Burchardt et al., 1999; Charnock-Jones et al., 1993; Cheung et al., 1995; Poltorak et al., 1997; Whittle et al., 1999). It is secreted by some cancer cells lines in the medium and can be purified using a heparin-Sepharose affinity chromatography. VEGF_{145a} displays a higher affinity for matrix components than VEGF_{165a} (Kawamura et al., 2008b; Lange et al., 2003; Poltorak et al., 1997). Interestingly this does not seem to be related to interactions with heparin, because heparitinase treatment does not release VEGF_{145a} from ECM (Poltorak et al., 1997).

VEGF_{145a} binds to VEGF-R2 and to NRP2 but probably not to NRP1 (Gluzman-Poltorak et al., 2000; Poltorak et al., 1997) although this is still debated (Kawamura et al., 2008b). It induces endothelial cells proliferation and migration, although less efficiently than VEGF_{165a}. When transfected in tumour cells, it induces a significant blood vessels invasion *in vivo* (Kawamura et al., 2008b; Poltorak et al., 2000; Poltorak et al., 1997).

IV-6 VEGF_{162a} (E1-E5 ; E6a ; E6b ; E8a)

VEGF_{162a} was identified in human ovarian carcinoma cell line (Lange et al., 2003). It induces HUVECs mitogenesis with an intermediate activity as compared to VEGF_{165a} and VEGF_{145a}. It also triggers the formation of blood vessels *in vivo*. Interestingly, its affinity for HSPG is lower than the affinity of VEGF_{145a}, suggesting that the amino acid sequence encoded by E6b has some inhibitory effect (Lange et al., 2003).

IV-7 VEGF_{183a} (E1-E5 ; E6a truncated ; E7; E8a)

Although ubiquitously expressed (Jingjing et al., 2000), VEGF₁₈₃ has been discovered in the eye where it is synthesized by Müller cells (glial cell of the retina). Its expression is up-regulated under hypoxic conditions (Jingjing et al., 1999). It differs from VEGF_{189a} by the absence of the 6 amino acids encoded by the 3'-end of E6a, due to the presence of a conserved alternative splicing donor site (Lei et al., 1998). Except for a slightly reduced affinity for some extracellular components, it is considered to possess the same properties than VEGF_{189a} (Jingjing et al., 2001).

IV-8 VEGF_{111a} (E1-E4 ; E8a)

VEGF_{111a} is the only VEGF that does not possess the E5-encoded domain (Lambert et al., 2008; Mineur et al., 2007) as the entire sequence between E4 and E8a is spliced out (Fig 8).

It is the shortest and the more recently described variant. It was identified in many cells types upon “stress” in culture by either UV-B irradiation, exposure to chemotherapeutic drugs (Mineur et al., 2007) or cold shock and rewarming (Neutelings et al., 2013, in revision).

When produced in mammalian cells, VEGF_{111a} is secreted under its glycosylated form while, interestingly, a significant part of the other variants remain always non glycosylated (Mineur et al., 2007). This might influence its biological properties although it was never demonstrated.

VEGF_{111a} has pro-angiogenic activities (Fig 9). It initiates the phosphorylation of VEGF-R2 and the activation of the downstream ERK1/2 (Extracellular signal-regulated kinases phosphorylation 1/2) signalling pathway. It stimulates the proliferation of endothelial cells in culture and vasculogenesis in a model of embryoid body formation *in vitro*. It signals also through VEGF-R1 as illustrated by its capacity to induce monocyte migration. Its activity was also studied in a model of tumoural angiogenesis using HEK293 cells expressing a single VEGF variant and implanted in nude mice. In these conditions, VEGF_{121a} and VEGF_{165a} were shown to promote the formation of enlarged blood vessels inside the tumour mass. By sharp contrast, expression of VEGF_{111a} did not modify the intra-tumoural angiogenesis but induced the formation of a dense network of functional capillaries in the peritumoural tissue. Beside demonstrating a strong activity *in vivo*, these observations also suggested that VEGF_{111a} is probably able to diffuse almost freely without any interaction with the ECM.

As another interesting and very specific property resulting from the absence of the E5-encoded sequence, VEGF_{111a} is resistant to degradation by plasmin, an enzyme with broad spectrum substrates, and by the cocktail of proteases present in skin ulcer exudates (Mineur et al., 2007). All these characteristics make VEGF_{111a} a variant with many potential clinical applications and implications in various pathologies. In acute or chronic ischemia (heart infarction, stroke, skin ulcer, tissues grafting, ...) its use could potentially be beneficial for the patients by preventing endothelial cell apoptosis and stimulating the formation of new blood vessels. By contrast its endogenous expression could be detrimental in diseases where abnormal or excessive angiogenesis is observed (cancer, arthritis, ...).

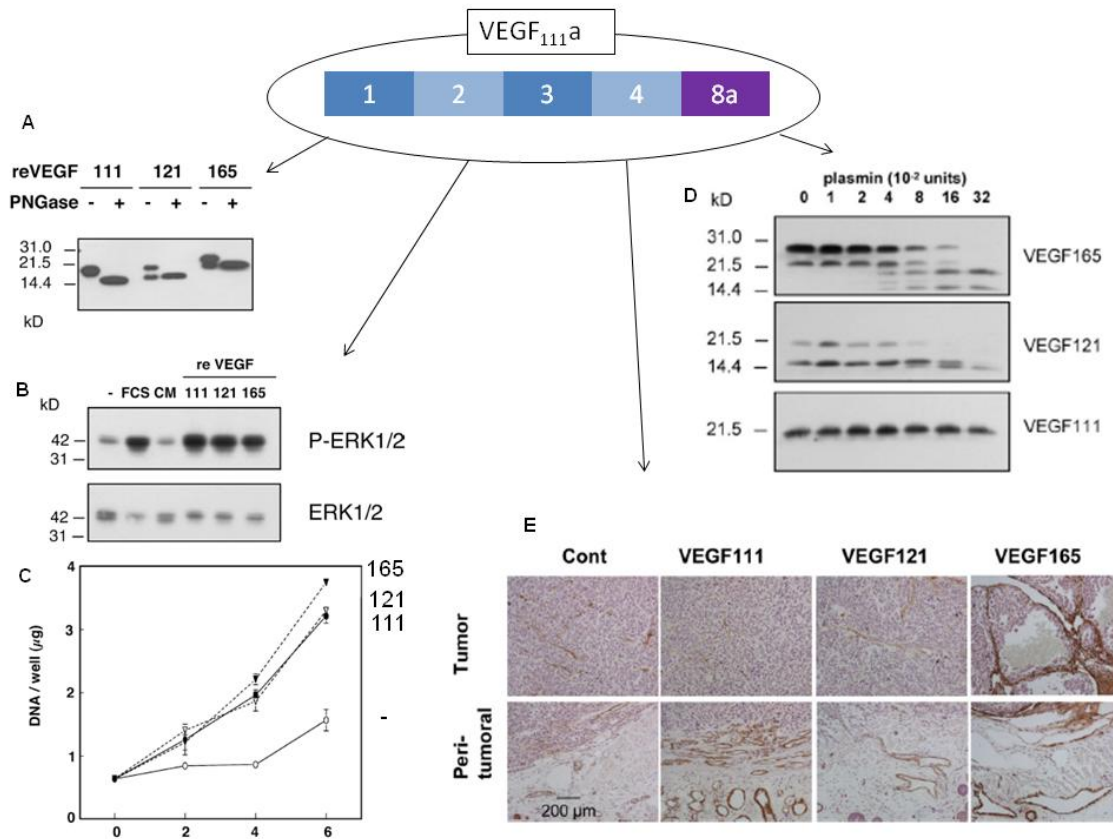


Figure 9 : Characterizations of VEGF_{111a}

(A) As demonstrated by western-blot analyses of VEGF variants treated with Peptide-N-Glycosidase F (PNGase), VEGF_{111a} is secreted only as a glycosylated protein while the “classical” variants (VEGF_{121a} and VEGF_{165a}), are identified as glycosylated and non glycosylated polypeptides. VEGF_{111a} is as efficient as VEGF_{121a} and VEGF_{165a} (B) for stimulating the phosphorylation of ERK1/2 and (C) the proliferation of endothelial cell (VEGF_{111a}, black circle, VEGF_{121a}, open triangle, VEGF_{165a}, black triangle and control, open circle). (D) VEGF_{111a} displays an increased resistance to proteolytic degradation by plasmin. (E) As compared to VEGF_{121a} and VEGF_{165a} that induce intratumoural vascularization, VEGF_{111a} stimulates the formation of a dense network of small capillaries in the surrounding normal skin. *From (Mineur et al., 2007)*

IV-9 VEGF_{xxx}b variants

IV-9-1 Discovery, generalities and expression

A study of VEGF mRNA isoforms in kidneys led to the identification of a new class of variants reported as anti-angiogenic and characterized by the presence of an alternative exon 8b (Bates et al., 2002; Bates and Jones, 2003). Although a recent controversy questioning their existence/biological significance (Catena et al., 2010; Harris et al., 2012), we felt that their description and study were nonetheless fully relevant to our work for three independent reasons:

- There are tens of publications from several laboratories describing their expression;

- Due to their properties, their use as recombinant proteins is promising for treating human pathologies, even if they are not significantly produced as physiological native proteins;
- Their characterization and comparison with other variants provide fundamental new knowledge concerning the function of the different domains alternatively present in the various VEGF variants.

In their original publication, Bates and co-workers found that this new variant was expressed in podocytes in normal kidneys but was down-regulated in tumour samples and cell lines (Bates et al., 2002; Cui et al., 2004). By sequencing, they identified a new terminal coding sequence that is present in the other variants but only in the 3'-UTR (Xu et al., 2011b). This new sequence, referred to as exon 8b (E8b) (Woolard et al., 2004), codes for six amino acids and a stop codon followed by a 3'-UTR. The alternative splicing mechanism leading to its formation has been studied. It has been shown that VEGF with E8b or E8a are generated as a result of the alternative use of 2 different splice sites (Fig 10). Beside VEGF_{165b} (E1-E5; E7; E8b) described in the original publication (Bates et al., 2002), others have been identified such as VEGF_{121b} (E1-E5 ; E8b), VEGF_{145b} (E1-E5 ; E6a ; E8b) and VEGF_{189b} (E1-E5 ; E6a ; E7; E8b) (Cui et al., 2004; Harper and Bates, 2008; Miller-Kasprzak and Jagodzinski, 2008; Rennel et al., 2009b; Woolard et al., 2004). As already mentioned, VEGF variants possessing E8a or the alternative E8b are referred to as VEGF_{xxx}a or VEGF_{xxx}b, respectively. The expression of this new class of variants was reported to be significant and it was even postulated that they could be more abundant in healthy tissues than the VEGF_{xxx}a isoforms (Bevan et al., 2008; Pritchard-Jones et al., 2007; Rennel et al., 2008; Varey et al., 2008; Woolard et al., 2004), which is however another controversy in the field.

VEGF_{xxx}a and VEGF_{xxx}b isoforms are generated by the selection of a proximal (PSS) or a distal (DSS) splice site, the latter being localized 66 bp further downstream in the terminal exon 8 (see Fig 10) (Woolard et al., 2004). Cascades of molecules, such as growth factors and splicing factors, are implicated in the choice of the splicing site. Studies in primary epithelial cell, podocytes and endothelial cells demonstrate that factors such as IGF1 and TNF α (Tumor Necrosis Factor α) favour the PSS, which leads to the synthesis of VEGF_{xxx}a, while TGF- β 1 favours DSS and secretion of VEGF_{xxx}b (Nowak et al., 2008).

IGF induces the PKC (Protein Kinase C) pathway (Fig 10A) and SRPK1 (Serine/Arginine Protein Kinase 1) activation, which induces the phosphorylation and the translocation of ASF/SF2 (also known SRSF1: Serine/Arginine-rich Splicing Factor 1) in the nucleus where it participates to the preferential selection of the PSS (Nowak et al., 2010). By contrast (Fig

10B), TGF- β 1 activates successively p38 and Clk1 (CDC-like kinase 1) pathways, which induces the phosphorylation of SRp55 (also known SRSF6) allowing its binding to the VEGF pre-mRNA, which favours the selection of the DSS and the synthesis of VEGF_{xxx}b (Manetti et al., 2011; Nowak et al., 2008). Endostatin and the E2F1 transcription factor could also participate to the selection of the DSS by triggering the activation of the splicing factor SC35 (Li et al., 2011; Merdzhanova et al., 2008; Merdzhanova et al., 2010). However, a positive correlation between the expression of VEGF_{xxx}a and E2F1 has been identified in colorectal cancer samples, suggesting that the relationship between these two factors is probably complex (Diaz et al., 2008). Finally, WT1 (Wilms Tumour protein 1) can bind to SRPK1 and down-regulate its expression, which represses the expression of VEGF_{xxx}a. Interestingly, in Deny Drash Syndrome, a urogenital disorder, WT1 is expressed as a mutated form unable to bind and to inhibit SRPK1 (Amin et al., 2011; Schumacher et al., 2007), which stimulates an overexpression of VEGF_{xxx}a responsible for renal failure.

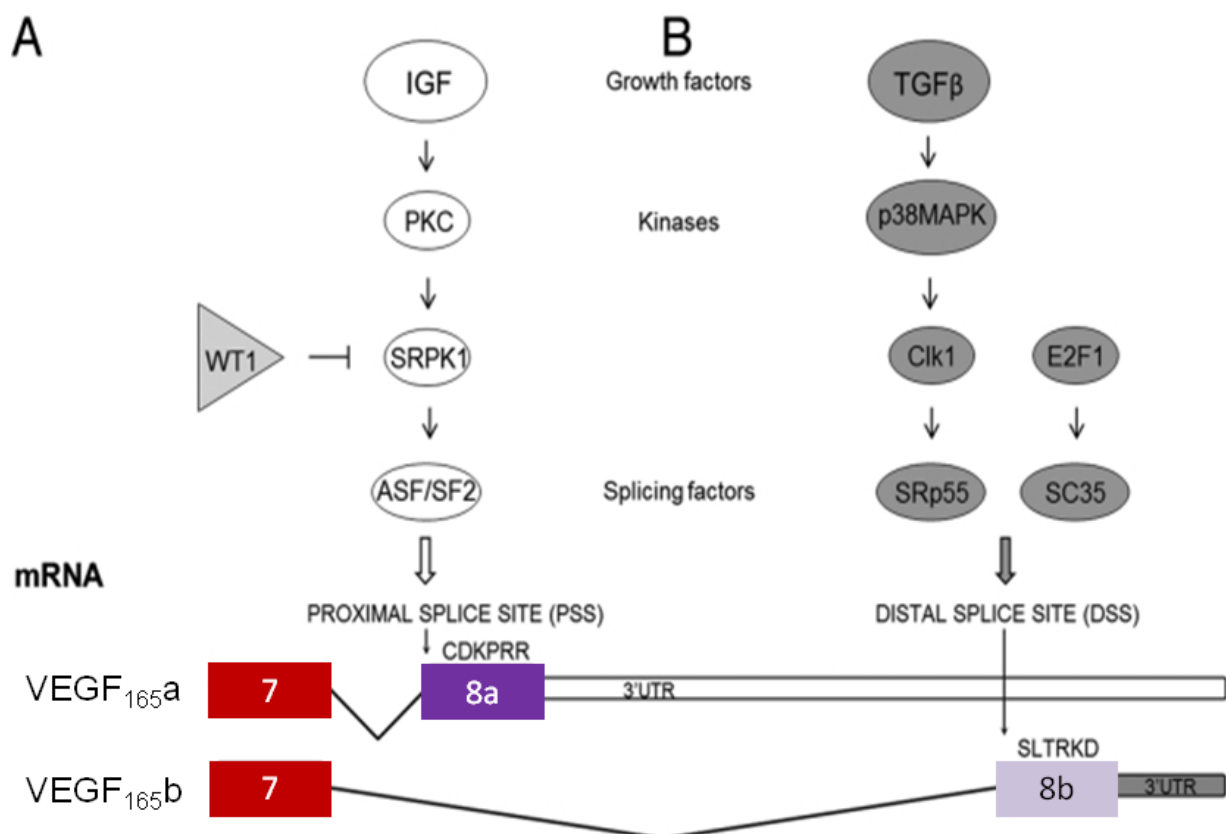


Figure 10 : Regulation of the alternative splicing in the terminal exon of the VEGF-A pre-mRNA

Several growth factors, kinases and splicing factors are implicated in pathways regulating the selection of a proximal (**A**) or a more distal (**B**) splice site, which leads to the synthesis of either VEGF_{xxx}a or VEGF_{xxx}b isoforms, respectively. *From (Peiris-Pages, 2012)*

VEGF_{165b} (E1-E5; E7; E8b) is the most investigated VEGF_{xxx}b isoform. It has been produced as a recombinant protein (Fig 11A) (Bates et al., 2002; Catena et al., 2010). It is efficiently secreted (Leung et al., 1989), forms dimers (Bates et al., 2002; Woolard et al., 2004), and has high affinities for VEGF receptors (Hua et al., 2010). An antibody targeting the 6 amino acids encoded by E8b has been produced and used to detect, by immunohistochemistry or ELISA, the presence of VEGF_{165b} in kidney and plasma samples (Bills et al., 2009; Woolard et al., 2004).

The 6 amino acids encoded by E8b (Ser-Leu-Thr-Arg-Lys-Asp or “SLTRKD”) largely differ from those derived from E8a (Cys-Asp-Lys-Pro-Arg-Arg or “CDKPRR”) (Bates and Jones, 2003), which has potential functional implications. In VEGF_{165a}, the Cys residue encoded by E8a is expected to form a disulfide bond with Cys¹⁴⁶ (derived from E7) (Claffey et al., 1995). This brings the two terminal Arg encoded by E8a close to the basic residues derived from E6, which forms a highly basic 3D-domain. By sharp contrast, the domain encoded by E8b does not contain a Cys and ends with an Asp acidic residue (Cebe-Suarez et al., 2008), two features that could strongly modify the 3D-conformation and the properties of VEGF_{165b} as compared to VEGF_{165a}.

VEGF_{165b} binds to VEGF-R1 and VEGF-R2 (Fig 11B and 11C) (Hua et al., 2010; Woolard et al., 2004) but not to NRP1, heparin or HSPG (Cebe Suarez et al., 2006; Kawamura et al., 2008b). Surprisingly, however, it has been shown in independent studies that endothelial cells treatment by VEGF_{165b} induces only a faint and transient phosphorylation of VEGF-R2 and a very limited activation of ERK and Akt downstream signalling pathways (Catena et al., 2010; Cebe Suarez et al., 2006; Magnussen et al., 2010; Manetti et al., 2011; Woolard et al., 2004). Other studies have further shown that impaired phosphorylation of VEGF-R2 affects several Tyr residues (Cebe Suarez et al., 2006; Kawamura et al., 2008b; Magnussen et al., 2010). The involved mechanism is not yet fully understood. According to a first hypothesis, it could be related to the lack of binding of VEGF_{xxx}b isoforms to NRP1. This hypothesis is however hampered by the fact that VEGF_{xxx}a variants that have no affinity for NRP1 are however strong inducers of VEGF-R2 phosphorylation. Another more appealing hypothesis suggests that VEGF_{165b} would not be able to dictate the perfect orientation of the two VEGF-R2 molecules forming a functional dimer, which would affect tyrosine “trans-phosphorylation” and explain the quasi absence of activation of downstream pathways (Fig 11D). In this context it is not surprising that VEGF_{165b} is not able to trigger endothelial cells proliferation (Fig 11E), migration (Fig 11F) and tube formation *in vitro* or angiogenesis (Fig 12A) and vascular dilatation *in vivo* (Bates et al., 2002; Manetti et al., 2011; Rennel et al., 2008). The

low level of activation of these cascades seems however sufficient to have a biological role since VEGF_{165b} treatments promote survival of endothelial cell *in vitro* (Bevan et al., 2008; Magnussen et al., 2010; Woolard et al., 2004). Besides this protective function it was reported that VEGF_{165b} is able to repress the VEGF_{xxx}a-induced angiogenesis by a mechanism that would involve a competition for VEGF-R2.

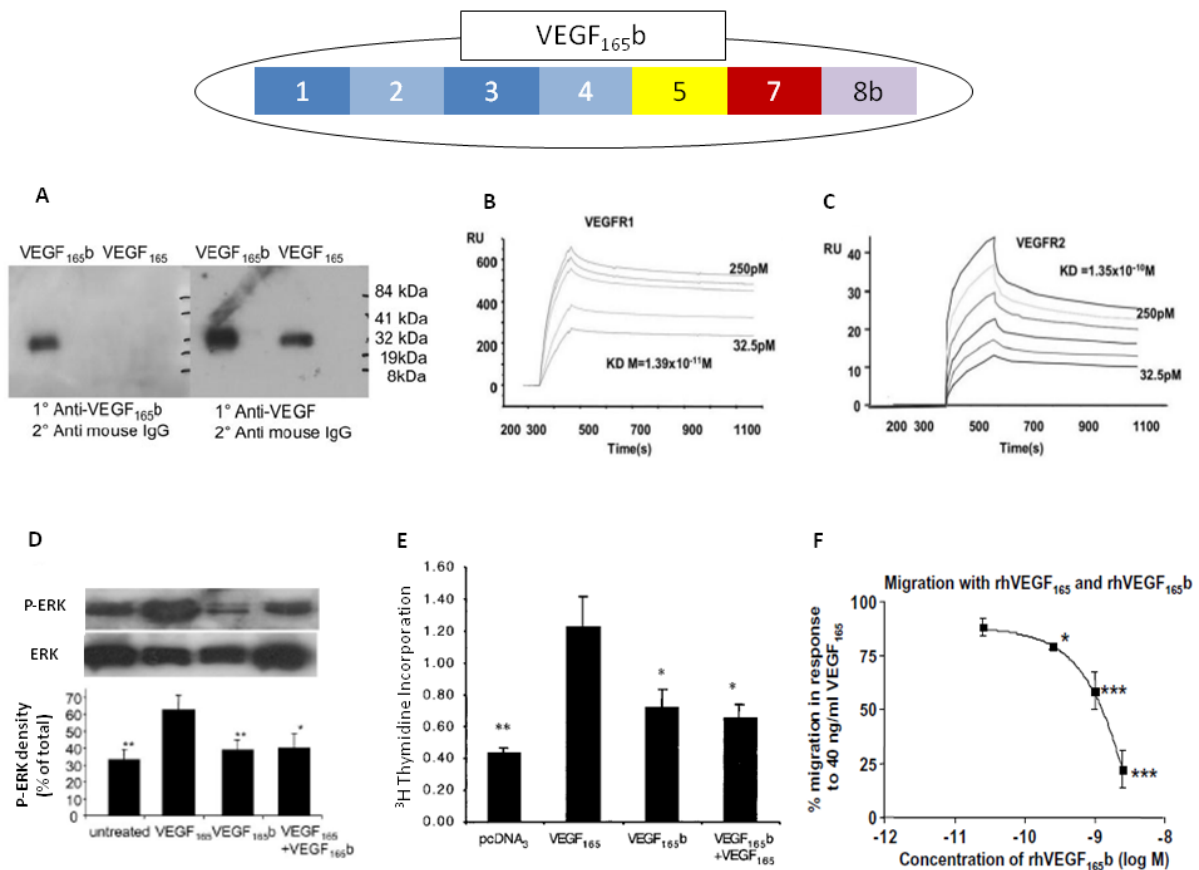


Figure 11 : *In vitro* effect of VEGF_{165b} on angiogenesis

VEGF_{165a} and VEGF_{165b} can both be evidenced by Western Blotting using an antibody targeting the N-terminus of the molecules, while only VEGF_{165b} can be visualized by an antibody raised against the E8b-derived sequence (A). VEGF_{165b} is able to bind to VEGF-R1 (B) and VEGF-R2 (C) as demonstrated by Surface Plasmon Resonance. (D) However, experiments performed *in vitro* on endothelial cells demonstrated that VEGF_{165b} cannot activate ERK pathway and inhibits the VEGF_{165a}-induced phosphorylation as shown by western-blot and the corresponding quantification. (E) VEGF_{165b} can repress VEGF_{165a}-induced endothelial cells proliferation when both variants are mixed in an equimolar amount as shown by ³H-thymidine incorporation. (F) VEGF_{165b} has the property to inhibit VEGF_{165a} induced endothelial cells migration in a dose-dependent manner as shown by the decrease percentage of cell migration relative to VEGF_{165a} taken as 100%. (D E, F) The statistical significances are reported by comparison to the treatment with VEGF_{165a} alone. **From (Bates et al., 2002; Hua et al., 2010; Rennel et al., 2008; Woolard et al., 2004).**

This antagonistic effect regarding the pro-angiogenic isoforms of VEGF was also investigated and confirmed *in vivo* in models of pathological neovascularization in the eye (Konopatskaya et al., 2006; Magnussen et al., 2010; Rennel et al., 2009b) and in tumours

(Fig 12B) (Peiris-Pages et al., 2010; Rennel et al., 2008; Rennel et al., 2009a; Rennel et al., 2009b). A small number of publications report however a weak but significant pro-angiogenic effect of VEGF_{121b} and VEGF_{165b} in a matrigel plug assay *in vivo* (Catena et al., 2010), which led to the hypothesis that the inhibitory effect of VEGF_{165b} would be limited to situations where the pro-angiogenic VEGF_{xxx}a isoforms are highly expressed. It was also shown that VEGF_{165b} is able to increase vascular permeability by signalling through VEGFR1, although less efficiently than VEGF_{165a} (Glass et al., 2006) that acts mainly through VEGFR2 (Whittles et al., 2002).

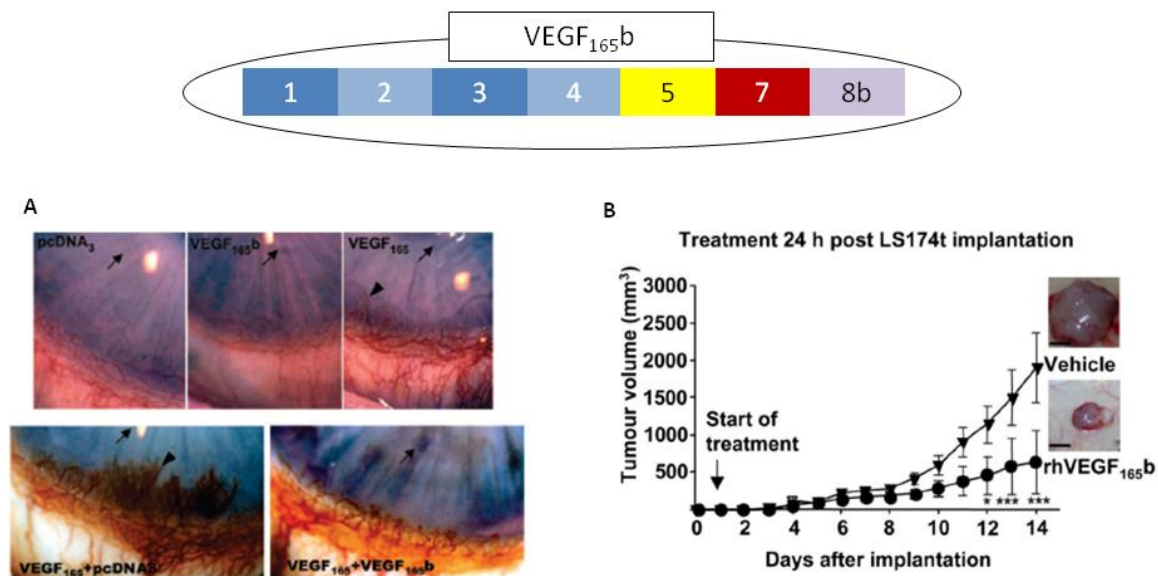


Figure 12 : *In vivo* effect of VEGF_{165b} on angiogenesis

(A) Unlike VEGF_{165a}, VEGF_{165b} does not induce ocular vascularization (upper panel). When present in equimolar concentration VEGF_{165b} inhibits the VEGF_{165a}-induced effect (lower panel). **(B)** LS174t carcinoma cells express high levels of VEGF_{165a}. They form vascularized tumours when grafted in nude mice. By contrast, chronic injection of recombinant VEGF_{165b} reduces tumor growth and vascularisation. *From (Rennel et al., 2008; Woolard et al., 2004)*

IV-9-2 VEGF_{xxx}b/VEGF_{xxx}a ratio in health and disease

The VEGF_{xxx}b/VEGF_{xxx}a ratio plays a significant role in the maintenance of the physiology of the organ in adulthood (Oltean et al., 2012b). It is also developmentally regulated in ovaries, testes and eyes (Artac et al., 2009; Baba et al., 2012; Baltés-Breitwisch et al., 2010; Caires et al., 2012; McFee et al., 2012). In placenta, where angiogenesis is active, VEGF_{xxx}b represents only 1.5% of the total VEGF (Bevan et al., 2008).

VEGF_{xxx}b isoforms are down-regulated in tumours as compared to healthy tissues in favour of VEGF_{xxx}a (Bates et al., 2002; Bevan et al., 2008; Rennel et al., 2008). VEGF_{xxx}b are also

the main variants expressed in normal eye but their concentration decreases during the proliferative angiogenesis occurring in the vitreous of diabetic patients (Hua et al., 2010; Perrin et al., 2005). By contrast, in glaucoma, a non-angiogenic pathology where VEGF is over-expressed, the VEGF_{xxx}b isoforms are the most abundant (Ergorul et al., 2008). All these information underscore a shift from VEGF_{xxx}b to VEGF_{xxx}a which is responsible for pathological blood vessels formation (Harper and Bates, 2008). This hypothesis is however not supported in breast tumours where up-regulation of VEGF_{xxx}b isoforms has been observed (Catena et al., 2010). A decreased VEGF₁₆₅b/VEGF₁₆₅a ratio is also involved in mesangial sclerosis and renal failure in patients suffering from Denis Drash Syndrome (Schumacher et al., 2007). An increased expression of VEGF₁₆₅b is involved in systemic sclerosis (Manetti et al., 2011), a chronic disease characterized by alterations of angiogenesis and vascular repair, which affects skin and internal organs (Manetti et al., 2010).

IV-9-3 VEGF_{xxx}b in clinic

Bevacizumab is an antibody trapping VEGF-A molecules (see paragraph VII-1). Today, it is the gold-standard treatment for inhibiting angiogenesis. Besides a limited effect, it has also specific disadvantages. It targets both VEGF_{xxx}a and VEGF_{xxx}b isoforms, which potentially reduces its anti-angiogenic properties. Bates and collaborators proposed to use the VEGF_{xxx}b/VEGF_{xxx}a ratio as a predictive biomarker for bevacizumab efficacy in metastatic colorectal cancer (Bates et al., 2012). Using samples of the phase III study (Giantonio et al., 2007), they have demonstrated a significant improvement of the survival of patients with a low VEGF_{xxx}b/ VEGF_{xxx}a ratio as compared to the patients with a high ratio.

When used at high doses in the eye for treating macular degeneration, bevacizumab can alter the viability of retinal pigment endothelial cells (Spitzer et al., 2006). Using recombinant VEGF_{xxx}b variants as therapeutic molecules to reduce pathological angiogenesis is an interesting concept because it inhibits angiogenesis while being cytoprotective for retinal pigment endothelial cells, even used at very high concentrations (Bates and Harper, 2005; Harper and Bates, 2008). The most promising effects were observed in *in vivo* models mimicking eyes diseases such macular degeneration and retinopathy of prematurity (ROP). In a choroidal neovascularization model (CNV), VEGF₁₆₅b limits the excess of abnormal blood vessels induced by laser exposure (Hua et al., 2010). Similarly, a benefit of VEGF₁₂₁b and VEGF₁₆₅b treatment on the neovascularization has been reported in several model of oxygen deprivation (Konopatskaya et al., 2006; Magnussen et al., 2010; Rennel et al., 2009b).

VEGF_{165b} has however its own disadvantages, such as a short half-life *in vivo* (Rennel et al., 2008). This could be improved however by increasing its resistance to degradation by endogenous proteases. An alternative would be to induce its synthesis *in vivo* by the host machinery by favouring its expression at the expense of the VEGF_{xxx}a isoforms, a therapeutic goal that could be achieved by regulating the alternative splicing of the VEGF pre-mRNA (Oltean et al., 2012a). For instance, SRPIN340, an antagonist of SRPK1, improves symptoms in a rat model of ROP (Nowak et al., 2010) and knocking down SRPK1 in colorectal tumor cell lines decreases their growth (Amin et al., 2011).

IV-10 Other variants

VEGF₁₄₈ results from the skipping of E6 and of a sequence encompassing E7b to the beginning of E8a, which further changes the reading frame of the 3'-end of the mRNA and leads to a novel carboxy-terminal amino acid sequence (Harper and Bates, 2008; Whittle et al., 1999; Zygalaiki et al., 2005). Alternative start codons upstream the canonical ATG codon can also be used, giving rise to isoforms longer than classical VEGF (Tee and Jaffe, 2001). However they do not display activity and their relative importance is still questionable.

Some artificial variants were also created to better understand the role of E6b and E8a as, for example, VEGF₁₃₈ (E1-E5; E6b; E8a), VEGF₁₈₂ (E1-E5; E6b; E7; E8a) or VEGF₁₅₉ (E1-E5; E7) (Cebe Suarez et al., 2006; Houck et al., 1991; Lange et al., 2003).

V- Role of the domains encoded by the exons of VEGF

Because of the very active and dynamic mechanism of alternative splicing affecting the VEGF-A pre-mRNA, differences between the VEGF variants directly depends on the presence in the mRNA of specific exon(s) or part of. For this reason, protein domains are usually described in direct relationship with their exonic origin. Their specific functions are briefly summarized here.

Exons 1 and 2

The two first exons code for the ATG start codon and for the 26 hydrophobic amino acids sequence form the signal peptide (Houck et al., 1992; Tischer et al., 1991). This sequence is therefore cleaved during the secretion process and absent from the mature forms.

Exon 3

The binding site for VEGF-R1 is encoded by E3, with a special importance of three amino acids: Asp⁶³, Glu⁶⁴ and Glu⁶⁷ (Keyt et al., 1996b). Two Cys residues (Cys⁵¹ and Cys⁶⁰) required for the formation of functional VEGF dimers are also part of the E3-derived sequence (Harper and Bates, 2008; Muller et al., 1997).

Exon 4

The E4-derived sequence contains the binding domain for VEGF-R2, with Arg⁸², Lys⁸⁴ and His⁸⁶ playing a critical role (Keyt et al., 1996b), and the only glycosylation site (Asn⁷⁵) present in VEGF-A molecules (Claffey et al., 1995; Neufeld et al., 1994).

Exon 5

The E5-encoded domain contains the main site of cleavage by plasmin (between Arg¹¹⁰ and Ala¹¹¹) (Keyt et al., 1996a; Lauer et al., 2002). The amino-terminal peptide resulting from the digestion possesses 110 amino acids, is still dimerized (Houck et al., 1992) and able to bind to VEGF-R1 and VEGF-R2 (Plouet et al., 1997). It is still active but much less than the intact VEGF_{165a} (Mineur et al., 2007). This domain contains also cleavage sites for MMPs (Lee et al., 2005). For instance in human, MMP3 cleaves VEGF_{165a} into VEGF₁₁₄ (between Glu¹¹⁴ and Asn¹¹⁵). This cleaved form triggers vascular dilatation while a mutated MMPs-resistant VEGF_{165a} generates anarchic hyper-branching. This illustrates the importance of taking into consideration the protease micro-environment when studying the effect and properties of VEGF isoforms (Coussens and Werb, 2002).

Exon 6a

The E6a-derived sequence plays a main role in binding to heparin and proteoglycans because of the presence of 12 basic amino acids (Tischer et al., 1991). This domain was also reported to have affinity for NRP1 (Herve et al., 2008; Jia et al., 2001) and NRP2 (Gluzman-Poltorak et al., 2000). It further contains a cleavage site by uPA (urokinase-type Plasminogen Activator) corresponding to its carboxy-terminal sequence (Tyr-Lys-Ser-Trp-Ser-Val), absent in VEGF₁₈₃ (Jingjing et al., 1999).

Exon 6b

VEGF₁₆₂ (E1-5 ; E6a ; E6b ; E8a) possesses significantly less affinity for ECM than VEGF₁₄₅ (E1-5 ; E6a ; E8a) but more than the artificial recombinant VEGF₁₃₈ (E1-5 ; E6b ; E8a) (Lange et al., 2003). This suggests that the E6b-derived sequence has no affinity for ECM components and is even able to limit the affinity of the E6a domain for matrix components.

Exon 7

The E7 domain possesses 3 accessory sites of cleavage by plasmin (Arg¹²³/Arg¹²⁴, Lys¹²⁵/His¹²⁶ and Lys¹⁴⁷/Ala¹⁴⁸) (Lauer et al., 2002) and two additional cleavage sites by MMPs (Ser¹²¹/Gln¹²² and Lys¹³⁶/Cys¹³⁷) (Lee et al., 2005). An affinity for heparin (Krilleke et al., 2007) and VEGF-R1 (Allain et al., 2012) has been reported. It contains also the first identified binding site for NRP1 (Soker et al., 1997).

Exon 8a

The CDKPRR sequence derived from E8a is currently considered as the main binding site to NRP1 by some authors (Pellet-Many et al., 2008) as suggested by the use of different synthetic peptides (Allain et al., 2012).

Exon 8b

Substitution of the CDKPRR sequence (E8a) by the SLTRKD sequence (E8b) strongly modifies the biological properties of VEGF-A variants (Bates et al., 2002; Catena et al., 2010) by mechanisms that would involve modifications of the 3D-structure of the entire molecule and alteration of pockets formed by positively charged amino acids.

VI- VEGF-receptors and co-receptors

As already briefly mentioned, the regulation of cell phenotype by VEGF-A variants involves 2 transmembrane tyrosine kinase receptors and several co-receptors in charge of modulating their availability and presentation to the receptors.

VI-1 Vascular Endothelial Growth Factor Receptor 1

The Vascular Endothelial Growth Factor Receptor 1 (VEGF-R1, initially described as FLT-1 or Fms-Like Tyrosin Kinase-1) was the first described VEGF receptor. It was identified as an endothelial cell surface protein able to complex with VEGF and possessing similarities with the PDGF receptor (Plouet and Moukadiri, 1990a; Seetharam et al., 1995). Further characterizations showed that VEGFR-1 is a transmembrane receptor containing an extracellular region (7 IgG-like domains), a transmembrane sequence and an intracellular tyrosine kinase domain (Shibuya, 1995). Soluble and truncated versions also exist and are referred to as sVEGF-R1. They are produced both by alternative splicing of the pre-mRNA and by proteolytic processing (Cai et al., 2006; Shibuya, 2001). They play an anti-angiogenic role by sequestering VEGF-A in the extracellular space, which prevents its binding on

transmembrane receptors present at the cell surface. Like the full-size VEGF-R1, sVEGF-R1 can also act as inhibitor by forming non-functional heterodimer with VEGF-R2 (Cudmore et al., 2012; Kendall and Thomas, 1993; Kendall et al., 1994).

VEGF-R1 binds with high affinity (15 pM) to VEGF-A variants through the IgG loop 2 (Davis-Smyth et al., 1996; Tanaka et al., 1997). The initial binding of VEGF-A on a single VEGF-R1 molecule induces the recruitment of a second VEGF-R1 to form an active dimer. This induces conformational changes allowing trans-phosphorylation of specific tyrosine residues and activation of downstream signalling pathways (Lemmon and Schlessinger, 2010). However, despite the presence of several potential tyrosine phosphorylation sites (Ito et al., 1998), VEGF-R1 is only slightly phosphorylated in endothelial cells upon VEGF-A exposure (de Vries et al., 1992; Meyer et al., 2006). VEGF-R1 is therefore considered as a decoy receptor in charge of repressing excessive angiogenesis. This is illustrated *in vivo* in mouse models. VEGF-R1^{-/-} embryos die *in utero*, due to hyperproliferation of endothelial cells and severe disorganisation and dysfunction of the vascular system (Fong et al., 1995) while the deletion of its tyrosine kinase domain has no effect on angiogenesis (Hiratsuka et al., 1998). In the same context, it has been postulated that preventing interactions between VEGF-A and VEGF-R1 would favour the binding to VEGF-R2 and stimulate angiogenesis (Ho et al., 2012). This could be achieved by PlGF as this VEGF family member binds exclusively and with very high affinity to VEGF-R1 therefore competing with VEGF-A for VEGF-R1, and increasing the amount of VEGF-A available for VEGF-R2 (Park et al., 1994).

Beside the control of angiogenesis, VEGF-R1 plays also a role in the inflammatory response, as shown in cancer, by participating to the recruitment of bone marrow-derived monocytes (Hiratsuka et al., 2001) and macrophage chemotaxis through interactions with PlGF (Clauss et al., 1996; Fischer et al., 2008) but also with VEGF-A isoforms (Barleon et al., 1996; Hiratsuka et al., 1998; Mineur et al., 2007).

In vivo, VEGF-R1 expressed at the surface of macrophages increases their recruitment to wound sites (Lauer et al., 2000) and favours the healing process while sVEGF-R1 seems to delay tissue repair likely by inhibiting inflammatory cells chemotaxis and angiogenesis (Eming et al., 2004).

VI-2 Vascular Endothelial Growth Factor Receptor 2

VEGF-R2, initially identified as KDR (Kinase-insert Domain Receptor) or Flk-1 (Foetal liver kinase-1), is a 210-230 kD glycoprotein with similarities to VEGF-R1 (Koch et al., 2011). It is the main receptor of VEGF in the regulation of angiogenesis (Gille et al., 2001; Terman et al., 1992) as demonstrated by using mutated VEGF variants. An absence of binding to

VEGF-R1 does not affect the pro-angiogenic properties of the mutated VEGF. By contrast, mutations preventing interactions with VEGF-R2 totally abolish the VEGF angiogenic activity (Keyt et al., 1996b). The VEGF-A-VEGF-R2 signalling is central to the regulation of endothelial cell differentiation, proliferation and migration, but also to blood vessel homeostasis and functions (formation, fenestration, maintenance (survival), permeability...) (Fig 13) (Ferrara et al., 2003). The critical function of VEGF-R2 was confirmed *in vivo* since VEGF-R2^{-/-} embryos die at 8.5 - 9.5 dpf, at a development time and with alterations resembling those of VEGF-A^{-/-} embryos (Shalaby et al., 1995).

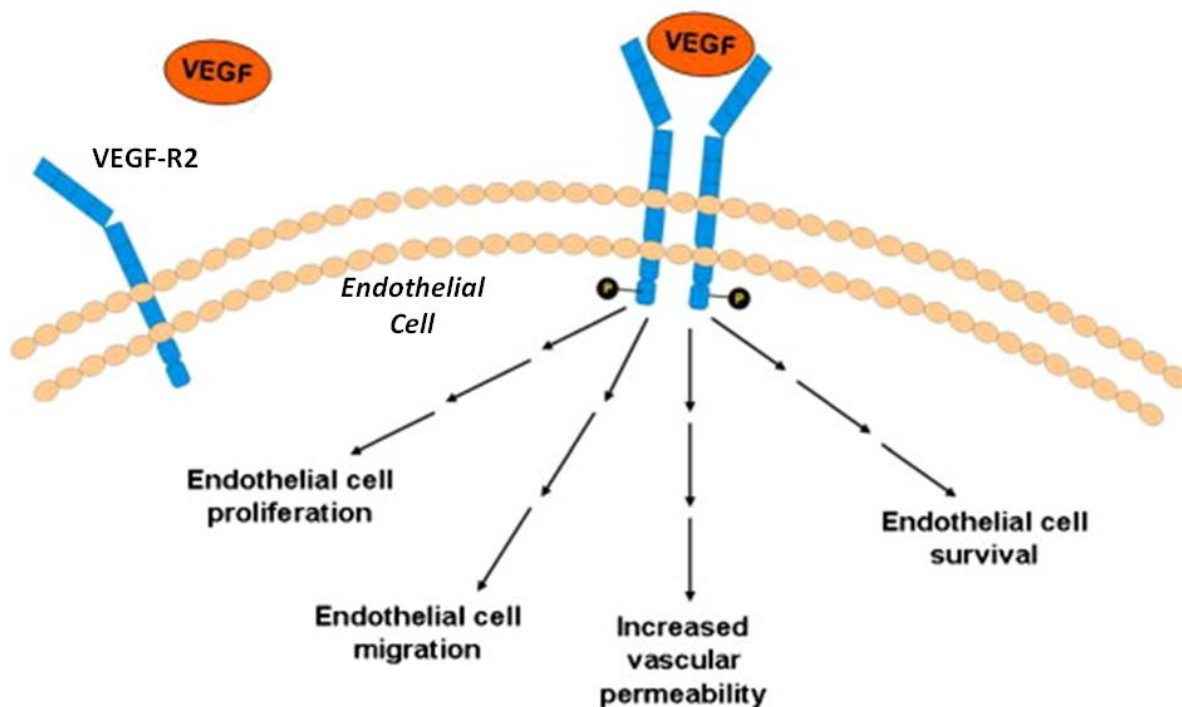


Figure 13 : Effect of VEGF through VEGF-R2 on endothelial cells

The effects of VEGF-A on endothelial cells is mainly mediated by VEGF-R2. VEGF-A binding on one molecule of VEGF-R2 induces the recruitment of a second VEGF-R2 monomer. Their dimerization is a key step for transphosphorylation of specific tyrosines residues and activation of downstream signalling pathways. Integration of these signals is central for regulating endothelial cell phenotype and vessels homeostasis. **From (Farhat et al., 2012)**

VEGF-R2 is mostly expressed in vascular endothelial cells although it can be found also in lymphatic endothelial cells, neurons, cancer cells and macrophages (Bellon et al., 2010; Dineen et al., 2008; Silva et al., 2011; Smith et al., 2010). Its expression is increased in activated endothelial cells and during sprouting angiogenesis, being more elevated in “tip cells” than in “stalk cells” (Gerhardt et al., 2003). Similarly to VEGF-R1, soluble versions, referred to as sVEGF-R2, have been identified (Ebos et al., 2004; Wen et al., 1998). Beside

potential sequestration of VEGF, these soluble variants seem to regulate mural cells migration and vessels coverage (Lorquet et al., 2010).

Activation

VEGF-R2 interacts with VEGF-A via its IgG-like domains 2 and 3. The reported affinity between the two proteins is high (750 pM) although lower than with VEGF-R1 (15 pM) (Millauer et al., 1993; Terman et al., 1992). The initial interaction between VEGF and VEGF-R2 triggers the recruitment of a second receptor molecule, which allows trans-phosphorylation of several tyrosine residues within the dimer and activation of several downstream signalling pathways (Fig 13) (Stuttfield and Ballmer-Hofer, 2009). Interestingly, the formation of VEGFR1-VEGFR2 heterodimers have been reported, which could represent another level of regulation by VEGF-R1 of the VEGF-R2 induced effects (Cudmore et al., 2012; Huang et al., 2001). After activation, the VEGF-R2/VEGF complex is rapidly internalized by clathrin-mediated endocytosis, which does not hamper, and even perhaps increases, downstream signalling (Lampugnani et al., 2003). It can be then recycled to the plasma membrane (Zwang and Yarden, 2009) or degraded, depending on the type of endocytosis vesicles involved.

All phosphorylated Tyr are not equivalent as they trigger different signalling cascades (Matsumoto et al., 2005; Takahashi et al., 2001).

Tyr¹¹⁷⁵

Tyrosine¹¹⁷⁵ in human VEGF-R2 (Tyr¹¹⁷³ in mouse) is probably the most important tyrosine for mediating the VEGF-A effects. Its replacement by a phenylalanine residue has been investigated *in vivo*. VEGF-R2^{Phe1173} homozygous embryos die at 9.5 dpf because of defects similar to those observed in VEGF-R2^{-/-} embryos (Sakurai et al., 2005). Tyr¹¹⁷⁵ phosphorylation allows the binding of several intracellular molecules (PLC γ , SHB, Sck) that initiate intracellular signalling (Fig 14) (Cunningham et al., 1997; Holmqvist et al., 2004; Takahashi et al., 2001; Warner et al., 2000). For example, PLC γ (Phospholipase C gamma) is responsible for the activation of PKC (protein kinase C) and, consequently, ERK_{1/2} (Takahashi et al., 2001). This leads to endothelial cells proliferation. SHB (SH2-domain-containing adaptor protein B) and Sck (Src homology and collagen homology related adaptor protein) induce FAK (Focal Adhesion Kinase) phosphorylation and contribute to cells attachment and migration (Abu-Ghazaleh et al., 2001; Holmqvist et al., 2003). Finally, Sck controls Ras activation and cell proliferation (Meadows et al., 2001).

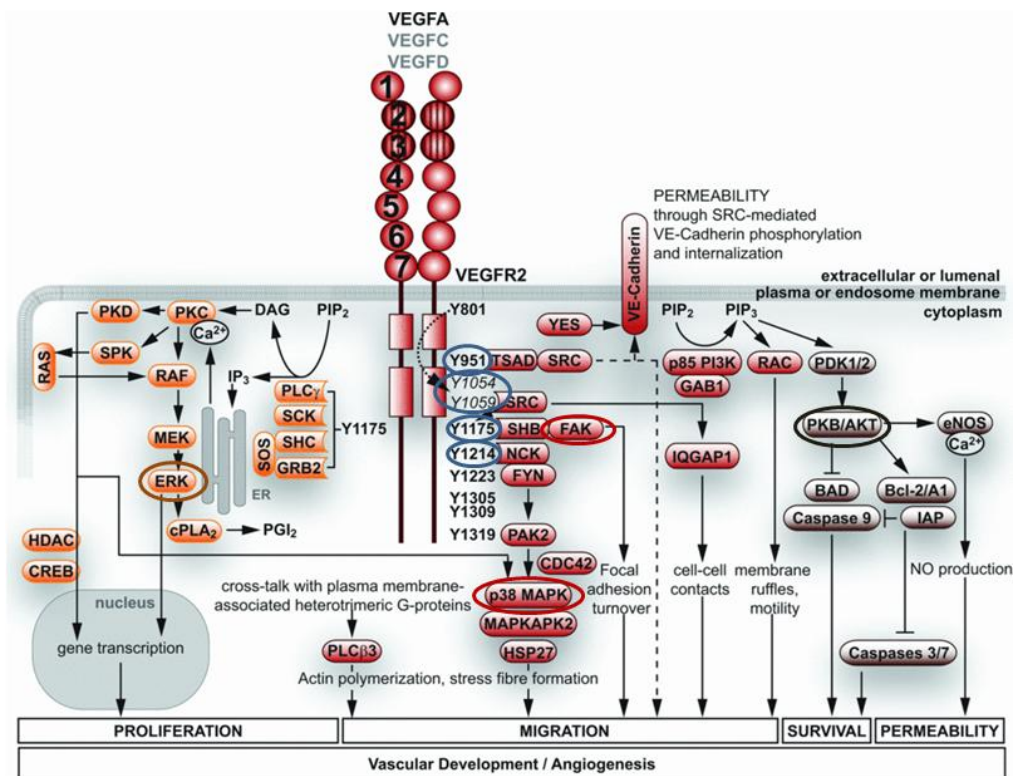


Figure 14 : VEGF-R2 phosphorylation sites, their related signalling pathways and their effects on endothelial cell phenotype and angiogenesis.

Upon interactions with VEGF-A, VEGF-R2 is phosphorylated on several tyrosine residues. Tyr¹¹⁷⁵ is the most important phosphorylation site as it activates, directly or indirectly, several key factors (PLC γ , ERK, FAK, p38...) that regulate endothelial cell proliferation and migration. Tyr⁹⁵¹, Tyr¹⁰⁵⁴, Tyr¹⁰⁵⁹ and Tyr¹²¹⁴ are implicated in vessels migration. It is not completely clear which tyrosine residue(s) is (are) related to Akt pathway. Main tyrosine sites and main downstream molecules studied in the literature are circled. **From (Koch et al., 2011)**

Tyr⁹⁵¹

Tyr⁹⁵¹ is phosphorylated during angiogenesis, where it plays a role in migration and actin reorganization via activation of TSA δ (T-cell-Specific Adapter molecule) (Matsumoto et al., 2005). However, its mutation (into Phe) does not impair mice development showing that this phosphorylation event and its downstream cascades are not critical (Koch et al., 2011).

Tyr¹⁰⁵⁴-Tyr¹⁰⁵⁹

Tyr¹⁰⁵⁴ and Tyr¹⁰⁵⁹ are also crucial residues for VEGF-R2 activity because they are required for complete receptor internalization and activation (Dougher and Terman, 1999; Kendall et al., 1999). Indeed, Tyr¹⁰⁵⁹ allows a maximal phosphorylation of Tyr¹¹⁷⁵ by a positive feedback involving the binding Src and the activation IQGAP1 pathway (IQ-motif-containing GTPase-

activating protein 1). This finally regulates cell-cell contacts, proliferation and migration (Meyer et al., 2008; Yamaoka-Tojo et al., 2006).

Tyr¹²¹⁴

Tyr¹²¹⁴ (Tyr¹²¹² in mouse), by recruiting the Nck adaptor molecule (non-catalytic region of tyrosine kinase adaptor protein 1) and the Fyn tyrosine kinase, plays a role in the activation of the p38 mitogen-activated protein kinase (MAPK) pathway (Lamallice et al., 2006). However, VEGF-R2^{Phe1212} homozygous mice are viable and fertile (Sakurai et al., 2005). By sharp contrast however, p38^{-/-} mice embryos die at 10.5-11.5 dpf because of vascular abnormalities (Aouadi et al., 2006) and VEGF_{165a} efficiently stimulates p38 phosphorylation in endothelial cell expressing only the VEGF-R2^{Phe1214} mutant (Kawamura et al., 2008a). These conflicting data most probably suggest that other phosphorylated tyrosine can also triggers the p38 pathway.

Other regulatory pathways

Although PI3K (phosphatidylinositol 3-kinase) is a key factor for VEGF-A induced regulation, the mechanisms leading to its activation remain poorly understood (Koch et al., 2011). PI3K regulates endothelial cells migration and survival through Rac and Akt, respectively (Datta et al., 1999). Via eNOS, it regulates also vessels permeability, the first identified role of VEGF-A, which is an essential process for normal tissue homeostasis and during the first steps of angiogenesis (Bates and Harper, 2002). Increased permeability can result from the formation of transendothelial pores and/or from the destabilization of the junctions formed between endothelial cells (Garrido-Urbani et al., 2008). Other cascades involving Src and YES can also regulate cell-cell adhesions through the β -catenin/VE-cadherin pathway (Roura et al., 1999; Wallez and Huber, 2008).

VI-3 Neuropilin 1

Neuropilin 1 (NRP1) is a 130 kD transmembrane protein that was initially identified in neural central system as a receptor for semaphorin 3A/Collapsin1 (Sema3A), a secreted polypeptide playing a role in nerve guidance during development (He and Tessier-Lavigne, 1997; Kolodkin et al., 1997). It can also bind VEGF-A variants at the level of two coagulation factor V/VIII homology domains, referred to as B1 (b1) and B2 (b2), present in the large extracellular region (Fig 15) (Appleton et al., 2007; Pellet-Many et al., 2008). In the recent years, many ligands for NRP1 have been identified (Bagri et al., 2009). The molecule contains also a transmembrane and a small cytoplasmic domain containing a PDZ-binding

motif (SEA domain) but lacking intrinsic catalytic function (Fujisawa et al., 1997). Association between this SEA intracytoplasmic motif and an adaptor molecule named synectin (or GIPC) would allow signalling from NRP1 to intracellular pathways of regulation (Cai and Reed, 1999). Phosphorylations on serine and threonine residues have also been suggested (Shintani et al., 2009) and could participate in the NRP1-induced regulation although it is considered that the main functions of NRP1 rely on its activity as a co-receptor. Soluble variants resulting from AS mechanisms have also been identified and would act as anti-angiogenic factors (Cackowski et al., 2004). It can be also post-translationally modified, in a cell type specific manner, by the addition on Ser⁶¹² of either a chondroitin sulfate or a heparan sulphate chain, which can modify its affinity for ligand (Pellet-Many et al., 2008; Shintani et al., 2006).

In the specific field of angiogenesis, it has been shown that NRP1 is expressed at the endothelial cells surface, especially in arteries (Herzog et al., 2001; Soker et al., 1998), and in pericytes (Shintani et al., 2006). It is also upregulated in many tumours and transformed cell lines (Bielenberg et al., 2006; Frankel et al., 2008; Jubb et al., 2012b; Klagsbrun et al., 2002), especially in cells with a high metastatic potential (Bachelder et al., 2001; Latil et al., 2000). NRP1 is also present at the surface of immune cells such as naive T-cell and dendritic cells where it plays a role in the regulation of the immune response (Prud'homme and Glinka, 2012; Tordjman et al., 2002).

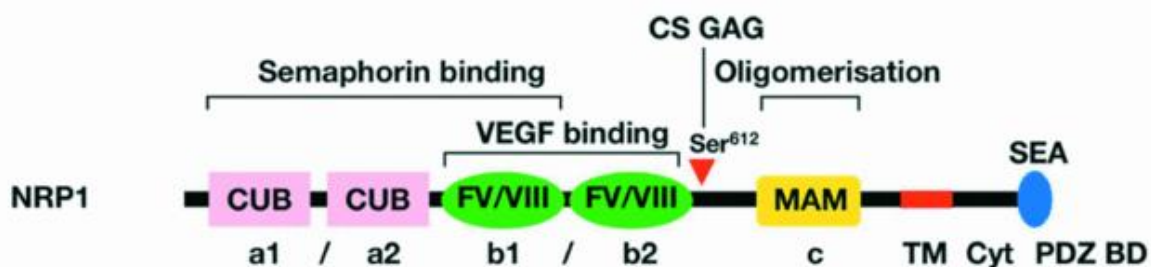


Figure 15 : Schematic structure of Neuropilin 1

Neuropilin 1 is a transmembrane co-receptor containing different domains. An extracellular region contains two CUB domains (a1, a2), two coagulation factor V/VIII homology domains (FV/VIII; b1, b2) and a MAM domain, implicated in oligomerization (c). Domains a1, a2 and b1 are involved in Semaphorin binding while b1 and b2 are involved in VEGF binding. In the extracellular portion, a glycosylation site (CS GAG: Chondroitin Sulfate Glycosaminoglycans) located on Ser⁶¹² domain is identified. The co-receptor domain is also composed of a transmembrane sequence (TM) and a short cytoplasmic regions (cyt) containing the PDZ binding domain (BD), critical for NRP1 function and formed by the SEA sequence. CUB: Complement protein subcomponents C1r/C1s, Urchin embryonic growth factor and Bone morphogenic protein domain, MAM: Meprin/A5-protein/PTPmu domain. **From (Pellet-Many et al., 2008)**

NRP1 is crucial during development, as illustrated in NRP1^{-/-} embryos that die at 12.5-13.5 dpf largely because of vascular problems (Kawasaki et al., 1999). Similar alterations were observed in mouse embryos where NRP1 expression was repressed in endothelial cells only and in the zebrafish model by the use of NRP1-specific morpholinos, demonstrating the critical importance of NRP1 for the development of the cardiovascular system (Gu et al., 2003; Lee et al., 2002).

NRP1-NRP2 double KO mice die at 8.5 dpf with even more severe vascular defects (Takashima et al., 2002) while overexpressing NRP1 triggers an excess of capillary growth and anarchic sprouting leading to mortality *in utero* (Kitsukawa et al., 1995).

VI-3-1 NRP1 in angiogenesis and cancer

As already briefly mentioned, NRP1 could potentially have a direct signalling activity upon ligand binding. It is considered however that its role as a co-receptor is probably the most significant, especially in endothelial cells.

Co-receptor activity

Initially NRP1 was considered only as a co-receptor “presenting” VEGF variants to VEGF-R2, as demonstrated for VEGF_{165a} and VEGF_{121a} for example (Pan et al., 2007b; Shraga-Heled et al., 2007). However, NRP1 is also central to the formation of multi-molecular complexes containing specific VEGF variants (mostly VEGF_{165a} and VEGF_{189a}), VEGF-R2 and sometimes heparin and HSPG (Fig 16). These associations strengthen the interaction between VEGF and VEGF-R2, which increases the activation of signalling pathways regulating endothelial cell phenotype (Becker et al., 2005; Oh et al., 2002; Soker et al., 2002; Whitaker et al., 2001). As compared to VEGF_{121a}, an isoform unable to initiate the formation of such complexes, VEGF_{165a} induces a stronger phosphorylation of p38 in endothelial cells, an increased branching of vessels and a most efficient recruitment of pericytes (Cebe-Suarez et al., 2008; Grunstein et al., 2000; Kawamura et al., 2008a). These properties are inhibited by a blocking antibody for NRP1, further confirming its crucial role in modulating angiogenesis (Pan et al., 2007a). In another example, NRP1 downregulation during wound healing delays the repair process by reducing blood vessel formation (Gu et al., 2003; Matthies et al., 2002). Surprisingly, however it seems that VEGF-induced vascular permeability is not influenced by NRP1 (Pan et al., 2007a).

Expression of NRP1 in “tip cells” has been described as a key element controlling sprouting, by regulating filopodia formation and guiding the direction of migration (Gerhardt et al., 2004). It has also been shown that VEGF_{165a} can induce the formation of complexes

involving VEGF-R2 and NRP1 molecules expressed on the surface of adjacent cells (VSMC), a process probably required in “tip cell” guidance (Cebe-Suarez et al., 2008; Gerhardt et al., 2003).

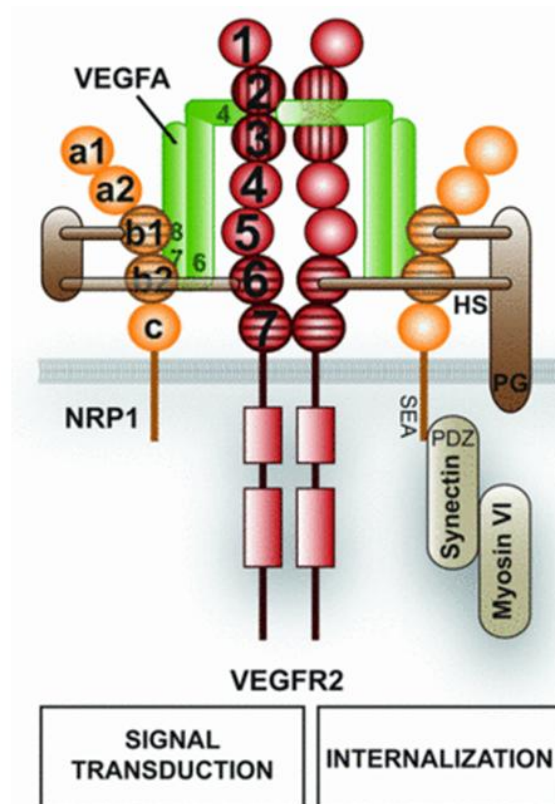


Figure 16 : VEGFR2-VEGF-NRP1-HSPG tetrameric complex

VEGF_{165a} or VEGF_{189a} (green) can form a complex with VEGF-R2 (red), NRP1 (orange) and HSPG (brown). The E4-encoded domain of VEGF is required for binding to VEGF-R2. The E6, E7 and E8 domains are involved in binding to NRP1 while interactions with HSPG/heparin are mediated by the E6 and E7-derived basic amino acids. This complex strengthens the signalling downstream of VEGF-R2 phosphorylation. Other functions or properties of NRP1 rely on its intracytoplasmic domain through interactions between the SEA sequence and synectin, which would participate in the control of internalization and degradation or recycling of VEGF-R2. **From (Koch et al., 2011)**

Besides influencing signalling, NRP1 affects also VEGF-R2 internalization, trafficking and degradation (Ballmer-Hofer et al., 2011). When cells are treated with VEGF_{165a}, complexes between NRP1 and VEGF-R2 can be recycled to the plasma membrane through Rab11 vesicles. By contrast, VEGF_{165b}, which does not bind NRP1, induces internalization in Rab7 vesicles leading to the receptor degradation (Ballmer-Hofer et al., 2011). The SEA domain, by interacting with synectin, plays a critical role in the recycling process (Berger and Ballmer-Hofer, 2011). It has been also suggested that these complexes regulations involving NRP1, VEGF and VEGF-R2 probably operate in other cell types such as pericytes and glioma cells

(Hamerlik et al., 2012; Liu et al., 2005). They are also possibly involved in tube formation by renal epithelial cells (Karihaloo et al., 2005).

Direct signalling activity

It was suggested that NRP1-VEGF binding, without any further interaction with VEGF-R2, could regulate endothelial cells attachment and migration, but not proliferation (Murga et al., 2005; Wang et al., 2003). The SEA-carboxyterminal sequence and its interacting partner, synectin, are essential for these regulations as demonstrated in zebrafish where expression of NRP1 lacking the SEA-motif or, alternatively, the knockdown of synectin, alter blood vessels formation (Wang et al., 2006). p38 is the downstream signalling pathway involved in this process (Ballmer-Hofer et al., 2011; Evans et al., 2011). It has been suggested also that NRP1 could participate in cell adhesion independently of binding to any growth factor (Murga et al., 2005; Shimizu et al., 2000).

NRP1 expression in cancer correlates with poor prognosis, advanced disease state and invasiveness (Hansel et al., 2004; Kawakami et al., 2002; Wang et al., 2012). In absence of VEGF-R2 expression by cancer cells, it was shown that VEGF-NRP1 interactions can regulate however their adhesion, chemotaxis and proliferation *in vitro* and *in vivo* (Bachelder et al., 2001; Herve et al., 2008; Yaqoob et al., 2012). In fibrosarcoma, hypoxia drives NRP1 expression, which stimulates tumour growth through induction of vascular mimicry (Misra et al., 2012). Interestingly, NRP1, in its chondroitin sulphate modified form, could stimulate invasion of human glioblastoma through downstream activation of the p130^{cas} pathway (Frankel et al., 2008).

VI-3-2 Potential use in therapy

Different strategies for inhibiting the VEGF-NRP1 interactions have been tested and evaluated for their efficiency in reducing tumour growth, either directly or indirectly by altering angiogenesis.

- Blocking NRP1 antibodies inhibit angiogenesis *in vivo* and synergizes with an anti-VEGF antibody for reducing tumour growth and blood vessels organization and maturation, particularly by inhibiting pericytes recruitment (Pan et al., 2007a).
- Soluble forms of NRP1 could be used as VEGF trap. Their effects are either direct, by inhibiting cancer cells migration for example (Cackowski et al., 2004; Gagnon et al., 2000), or indirect, by repressing intratumoural angiogenesis (Yamada et al., 2001).
- VEGF mimetic peptides have been also used for the same purpose. A synthetic peptide analogous to the E8a-encoded domain reduces the growth of tumours formed by MDA-

MB231 cells by controlling blood vessel density (Starzec et al., 2006). Other peptides were also evaluated such as those mimetic of the E6a- (Jia et al., 2001) or E7-derived sequences (Soker et al., 1997), or Tufstin (NH₂-Thr-Lys-Pro-Arg-COOH), a peptide with affinity for the b1 domain of NRP1 implicated in VEGF binding (Vander Kooi et al., 2007; von Wronski et al., 2006).

As many aggressive tumour cells are characterized by high levels of NRP1 expression, such peptides conjugated to cytotoxic drugs could be used for targeted therapy, although potential side effects on endothelial cells have to be carefully considered and evaluated (Prud'homme and Glinka, 2012). Promising data have also been observed with peptides coupled to a photosensitizer molecule (Benachour et al., 2012; Tirand et al., 2006).

VI-4 Neuropilin 2

NRP2 displays many similarities with NRP1, such as a 44% sequence identity, high expression levels in the nervous system (Chen et al., 1997; Fujisawa et al., 1997; Kolodkin et al., 1997) and implication, as a co-receptor, in the regulation of angiogenesis (Gluzman-Poltorak et al., 2000; Sulpice et al., 2008). Additionally, NRP2 possesses also a small cytoplasmic domain lacking intrinsic catalytic function (Fujisawa et al., 1997), can be produced as soluble factor (Rossignol et al., 2000) and is upregulated in cancer and is associated with aggressiveness and poor outcomes (Chen et al., 1997; Fakhari et al., 2002; Goel et al., 2012; Handa et al., 2000; Jubb et al., 2012a). It interacts with VEGF-R1 (Gluzman-Poltorak et al., 2001) and induces the formation of NRP2-VEGF₁₆₅a-VEGF-R2 complexes. Their effects on endothelial cells survival and migration have been reported (Favier et al., 2006).

NRP2 possesses however specific properties and function. It is mainly expressed in veins and lymphatics (Herzog et al., 2001; Yuan et al., 2002). *Nrp2*^{-/-} mice are viable with normal veins and arteries but display a reduced network of small lymphatic vessels and capillaries (Yuan et al., 2002). A reduction of VEGF-induced neo-angiogenesis in *NRP2*^{-/-} mice has also been reported (Shen et al., 2004). Its b domains can interact with PlGF and VEGF-A variants (Geretti et al., 2007; Gluzman-Poltorak et al., 2000), but with a lower affinity than the corresponding domain of NRP1 because of the absence of critical acidic residues. NRP2 forms also complexes with VEGF-C or VEGF-D and VEGF-R3, which explains its role in lymphangiogenesis (Karpanen et al., 2006). As for NRP1, treatments with NRP2 antibodies or soluble NRP2 reduce lymphangiogenesis, tumour growth and metastasis (Caunt et al., 2008; Geretti et al., 2010).

VI-5 Heparan Sulfate Proteoglycans and heparin

VI-5-1 Structure

The basic proteoglycan unit consists of a "core protein" with one or more glycosaminoglycan (GAG) chain(s) covalently attached on a Ser residue in an appropriate consensus sequence. Proteoglycans can be categorized depending upon the nature of their GAG chains (heparan, chondroitin, dermatan or keratan sulfate), which may be cell type specific. Heparan sulfate is a glycosaminoglycan structurally closely related to heparin. It consists of a variable number of repeating "glucuronic acid - glucosamine" disaccharide units that can be further modified and partially sulfated. It is mostly found at the cell surface and in the ECM (Esko and Selleck, 2002).

VI-5-2 Role in angiogenesis and cancer

VEGF was initially identified as a heparin and heparin sulphate proteoglycan (HSPG)-binding factor (Ferrara and Henzel, 1989; Senger et al., 1983). Later it was demonstrated that VEGF binding to heparin (Cebe Suarez et al., 2006; Houck et al., 1992) and HSPG (Kawamura et al., 2008b) was isoform-specific. These differences in affinities for HSPG are responsible for the variable capacity of the VEGF-A isoforms to be immobilized in the ECM. As an example, VEGF_{189a} forms stable complexes with heparin and is efficiently trapped and stored in the ECM and at the cell surface (Park et al., 1993) while VEGF_{121a} does not interact with heparin and is therefore more "diffusible". VEGF_{165a} displays intermediate properties (Houck et al., 1992). The simultaneous expression of the three isoforms by tumour cells generates a VEGF gradient that stimulates the formation of a well-organized vascular network (Grunstein et al., 2000). However, a more recent study demonstrates that the binding to heparin is not essential for the localization of the blood vessels in response to VEGF isoforms (Springer et al., 2007).

HSPG have affinity for VEGF-R1, VEGF-R2 and NRP1, but not NRP2 (Park and Lee, 1999; Vander Kooi et al., 2007; Xu et al., 2011a). It was initially reported that HSPG increased the binding of VEGF to its receptors and co-receptor NRP1 (Dougher et al., 1997; Fuh et al., 2000; Gitay-Goren et al., 1992; Tessler et al., 1994), but this was not confirmed in another study for VEGF-R1 and VEGF-R2 (Keyt et al., 1996b). As previously mentioned, HSPG and heparin potentiate VEGF signalling by facilitating the formation of VEGFR2-VEGF-NRP1 complexes at the surface of endothelial cells (Ashikari-Hada et al., 2005; Kawamura et al., 2008a).

VI-6 Other receptors for VEGF

Some VEGF variants, especially the longer variants with affinities for HSPG, present also affinity for other receptors such as integrins, which are transmembrane heterodimers regulating the interactions of cell with the ECM and, therefore, cell adhesion, migration and survival (Chen et al., 2010; Herve et al., 2008; Hutchings et al., 2003). For instance, VEGF can form complex with $\alpha_v\beta_3$, which regulates p38 and FAK pathways activation and affects cell adhesion and migration (Borges et al., 2000; Mahabeleshwar et al., 2006).

VII- Benefits and pitfalls of inhibiting angiogenesis in clinic

The concept of inhibiting angiogenesis for starving tumour and fighting cancer is an old concept (Folkman, 1972). A proof-of-concept study using a blocking antibody targeting VEGF-A was published two decades ago (Kim et al., 1993) and confirmed later in different experimental models (Borgstrom et al., 1998; Borgstrom et al., 1996; Mesiano et al., 1998; Warren et al., 1995).

It rapidly became clear however that using VEGF inhibitors as a monotherapy was efficient only transiently and had only very limited effect on long term outcome. By contrast, treatments combining “classical” chemotherapeutic agents and anti-VEGF molecules currently seem more promising (Ferrara et al., 2007; Garcia et al., 2008; Micha et al., 2007). A concept of vasculature “normalization” explains this synergistic therapeutic effect (Jain, 2005). In tumours, there is an excessive expression of pro-angiogenic molecules, which alters the balance between pro- and anti-angiogenic factors (Fig 17). As a result, the vasculature is poorly organized and vessels remain immature, tortuous and permeable. This has several consequences. The interstitial fluid pressure in the tumour is higher than in the other tissues, which strongly limits the access of chemotherapeutic drugs in the tumour mass. This causes also local hypoxia, which further stimulates pro-angiogenic pathways and contributes to keep abnormal vasculature in the tumour (Fig 17B).

Anti-angiogenic treatments, by restoring a correct balance, tend to destroy preferentially immature vessels and to normalize the vasculature, which reduces intra-tumoural pressure and hypoxia (Fig 17C) and facilitates the delivery of cytotoxic drugs to cancer cells (Jain, 2001). The use of anti-angiogenic molecules requires however a careful dosage because, when use in excess, they can also lead to the destabilization of mature and normal vessels (Fig 17D, upper panel) (Jain and Carmeliet, 2012). In the best case, it may result in tumour regression but usually associated with a reduction of the efficacy of the chemotherapy. In the

worst case, the induced hypoxia could favour metastases and/or stimulate cancer cells to activate alternative pathways for improving their resistance to the treatment. Some of these anti-angiogenic molecules are listed in Table 1 and will be briefly described. They can either target directly VEGF or VEGF-receptors and co-receptors. These compounds can also be used with some success for curing eye diseases due to excessive angiogenesis.

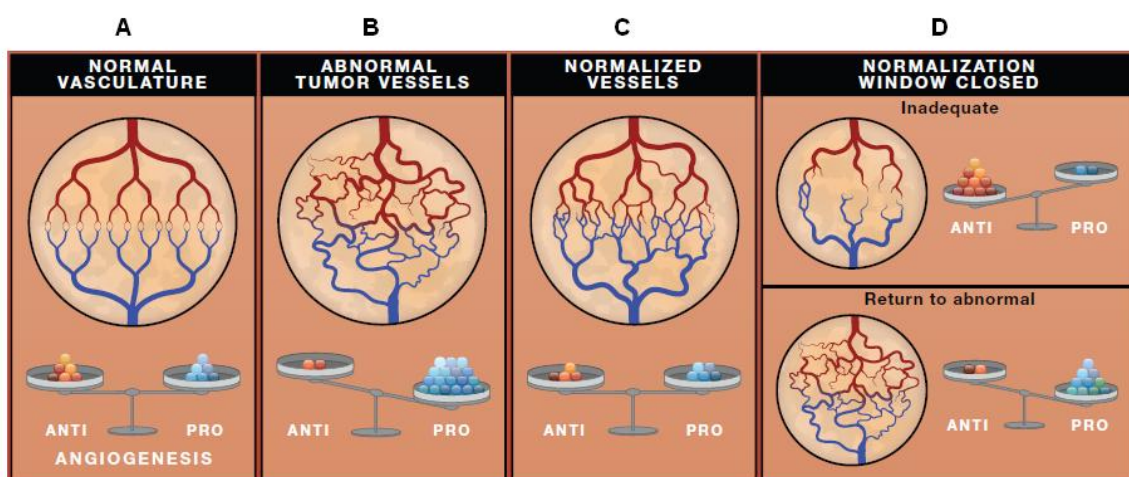


Figure 17 : Blood vessels organization according to the balance between pro- and anti-angiogenic molecules

Normal vasculature homeostasis results from an optimal balance between pro- and anti-angiogenic factors (A). In tumours, blood vessels network is anarchic because of a large excess of pro-angiogenic molecules (B). Restoring a correct balance with optimal dosage of anti-VEGF drugs normalizes the blood vessel network (C). Too high concentrations of anti-angiogenic factors strongly affect the vasculature (D, upper panel) and stopping the therapy leads to a rapid return to abnormal vessel organization (D, lower panel). *From (Jain and Carmeliet, 2012)*

VII-1 Bevacizumab (Avastin®)

Bevacizumab (Avastin®) is a humanized monoclonal IgG1 antibody raised against the E2-E4 encoded sequence of VEGF-A (Presta et al., 1997). Therefore it recognizes both the pro- and anti-angiogenic isoforms as well as the aminoterminal part of cleaved molecules (Gutierrez et al., 2008; Muller et al., 1998; Varey et al., 2008). Bevacizumab is currently the most widely used anti-angiogenic molecule (Jain and Carmeliet, 2012). It can be used as a single agent in second line treatment of glioblastoma but its association with cytotoxic molecules has been approved by the FDA (Food and Drugs Administration of the USA) for treating several cancers, such as advanced colorectal cancer (Escudier et al., 2007; Ferrara et al., 2005; Hurwitz et al., 2004; Rini et al., 2008). As another example, the combination of Avastin and docetaxel was evaluated in metastatic breast cancer. This combined treatment was reported to increase the survival of patients up to 6.0 months as compared to docetaxel alone (Ramaswamy et al., 2006). This synergistic effect seems however to be specific of

some cancer types as the benefit is modest or absent in advanced and metastatic pancreatic cancer (Hayes, 2011; Kindler et al., 2010; Van Cutsem et al., 2009). Furthermore, the initial observation of the positive effect of Avastin for the treatment of metastatic breast cancer has been recently contested (Hayes, 2011)

VII-2 Ranitizumab (Lucentis®)

Ranitizumab, a humanized Fab fragment derived from bevacizumab, is also able to recognize all the VEGF variants (Ferrara et al., 2006). In addition to be much smaller than the parent molecule, it has been designed to have a stronger affinity to VEGF. Its efficiency has been proved in the context of eyes diseases and it is currently the gold reference for the treatment of AMD.

VII-3 VEGF trap (Aflibercept®)

This VEGF decoy is formed by a fusion of extra-cellular domain 2 of VEGF-R1 and domain 3 of VEGF-R2 thanks to the Fc domain of IgG1 (Holash et al., 2002; Teng et al., 2010). It is currently approved as a therapy for AMD and it displays efficacy when combined with chemotherapeutic agents in improving survival of patients with metastatic colorectal cancer (Van Cutsem et al., 2012)

Table 1: Non-exhaustive list of VEGF and VEGF receptors inhibitors

Name	Brand name	Type	Application
Bevacizumab	Avastin	Anti-VEGF Humanized antibody	Cancer
Ranitizumab	Lucentis	Anti-VEGF Humanized antibody fragment	Ocular neo-angiogenic diseases
VEGF-trap	Aflibercept	Extracellular domains of VEGF-R1 and -R2 fused by Fc	Ocular neo-angiogenic diseases, Cancer
Sunitinib	Sutent	Multi-target RTK inhibitor	Cancer
Sorafenib	Nexavar	Multi-target RTK and Raf pathway inhibitor	Cancer
Pazopanib	Votrient	Multi-target RTK inhibitor	Cancer
Axitinib	Inlyta	Multi-target RTK inhibitor	Cancer
Pegaptanib	Macugen	Aptamer anti-VEGF _{165a}	Ocular neo-angiogenic diseases
MNRP1685A		NRP1 antibody	Cancer

VII-4 Pegaptanib (Macugen®)

Pegaptanib is an aptamer with a specific affinity for VEGF_{165a}. When injected in the eye it represses pathological neovascularisation (Ng et al., 2006). As opposed to bevacizumab (Varey et al., 2008), it has the advantage of not recognizing VEGF_{165b}, the variant that permits the survival of endothelial cells but not their proliferation (Magnussen et al., 2010). It is proposed as an alternative to bevacizumab or ranitizumab for the treatment of eyes diseases (Adamis et al., 2006).

VII-5 VEGF-R2 TKI

Several VEGF-R2 tyrosine kinase inhibitors (VEGF-R2 TKI) are currently in development: Sunitinib (Sutent®), Sorafenib (Nexavar®), Pazopanib (Votrient®) or Axitinib (Inlyta®). All of them target VEGF-R2, but some of them can inhibit other tyrosine kinase receptors. They have been proved to display efficacy in cancer therapy by preventing the intracellular phosphorylation of the VEGF-R2 (Escudier et al., 2009; Rini et al., 2009; Sternberg et al., 2010). Amongst them, Sorafenib has the additional advantage to target also downstream signalling pathways (c-Raf, B-Raf) of the VEGF-R2 (Adnane et al., 2006).

VII-6 Resistance and side effects

The use of anti-angiogenic factors in cancer therapy has been so far disappointing for several reasons (Table 2) (Kerbel, 2012; Miller et al., 2005). Resistance to treatment has been reported many times. It could be related to the lack of sensitivity to VEGF of the mature vessels feeding the tumours (Fig 4) (Bergers et al., 2003; Sitohy et al., 2012). The activation of alternative pro-angiogenic pathways, such as the cascade triggered by c-Met, is another mechanism of resistance to current therapies (Casanovas et al., 2005; Huang et al., 2010; Shojaei et al., 2010; You et al., 2011). Another problem relates to dangerous side effects such as thrombo-embolism, hypertension and proteinuria (Kabbinavar et al., 2003; Launay-Vacher and Deray, 2009; Mir et al., 2011). The absence of reliable biomarker that could allow an evaluation of the efficacy of anti-angiogenic drugs and their price, especially for Avastin®, are other features that prevent further development and use. Finally, any interruption in the treatment leads to a rapid reformation of the previous vasculature network because the remaining of dead vessels (channels, ECM including basement membrane, surviving pericytes...) serve as preferential scaffolds for neo-angiogenesis (Mancuso et al., 2006). Other adverse effects such as an increase of metastasis have been observed after a short-term treatment with Sunitinib (Ebos et al., 2009).

Table 2 : Major Problems of Anti-angiogenic therapies	
Disappointing results	Resistance to treatment, limited effect (if any) in Phase III studies
Adverse side effects	Re-growth of tumor after stopping treatment, hypertension, proteinuria
Cost	Excessive price (Avastin)
No biomarker available	Absence of control of the efficacy

From Conference of X. Pivot, Fourth Congress of French Society of Angiogenesis

VII-7 Endocan: a potential biomarker of the expression of VEGF by tumours

The identification of biomarkers allowing the evaluation of the progression of neovascularisation in cancer and during anti-VEGF treatment is needed. Endocan, also referred to as ESM-1 (Endothelial cell-Specific Molecule 1), is a secreted proteoglycan composed of a 165 amino acids core protein covalently linked to one dermatan sulphate side chain (Bechard et al., 2001; Bechard et al., 2000). Its expression is induced by VEGF (Abid et al., 2006; Recchia et al., 2010; Rennel et al., 2007; Strasser et al., 2010) and in cancer, especially during the switch from dormant to fast-growing angiogenic tumours (Almog et al., 2009). Increased endocan concentrations have been measured in serum of patients with lung and renal cancers, as compared to healthy subjects (Leroy et al., 2010; Scherpereel et al., 2003). All these observations suggest that circulating endocan could be a biomarker of neo-angiogenesis and tumour aggressiveness.

VIII- Stimulation of angiogenesis for the treatment of ischemic diseases

While cancers and many eyes diseases could be cured by anti-angiogenic therapies, several clinical conditions are directly or indirectly related to insufficient perfusion, either acute (stroke, heart infarction, tissues grafting) or chronic (angina, skin ulcers...).

Wound healing delay

During tissue repair, hypoxia, pro-inflammatory cytokines and growth factors trigger VEGF secretion by keratinocytes and infiltrating inflammatory cells (Detmar et al., 1995; Frank et al., 1995; Fukumura et al., 1998; Kishimoto et al., 2000). This leads to vascular permeability, local angiogenesis and to the recruitment of additional inflammatory cells and bone-marrow derived endothelial progenitor cells (Brown et al., 1992; Eming and Krieg, 2006; Galiano et al., 2004). Reduced concentrations of VEGF-A delay the healing process. This is illustrated

in a model of normal mice treated with a blocking VEGF antibody (Howdieshell et al., 2001) and in diabetic (db/db) mice where low levels of VEGF in the skin largely participate to the impaired tissue repair. Moreover, treating db/db mice with VEGF_{165a} accelerates healing (Corral et al., 1999; Galiano et al., 2004; Romano Di Peppe et al., 2002; Roth et al., 2006). However, this effect is restricted to mice with a delay phenotype as animals overexpressing VEGF do not heal better than their wild-type controls (Hong et al., 2004).

Based on these data it was suggested that VEGF could be used to accelerate the healing process of chronic ulcers that are frequent in diabetic patients and in patients with venous problems. The first experimental evaluations were however disappointing. Several hypotheses have been made to explain this absence of efficacy, such as bad access of VEGF to endothelial cells in the wound bed or degradation of VEGF by the proteases-rich environment (Keyt et al., 1996a; Lauer et al., 2000; Lauer et al., 2002). In this context, the use of variants that are more resistant to proteolysis and more “diffusible” such as VEGF_{111a} could help solving these limitations (Lauer et al., 2002; Mineur et al., 2007).

SCIENTIFIC CONTEXT AND AIMS OF THE WORK

Scientific context

VEGF-A, a major regulator of angiogenesis, is involved in physio-pathological processes such as development, menstrual cycle, wound healing, cancer and several eyes diseases. Its expression is regulated at the transcriptional level by activation of its promoter but also by post-translational mechanisms, mainly in hypoxic conditions. Alternative splicing of the pre-mRNA is also a potent regulator of VEGF-A activity as it induces the production of several VEGF variants possessing specific properties. While the role of the constant amino-terminal portion encoded by exons 1 to 4 is currently well defined, the functions of the alternative carboxy-terminal domains have to be deeply characterized in order to better understand why the different VEGF variants have very specific properties regarding the regulation of angiogenesis.

Aims of the work

This work, aiming at better defining the roles and potential cooperation of the domains encoded by the E5 to E8a/E8b terminal exons, can be divided in 4 different but related steps:

- Production and purification of relevant VEGF variants
- Characterization at a biochemical level by determining:
 - their affinity to VEGF receptors and co-receptors
 - their resistance to proteolysis.
- Evaluation of their role on angiogenesis by measuring their effects
 - on various endothelial cell types *in vitro*
 - on tumoural angiogenesis *in vivo*.
- Preliminary characterizations regarding potential clinical applications of our studies are also provided.

MATERIAL AND METHODS

I- Cell culture and transfected cell lines

HEK293 cells were cultured in DMEM (BioWhittaker, Walkersville, MD, USA) containing 10% FBS (Foetal Bovine Serum), penicillin (100 IU/ml) and streptomycin (100 IU/ml) except otherwise indicated. Hygromycin B (100 µg/ml, Roche, Basel, Switzerland) was added to the medium for selection of cells stably transfected with the various expression vectors. Human Umbilical Vascular Endothelial Cells (HUVECs) were cultured on a gelatin coat in M200 medium (Cascade Biologic, Portland, OR, USA) supplemented with LSGS kit (Cascade Biologic) and penicillin. Porcine aortic endothelial cells (PAEC) were cultured in Ham's F-12 (Bio Whittaker) supplemented with 10% FBS, penicillin and fungizone (0.5 µg/ml). For cells overexpressing human VEGF-R1 (PAEC-R1), VEGF-R2 (PAEC-R2) or NRP1 (PAEC-NRP1) (Becker et al., 2005; Waltenberger et al., 1994), G418 (0.5 mg/ml) was used to maintain selection. In order to produce PAEC-R2 further expressing human NRP1, a full length NRP1 cDNA was cloned into the pcDNA4/T0 vector (Invitrogen, Carlsbad, New-Mexico, USA) and the construct was transfected into PAEC-R2 using cationic lipids (GeneJuice Transfection Reagent, Novagen, UK). Cells were then selected in Ham's F-12 containing Zeocin (Invitrogen, Belgium) at 150 µg/ml.

For quantifying the secretion of endocan HUVEC were seeded in M200 supplemented with LSGS on a gelatin-coated 12 wells-plate. At 80% of confluence, cells were starved in M200 containing 0.2% FBS for 4h before the addition of VEGF isoforms (at 1nM). Conditioned media were sampled after 24h and 48h.

II- Chemicals and antibodies

Human plasmin, Evans' blue and formamide were obtained from Sigma-Aldrich (St-Louis, MO, USA). The following antibodies were used for Western blot: anti-ERK 1/2 (rabbit polyclonal, M-5670) and anti-phospho ERK 1/2 (mouse monoclonal, M-8159) were purchased from Sigma-Aldrich; anti-VEGF (rabbit polyclonal, SC-152) was purchased from Santa Cruz Biotechnology (Santa Cruz, CA, USA); anti-human VEGF-R2 (clone 55B11, rabbit); anti-phospho Tyr1175 of VEGF-R2 (rabbit), anti-Akt (rabbit) and anti-phosphoAkt (rabbit) were purchased from Cell Signalling Technology (Danvers, MA, USA). Goat anti-Rabbit antibody coupled to peroxidase (Cell Signalling Technology) was used for rabbit antibodies. Other secondary antibodies were purchased from Dako (Glostrup, Denmark).

Mimetic peptides A7R (NH₂-Ala-Thr-Trp-Leu-Pro-Pro-Arg-COOH) (Starzec et al., 2006) and R8R (NH₂-Arg-Pro-Lys-Lys-Asp-Arg-Ala-Arg-COOH) were obtained from Polypeptide Group (Strasbourg, France).

III- Cloning, production and purification of VEGF variants recombinant proteins

Cloning of VEGF_{111a}, VEGF_{121a} and VEGF_{165a} cDNAs and transfection of HEK293 cells were described elsewhere (Mineur et al., 2007). The coding sequence of VEGF_{111b}, VEGF_{121b}, VEGF_{155a}, VEGF_{155b}, VEGF_{165b}, VEGF_{179a} and VEGF_{179b} cDNAs were chemically synthesized (Genscript, Piscataway, NJ, USA), subcloned in a pCEP-4 vector and transfected into HEK293 cells using FuGENE 6 transfection reagent (Roche). Hygromycin-resistant transfected cells were cultured up to 90% confluence in medium supplemented with 10% FBS. For VEGF production it was replaced by medium containing 1% FBS and cultures were continued for 2 additional days. VEGF variants were then purified from conditioned media by affinity chromatography using Bevacizumab (Avastin, Roche) coupled to Affi-Gel Hz (Biorad, Hercules, CA, USA) as described by the manufacturer. After sample loading and washing (Tris 0.05 M, NaCl 0.15M, pH 7.5), VEGF was eluted (Glycine 0.1M, pH 3.5) and the recovered fractions were immediately neutralized with 1:10 volume of 1M Tris. Some VEGF variants were also purified by affinity chromatography using heparin-sepharose (CL6B, GE Healthcare). After sample loading and washing (H₂PO₄⁻-HPO₄²⁻ 0.01 M, NaCl 0.25M, pH 7.3), VEGF were eluted with increasing concentrations of NaCl (0.5M, 1M, 1.5M and 2M). Purity and concentration were evaluated after SDS-PAGE (15% acrylamide) and Sypro Ruby (BioRad) staining (see chapter IV-2). Proteins were dialysed against HBS-EP buffer (GE Healthcare, Little Chalfon, UK) for Surface Plasmon Resonance or diluted in PBS for other purposes.

IV- Analytical procedures

IV-1 Western blot

Western blot analyses were used to evaluate the quality and the purity of the different VEGF variants and to determine the phosphorylation and activation of VEGF-R1, VEGF-R2 and downstream signalling molecules. Proteins were separated by SDS-PAGE (Sodium Dodecyl Sulfate PolyAcrylamide Gel Electrophoresis) and transferred onto polyvinylidene difluoride membranes (Perkin Elmer, Waltham, MA, USA) by electroblotting. Membranes were blocked for 1 hour in PBS-Tween (0.05%) buffer supplemented with 3 % fat free dry milk before probing with the primary antibodies. After washing in PBS-Tween, membranes were

incubated with the appropriate HorseRadish Peroxydase (HRP)-conjugated secondary antibodies. Signals were detected by chemiluminescence using the ECL Western Blotting Analysis Substrate (Thermo, Fischer Scientific Waltham, MA, USA) and x-ray film exposure before quantification using the Fluor-S Multimager and Quantity One software (Bio-Rad Laboratories, Hercules, CA, USA).

IV-2 Sypro Ruby

After SDS-PAGE separation, gels were fixed (30 min) in a solution containing 50% methanol and 7% acetic acid for half an hour, stained in Sypro ruby solution for 4 hours and washed in a solution containing 10% methanol and 7% acetic acid for 30 min. The quantification was performed using the Fluor-S Multimager and Quantity One software. The VEGF concentrations were evaluated by comparison to BSA (Bovine Serum Albumine) samples of defined concentrations run on the same gel.

IV-3 Quantification by ELISA

VEGF concentrations were also evaluated by ELISA using either panVEGF or VEGF_{165b} Duoset (R&D systems). Endocan concentration was assessed using JDIYEK ELISA kit (Lunginnov, Lille, France).

IV-4 Mass Spectrometry

The amino acids terminal sequence of VEGF variants was analyzed by MALDI-TOF (Matrix-Assisted Laser Desorption/Ionisation and time-of-flight mass spectrometry) process at the GIGA-Proteomic Platform (University of Liège).

V- Binding to VEGF-receptors and co-receptors

V-1 Surface Plasmon Resonance

Surface Plasmon Resonance (SPR) analyses were performed on a Biacore X-100 system (GE Healthcare) as previously described (Fig 18) (Herve et al., 2008). Briefly, Fc chimera human VEGF-R1 or VEGF-R2 and Fc chimera Rat NRP1 or NRP2 (R&D Systems, Minneapolis, MN, USA) were bound to the CM5 Sensorchip (GE Healthcare) using goat polyclonal antibodies against Human Fc (Sigma-Aldrich) fixed by amine binding to the chip. Biotinylated heparin was coupled to a carboxymethylated dextran pre-immobilized with streptavidin (Sensorchip SA, GE Healthcare). For routine evaluation the samples were diluted in HBS-EP buffer and injected for the indicated period of time (100-300 sec) followed by washing in HBS-EP (150-600 sec) in order to evaluate the association and dissociation curves, respectively. For more quantitative measurements (BIAevaluation software 4.1, GE

Healthcare), increasing concentrations of samples (0.4, 1.3, 4.0, 13.0 and 40.0 nM) were successively injected on the chip.

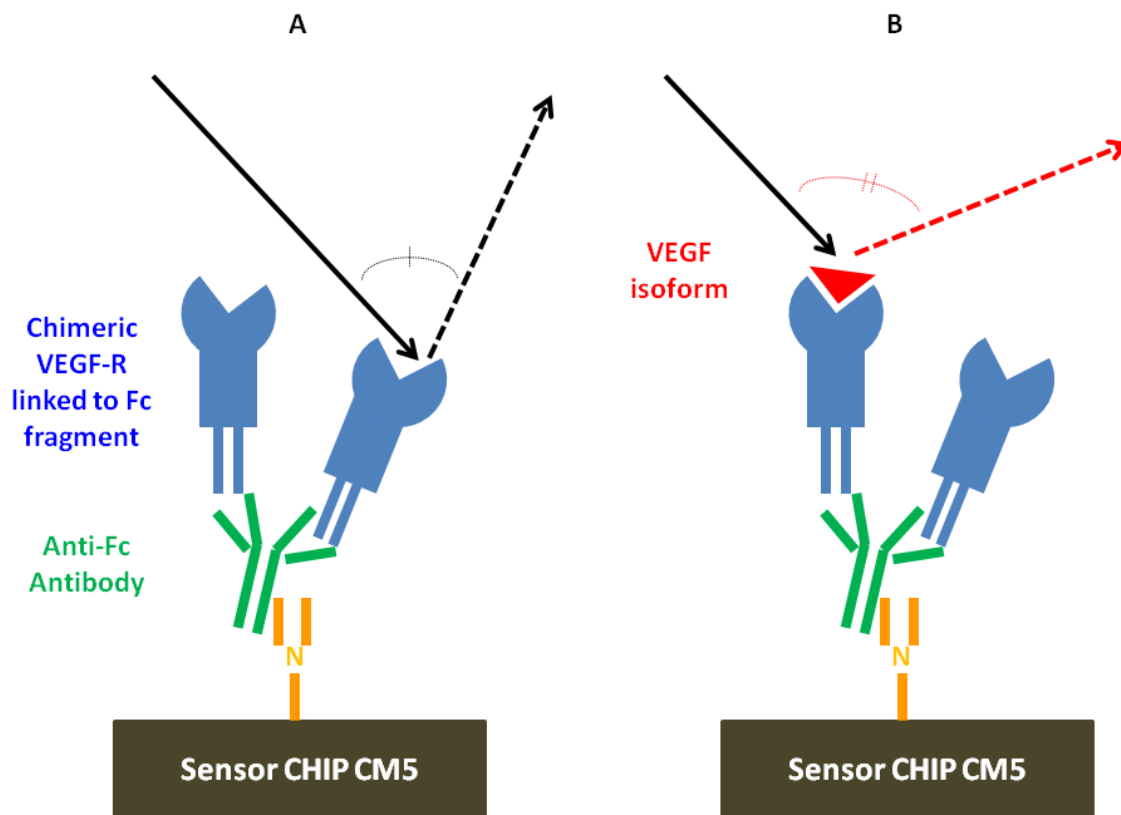


Figure 18 : Surface Plasmon Resonance analyses

VEGF (co-)receptors (blue) are bound to the chip using anti-human Fc antibodies (green) immobilized on the chip (grey) by amine bonds (orange). **(A)** In absence of any ligand an incident light is refracted with specific characteristics, here shown by the black dotted lines. **(B)** After binding of a ligand (VEGF here, red triangle), the angle of the refraction of the light is modified (red dotted line). This modification can be measured, quantified and used to evaluate the association and dissociation parameters. VEGF-R: VEGF-Receptor

V-2 Solid Phase Assay

For direct binding evaluation, solid phase assays were performed by coating 110 ng of VEGF in 50 μ l PBS-Tween 0.1% containing BSA 0.1% on a flat bottom polystyrene plate (Maxisorp, Nunc Thermo Scientific) overnight at 4°C. After blocking (PBS-tween-BSA for 24h at 4°C) and washing (PBS-Tween-BSA), VEGF-R2-Fc (0.5 μ g/ml), NRP1-Fc (0.5 μ g/ml) + heparin (1 μ g/ml) or NRP2-Fc (0.5 μ g/ml) + heparin (1 μ g/ml) were added in 50 μ l of buffer for 1 hour at room temperature. Diluted (1/1200) biotinylated antibody against Human Fc (Sigma-Aldrich) was then added and incubated for 30 min at room temperature. Streptavidin-HRP and ABTS substrate (RnD systems) were then added. The Optical Density (OD) was measured at 415 nm after 30min of reaction.

For competition assays, the surface of flat bottom polystyrene wells was treated overnight at 4°C with 100 µl of 2 µg/ml anti-Fc IgG in phosphate buffer saline (PBS, Sigma). After washing and saturation of non-specific interactions with bovine serum albumin (BSA, Sigma), purified recombinant rat NRP1-Fc (20 ng/well in 50 µl PBS-Tween-80 containing BSA 0.5% (PBT), R&D Systems, Abingdon, UK) was added in the wells. Then peptides solution (50 µl in PBT from 0.01 to 300 µM, final concentration) or VEGF (from 5 to 450 nM, final concentration) and biotinylated VEGF_{165a} (1nM, final concentration, R&D Systems) diluted in PBT containing 2 µg/ml of heparin were successively added. After overnight incubation at 4°C, the wells were washed and treated with Streptavidin-HRP and ABTS substrate.

VI- Resistance to degradation

20ng of the different VEGF variants were treated with increasing concentrations of plasmin (0-32 x 10⁻² IU) or of exudates from skin ulcer and incubated at 37°C for 4, 24 and 48 hours. The products of the reactions were analyzed by western blot as described above.

VII- Angiogenesis *in vitro*

VII-1 Phosphorylation assay

PAEC (Porcine Aortic Endothelial Cells) control, PAEC-R1, PAEC-R2, PAEC-NRP1, PAEC-R2-NRP1 and HUVECs were seeded in 6-well plates and allowed to spread overnight. Cells were then starved for 18 h (PAEC) or 6 h (HUVECs) in appropriate medium deprived of FBS. VEGF variants were added at the indicated concentration and time according to the protocol previously described (Catena et al., 2010; Woolard et al., 2004). Serum-free media and media containing 10% FBS were used as controls. Reactions were stopped by placing cells on ice, immediate washing with ice-cold PBS and lysis in 200 µl of Laemmli buffer. The lysates were sonicated and stored at -20°C until western blot analysis. Quantifications of the signal were performed and the relative phosphorylation indexes (phosphorylated protein/total protein) were calculated. Due to large differences in the levels of phosphorylation, films obtained after different times of exposure were quantified, samples providing intermediate intensities being used as internal comparative calibration signals. To facilitate the comparison between all the samples, the phosphorylation index calculated for VEGF_{165a} was arbitrary set at 1.

VII-2 Proliferation and survival assay

WST-1 and [³H]-thymidine incorporation assays were performed to measure cell proliferation and survival. Different media and time were tested in preliminary experiments for defining the optimal conditions for the different assays.

For the WST-1 assays, 3x10³ HUVECs were seeded overnight in gelatin-coated 96-wells plates (Greiner Bio-One, NC, USA) in M200 supplemented with LSGS. Cells were washed with PBS and incubated in M200 containing 0.5% FBS in the presence or absence of VEGF variants (250 pM). Two days later, 10 µl of WST-1 reagent were added to each well. After 2 hours, the optical density was measured at 450 nm.

For [³H]-thymidine incorporation assays, 1.5x10⁴ HUVECs were seeded overnight in gelatin-coated 24-wells plates in M200 supplemented with LSGS. Cells were washed with PBS and further cultured for 24 h in M200 containing 0.5% FBS for the evaluation of proliferation (or 0.1% for the survival assay) supplemented or not with VEGF (250 pM). [³H]-thymidine (1 µM final concentration, 2.5 Ci/mol, Perkin Elmer, Waltham, MA, USA) was then added to the culture medium and the 10 % TCA-precipitable radioactivity was measured 24 h later.

VII-3 Migration assay

The capacity of VEGF variants to induce migration of HUVEC was evaluated using the Boyden Chamber assay. VEGF variants (1nM in 500 µl of M200 supplemented with 0.001% FBS) were placed in the bottom chamber of a 24-wells plate. Inserts with 8 µm diameter pores (Millipore) were coated with attachment factor (Invitrogen) for 1 hour at 37°C and then placed in wells before seeding serum-starved HUVEC in the top chamber (100.000 cells in M200 / 0.001% FBS). After 8 to 16h at 37°C for allowing cells to migrate from the top to the bottom chamber, the inserts were washed twice with PBS and fixed in PFA 4% for 20 min. Using a cotton swab, cells of the upper chamber were removed before staining with Hoechst (Invitrogen) for 5 min. Cells which migrated from top to bottom chamber were counted in 10 fields and the percentage of migration were calculated using the following formula. Percentage of migration = (Cells per Field*1/0.0028637/1x10⁵)x10. (0.0028637) represents the area of the insert visible by 1 field of view.

VIII- VEGF Half-life in vivo

Six week-old C57bl6 mice were divided into twelve groups (4-6 mice per group). They received intravenous, intraperitoneal or subcutaneous injections of VEGF_{111a}, VEGF_{111b},

VEGF_{165a} and VEGF_{165b} (5 µg in 100µl). Blood samples were collected in the tail using heparitinized capillaries (Hirschmann Laborgerate, Eberstat, Germany) directly and 0.5, 1, 2, 4 and 8 hours after injection. After centrifugation at 11,7000 rpm for 5 minutes using Autocrit ULTRA-3 centrifuge (BD, Franklin Lakes, NJ, USA), plasma were collected and stored at -20°C before further analysis. VEGF concentrations were evaluated using panVEGF and VEGF_{165b} Duo set ELISA kit (R&D systems). Half-life was evaluated by constructing exponential regression using Excel software (Redmonds, WA, USA), $y=a*\exp^{(bx)}$, where “a” and “b” are the maximal concentration and the exponential constant, respectively. Half-life were then calculated according to the following formula : $t_{1/2}=\ln(2)/b$.

IX- Angiogenesis *in vivo*

Experimental protocols were approved by the local animal ethical committee (University of Liège, approval document n° 1125). 2×10^6 HEK293 cells transfected with the empty vector or expressing human VEGF variants were mixed with 200µl of Matrigel depleted in growth factors (Becton Dickinson, Franklin Lakes, NJ, USA) and injected subcutaneously in the flank of nude mice (6-week-old Swiss Nu/Nu, Charles River Laboratories, Wilmington, MA, USA) as described by Mineur and collaborators (Mineur et al., 2007). Four to 19 mice were used per group. Three weeks later, animals were sacrificed and dissected. Tumours and peritumoural tissues were collected and used for RNA purification and RT-PCR amplification, protein analysis and histological and immunohistochemical evaluations. VEGF mRNAs expression in the tumours was evaluated by RT-PCR using panVEGF primers (specific for sequences corresponding to exons 2 and 4, thus common to all isoforms) or VEGF_{xxx}a, VEGF_{111b}, VEGF_{121b} and VEGF_{155-165-179b} specific primer pairs (Table 3). VEGF_{xxx}b protein levels were quantified in protein extracts using VEGF_{165b} specific ELISA (R&D Systems). Angiogenesis was evaluated by measuring CD31 mRNA expression by RT-PCR (Table 3).

For immunohistochemistry analyses, anti-mouse CD31 (rabbit antiserum, at dilution 1:20, Dianova, Hambourg, Germany), anti-collagen IV (in-house developed rabbit anti-serum, at dilution 1:100), anti- α smooth muscle actin (α -SMA, mouse monoclonal, at dilution 1:400, Sigma-Aldrich) and anti-VEGF (1:50) were used. Secondary antibodies were obtained from Dako. The CD31 labelling of vessels in tumoural and peritumoural mouse tissues was quantified as the positive area relative to the total area by using Image J Software (National Institute of Mental Health, Bethesda, MD, USA).

Table 3 : mRNA primers and amplicons size

Primers name	Primers sequences (5' to 3')	Size (bp)	mRNA
P1 (forward) P2 (reverse)	CTG CTC TAC CTC CAC CAT GCC AA AGG GGC ACA CAG GAT GGC TTG AA	197	PanVEGF
P3 (forward) P4 (reverse)	CCT GGT GGA CAT CTT CCA GGA GTA CTC ACC GCC TCG GCT TGT CAC A	245 275 377 407 449	VEGF _{111a} VEGF _{121a} VEGF _{155a} VEGF _{165a} VEGF _{179a}
P5 (forward) P6 (reverse)	CCT GGT GGA CAT CTT CCA GGA GTA TCC TGG TGA GAG ATC TGC ATT CAC	237	VEGF _{111b}
P7 (forward) P8 (reverse)	CCT GGT GGA CAT CTT CCA GGA GTA GTC TTT CCT GGT GAG AGA GTT TTC TT	273	VEGF _{121b}
P9 (forward) P10 (reverse)	CCT GGT GGA CAT CTT CCA GGA GTA CGA TCG TTC TGT ATC AGT CTT TCC T	368 398 440	VEGF _{155b} VEGF _{165b} VEGF _{179b}
P11 (forward) P12 (reverse)	GTT CAC CCA CTA ATA GGG AAC GTG A GAT TCT GAC TTA GAG GCG TTC AGT	212 269*	28S
P13 (forward) P14 (reverse)	CAA GGC GAT TGT AGC CAC CTC CA CCA ACA ACT CCC CTT GGT CCA GA	209	CD31

RT-PCR using P3-P4 allows to measure the amplification product of the 5 studied VEGF_{xxx}a variants, which are discriminated according to their size after migration on SDS-PAGE. VEGF_{111b} and VEGF_{121b} are amplified using the P5-P6 and P7-P8 primers, respectively. RT-PCR using P9-P10 allows to measure the amplification product of 3 of the 5 studied VEGF_{xxx}b variants, which are discriminated according to their size after migration on SDS-PAGE. CD31 is amplified using the P13-P14 primers. *internal control. bp: base pairs.

X- Inhibition of Neoangiogenesis

IX-1 Choroidal Neovascularization assay (CNV)

Six week-old C57bl6 mice were anesthetized by intraperitoneal injection of 0.1 ml of a 50:50 mixture of ketamine hydrochloride (20 mg/ml) and xylazine hydrochloride (100 mg/ml, Phoenix Pharmaceutical, St Joseph, MO, USA). They received 2 to 4 photocoagulation lesions per eye delivered with a diode green laser (λ - 810nm, 250mV, 75ms, 75 μ m, 2 to 4 lesions/eye 250mW, IRIDEX Oculight GLX, Mountain View, CA, USA). Eyes were immediately treated with intravitreal (IVT) injection of 2 μ l PBS containing 10 ng of VEGF₁₁₁b (15 lesions) or VEGF₁₆₅b (25 lesions) in one eye and 2 μ l of PBS (22 lesions) in the other, as negative control (Hua et al., 2010). Injections were performed using a 33-gauge needle (Nanofil, World Precision Instruments, Sarasota, FL, USA) after dilatation of the pupils using 2.5% phenylephrine hydrochloride and 0.8 % tropicamide. Injections were repeated on day 7. On day 14, mice were sacrificed. Choroids were dissected, fixed in 4% PFA and stained with a specific endothelial cell marker (isolectin B4, 1:100, Vector Laboratories, Burlingame, CA, USA). Areas of pathological neovascularization were measured using Image J software.

IX-2 Oxygen Induced Retinopathy assay (OIR)

For oxygen induced retinopathy (OIR), Sprague Dawley® rats (n=6 per group) were exposed at birth to 7 cycles of atmosphere at 50% O₂ for 24 hours followed by another 24 hours of atmosphere at 10 % oxygen (Penn and Rajaratnam, 2003; Penn et al., 1994). After 14 days animals were placed at room air (21% oxygen). At this time point, they received 10ng of VEGF₁₁₁b in 2 μ l PBS in one eye and 2 μ l PBS in the other as described for CNV. On day 20, pups were sacrificed and retinas were dissected and stained as previously described for CNV (Hua et al., 2010). A clock hour analysis method (Penn et al., 1994) was performed to quantify intravitreal neovascularization (IVNV). Arterial tortuosity, vessels' diameter and avascular areas were analysed using Image J software.

IX-3 Cytoprotection assay

Fresh retinal pigment epithelial cells (RPE) and arising spontaneously transformed retinal pigment epithelial cells (ARPE19) were used to evaluate the cytoprotective effect of VEGF variants against toxic doses of ketocholesterol. 15x10³ ARPE19 or 12x10³ primary RPE cells were seeded in a 96-wells plate in full DMEM-Glutamax overnight. Cells were starved in absence of FBS and treated with 2.5nM of VEGF isoforms or EGF, used as a positive control (5-wells per condition). 24h later, cells were treated with 14 to 40 μ M of

Ketocholesterol. After 24h, cell activity was measured by WST-1 reagent (Roche) or LDH (Lactate Dehydrogenase) released in culture media (Promega, Madison, WI).

XI- Permeability *in vivo*

Vascular permeability *in vivo* was evaluated by using a Miles and Miles modified assay (Sounni et al., 2010) using 6 to 8 week-old BALB/C mice. The backs of the animals were shaved 2 days before the experiment. 10µl of VEGF isoforms (50 ng) were injected intradermally in the back of anesthetized mice (n=5 for VEGF_{121a} and VEGF_{121b}; n=6 for VEGF_{111b}, VEGF_{155a}, VEGF_{155b} and VEGF_{165b}; n=7 for VEGF_{111a} and VEGF_{165a}). Five minutes later, Evans' blue dye was injected intravenously (30 mg/kg in 100 µl PBS). After 30 minutes, mice were perfused intracardiacally with 20 ml of PFA 1%. The skin surrounding the site of injection (~20 mm²) was then excised, weighed and the Evans' blue dye was then extracted in 1 ml of formamide at 65°C during 48h. The blue staining was quantified (620 nm) and normalized for skin weight.

XII- Effects of VEGF variants on mouse physiology

VEGF_{111a}, VEGF_{111b}, VEGF_{165a} and VEGF_{165b} (4 µg in 200 µl PBS) and PBS were injected daily subcutaneously in six week-old C57Bl6 mice (n=5 per group). Animals were monitored every day by a general examination controlling animal behaviour, colour of the mucosae and hydration level (pinching test). Mice were also weighed every three days. After 14 days of treatment, the mice were sacrificed and blood was collected. The total blood fractions were used for blood cell counting and characterization (CELL-DYN 3700, Abbott Laboratories, IL, USA). ALT (Alanine Transaminase) and AST (Aspartate Transaminase) hepatic markers were quantified in serum (Department of Biochemistry, Faculty of Veterinary Medicine, University of Liège). Finally isolated cells were used for FACS (Fluorescence Activated Cell Sorting) analysis to evaluate the proportion of specific bone-marrow derived cells population. The following markers were used: GR1 (Granulocytes), CD45b (Lymphocytes), CD11b (Macrophages), TER119 (Erythrocytes) and CD3 (Lymphocytes T). Spleen and liver were collected and weighed while tissues near the site of chronic injections were also recovered, fixed and evaluated for their blood vessels content by immunohistochemistry using a CD31 antibody.

RESULTS

I- Production of purified recombinant VEGF-A variants

Recombinant human VEGF variants (VEGF_{111a}, VEGF_{111b}, VEGF_{121a}, VEGF_{121b}, VEGF_{155a}, VEGF_{155b}, VEGF_{165a} and VEGF_{165b}, Fig 19A) were produced using HEK293 cells transfected with pCEP4 vector containing the appropriate cDNA. These cells were selected for their low to undetectable intrinsic expression of VEGF. VEGF_{111b} (E1-E4 & E8b), VEGF_{155a} (E1-E4 & E7-E8a) and VEGF_{155b} (E1-E4 & E7-E8b) are artificial variants never described *in vivo*. All these variants were efficiently produced as described in Material and Methods. After purification, they were analyzed by SDS-PAGE under reducing conditions followed by Sypro Ruby staining or by Western blot analysis (Fig 19B, 19C). VEGF_{111a}, VEGF_{155a} and VEGF_{155b} appeared as single products corresponding to the glycosylated monomer while VEGF_{111b}, VEGF_{121a}, VEGF_{121b}, VEGF_{165a} and VEGF_{165b} were expressed as glycosylated and non-glycosylated polypeptides. The increased glycosylation for variants that do not possess the E5-encoded domain was not expected as the single glycosylation site was reported to be in the E4-encoded sequence (Claffey et al., 1995), which is present in all the produced variants. No correlation could be established between the glycosylation rate and the level of VEGF expression (data not shown). Western blots were probed with anti-pan VEGF antibody (Fig 19C, upper panel) or anti-VEGF_{xxx}b antibody (Fig 19C, lower panel), which recognized only the recombinant VEGF_{xxx}b isoforms as expected.

Quantification of the concentration of the VEGF-A isoforms by the panVEGF ELISA was not fully satisfactory because the antibodies used in the ELISA have not an identical affinity for all the variants when quantified in their native form. Indeed, VEGF_{121a} and VEGF_{165a} were efficiently detected while the sensitivity of the assay was reduced for VEGF_{111a}, VEGF_{111b}, VEGF_{155a} and VEGF_{165b} leading to underestimation of their concentration. The VEGF_{xxx}b ELISA was specific as it allowed quantification of VEGF_{111b} and VEGF_{165b} and did not provide any signal for VEGF_{xxx}a variants.

Gel staining after SDS-PAGE was therefore used for determining the concentration of all the variants. In this assay, we compared in the same run all the VEGF variants to a BSA curve. Depending on the selected cell lines and on the VEGF isoform, the complete production and purification processes allow the recovery of purified recombinant protein at a final concentration ranging from 20 to 150 µg/ml.

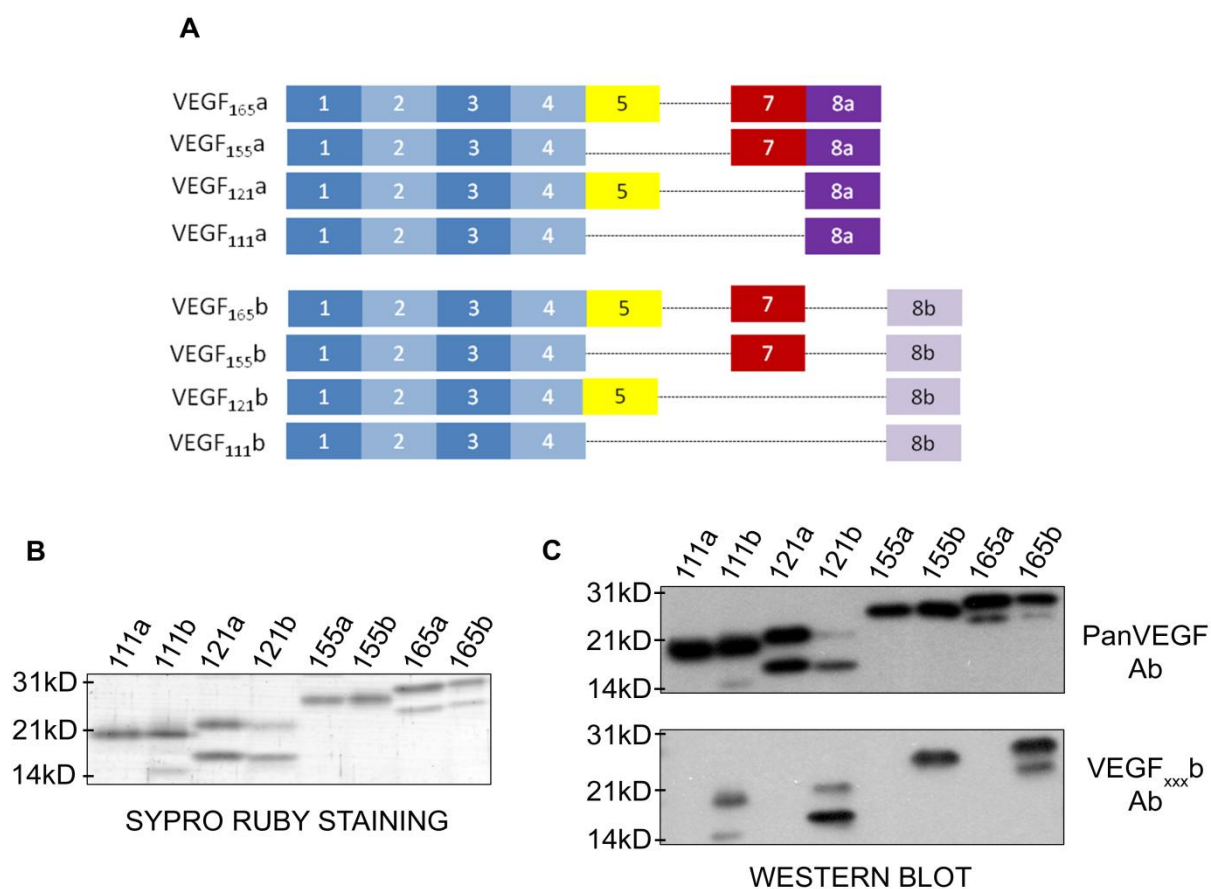


Figure 19 : Structure and analysis of the various recombinant VEGF isoforms

(A) Structure of the human VEGF-A variants used in this part of the work. Exons are represented by boxes and are not drawn to scale. Dotted lines identify the lacking exons in the various isoforms. E6a and E6b are absent from all the isoforms presented here. **(B)** SDS-PAGE analysis of the recombinant VEGF variants after production and purification by affinity chromatography using Avastin-Sepharose. Gel was stained with Sypro Ruby. **(C)** Representative Western blot of the purified VEGF variants using primary antibody against all VEGF isoforms (Pan VEGF, upper panel) and VEGF_{xxx}b (lower panel). Ab: Antibody.

These VEGF preparations were then used for further biochemical and biological characterizations performed in our laboratory or in collaboration with other laboratories. For instance, recombinant VEGF_{111a} was used to improve vascularization of xeno-transplantation of ovarian tissue *in vivo* (Labied et al., 2013) (see annex 2).

II- Receptors binding assay

II-1 Surface Plasmon Resonance

Surface Plasmon Resonance was used to evaluate the ability of the various VEGF variants to bind to VEGF receptors, VEGF-R1 and VEGF-R2, and their co-receptors, NRP1, NRP2 and heparin. This assay also allowed to evaluate the potential formation of complexes between VEGFR-2, VEGF and NRP1 or between NRP1, VEGF and heparin for example.

II-1-1 Binding to VEGF-R1

Increasing concentration of VEGF_{111a}, VEGF_{111b}, VEGF_{165a} and VEGF_{165b} were injected on VEGF-R1 coated chip. As expected from the presence of E3 encoded domain, which contains the binding site for VEGF-R1 (Fig 20A), all these isoforms displayed rapid association to the receptor followed by a slow dissociation rate (illustrated for VEGF_{111a} and VEGF_{165b}, Fig 20B, 20C). Dissociation constant (Kd) were quantified. Values were measured within the 1.4 to 4.5×10^{-10} range, which is in accordance with published data reporting high affinity of VEGF for VEGF-R1. The addition of soluble heparin (1 μ g/ml) and/or soluble NRP1 (10nM) did not significantly modified the calculated values.

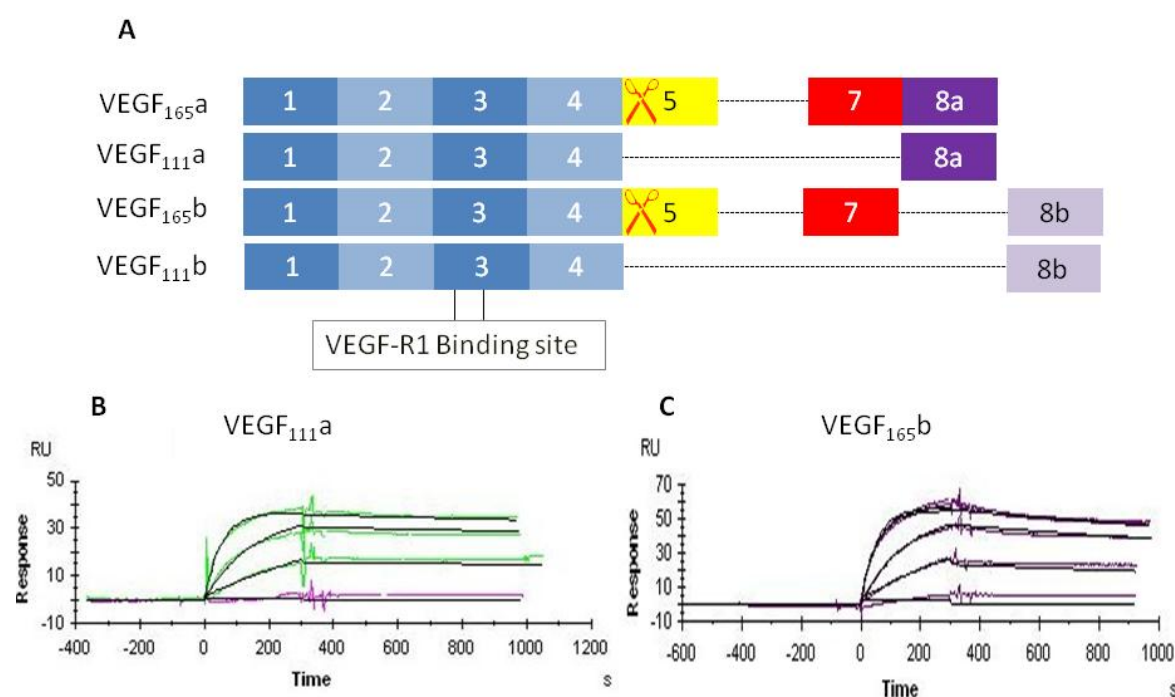


Figure 20 : Binding of VEGF isoforms to VEGF-R1

(A) In VEGF-A, the binding domain for VEGF-R1 is encoded by E3. (B, C) Sensorgrams obtained using VEGF-R1 coated chip. 0, 4, 10 and 40 nM of VEGF_{111a} (B) or VEGF_{165b} (C) were injected for ~250 seconds followed by injection of HBS-EP buffer in order to visualize the dissociation rate. RU: Response in arbitrary units.

II-1-2 Binding to VEGF-R2

VEGF_{111a}, VEGF_{111b}, VEGF_{121a}, VEGF_{121b}, VEGF_{155a}, VEGF_{155b}, VEGF_{165a} and VEGF_{165b} were able to bind to VEGF-R2 with similar K_d within a range from 1×10^{-10} to 1×10^{-11} M (illustrated for VEGF_{111a} and VEGF_{165b}, Fig 21B, C). These results were in accordance with published data (Hua et al., 2010; Waltenberger et al., 1994). Interestingly, we reproducibly observed a higher association rate for VEGF_{111a} ($K_a=2.6 \times 10^{11}$) as compared to VEGF_{165a} ($K_a=0.15 \times 10^{11}$).

Addition of heparin (1 μ g/ml) to VEGF_{165a} (10nM) did not modify the affinity of the ligand for its receptor. However, when VEGF_{165a} was used at a lesser concentration (4nM), heparin increased the response by a factor of about 2 (data not shown).

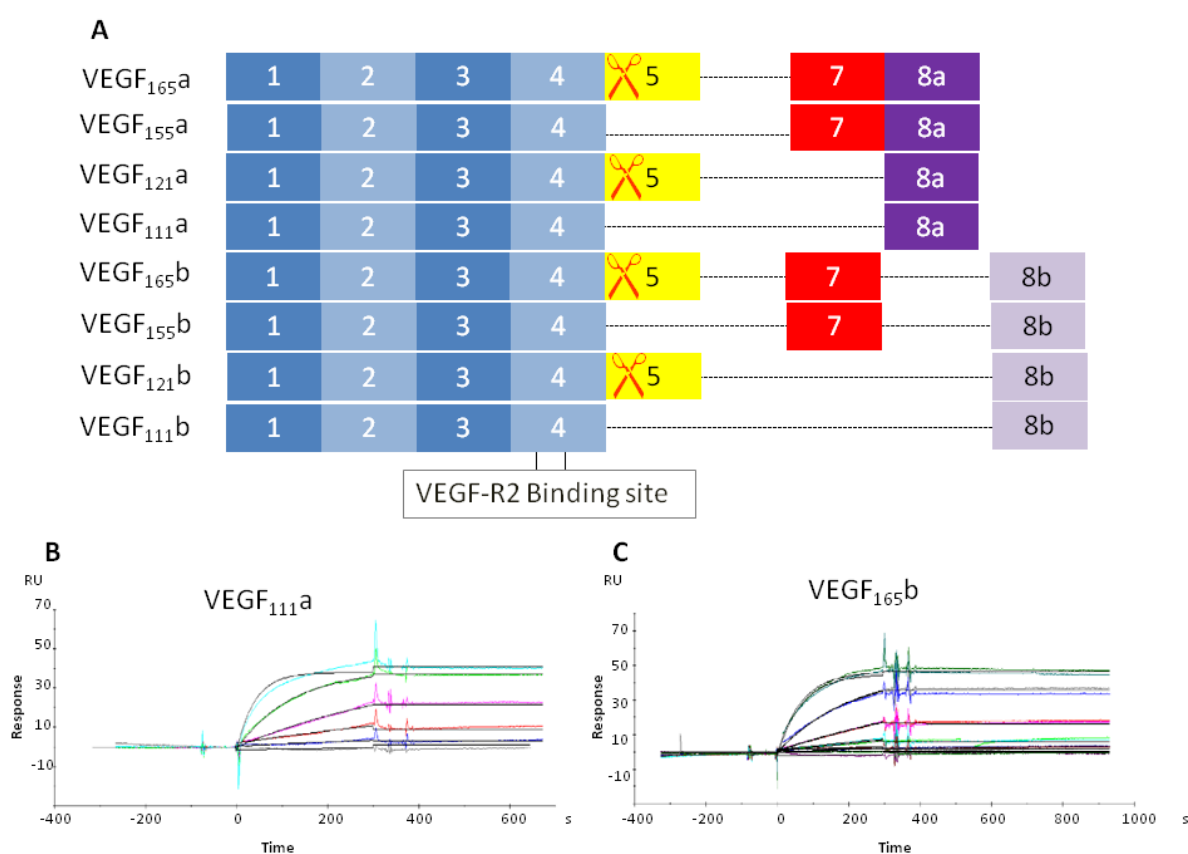


Figure 21 : Binding of VEGF the various isoforms to VEGF-R2 depends on the presence of E4-encoded domain

(A) The VEGF-R2 binding site is located in the E4-encoded domain. **(B, C)** Sensorgrams obtained using VEGF-R2 coated chip. 0, 1, 4, 10 and 40 nM of VEGF_{111a} **(B)** and VEGF_{165b} **(C)** were injected for ~250 seconds followed by injection of HBS-EP buffer in order to visualize the dissociation rate. RU: Response in arbitrary units

II-1-3 Binding to NRP1

When NRP1 was immobilized on the chip, only VEGF_{165a} and VEGF_{121a} bound efficiently (Fig 22C, 22E). VEGF_{155a} was also able to bind but with a reduced association rate as visualized by the flattened slope of the curve (Fig 22D). The absence of interaction of VEGF_{xxx}b (illustrated only for VEGF_{165b} in Fig 22G) confirmed previous data describing the implication of the E8a-encoded sequence in binding to NRP1 (Cebe Suarez et al., 2006; Pan et al., 2007b). By contrast, the absence of interaction of VEGF_{111a} (Fig 22B) suggests that the E8a domain is not sufficient for binding. Since the presence of the entire E8a-encoded sequence was confirmed by mass spectrometry analysis of VEGF_{111a} (data not shown), it suggests that the E8a-domain must cooperate with another domain for efficient binding. Because the only difference between VEGF_{111a} (non-binder) and VEGF_{121a} (binder) is the presence of the domain encoded by exon 5, its contribution to the binding capacity to NRP1 is likely.

The binding of VEGF to NRP1 coated sensorchips was stimulated by heparin only for VEGF_{155a} (1.5-fold) and VEGF_{165a} (4.5-fold) (not illustrated) suggesting a role for the E7 domain in the formation of multimolecular complexes. A role for the E5-encoded basic domain is also suggested when considering the marked difference between SPR responses obtained with VEGF_{155a} and VEGF_{165a}.

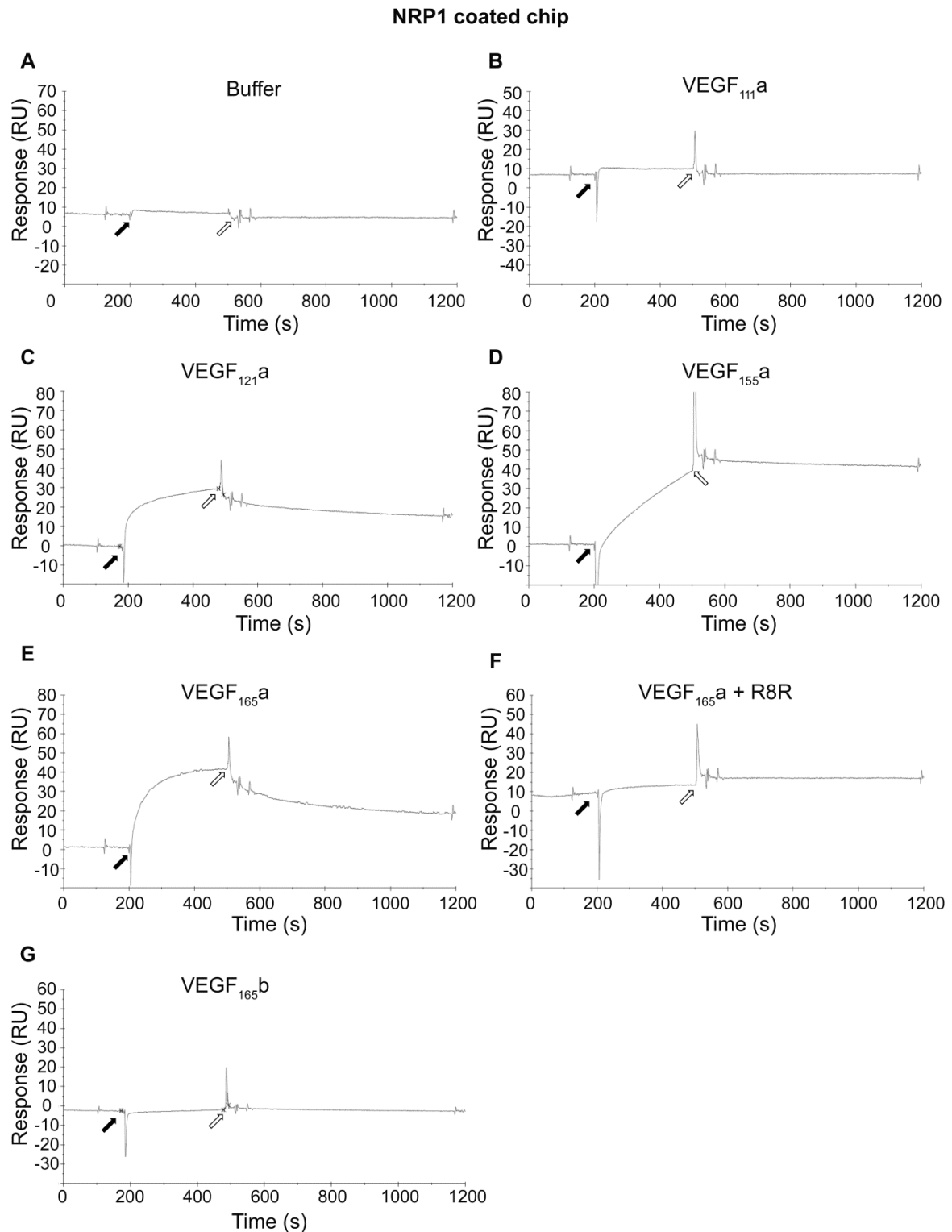


Figure 22 : Binding of VEGF variants to NRP1

Binding of VEGF variants (40nM) to NRP1 was measured by Surface Plasmon Resonance. **(A)** HBS-EP control buffer, **(B)** VEGF_{111a}, **(C)** VEGF_{121a}, **(D)** VEGF_{155a}, **(E)** VEGF_{165a} alone or **(F)** in combination with the R8R peptide (300 μ M, mimicking the E5 encoded sequence) and **(G)** VEGF_{165b} were injected (black arrow) for ~250 seconds followed by injection of HBS-EP buffer (open arrow) in order to visualize the dissociation rate. RU: Response in arbitrary units.

II-1-4 Binding to NRP2

None of the tested VEGF-A variants (VEGF_{111a}, VEGF_{111b}, VEGF_{165a} and VEGF_{165b}) had a significant direct affinity for NRP2. When heparin (1 µg/ml) was co-injected, only VEGF_{165a} was able to form stable complexes (illustrated for VEGF_{111a} and VEGF_{165a} in Fig 23A and 23B).

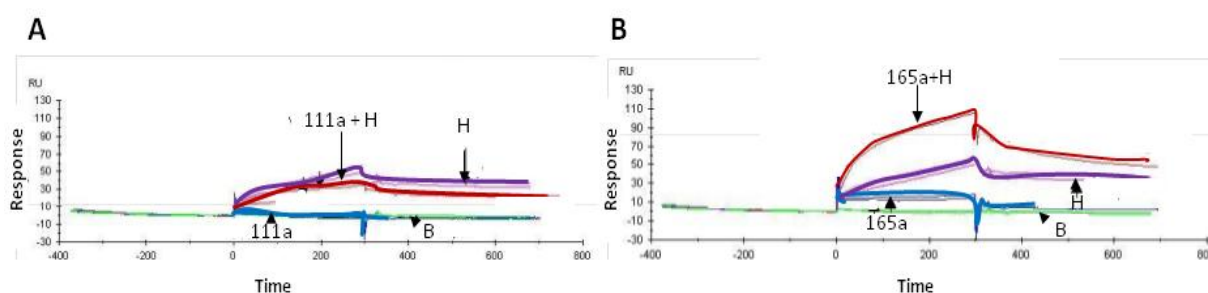


Figure 23 : Binding of VEGF variants to NRP2

The binding of VEGF_{111a} (**A**) and VEGF_{165a} (**B**) (both at 40 nM) to NRP2 was evaluated in absence or presence of heparin (1 µg/ml). HBS-EP control buffer (green), VEGF with (red) or without heparin (blue), or heparin alone (violet) were injected for ~250 seconds followed by injection of HBS-EP buffer in order to visualize the dissociation rate. RU: Response in arbitrary units; B: Buffer ; H: Heparin ; 111a: VEGF_{111a} ; 165a: VEGF_{165a}.

II-1-5 Binding to heparin

Some VEGF variants have been reported to interact with heparan sulfate proteoglycans through their E7-encoded domain (Kawamura et al., 2008b). SPR experiments indicated that the injection of VEGF_{xxx}a variants to biotinylated heparin coupled to a streptavidin-coated sensorchip resulted in a significant binding of VEGF_{165a} and VEGF_{155a}, although at a considerably lesser extent, while the other variants failed to bind, which confirms the importance of the sequence encoded by exon 7 (Fig 24). However, VEGF_{165b} and VEGF_{155b} (illustrated for VEGF_{165b} in Fig 24F), two variants possessing the sequence encoded by exon 7, also failed to bind to heparin, demonstrating a direct implication of the E8a domain or an inhibitory function of the E8b sequence on this interaction. Moreover, the important difference between VEGF_{155a} and VEGF_{165a} suggests a role for the E5-encoded domain. These data were confirmed using heparin-sepharose affinity chromatography (data not shown).

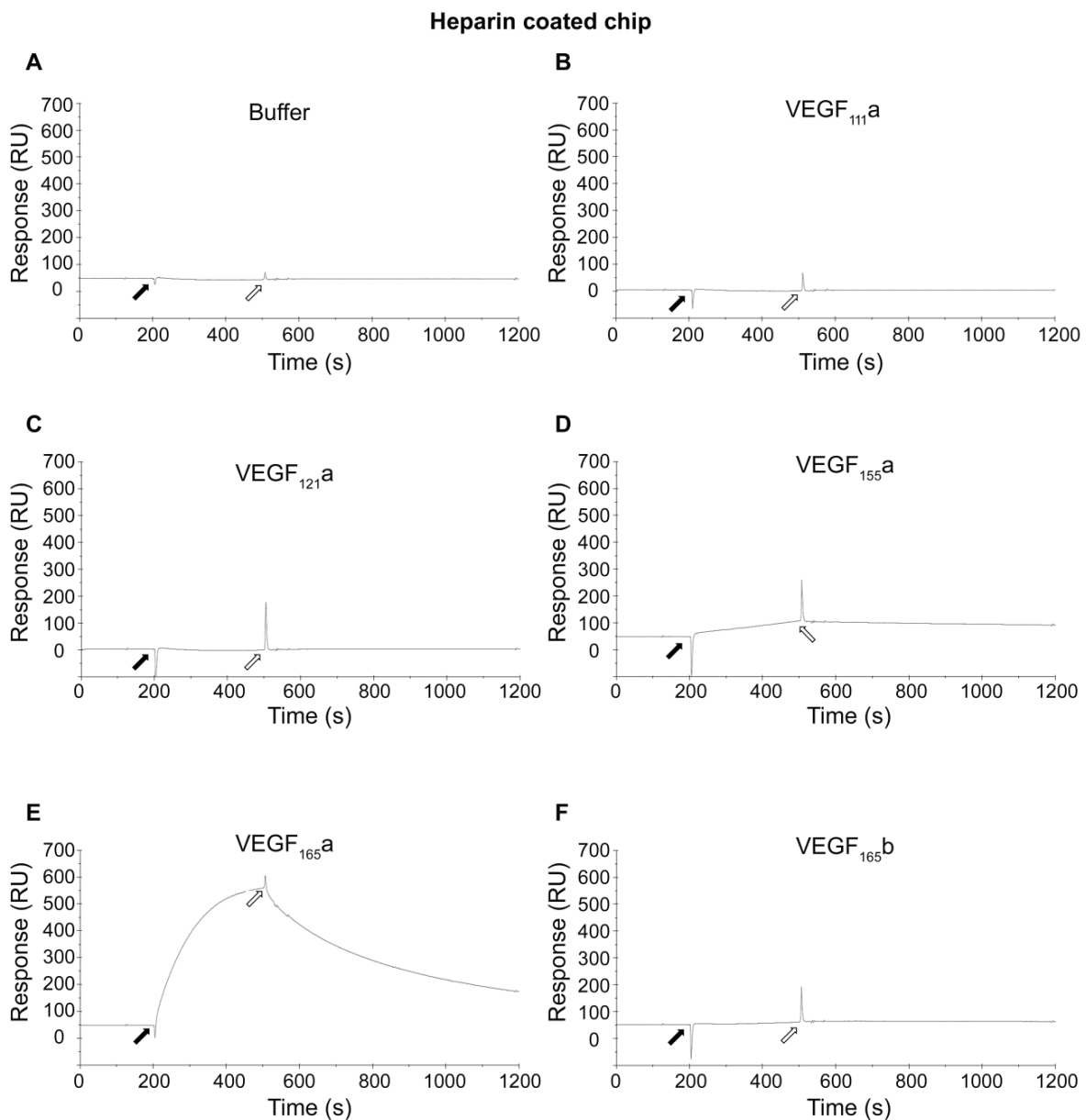


Figure 24 : Binding of VEGF variants to heparin

Binding of VEGF variants (200 nM) to heparin was measured by Surface Plasmon Resonance. **(A)** HBS-EP buffer, **(B)** VEGF_{111a}, **(C)** VEGF_{121a}, **(D)** VEGF_{155a}, **(E)** VEGF_{165a} and **(F)** VEGF_{165b} were injected (black arrow) for ~250 seconds followed by injection of HBS-EP buffer (open arrow) in order to visualize the dissociation rate. RU: Response in arbitrary units.

Simultaneous injection of VEGF_{165a} (40nM) and soluble NRP1 (15nM) on the heparin chip (Fig 25) strongly improves the binding (566 RU) as compared to VEGF_{165a} (132 RU) and NRP1 (131 RU) alone. Such synergy was not observed when soluble NRP1 was injected concomitantly with VEGF_{121a}, confirming data previously observed with the NRP1 chip.

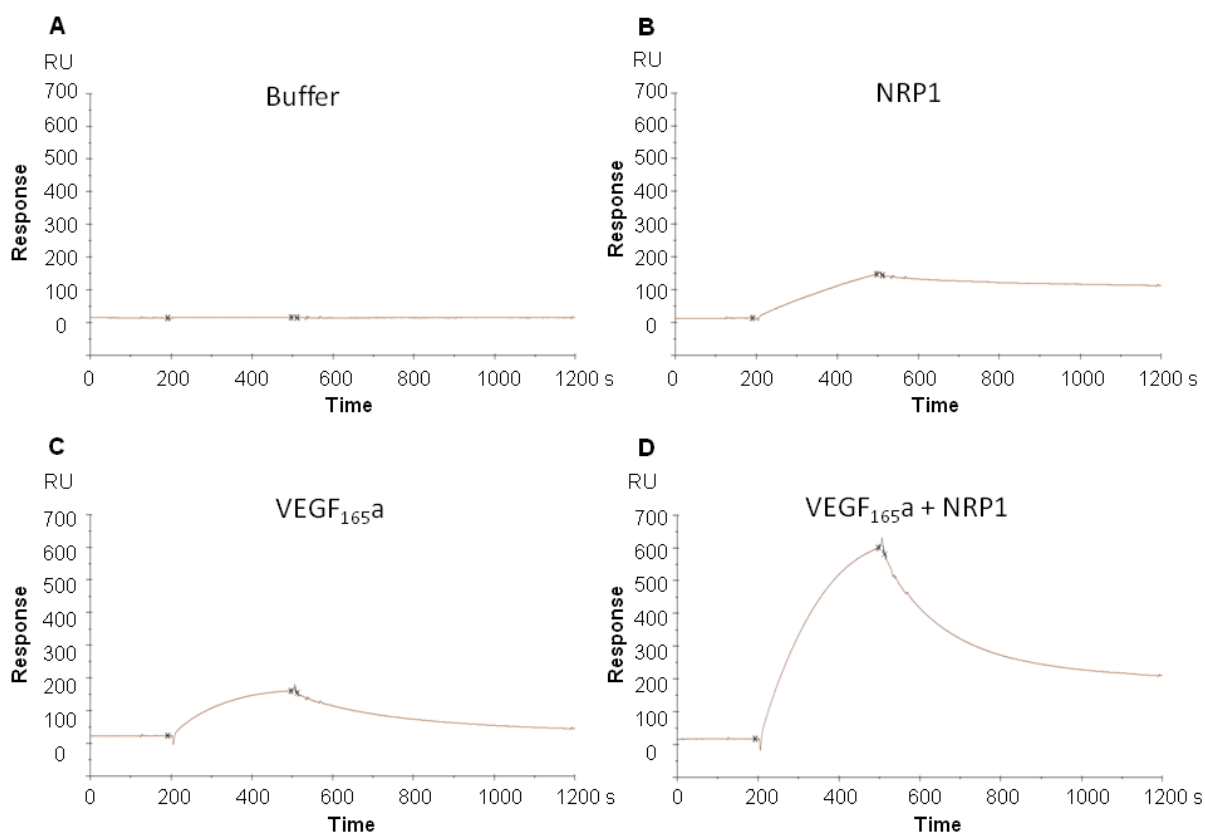


Figure 25 : Reinforcement of binding to heparin in presence of sNRP1

Binding of VEGF_{165a} (40 nM) and soluble NRP1 (15nM), separately or concomitantly, to heparin was measured by Surface Plasmon Resonance. **(A)** HBS-EP buffer, **(B)** soluble NRP1, **(C)** VEGF_{165a} and **(D)** mixture of VEGF_{165a} and soluble NRP1 were injected for ~250 seconds followed by injection of HBS-EP buffer in order to visualize the dissociation rate. RU: Response in arbitrary units.

II-1-6 VEGFR2-VEGF multimolecular complexes

The formation of multimolecular complexes between VEGF-R2, NRP1, heparin (H) and VEGF variants was also evaluated. The different VEGF variants (20 nM) and NRP1 (20 nM) were sequentially injected in the absence or presence of heparin (1 µg/ml) on a VEGF-R2 sensorchip (Fig 26). As expected, the initial injection of VEGF induced a response on the sensorgram (illustrated here for VEGF_{165a} (Fig 26A), VEGF_{121a} (Fig 26D) and VEGF_{165b} (Fig 26H) for example). When VEGF_{165a} is already bound on VEGF-R2, subsequent injection of NRP1 alone (Fig 26A) had only a limited effect but resulted in a sharp additional response in the presence of heparin (compare Fig 26B to Fig 26A). When VEGF_{165a} was omitted the response to NRP1 + H was much more modest (compare Fig 26C to Fig 26B), indicating weaker or less numerous protein interactions and underscoring the importance of VEGF_{165a} in the formation of large complexes with VEGF-R2. VEGF_{155a}, the only other tested isoform possessing both the E7 and E8a-derived sequences, was also able to induce the formation of complexes with NRP1 in presence of heparin (not shown). By sharp contrast, none of the other isoforms was able to significantly mediate the interactions between VEGF-R2 and NRP1 as shown by a similar response to NRP1+H in presence or absence of VEGF as illustrated for VEGF_{121a} and VEGF_{165b} (compare Fig 26D and Fig 26H to Fig 26C).

To address the question of a potential competition between the various VEGF variants, successive injections on VEGF-R2 chips were performed. As an example, a saturating amount of VEGF_{165a} (80 nM) was injected first followed by sequential injections of VEGF_{165b} (20nM) and NRP1+heparin. In these conditions, VEGF_{165a} could efficiently bind to VEGF-R2 and induce the formation of VEGFR2-VEGF-NRP1-heparin complexes (Fig 26E). By contrast, when VEGF_{165b} (80nM) was injected first only a limited amount of VEGF_{165a} could be immobilized and the formation of the complex was strongly inhibited (Fig 26F). Similar data were obtained when VEGF_{121a} (Fig 26G) or VEGF_{155b} (not shown) were used in place of VEGF_{165b} for the first injection, again demonstrating a competition of these variants with VEGF_{165a} for binding to VEGF-R2 and further confirming that VEGF_{165a} is able to promote the formation of complexes while VEGF_{155b}, VEGF_{165b} and VEGF_{121a} are not efficient (summarized in Fig 26I).

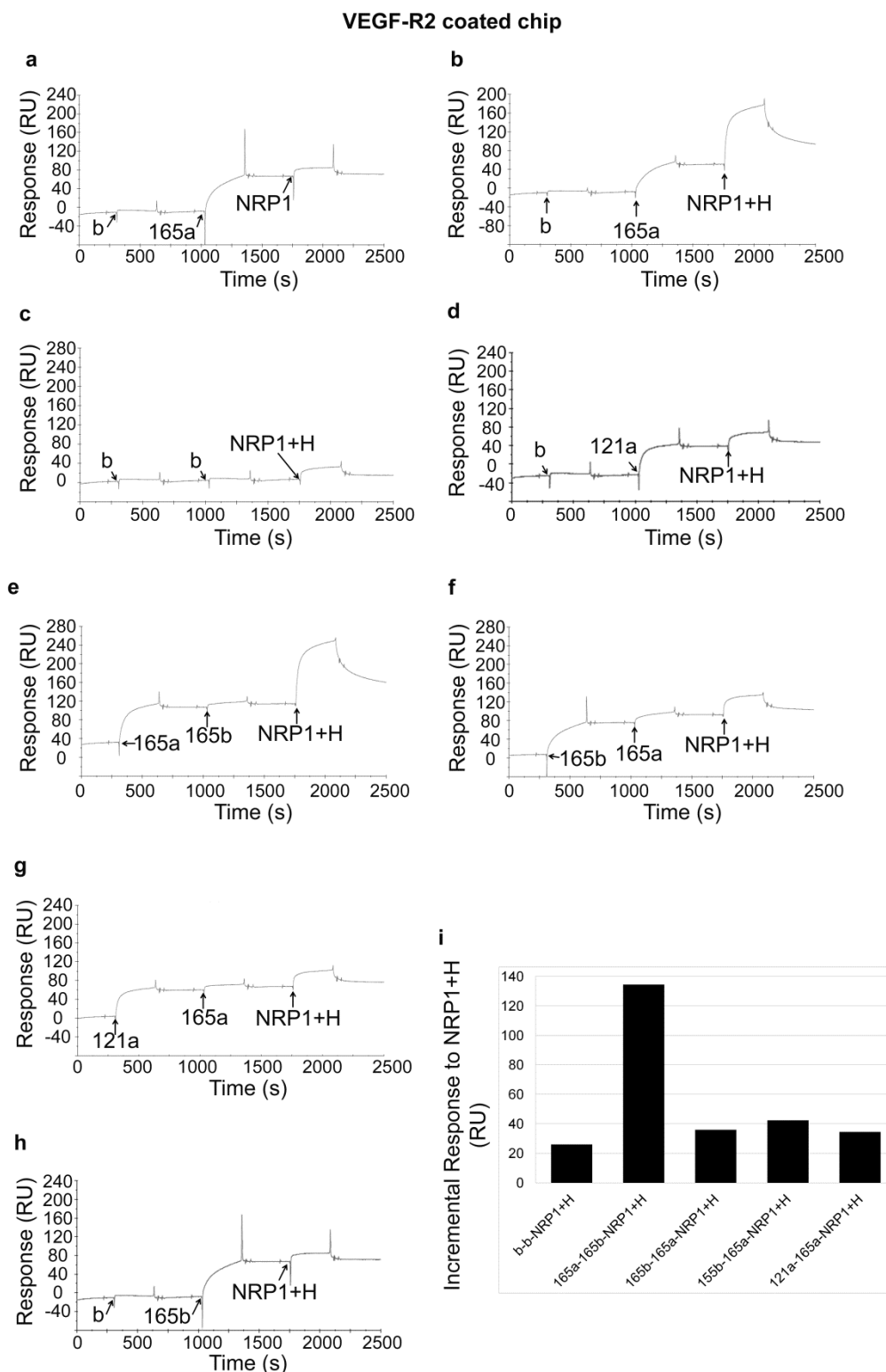


Figure 26 : Ability of VEGF variants to form VEGFR2-VEGF-NRP1-heparin complexes

(A-H) The formation of the VEGFR2-VEGF-NRP1-heparin complexes was measured by Surface Plasmon Resonance. VEGF-R2 was coated on the sensorchip and successive injections were made as indicated on the drawings. (I) Increment of response induced by addition of NRP1+heparin after injection of various VEGF variants. b: HBS-EP buffer; 121a: VEGF_{121a}; 165a: VEGF_{165a}; 165b: VEGF_{165b}; NRP1: neuropilin-1; H: heparin.

The effect of PIGF on the formation of VEGF-R2-NRP1-heparin complexes was also investigated. Surprisingly, despite an absence of direct binding of PIGF to VEGF-R2, it reduced the binding of NRP1 to VEGF-R2 (Fig 27). All the data obtained by Surface Plasmon Resonance are summarized in Table 4.

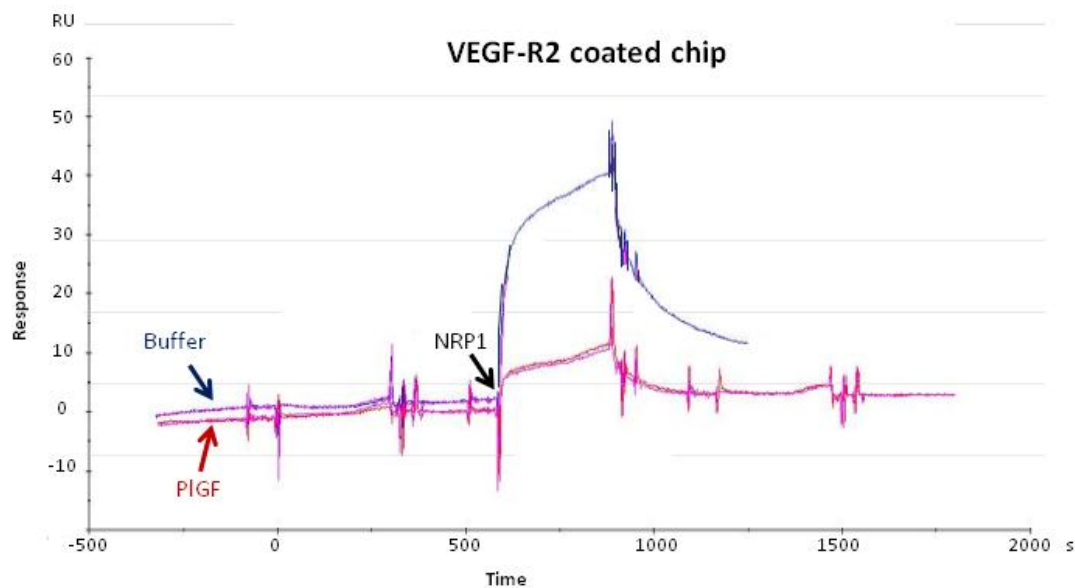


Figure 27 : PIGF inhibits direct binding of NRP1 to VEGF-R2

The influence of PIGF on formation of the VEGFR2-NRP1-heparin complexes was measured in duplicate by Surface Plasmon Resonance on VEGF-R2 coated sensorchips. Successive injections consisted in either HBS-EP Buffer followed by NRP1 + heparin (blue) or PIGF and then NRP1 + heparin (red).

Table 4 : Summary of the ability of the VEGF variants to bind to VEGF receptors and co-receptors

	Presence of the relevant exon-encoded domain	Direct binding on					Formation of complexes including:		
		VEGF-R1	VEGF-R2	NRP1	NRP2	H	NRP2+H	NRP1+H	VEGFR2+NRP1+H
VEGF _{111a}	E1-4 ; E8a	Yes	Yes	No	No	No	No	No	No
VEGF _{111b}	E1-4 ; E8b	Yes	Yes	No	No	No	No	No	No
VEGF _{121a}	E1-4 ; E5 ; E8a	nd	Yes	Yes	nd	No	nd	Yes	No
VEGF _{121b}	E1-4 ; E5 ; E8b	nd	Yes	No	nd	No	nd	No	No
VEGF _{155a}	E1-4 ; E7 ; E8a	nd	Yes	Yes	nd	Yes	nd	Yes	Yes
VEGF _{155b}	E1-4 ; E7 ; E8b	nd	Yes	No	nd	No	nd	No	No
VEGF _{165a}	E1-4 ; E5 ; E7 ; E8a	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
VEGF _{165b}	E1-4 ; E5 ; E7 ; E8b	Yes	Yes	No	No	No	No	No	No

nd: not determined; E: exon; H: heparin

II-2 Solid phase assay

Data obtained in the SPR model were further validated in a solid phase ELISA assay using VEGF_{111a}, VEGF_{111b}, VEGF_{165a}, VEGF_{165b} and PIGF-coated plates. VEGF-R2 bound efficiently to all variants while only VEGF_{165a} was able to interact with NRP1 or NRP2 in presence of heparin, as expected from the SPR data (Fig 28). As expected, PIGF bound to NRP1 but not to VEGF-R2 and NRP2. In another experimental setting, a solid phase assay was also used for evaluating the competition for immobilized NRP1 between fixed concentration of biotinylated VEGF_{165a} and increasing amount (from 5 to 450 nM) of other VEGF variants. As a control, we first verified that VEGF_{165a} was able to completely inhibit the binding of biotinylated VEGF_{165a}. By contrast, none of the other variant was able to compete with VEGF_{165a} for NRP1, except for a slight effect of VEGF_{155a} at 40 nM, again in agreement with the SPR results (not illustrated).

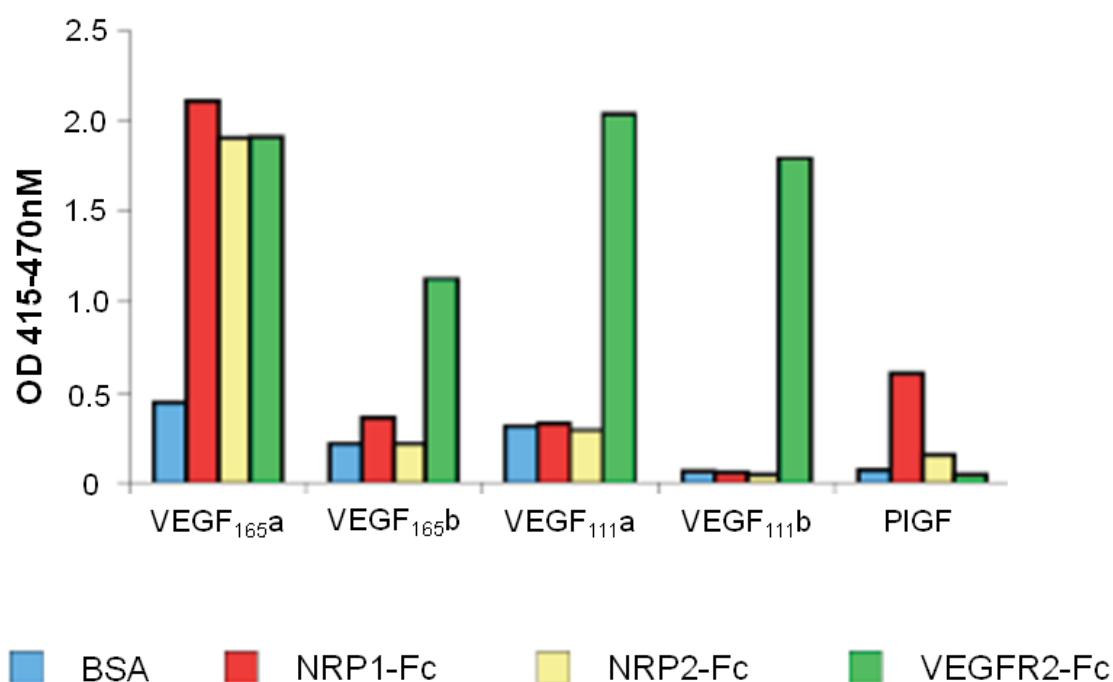


Figure 28 : Binding of VEGF variants to VEGF-R2, NRP1 and NRP2 as determined in a solid phase assay

96-wells plates were coated with PIGF, VEGF_{111a}, VEGF_{111b}, VEGF_{165a} or VEGF_{165b}, washed and incubated with solution containing BSA (negative control) or Fc-coupled VEGF-R2 (VEGF-R2-Fc), NRP1 (NRP1-Fc) or NRP2 (NRP2-Fc) in presence of heparin. After washing and incubation with HRP-coupled anti-Fc antibody, the relative amounts of bound protein were detected by quantifying the HRP activity immobilized in the wells. PIGF: Placental Growth Factor, BSA: Bovine Serum Albumine, OD: Optical Density.

II-3 Effect of mimetic peptides of E5 and E8a encoded domain on VEGF binding to NRP1

The study of the various VEGF isoforms by Surface Plasmon Resonance and solid phase assay suggested the implication of the E5- and E8a-encoded domains for NRP1 binding. This hypothesis was further investigated by using synthetic peptides. Peptides mimicking the E8a domain, A7R, (Starzec et al., 2007; Starzec et al., 2006) or the E5 domain (R8R) were used. They fully inhibited the binding of VEGF_{165a} on NRP1 immobilized on SPR sensorchip (illustrated for R8R, compare Fig 22F to Fig 22E), confirming previous data. They also prevented the formation of the super-complexes involving VEGF-R2, NRP1, VEGF_{165a} and heparin (Compare Fig 29A to 29B, for effect of A7R and 29A to 29C for effect of R8R), confirming that these two domains are required.

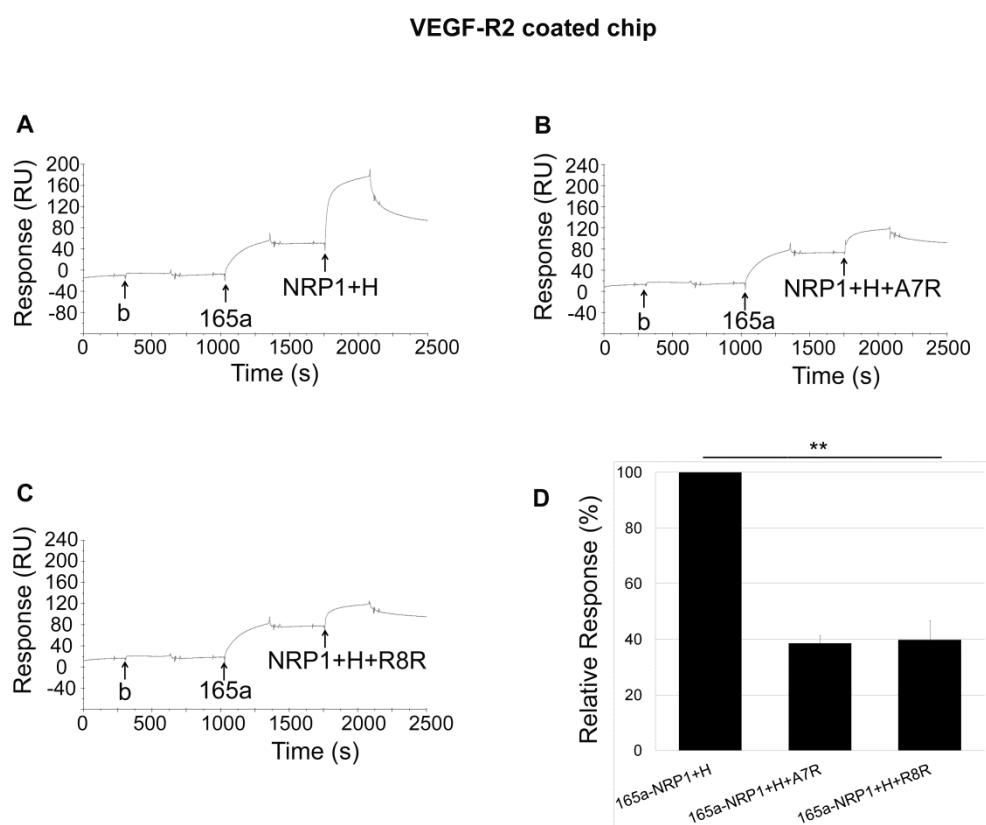


Figure 29 : Effect of peptides mimicking the E5- (R8R) or the E8a- (A7R) derived domains on the formation of VEGFR2-VEGF_{165a}-NRP1-heparin super-complexes

(A-C) The formation of the VEGFR2-VEGF_{165a}-NRP1-heparin super-complexes was assessed by Surface Plasmon Resonance. VEGF-R2 was coated on the sensorchip and successive injections were made as indicated on the drawings. **(D)** Quantification of the response induced by the addition of NRP1+H in the absence or presence of mimetic peptides (A7R and R8R). Results are expressed in percentage of values recorded in absence of peptide. b: HBS-EP buffer; H: heparin.

These properties were further investigated in a solid phase assay where NRP1 was immobilized in the well. Pre-treatment with A7R, R8R or a peptide with the sequence encoded by exon 8a totally inhibited the binding of biotinylated VEGF_{165a} on immobilized NRP1 (Fig 30) whereas a peptide with the sequence encoded by E8b had no effect. Altogether these results clearly demonstrated the importance of the E5- and E8a-encoded domains for VEGF binding to NRP1, the E8b sequence being not involved.

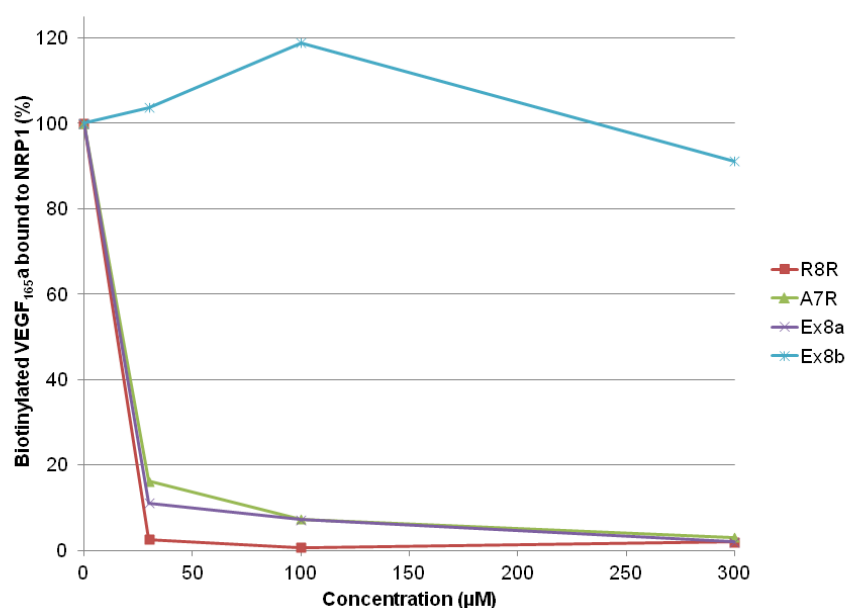


Figure 30 : Effect of mimetic peptides on the binding of VEGF_{165a} on NRP1

Biotinylated VEGF_{165a} was incubated in 96-wells plates previously coated with NRP1 and pre-treated with increasing concentrations (0 to 300 nM) of peptides mimetic of the domain encoded by exon 8a (Ex8a, A7R), exon 8b (Ex8b) or exon 5 (R8R). After washing and incubation with HRP-coupled streptavidin, quantification of the immobilized HRP activity was used to evaluate the relative level of VEGF_{165a} bound to NRP1. Data are expressed comparatively to the values obtained in absence of peptides, taken as 100%.

III- Resistance of VEGF isoforms to proteolysis

As we have shown in chapter II, the C-terminal domains of VEGF are required for the formation of complexes with NRP1 and heparin while the VEGF-R1 and VEGF-R2 binding sites are located more NH₂-terminally. As a result, any proteolytic cleavage in the middle of the VEGF molecule should strongly affect its overall biological activity, underscoring the importance of evaluating the sensitivity to proteases of the different variants. The various VEGF isoforms were incubated for increasing times with increasing concentrations of plasmin and analyzed by Western blot using an antibody specific for a N-terminal epitope (Fig 31A). Both glycosylated and non-glycosylated forms of VEGF_{165a} and VEGF_{165b} were rapidly converted into smaller products, likely corresponding to the VEGF₁₁₀ fragment obtained after cleavage at a previously described site in the E5-derived sequence (Arg¹¹⁰/Ala¹¹¹, (Keyt et al., 1996a)). As expected from the absence of this sensitive region, VEGF_{111a} and VEGF_{111b} were resistant to degradation, even at the highest concentrations and the longest incubation times (Fig 31A), and VEGF_{111b} fully kept its E8b-encoded terminal domain, as shown by using a specific anti-E8b domain antibody (Fig 31B). In spite of the lack of the E5-sequence, cleavage products of VEGF_{155a} and VEGF_{155b} already appeared with $2-4 \times 10^{-2}$ IU of plasmin. The size of the two degradation products observed was compatible with a cleavage occurring in the sequence encoded by E7. This was further supported by the loss of immunoreactivity to the VEGF_{xxx}b antibody of the plasmin-treated VEGF_{155b} (Fig 31C), suggesting that the E7-encoded domain might become more exposed to plasmin in absence of the E5-sequence. The situation for the VEGF₁₂₁ isoforms was more complex since VEGF_{121a} was cleaved by plasmin while VEGF_{121b} was not although it did possess the E5-derived domain. This suggests that the alternative use of the sequence encoded by E8a or E8b affects the three-dimensional structure of the molecules and the accessibility to the proteolytic enzymes.

VEGF_{111a}, VEGF_{111b}, VEGF_{165a} and VEGF_{165b} were also incubated with fluids collected from non-healing wound of three patients with a chronic skin ulcer (Fig 31D) as these exudate are known to be rich in various proteases including plasmin (Palolahti et al., 1993) and metalloproteinases (Yager et al., 1996). After 24h of treatment, VEGF_{111a} and VEGF_{111b} remained intact whereas VEGF_{165a} and VEGF_{165b} were degraded likely into VEGF₁₁₀.

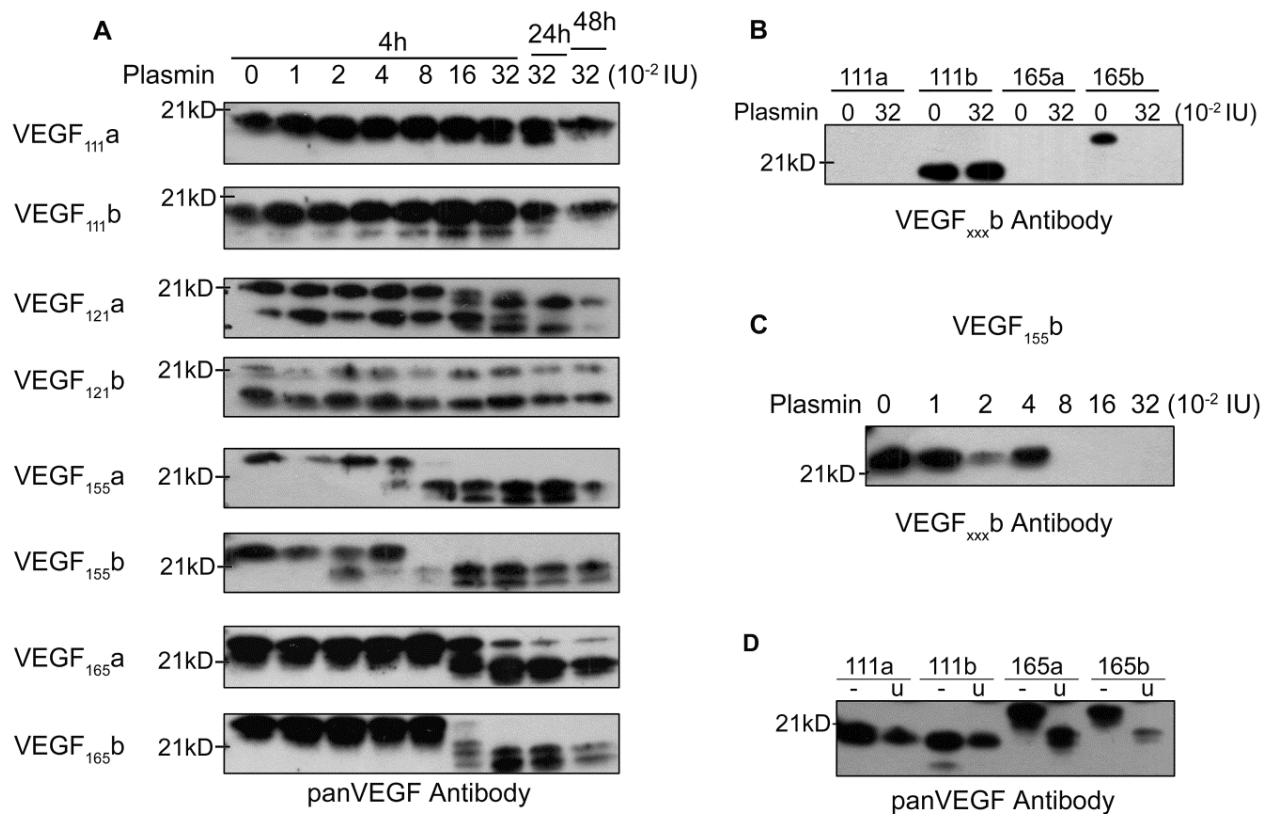


Figure 31 : Effect of treatment by plasmin and exudate from skin ulcer on VEGF variants

(A) 20ng of VEGF variants were treated with increasing amounts of plasmin (expressed in 10⁻² IU) for the indicated times at 37°C. The products of the reactions were analyzed by Western blot using a panVEGF antibody. **(B, C)** VEGF variants were treated for 4 h with the indicated concentrations of plasmin before Western blot analysis using an anti-VEGF_{xxx}b antibody. **(D)** VEGF variants were incubated for 4 h in PBS (-) or in exudate from skin ulcer (u) before Western blot analysis using a panVEGF antibody. 111a: VEGF_{111a}, 111b: VEGF_{111b}, 165a: VEGF_{165a}, 165b: VEGF_{165b}, IU: International Unit.

IV- *In vitro* assay

IV-1 Effect of VEGF variants on VEGF signalling

The effects of the VEGF variants were extensively characterized in various culture conditions. Only some data will be presented here to illustrate specific features and findings. Two cell models were used for evaluating angiogenesis in culture. Porcine Aortic Endothelial Cells (PAEC) do not express VEGF receptors and co-receptors at their surface. They were stably transfected with an empty vector (PAEC control) or with expression vectors for human NRP1 (PAEC-NRP1), VEGF-R1 (PAEC-R1), VEGF-R2 (PAEC-R2) or VEGF-R2 and NRP1 (PAEC-R2-NRP1) (Becker et al., 2005; Miao et al., 1999; Waltenberger et al., 1994). The second model used HUVEC, primary human endothelial cells that express VEGF-R1, VEGF-R2, NRP1 and HSPG at their surface.

IV-1-1 VEGF variants do not regulate endothelial cells through direct interactions with NRP1

For evaluating any potential direct effect of VEGF variants, PAEC cells, either control or expressing NRP1, were treated with VEGF isoforms. The activation of ERK1/2 was measured as it is one of the main pathways regulating endothelial cells proliferation. An increased phosphorylation was induced by FBS, used as a positive control independent of NRP1 signalling. None of the VEGF variants was active, confirming that these cells are not responsive and that no direct effect can be mediated by NRP1 (Fig 32).

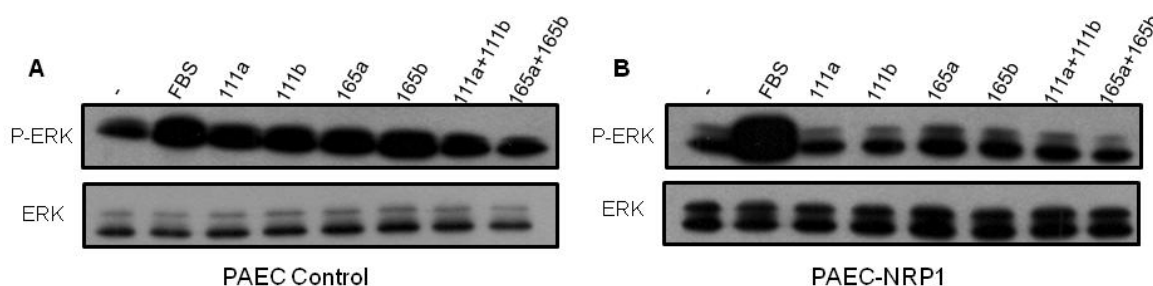


Figure 32 : Evaluation of the effect of VEGF variants on ERK phosphorylation in PAEC either control or expressing NRP1

(A) PAEC-Control and (B) PAEC-NRP1 were treated by addition of FBS or with 1 nM of VEGF variants for 10min in serum free medium. Protein extracts were then analyzed by Western blot using antibodies against ERK1/2 (ERK) or phospho-ERK1/2 (P-ERK). -: Control medium; FBS: medium containing Foetal Bovine Serum; 111a: VEGF_{111a}; 111b: VEGF_{111b}; 165a: VEGF_{165a}; 165b: VEGF_{165b}; 111a+111b: VEGF_{111a} and VEGF_{111b} added both at 1nM; 165a + 165b: VEGF_{165a} and VEGF_{165b} added both at 1nM.

IV-1-2 VEGF variants act through VEGF-R2 but not through VEGF-R1

The presence of VEGF-R1 at the cell surface of PAEC did not result in any marked specific response triggered by VEGF variants (Fig 33A). By contrast, the presence of VEGF in the culture medium induced a rapid phosphorylation of VEGF-R2 in PAEC-R2 (Fig 33B). Most interestingly, the level of phosphorylation was highly variant-specific and was correlated to the level of ERK1/2 and Akt phosphorylation. Co-treatment of VEGF_{111a} and VEGF_{111b} or of VEGF_{165a} and VEGF_{165b} did not result in any synergistic or antagonistic effects.

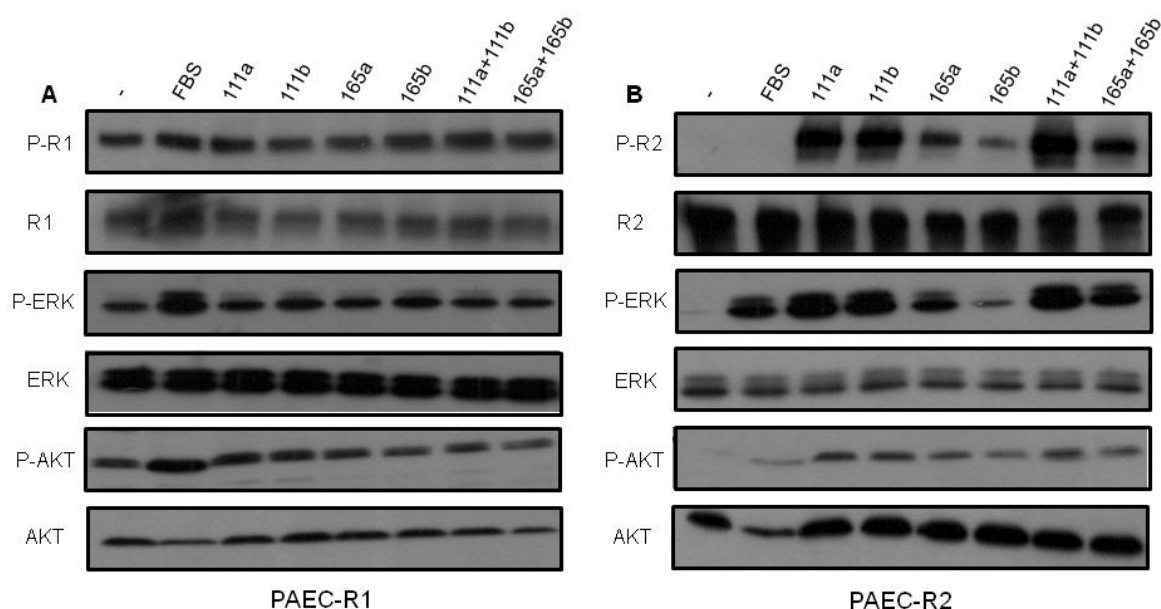


Figure 33 : Effect of VEGF variants on VEGF-R1/R2 phosphorylation and signalling pathways activation in PAEC-R1 and PAEC-R2

PAEC-R1 (**A**) and PAEC-R2 (**B**) were treated with FBS or with 1 nM of VEGF variants for 10 min in serum free medium. Protein extracts were analyzed by Western blot using (**A**) antibodies against VEGF-R1 (R), phospho-VEGFR1 (P-R1), ERK1/2 (ERK), phospho-ERK1/2 (P-ERK), AKT or phospho-AKT (P-AKT) and (**B**) VEGF-R2 (R2), phospho-VEGFR2 (Tyr1175, P-R2), ERK1/2, phospho-ERK1/2, AKT or phospho-AKT. -: Control medium; FBS: medium containing Foetal Bovine Serum; 111a: VEGF_{111a}; 111b: VEGF_{111b}; 165a: VEGF_{165a}; 165b: VEGF_{165b}; 111a+111b: VEGF_{111a} and VEGF_{111b} (both at 1nM); 165a + 165b: VEGF_{165a} and VEGF_{165b} (both at 1nM).

IV-1-3 NRP1 potentiates the VEGF-R2 phosphorylation induced by VEGF_{165a}

The effects of the 8 VEGF variants were also studied in parallel on PAEC-R2 and PAEC-R2-NRP1 for evaluating the activity of NRP1 as a co-receptor stimulating VEGF-R2 phosphorylation and activation of downstream signalling factors. The shortest VEGF isoforms, whatever the composition of the terminal exon (VEGF_{111a/b} and VEGF_{121a/b}), were the strongest inducers of VEGF-R2 phosphorylation in PAEC-R2, while VEGF_{165a} was active but to a lesser extent (Fig 34A). VEGF_{155a}, VEGF_{155b} and VEGF_{165b} were barely active, although they possess the VEGF-R2 binding sequence. A similar pattern of phosphorylation/activation was observed for ERK1/2 (Fig 34A, 34C). The results obtained in PAEC-R2-NRP1 cells (Fig 34B, 34D) were similar to those in PAEC-R2, with the significant exception that VEGF_{165a} was as active in these cells as the short VEGF isoforms.

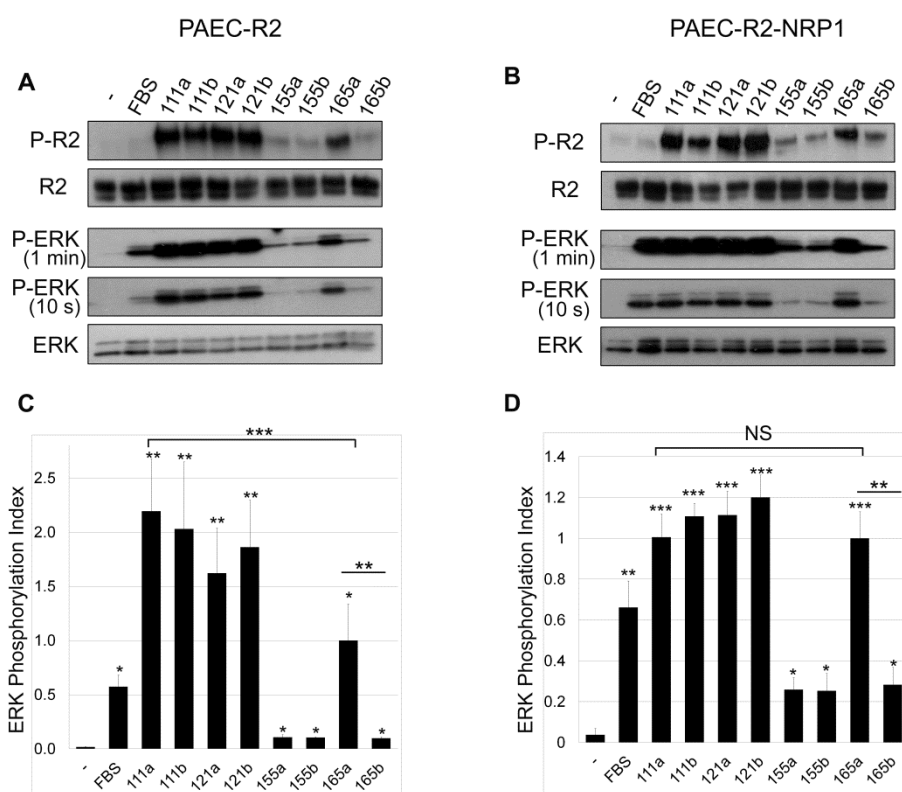


Figure 34 : Effect of VEGF variants on PAEC-R2 and PAEC-R2-NRP1

(A) PAEC-R2 and (B) PAEC-R2-NRP1 were treated with 1 nM of VEGF variants for 10 min in serum free medium and analyzed by Western blot using antibodies against VEGF-R2 (R2), phospho-VEGFR2 (Tyr1175, P-R2), ERK1/2 (ERK) or phospho-ERK1/2 (P-ERK). For P-ERK two different film exposures are shown (10 s and 1 min). (C, D) The phosphorylation indexes (P-ERK/ERK) were calculated and compared to the index measured for VEGF_{165a} (arbitrary set at 1) in each cell line. FBS: Foetal Bovine Serum; 111a: VEGF_{111a}; 111b: VEGF_{111b}; 121a: VEGF_{121a}; 121b: VEGF_{121b}; 155a: VEGF_{155a}; 155b: VEGF_{155b}; 165a: VEGF_{165a}; 165b: VEGF_{165b}. *p<0.05, **p<0.01, ***p<0.001 (t-test of Student, sample versus control or between two specific conditions indicated by the bar).

IV-1-4 VEGF_{165a} is the most active isoform in HUVEC

HUVEC are characterized by the simultaneous expression at their surface of a relatively physiological number of VEGF-R1, VEGF-R2 and NRP1 (5,000 – 20,000 compared to 150,000 in the PAEC-R2 or PAEC-R2-NRP1 cells) (Herve et al., 2008; Waltenberger et al., 1994). This did not modify however their response to VEGF except for an increased relative stimulation of the VEGF-R2 signalling cascade specifically in presence of VEGF_{165a} (Fig 35A, 35B). This makes this isoform the most active in HUVEC and confirms the SPR and solide phase assay data showing that VEGF_{165a} is the only isoform able to interact significantly with NRP1 and to induce the formation of complexes with VEGFR2 and NRP1. This also suggests that in physiological situations where VEGF-R2 and NRP1 are less abundant than in transfected cells, VEGF_{165a} is more active than the other isoforms.

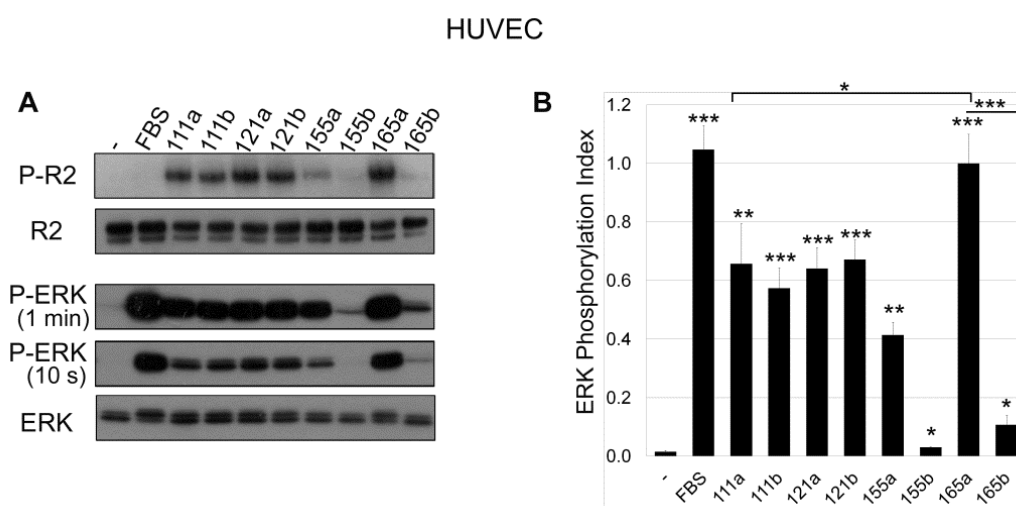


Figure 35 : Effect of VEGF variants on HUVEC

(A) HUVEC were treated with 1nM of VEGF variants for 10min in serum free medium and were analyzed by Western blot using antibodies against VEGF-R2 (R2), phospho-VEGFR2 (Tyr1175, P-R2), ERK1/2 (ERK) or phospho-ERK1/2 (P-ERK). For P-ERK two different film exposures are shown (10 s and 1 min). **(B)** The phosphorylation indexes (P-ERK/ERK) were calculated and compared to the index measured for VEGF_{165a} (arbitrary set at 1). FBS: Foetal Bovine Serum; 111a: VEGF_{111a}; 111b: VEGF_{111b}; 121a: VEGF_{121a}; 121b: VEGF_{121b}; 155a: VEGF_{155a}; 155b: VEGF_{155b}; 165a: VEGF_{165a}; 165b: VEGF_{165b}. *p<0.05, **p<0.01, ***p<0.001 (t-test of Student, sample versus control or between two specific conditions indicated by the bar).

To further characterize the specific activity of the different isoforms, HUVEC and PAE-R2 were also treated during increasing periods of time or with various concentrations of VEGF. Time-course experiments showed a maximal ERK1/2 phosphorylation 5 to 15 min after addition of any VEGF variant (Fig 36A, 36B). No effect was observed at 1 min and the phosphorylation was highly reduced at 30 min whatever the VEGF isoforms. Using various concentrations (0.1 to 3nM), we also confirmed that treatment with 1 nM of VEGF was the most appropriate concentration for comparing the effects of all the variants (data not shown). Indeed stimulation of phosphorylation was already detected after treatments at 0.1 nM in PAEC-R2 or at 0.3 nM in HUVEC while 3 nM was already a saturating concentration for both cell lines.

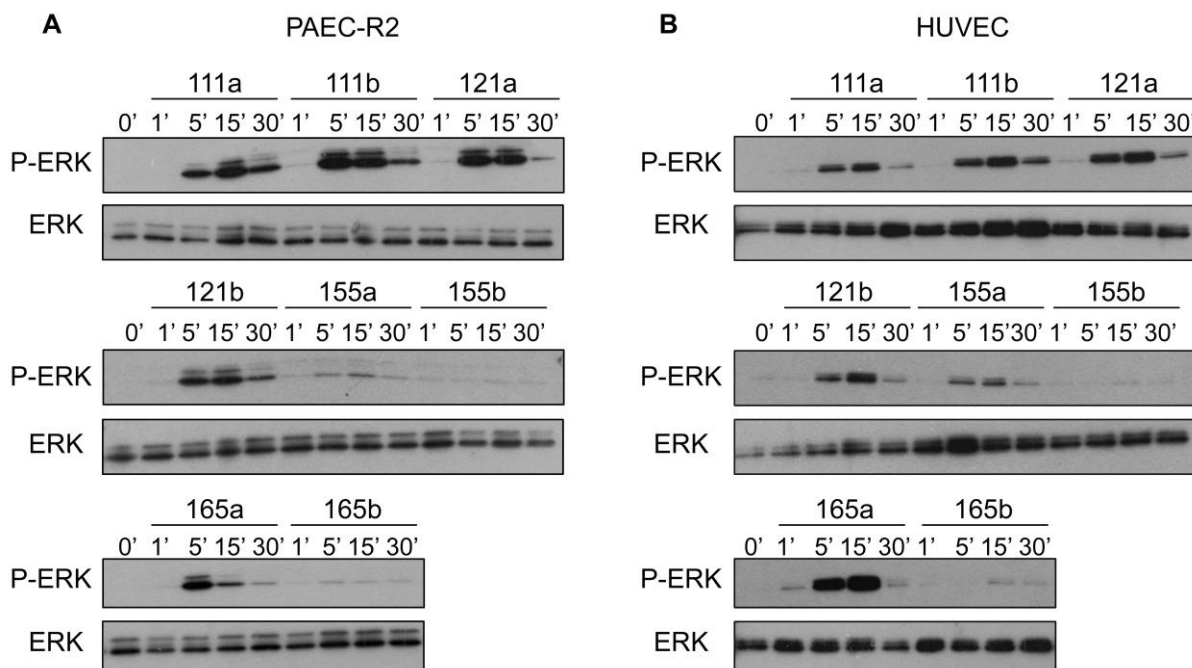


Figure 36 : Time-course experiments evaluating the effects of VEGF variants on ERK1/2 phosphorylation on endothelial cells

(A) PAEC-R2 and (B) HUVEC were treated with 1nM of VEGF variants for 0, 1, 5, 15 or 30 min in serum free medium. Protein extracts were then analyzed by Western blot using ERK1/2 (ERK) and phospho-ERK1/2 (P-ERK) specific antibodies

IV-1-5 VEGF_{165b} does not affect VEGF_{165a}-induced phosphorylation

VEGF_{165b} has been reported in the literature to be able to inhibit the VEGF_{165a}-induced activation of the VEGF-R2 signalling pathway (Woolard et al., 2004). Such inhibitory effect was however not observed in the previous experimental settings used with PAEC-R2 (Fig 33B). This was further investigated here in PAEC-R2 and HUVEC, using various types of treatments and different concentrations of VEGF_{165a} and VEGF_{165b} (Fig 37). Inhibition of the VEGF_{165a}-induced activation was never observed, even with cells pre-treated with VEGF_{165b} before the addition of VEGF_{165a} (Fig 37C, 37D).

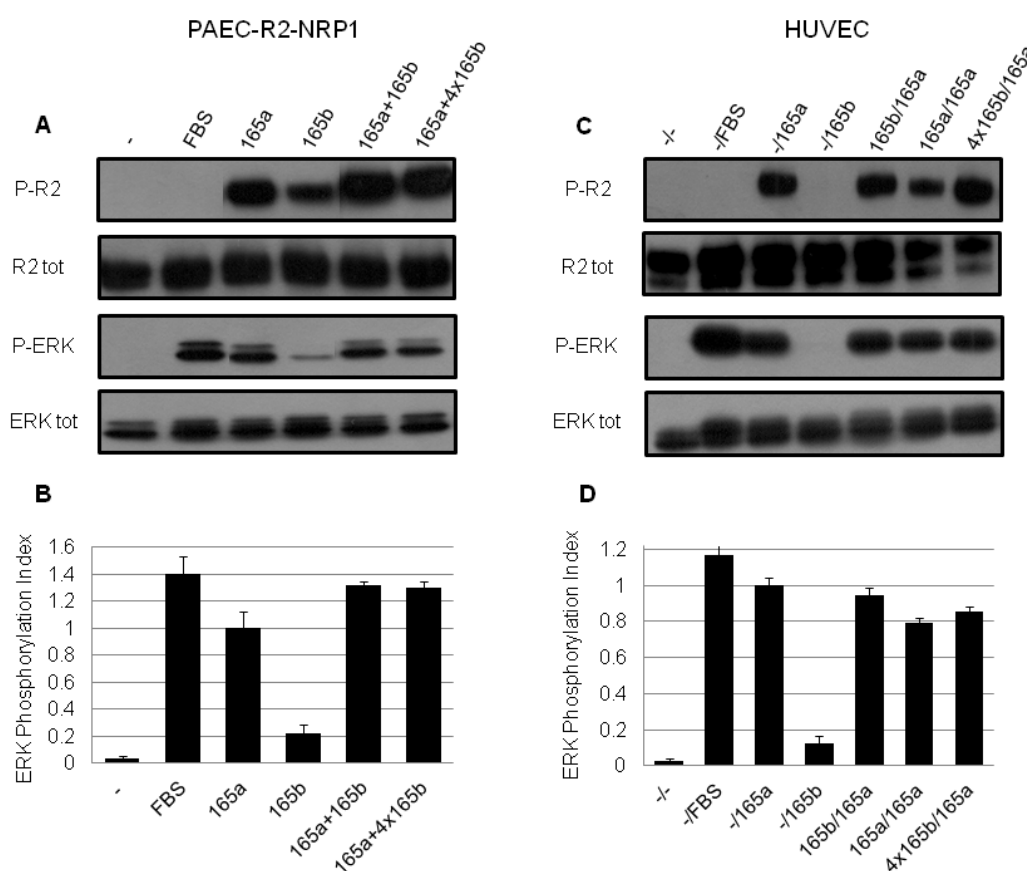


Figure 37 : Effect of VEGF_{165b} on VEGF_{165a}-induced phosphorylation of VEGF-R2 and ERK1/2

(A) PAEC-R2-NRP1 were treated with 1nM of VEGF_{165a} and VEGF_{165b}, added alone or together for 10min in serum free medium. (C) HUVEC were pre-treated without or with VEGF_{165a} or VEGF_{165b} for 15 min, before addition of VEGF_{165a} or VEGF_{165b} for 10 min. Cells were lysed and analyzed by Western blot using antibodies against VEGF-R2 (R2), phospho-VEGFR2 (Tyr1175, P-R2), ERK1/2 (ERK) or phospho-ERK1/2 (P-ERK). (B, D) The phosphorylation indexes (P-ERK/ERK) were calculated and compared to the index measured for VEGF_{165a} alone (arbitrary set at 1). FBS: Foetal Bovine Serum, 165a: 1nM VEGF_{165a}, 165b: 1nM VEGF_{165b}, 4x165b: 4nM VEGF_{165b}, 165b/165a: pre-treatment with VEGF_{165b} during 15' then addition of VEGF_{165a}.

IV-2 Effect of VEGF variants on endothelial cells proliferation and survival

Several preliminary experiments were performed to determine the best experimental conditions to evaluate the effects of VEGF on HUVEC survival and proliferation. Different conditions of medium and times of treatment were tested but the most critical parameter was the serum concentration. A concentration of 0.1% FBS for 48h was chosen for the survival assays while for the proliferation assays 0.5% for 48h was the best compromise, being high enough to prevent any side effect related to survival issues but too low to stimulate proliferation in absence of VEGF.

Using a WST-1 assay, we demonstrated that the proliferation rate was drastically increased by VEGF_{165a} and to a lesser extent by VEGF_{111a}, VEGF_{111b}, VEGF_{121a}, VEGF_{121b} and VEGF_{155a} while VEGF_{155b} and VEGF_{165b} had no stimulatory effect (Fig 38A). The effect of combining VEGF_{165a} (250 pM) with either VEGF_{165b} or VEGF_{155b} (1 nM) was also evaluated. Surprisingly, the effect of VEGF_{165a} was suppressed by the two VEGF_{xxx}b variants and the proliferation rate returned to control levels. These results were confirmed by using a [³H]-thymidine incorporation assay (data not shown).

It was previously suggested that VEGF_{165b} favours endothelial cells survival despite its reduced effect on VEGF-R2 signalling pathway (Woolard et al., 2004). This was clearly confirmed here as it had the same activity as VEGF_{165a} and VEGF_{111a} used as positive controls. VEGF_{111b} was also active (Fig 38B).

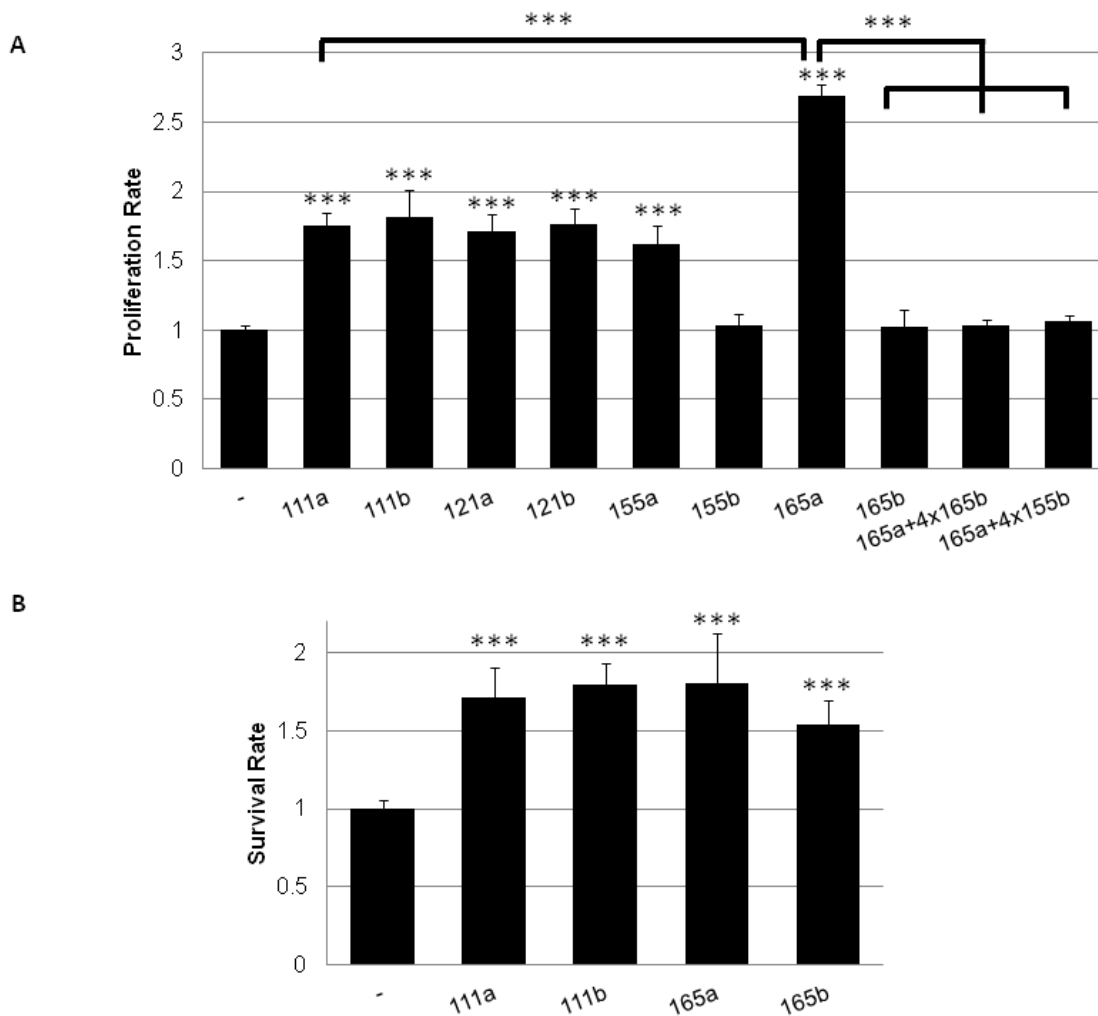


Figure 38 : Effect of VEGF variants on HUVEC proliferation and survival

HUVEC were seeded in complete medium during 16h. They were then washed before being cultured for 48h: **(A)** in a medium containing 0.5% FBS or **(B)** in a medium containing 0.1% FBS with or without 250pM of VEGF variants in order to evaluate **(A)** their proliferation or **(B)** their survival, respectively. -: Control medium; H: 1µg/ml heparin; FBS: Foetal Bovine Serum; 111a: VEGF_{111a}; 111b: VEGF_{111b}; 121a: VEGF_{121a}; 121b: VEGF_{121b}; 155a: VEGF_{155a}; 155b: VEGF_{155b}; 165a: VEGF_{165a}; 165b: VEGF_{165b}; 165a + 4x 155b: 250pM VEGF_{165a} mixed with 1nM VEGF_{165b}; 165a + 4x 165b: 250pM VEGF_{165a} mixed with 1nM VEGF_{155b}; *p<0.05, **p<0.01, ***p<0.001 (t-test of Student, sample versus control or between two specific conditions indicated by the bar).

IV-3 Effect of VEGF variants on endothelial cells migration

Various VEGF isoforms, alone or in combination, were evaluated for their capacity to induce the migration of HUVEC in Boyden chambers assay. A strong activity was observed for VEGF_{111a}, VEGF_{111b} and VEGF_{165a} (Fig 39). By contrast, VEGF_{165b} was not chemotactic and was further able to inhibit the VEGF_{165a}-induced migration. The addition of an antibody specific for the VEGF_{xxx}b isoforms inhibited the chemotactic activity of VEGF_{111b} and the inhibitory function of VEGF_{165b}, further strengthening the data obtained in cell proliferation assay.

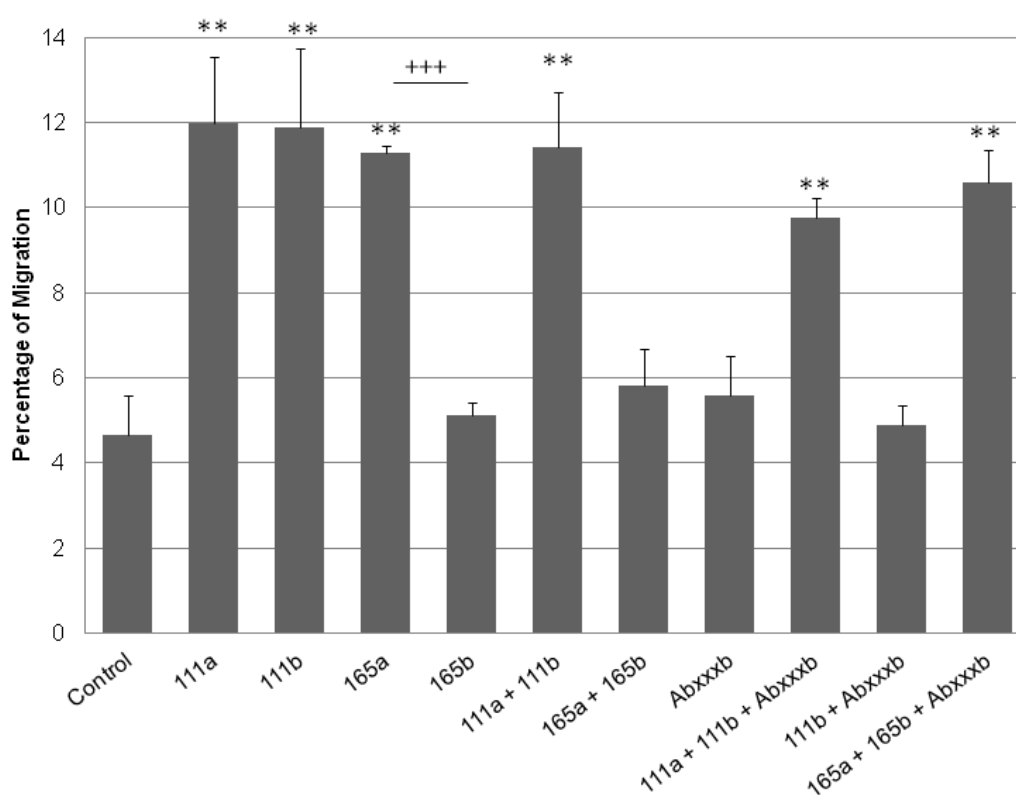


Figure 39 : Effect of VEGF variants on HUVEC migration

The chemotactic effect of VEGF variants were assessed in a Boyden chambers assay. VEGF isoforms were used alone (1 nM) or in association (1 nM each). In some conditions the VEGF_{xxx}b antibody was added (1 nM). The percentage of migrating cells was calculated as described in Material and Method. 111a: VEGF_{111a}, 111b: VEGF_{111b}, 165a: VEGF_{165a}, 165b: VEGF_{165b}, Abxxx b: Specific antibody directed against VEGF_{xxx}b isoforms. ** p<0.01 (t-test of Student, sample versus control), +++ p<0.001 (t-test of Student, between two specific conditions indicated by the bar).

IV-4 Role of exon 5 binding to NRP1 in VEGF effects *in vitro*

In VEGF-A, the E5-encoded domain is involved in binding to NRP1 and HSPG (Fig 22, 24, 28-30). Its role as an inducer of the VEGF-R2 signalling cascade was investigated in culture by the use of the R8R mimetic peptide. Endothelial cells were pre-treated with the R8R peptide before supplementing the medium with VEGF_{165a}. In PAEC-R2, the peptide did not modify the VEGF_{165a}-induced phosphorylation of VEGF-R2 (Fig 40A, 40C), which was expected as these cells do not express NRP1. By contrast, in similar conditions the peptide markedly reduced the VEGF-R2 activation in PAEC-R2-NRP1 (Fig 40B, 40D). Most importantly, R8R was also able to inhibit the VEGF_{165a}-induced proliferation of HUVEC (Fig 40E) to a rate similar to that observed with VEGF_{111a}, confirming the antagonistic effect of the E5-mimetic peptide and the implication of the E5-encoded domain on the NRP1 function.

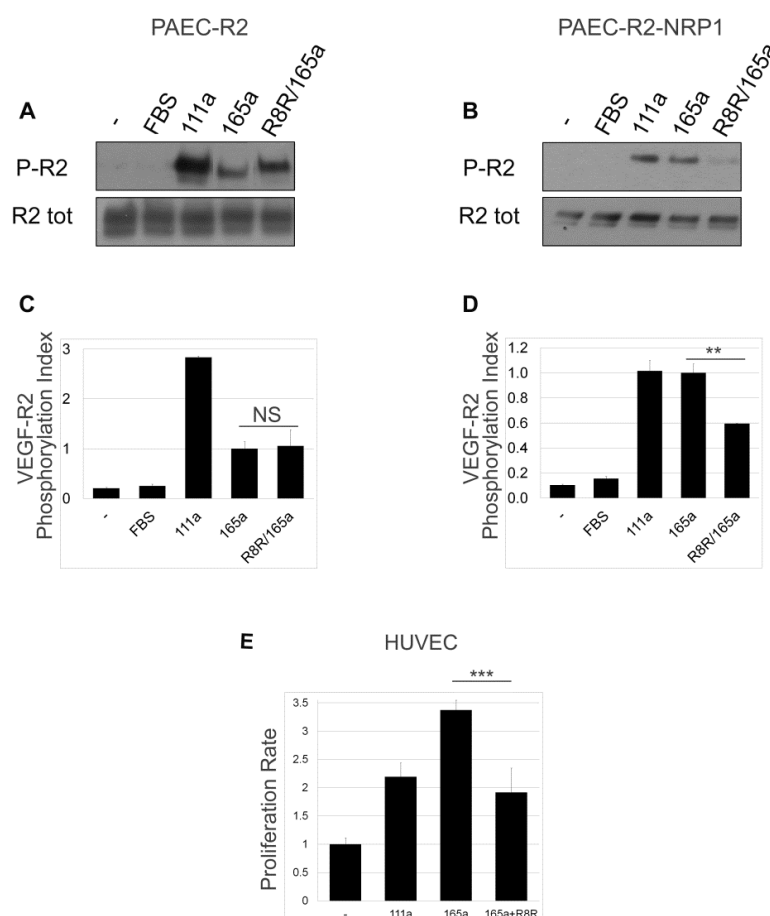


Figure 40 Effect of R8R on VEGF-induced signalling *in vitro*

(A) PAEC-R2 and (B) PAEC-R2-NRP1 were treated for 10 min at 37°C with 1 nM of VEGF_{111a} or 1 nM of VEGF_{165a} in the absence or presence of R8R (300 μM). Protein extracts were then analyzed by Western blot using VEGF-R2 (R2 tot) and phospho-VEGFR2 (P-R2) specific antibodies (C, D). Calculated P-R2/R2 ratio in (C) PAEC-R2 and (D) PAEC-R2-NRP1. (E) HUVEC proliferation was measured by WST-1 assay in absence of VEGF, in the presence of VEGF_{111a} (250 pM), in the presence of VEGF_{165a} (250 pM), or in the presence of both VEGF_{165a} (250 pM) and R8R (300 μM). Only statistics related to the effects of R8R are reported. **p<0.01, ***p<0.001 (t-test of Student).

IV-5 Cytoprotective effect of VEGF isoforms on RPE cells

VEGF_{165b} was reported to be cytoprotective in retina (Magnussen et al., 2010) as it protects retinal pigment epithelial cells (RPE cells) from apoptosis induced by toxic doses of ketocholesterol. This previously published protocol was used to assess the effect of 2.5nM of VEGF_{111a}, VEGF_{111b}, VEGF_{165a} or VEGF_{165b}.

In immortalized retinal ARPE19 cells, the addition of all isoforms, including VEGF_{165b}, induced a 1.5-fold increase of cell viability after ketocholesterol treatment, which is similar to the effect observed with EGF used as a positive control (Fig 41A). The protective effect was also indirectly confirmed by LDH release in the culture medium (Fig 41B). A similar trend was observed with primary RPE cells, although VEGF isoforms were slightly less active than EGF (Fig 41C). Altogether these data suggest that VEGF_{111a}, VEGF_{111b}, VEGF_{165a} and VEGF_{165b} conferred a survival advantage to the retinal epithelial cells, which could benefit to therapy of eyes diseases.

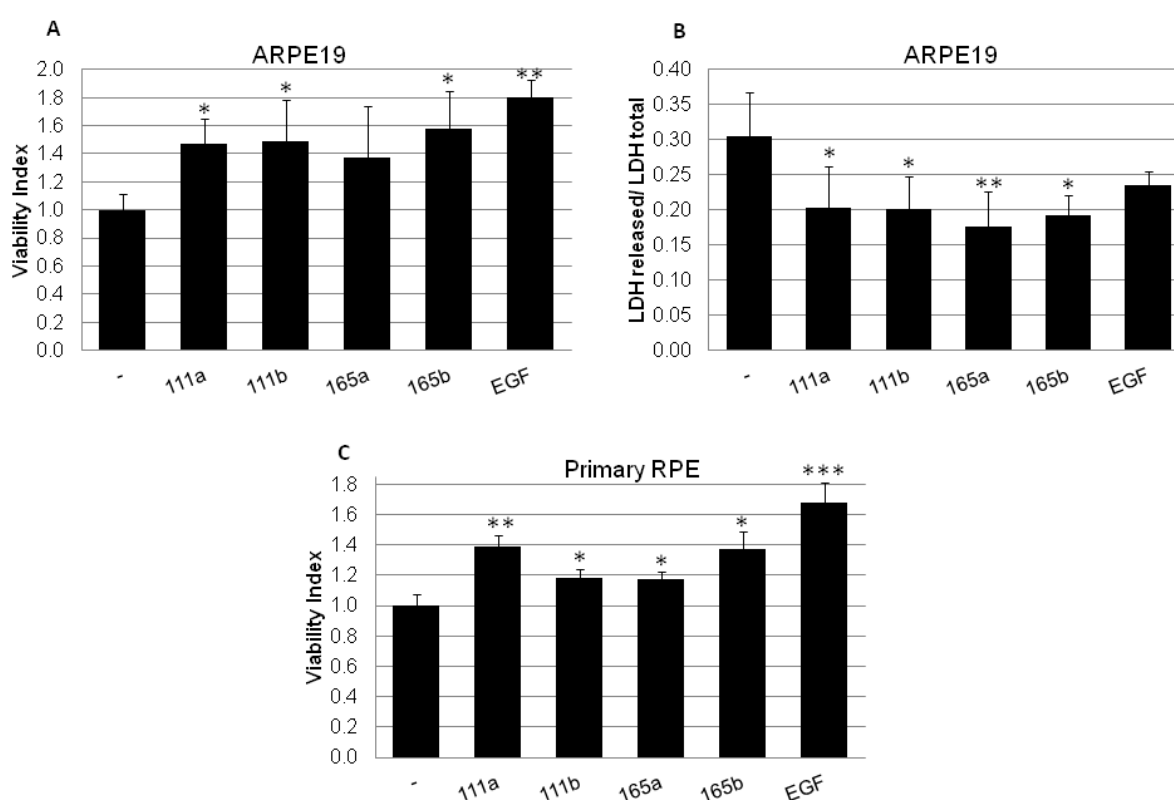
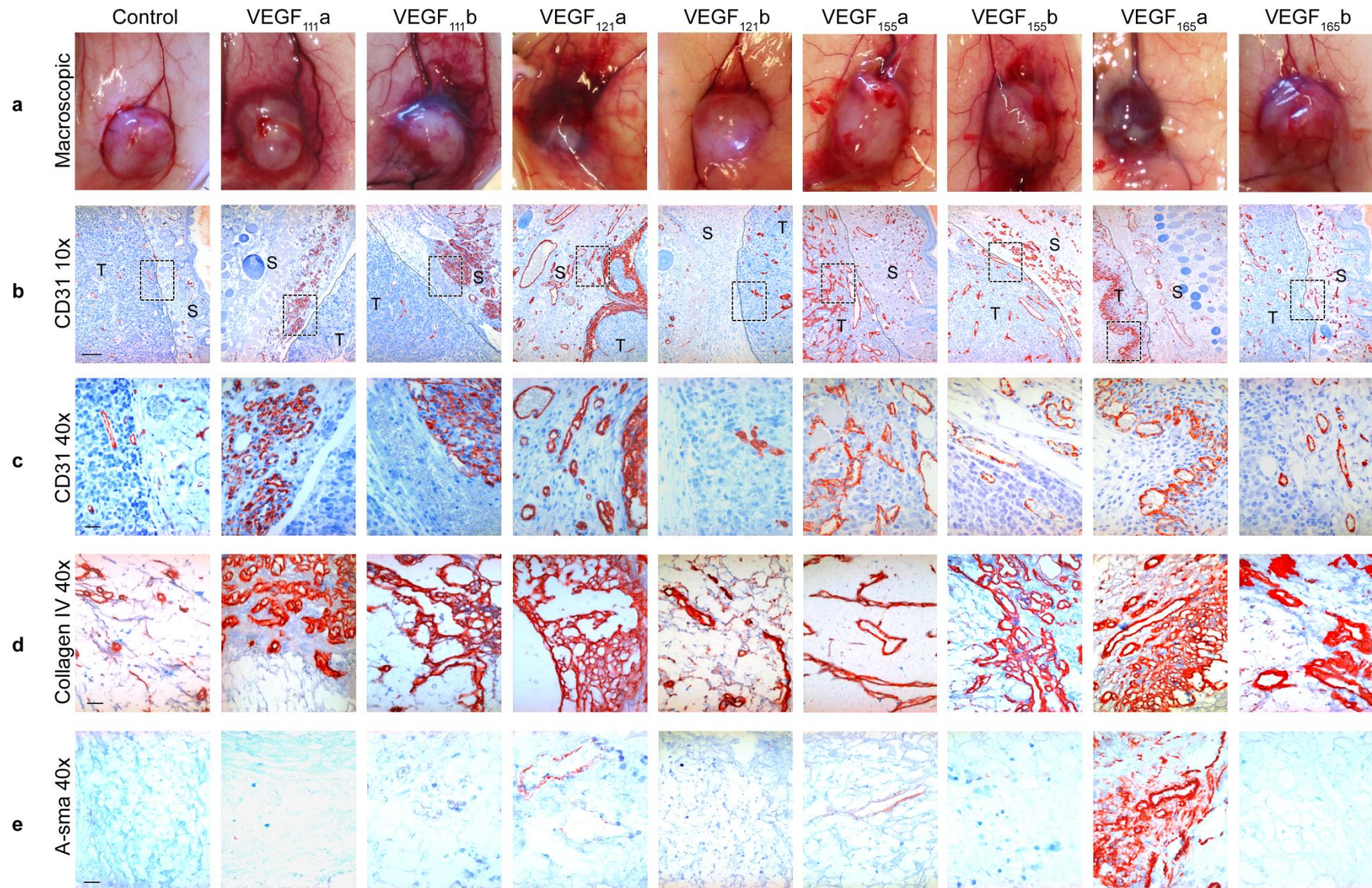


Figure 41 Effect of VEGF variants on cytoprotection of retinal epithelial cells

(A, B) ARPE19 and (C) RPE cells were treated with a toxic concentration of ketocholesterol (18 μ M) and VEGF variants or EGF as described in Material and Methods. Cells viability was evaluated using (A, C) The WST-1 colorimetric method and (B) measurement of the LDH released in the medium. ARPE19: Spontaneously Arising Retinal Pigment Epithelial Cells; Primary RPE: Primary Retinal Pigment Epithelial Cells, -: control, 111a: VEGF_{111a}, 111b: VEGF_{111b}, 165a: VEGF_{165a}, 165b: VEGF_{165b}, EGF: Epidermal Growth Factor. Statistical difference between control and treated cells: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, paired t-test.

V- VEGF isoforms generate different patterns of angiogenesis *in vivo*.

HEK293 cells transfected with the empty vector or expressing the various VEGF isoforms at a similar level *in vitro* were used to locally deliver recombinant VEGF variants in nude mice. Animals were weighed during the entire experiment. No significant weight variation was noted among the different groups, as it was previously observed for VEGF_{111a}, VEGF_{121a} and VEGF_{165a} (Mineur et al., 2007). After three weeks, mice were sacrificed and tumours were dissected. The overall level of human VEGF produced *in vivo* by HEK293 cells was measured in the tumours at the mRNA level. Primers (P1-P2) enabling amplification of sequence between E2 to E4 of the human but not the mouse transcripts were used (Table 3). No significant difference of VEGF mRNA levels was observed among the various groups injected with VEGF-expressing HEK293 cells while no signal was detected in the group injected with control cells (Fig 43A). Immunodetection using a VEGF antibody showed an intense and similar labelling in the tumour tissue for all the VEGF isoforms (data not shown) confirming the RT-PCR quantifications. By using primers specific for each of the VEGF_{xxx}a (P3-P4) or VEGF_{xxx}b subfamily (P5-P6, P7-P8 and P9-P10) (Table 3), we validated also the identity of the expressed VEGF variants (not illustrated).



Tumours and surrounding tissues were examined macroscopically. The most obvious differences were the intense reddish colour of the VEGF_{165a} and VEGF_{121a} tumours compared to the others, and the formation of a dense network of small capillaries in the dermis close to tumours, especially those expressing VEGF_{111a} or VEGF_{111b} (Fig 42A). The number of vessels, their size and their partition between the tumours and surrounding tissues were also evaluated by immunolabelling using anti-mouse CD31 antibodies (Fig 42B, 42C). Control tumours contained a low number of small blood vessels that were however functional based on the presence of red blood cells (not shown). As expected from macroscopic observation, vessels density was high within the tumour in the VEGF_{165a} and VEGF_{121a} mice, while it was scarce in VEGF_{111a}, VEGF_{111b} and VEGF_{121b} tumours. Slightly higher levels were induced by VEGF_{155b} and VEGF_{165b}, and intermediate levels were seen in VEGF_{155a} expressing tumours. To substantiate these observations, the surface of positive CD31 labelling was measured and expressed in the percentage of the total surface of the tumoural tissue present in the sections. It was significantly higher in VEGF_{121a} and VEGF_{165a}, and to a lesser extent in VEGF_{155a} tumours as compared to the control tumours (Fig 43B). VEGF_{165b} and VEGF_{155b} were active, although markedly less than their VEGF_{165a} and VEGF_{155a} counterparts, while VEGF_{111a}, VEGF_{111b} and VEGF_{121b} expression did not significantly increase the intratumoural CD31-positive surface, as compared to controls. By contrast, the ranking for the number of vessels in the skin adjacent to the tumours was VEGF_{111a} = VEGF_{111b} > VEGF_{121a} > VEGF_{155b} = VEGF_{165a} = VEGF_{165b} = VEGF_{155a} > VEGF_{121b} = control (Fig 42B, 42C and Fig 43C).

Figure 42 : Effects of VEGF variants on *in vivo* tumour angiogenesis using HEK293 cells expressing the various VEGF isoforms

Two millions HEK293 cells, transfected with the empty vector (control) or expressing the VEGF variants, were mixed with Matrigel and injected in the flanks of nude mice. **(A)** Macroscopic view of the tumours formed in each group. **(B)** CD31 immunostaining showing the presence of blood vessels in the tumour (T) and the adjacent skin (S) (scale bar = 100µm). **(C)** Enlarged view of the region delineated by the rectangle in each picture shown in **(B)** (scale bar = 25 µm). Staining of **(D)** type IV collagen and **(E)** α-SMA in regions where angiogenesis was the highest (scale bar = 25 µm). (Page 111)

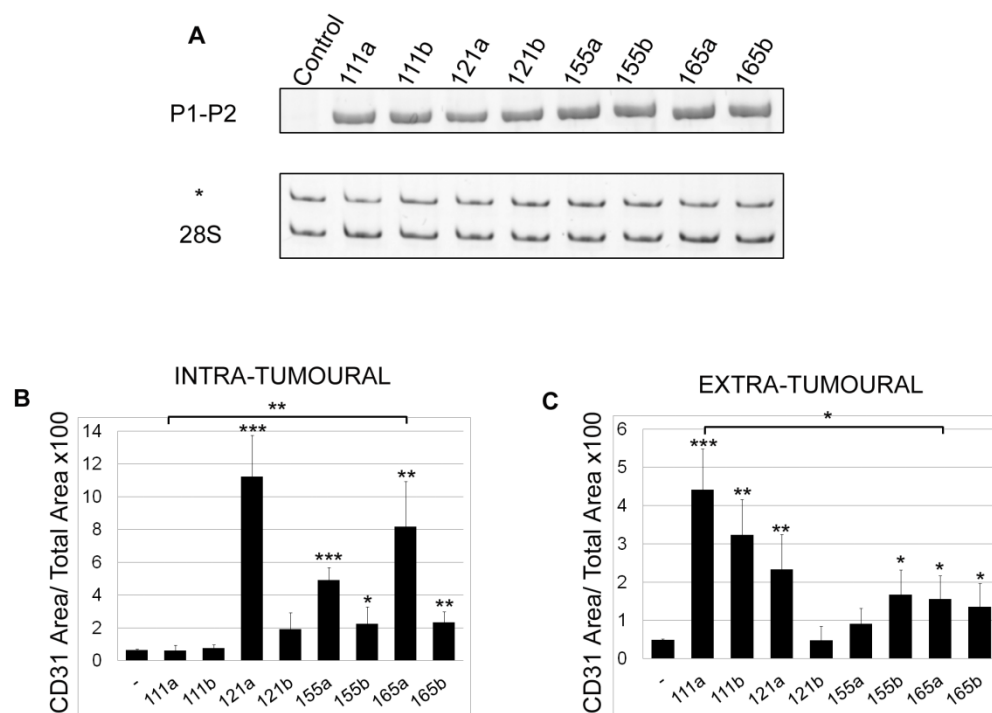


Figure 43 : Quantification of the effects of VEGF variants in tumour angiogenesis using HEK293 cells expressing the various VEGF isoforms

Two millions HEK293 cells, either control or expressing VEGF variants, were mixed with Matrigel and injected in the flank of nude mice. **(A)** The VEGF mRNA levels (upper panel) were measured by RT-PCR using primers P1 and P2 (see Table 1) that enable the amplification of all the VEGF variants with production of a single amplicon. The 28S rRNA was measured in parallel to normalize the quantities of RNA input in the reactions. * indicates the amplicon formed from an internal standard co-amplified with 28S rRNA to take into account potential variations of the PCR efficiency. Percentages of the CD31 stained surfaces in **(B)** the tumour or **(C)** the adjacent skin were quantified using Image J software. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ (unpaired t-test).

Maturation of the blood vessels was also investigated by immunostaining of the basement membrane (type IV collagen) and α -SMA positive pericytes. Whatever the conditions, the majority of the formed vessels were delineated by a basement membrane (Fig 42D). Striking differences were however observed by staining of α -SMA (Fig 42E). Positive cells were found mainly in the vessels growing in or around the tumours expressing VEGF_{165a}. They were also found although at a much reduced level, in the presence of VEGF_{155a} and VEGF_{121a}. They were almost totally absent in other samples, notably those expressing VEGF_{165b}.


Effect of tumour expressing VEGF variants on mice physiology

Toxicity triggered by HEK cells, either control or expressing VEGF_{111a}, VEGF_{111b}, VEGF_{165a} or VEGF_{165b}, on nude mice (4 mice per group) was evaluated using different parameters. The weekly monitoring showed healthy animals with a normal general examination, pink

mucosae, normal hydration and absence of ascite. After death, control of organs did not identify any hepatomegaly or splenomegaly in mice bearing VEGF tumours except for VEGF_{111a} mice which displayed a slightly higher spleen weight (1.20 ± 0.04 time the weight of the control spleen). Hepatic enzymes as well as complete blood counts were similar between the groups (not illustrated).

Diffusibility of VEGF variants in Matrigel *ex vivo*

The formation of dense network of small capillaries in healthy tissues close to the tumor and the absence of significant intra-tumoural vascularisation are highly specific to HEK293 cells expressing either VEGF_{111a} or VEGF_{111b}. This particularity is probably related to an increased “diffusibility” of these variants. As HEK293 cells forming tumours in mice are injected in suspension in Matrigel, we further evaluated the diffusion of VEGF variants out of Matrigel matrix. Solutions of Matrigel containing the different VEGF isoforms (1 nM) were poured in 12-wells plate and polymerized at 37°C. Serum free culture medium was then added in the wells and the VEGF progressively released from Matrigel into the medium was quantified by ELISA (Fig 44). Maximal concentrations, indicative of an equilibrium between the VEGF present in the Matrigel and in the medium, were found within 2-4 hours for VEGF_{111a} and later (8h-20h) for other tested isoforms. Although indirect, this semi-quantitative evaluation shows again an increased diffusion for VEGF_{111a}, VEGF_{111b} having not been evaluated in this assay.



	Peak of VEGF in the medium
VEGF _{111a}	2h-4h
VEGF _{121a}	8h-20h
VEGF _{155a}	8h-20h
VEGF _{165a}	8h-20h
VEGF _{165b}	8h-20h

Figure 44 : Diffusion of VEGF from Matrigel *in vitro*

Matrigel solution (200 µl) containing VEGF variants (1nM) were polymerized in 12-wells plate and covered by serum free medium (200µl). VEGF released in the culture medium was quantified by ELISA after increasing incubation times (2 to 20 hours). Maximum concentration in the conditioned medium was observed already after 2-4 hours for VEGF_{111a} and at later time points for the other isoforms.

Effect of the combination of VEGF_{xxx}a and VEGF_{xxx}b on angiogenesis *in vivo*

Based on our observations that VEGF₁₆₅b was able to significantly inhibit VEGF₁₆₅a-induced proliferation and migration *in vitro* (Fig 38A and Fig 39), we evaluated if a similar repression also occurred *in vivo*. A total number of 2×10^6 HEK293 cells expressing VEGF₁₆₅a and VEGF₁₆₅b were injected at ratios of 1:1 or 1:4 (Fig 45). The observed patterns of angiogenesis were intermediate to those observed when VEGF₁₆₅a or VEGF₁₆₅b were expressed alone and seemed to result from the actual abundance of each isoform rather than to inhibition of the effect of VEGF₁₆₅a by VEGF₁₆₅b. The observations were similar for VEGF₁₂₁a and VEGF₁₂₁b.

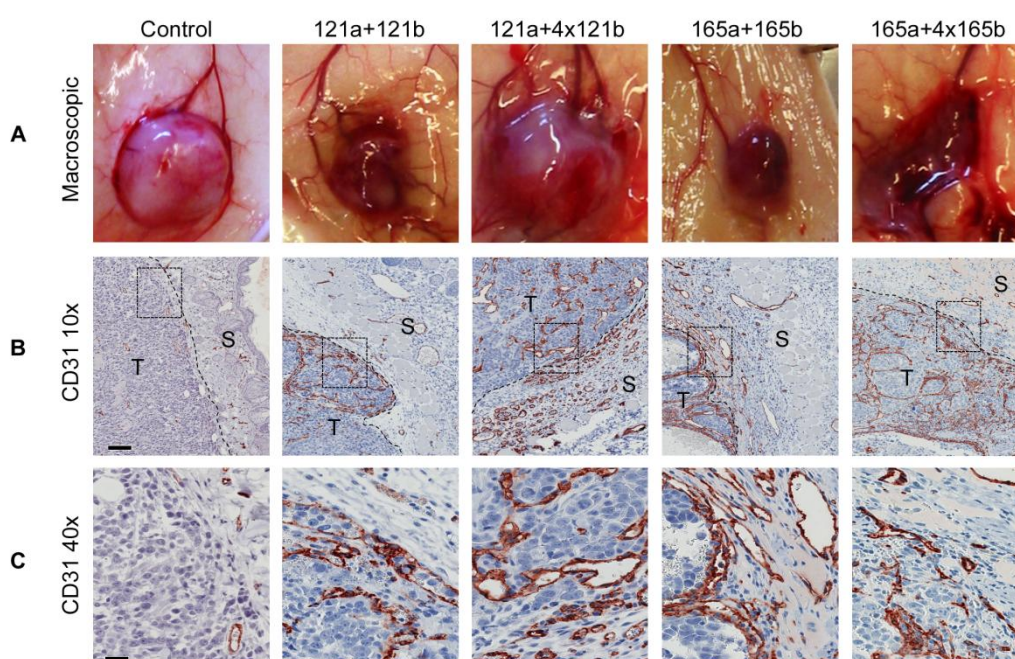


Figure 45 : Effects on tumour angiogenesis of co-expressing VEGF₁₆₅a and VEGF₁₆₅b or VEGF₁₂₁a and VEGF₁₂₁b

Two millions HEK293 cells were mixed with Matrigel and injected in the flank of nude mice. In addition to control cells, mixture of HEK293 cells expressing VEGF₁₆₅a and VEGF₁₆₅b were evaluated, either 1×10^6 each (165a + 165b) or 4×10^5 expressing VEGF₁₆₅a and 1.6×10^6 expressing VEGF₁₆₅b (165a + 4x165b). See Fig 40 for comparison with cells expressing only VEGF₁₆₅a or VEGF₁₆₅b. The same experiment was performed for VEGF₁₂₁a and VEGF₁₂₁b (A) Macroscopic view of the tumours obtained in each group. Control (n=5), 121a+121b (n=5), 121a+4x121b (n=5), 165a+165b (n=4), 165a+4x165b (n=5) (B) CD31 immunostaining on paraffin sections showing the tumour (T) and the adjacent skin (S) (scale bar = 100 μ m). Black lined rectangles delineate the areas of the sections represented in (C) at higher magnification (scale bar = 25 μ m).

VI- As Opposed to VEGF₁₆₅b, VEGF₁₁₁b does not inhibit pathologically induced neovascularization in the eyes.

As the pro-angiogenic effect of a VEGF_{xxx}b isoform was not initially expected, we further evaluated VEGF₁₁₁b in other *in vivo* models that previously allowed to demonstrate the specific properties of VEGF₁₆₅b in reducing neovascularization in ocular models (Hua et al., 2010; Magnussen et al., 2010).

VI-1 Choroidal Neovascularization

Choroidal neovascularization (CNV), a model of Age-related Macular Degeneration (AMD), was induced by LASER-photocoagulation in mice. The damaged eyes were then treated by injection of PBS, VEGF₁₁₁b or VEGF₁₆₅b. VEGF₁₆₅b injection significantly inhibited neovascularization as compared with PBS ($0.97 \pm 0.34 \times 10^4 \mu\text{m}^2$ vs $2.62 \pm 0.50 \times 10^4 \mu\text{m}^2$) (Fig 46A, 46B). By contrast, VEGF₁₁₁b did not inhibit neovascularisation and even induced a slight, although not statistically significant, increase of the neovascularized area ($4.76 \pm 1.28 \times 10^4 \mu\text{m}^2$) as compared to control eyes.

VI-2 Oxygen Induced Retinopathy

Oxygen Induced Retinopathy (OIR) in rat pups is a model of Retinopathy of Prematurity. In this assay, VEGF₁₆₅b reduced pathological angiogenesis similarly to what was observed in the CNV model (Magnussen et al., 2010) (Gammons et al., unpublished data). By contrast, treatment with VEGF₁₁₁b stimulated neo-vascularization as compared to PBS-treated eyes (Fig 46C). The diameter and the tortuosity of the vessels were however not affected.

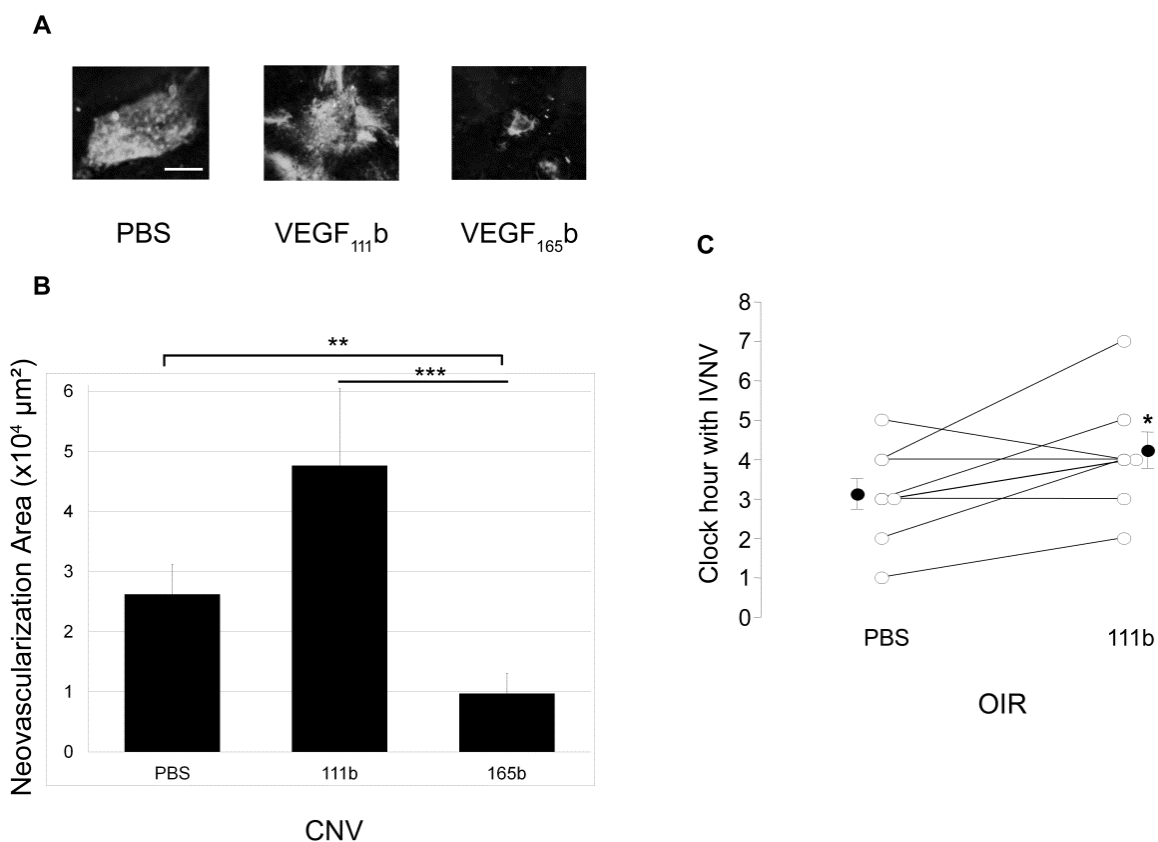


Figure 46 : Effect of VEGF₁₁₁b and VEGF₁₆₅b on pathologically induced neovascularization in eye models

(A, B) Choroidal Neovascularization was induced in mice by LASER impacts and the eyes were injected with PBS, VEGF₁₁₁b or VEGF₁₆₅b immediately and 7 days later. **(A)** Representative pictures of the choroid after isolectin B4 immunofluorescence staining (scale bar = 50 μm). **(B)** Quantification of the area of neovascularization. **(C)** Oxygen Induced Retinopathy was induced in rats. For each rat, one eye was injected with PBS and the other with 10 ng of VEGF₁₁₁b, allowing paired comparisons (represented by lines). Quantification of the number of Intravitreal Neovascularization (IVNV) per clock hour. Open circles represent quantifications in individual samples and black circles the mean. * p<0.05, (OIR, paired t-test of Student). ** p<0.01 ; *** p<0.001 (CNV, t-test of Student). CNV: Choroidal Neovascularization; OIR: Oxygen Induced Retinopathy; 111b: VEGF₁₁₁b; 165b: VEGF₁₆₅b.

VII- Effects of the different isoforms on vascular permeability *in vivo*

Based on data of a preliminary dose-response experiment using VEGF_{165a} (not shown), 50 ng of the different VEGF isoforms were injected intradermally followed by an intravenous delivery of Evans' blue dye. As compared to PBS controls, an increased permeability close to the site of injection was observed for VEGF_{111a}, VEGF_{111b}, VEGF_{121a}, VEGF_{155a} and VEGF_{165a} while the effect of the other variants was not statistically significant (Fig 47A). The total surface of skin displaying an increased permeability is also an interesting parameter. Although hard to precisely quantify because of the difficulties to define the exact border between affected and non-affected skin, it clearly appeared that VEGF_{111a} and VEGF_{111b} were active at a longer distance than the other isoforms as shown in a representative example for VEGF_{111a} and VEGF_{165a} (Fig 47B), suggesting higher diffusibility.

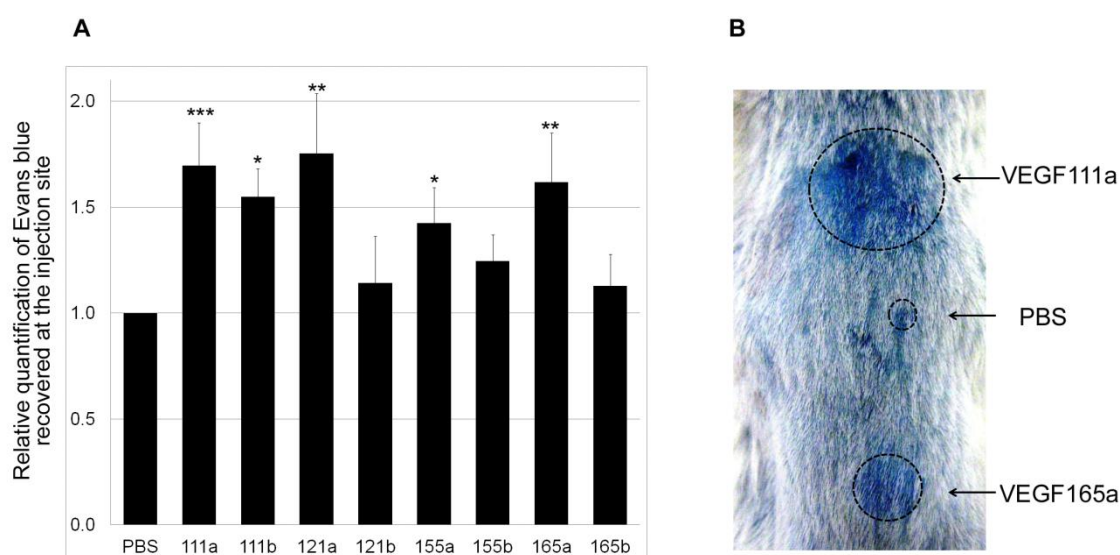


Figure 47: *In vivo* vascular permeability

A Miles and Miles modified assay was used to evaluate vascular permeability induced by the VEGF variants. **(A)** Quantification of the Evans' blue dye in the skin surrounding the site of injection (~ 20 mm²). The results were normalized for the weight of the skin samples and compared to the PBS control in each mouse. **(B)** Picture of the back of a mouse injected with VEGF_{111a}, VEGF_{165a} and PBS. Areas of increased vessel permeability were delineated with a black dotted line. 111a: VEGF_{111a}, 111b: VEGF_{111b}, 121a: VEGF_{121a}, 121b: VEGF_{121b}, 155a: VEGF_{155a}, 155b: VEGF_{155b}, 165a: VEGF_{165a}, 165b: VEGF_{165b}. * $p < 0.05$, ** $p < 0.01$ and *** $p < 0.001$, (t-test of Student).

VIII- Pharmacokinetic and toxicology of VEGF variants *in vivo*

VIII- 1 Half-life of VEGF variants *in vivo*

The half-life *in vivo* of VEGF_{111a}, VEGF_{111b}, VEGF_{165a} and VEGF_{165b} was evaluated after intra-venous (IV), intra-peritoneal (IP) or subcutaneous (SC) injections in mice. Their plasmatic concentration was quantified using an ELISA specific for human VEGF (Table 5A). After IV injection, half-life of VEGF_{165b} (12 ± 1 min) was the shortest and similar to the previously published values (12 min (Rennel et al., 2008); 13.2 min (Zhu et al., 2012)). The half-lives of the other isoforms were slightly higher, ranging between 20 and 30 min.

After IP injections, the isoforms with the longest and the shortest half-life were VEGF_{111a} and VEGF_{165b}, respectively, while after SC administration the ranking was VEGF_{111a} > VEGF_{111b} > VEGF_{165a} > VEGF_{165b}. Altogether, these data show that the variants possessing the 6 amino acids encoded by exon 8b have a reduced half-life as compared to the equivalent variants possessing the alternative E8a-derived sequence. Moreover, these results highlight that the lack of the sequence encoded by E5 and E7 in VEGF_{111a} confers an increased half-life *in vivo*, likely related to the resistance to degradation or to reduced interactions with the ECM.

Table 5 : Variations in the plasmatic concentrations of VEGF variants after different types of administration

A				B		
Half-life in blood stream (min)				Maximal Plasmatic concentration (ng/ml) after non-systemic injection		
	Method of injection				Method of injection	
	IV	IP	SC		IP	SC
VEGF _{111a}	21±2	113±39	100±13	VEGF _{111a}	35.0±8.1	37.2±11.8
VEGF _{111b}	29±8	38±5	72±19	VEGF _{111b}	31.7±10.1	36.6±6.1
VEGF _{165a}	28±4	48±5	52±12	VEGF _{165a}	9.6±3.1	8.0±3.7
VEGF _{165b}	12±1	14±5	25±12	VEGF _{165b}	11.5±4.2	4.7±1.7

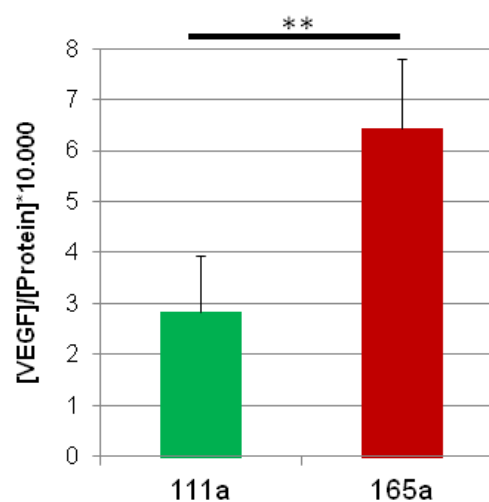
IV: Intravenous, IP: Intraperitoneal, SC: Subcutaneous.

The release from the site of injection into the blood stream is another critical parameter to be considered for evaluating the potential effects of VEGF variants *in vivo*. The maximal plasmatic concentrations were detected after 1 to 2 hours for all the variants. Marked differences were however observed when considering the actual concentration at the peak (Table 5B). Data clearly demonstrate that VEGF_{111a} and VEGF_{111b} can diffuse more efficiently than VEGF_{165a} and VEGF_{165b}.

The ability of VEGF_{111a} and VEGF_{165a} to diffuse *in vivo* was investigated in another model. The purified VEGF were injected under the skin of mice. After 8 hours tissues around the site of injection were recovered, total proteins were extracted and VEGF concentrations were determined. As compared to VEGF_{165a}, the local concentration of VEGF_{111a} was reduced confirming its increased diffusibility (Fig 48).

Figure 48 : VEGF_{111a} and VEGF_{165a} diffusion in the skin *in vivo*

VEGF_{111a} and VEGF_{165a} were injected subcutaneously. After 8h, proteins were extracted from the site of injection and the VEGF concentrations were measured. The results are reported as the ratio to total protein concentrations. ** p<0.01, t-test of Student.



VIII-2 Pathophysiological effects of VEGF variants *in vivo*

Xue and collaborators reported that daily subcutaneous injections of 4 µg of VEGF_{165a} for 14 days induced splenomegaly and hepatomegaly (Xue et al., 2008). Later, they observed the similar effects in mice bearing tumor overexpressing VEGF_{165a} together with increased hepatic parameters, ascite, anemia and bone-marrow defects (Xue et al., 2009). As we never saw such phenotype in our models of tumour angiogenesis, we decided to further characterize the effects of chronic injection of VEGF.

4 µg of VEGF (VEGF_{111a}, VEGF_{111b}, VEGF_{165a}, VEGF_{165b}) or PBS were daily injected during 14 days in the neck of C57Bl6 mice. Every day monitoring of animals showed that they were healthy (normal general aspect, pink mucosae, absence of ascite, normal

hydration, for example). No death was recorded during the experiment. At the end of the experiment, blood samples were collected and mice were sacrificed and dissected. Spleen and liver had a similar weight in all groups. Different organs and tissues were fixed and embedded in paraffin. Hematoxylin-eosin staining did not reveal any striking difference among the mice. Blood cell populations were similar in all the conditions and hepatic markers (ALT and AST) did not show any liver alteration induced by VEGF treatment. Altogether these data demonstrate that a prolonged treatment with VEGF injected at a dose more than 100 times higher than the physiological concentration did not induced anemia, inflammation, liver failure or any other obvious side effect.

Subcutaneous tissues close to the site of injection were also analyzed. They contained more blood vessels, as determined by CD31 immunostaining, for mice treated with VEGF_{111a}, VEGF_{111b} and VEGF_{165a} than in the VEGF_{165b} and PBS groups (not illustrated).

IX- Effect of the combination of VEGF_{111a} and VEGF_{165a} on angiogenesis *in vivo*

To evaluate any potential synergistic effects between VEGF_{111a} and VEGF_{165a} on angiogenesis *in vivo*, HEK293 cells expressing VEGF_{111a} or VEGF_{165a} were injected either simultaneously or alone as a control in nude mice. Tumours expressing both VEGF_{111a} and VEGF_{165a} were reddish and the adjacent skin invaded by numerous blood vessels (Fig 49A). An enlargement of the lateral thoracic vein was also seen, but at a lesser extent than with VEGF_{111a} alone. This is probably due to the number of cells expressing VEGF_{111a}: 2×10^6 in VEGF_{111a} group alone as compared to 1×10^6 in “VEGF_{111a}+VEGF_{165a}” group. Microscopically, invasion of small and immature vessels (CD31+, α -SMA-) in the peritumoural tissue and formation of large vessels surrounded by pericytes inside or close to the tumour (CD31+, α -SMA+) were observed which was indicative of an addition of the effects mediated by the two VEGF isoforms (Fig 49B, 49C).

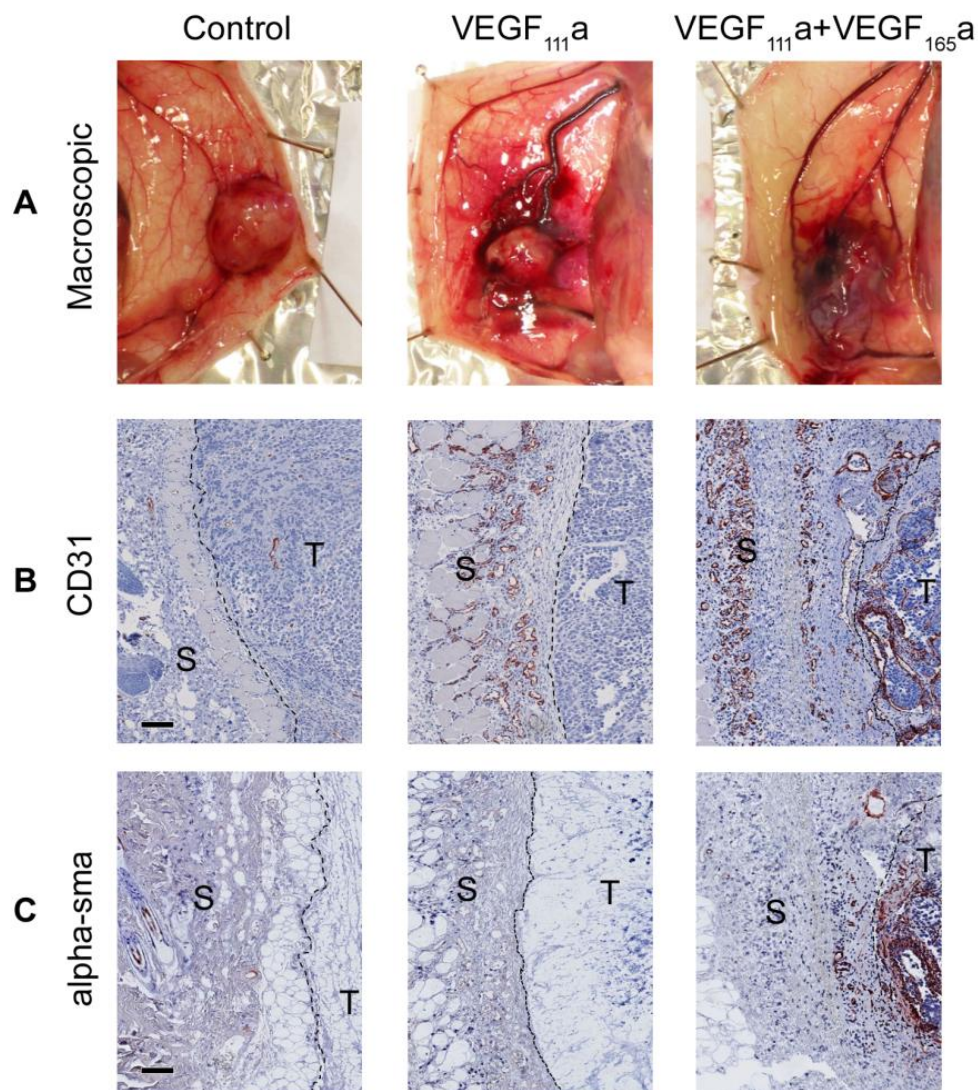


Figure 49 : Tumour angiogenesis by cells co-expressing VEGF_{111a} and VEGF_{165a}

Two millions HEK293 cells, transfected with the empty vector (control) or expressing one or both VEGF variants, were mixed with Matrigel and injected in the flanks of nude mice. **(A)** Macroscopic view of the tumours obtained in some groups. Control (n=4), VEGF_{111a} (n=4), VEGF_{111a} + VEGF_{165a} (1×10^6 HEK cells expressing VEGF_{111a} and 1×10^6 HEK cells expressing VEGF_{165a}, n=6). **(B)** CD31 immunostaining of paraffin sections showing the tumour (T) and the adjacent skin (S) (scale bar = 100 μ m). **(C)** α -SMA immunostaining showing the presence of pericytes (scale bar = 100 μ m).

X- Development of new VEGF variants

The development of efficient pro-angiogenic therapies would probably benefit from the use of VEGF variants possessing complementary specific properties. As an example the use of variants displaying different affinities for the ECM should favour the formation of VEGF gradients for recruiting and guiding vessel sprouts. The development of a VEGF variant able to stimulate the VEGF-R2 signalling cascade while displaying no affinity for VEGF-R1 would also be worth testing as VEGF-R1 is believed to be a competitor for VEGF-R2 when expressed as a soluble form or at the endothelial cell surface.

IX-1 VEGF_{179a} and VEGF_{179b}

VEGF_{189a} is mainly characterized by its high affinity for matrix components, due to the presence of the E6a-encoded domain (Houck et al., 1992; Park et al., 1993). This is a key property for forming gradient especially when co-expressed with more diffusible variants. It is however sensitive to proteolysis (Plouet et al., 1997). As VEGF_{111a} and VEGF_{111b}, are resistant to degradation presumably because of the absence of the E5-encoded domain, we produced VEGF_{179a} and VEGF_{179b} variants that are identical to VEGF_{189a} and VEGF_{189b}, excepted for the absence of the 10 amino acids coded by E5 (Fig 50A).

Their characterization is ongoing. As expected, both isoforms are mainly found associated with the cell layer in normal culture conditions but they can be released in the culture medium in the continuous presence of heparin (Fig 50B). For each variant 2 to 3 major products were identified by Western Blot: the full size glycosylated product (\approx 31 kD) and lower molecular weight bands (\approx 22 kD and 20 kD) likely corresponding to cleaved products. The size of these products together with the fact that only the native form of VEGF_{179b} is recognized by VEGF_{xxx}b antibody (Fig 50C) suggest that cleavages occur in the E6a-derived basic domain. We are currently developing a procedure, combining Avastin-Sepharose and Heparin-Sepharose Chromatography, for purifying the full-size VEGF_{179a} and VEGF_{179b} as illustrated in Fig 50D.

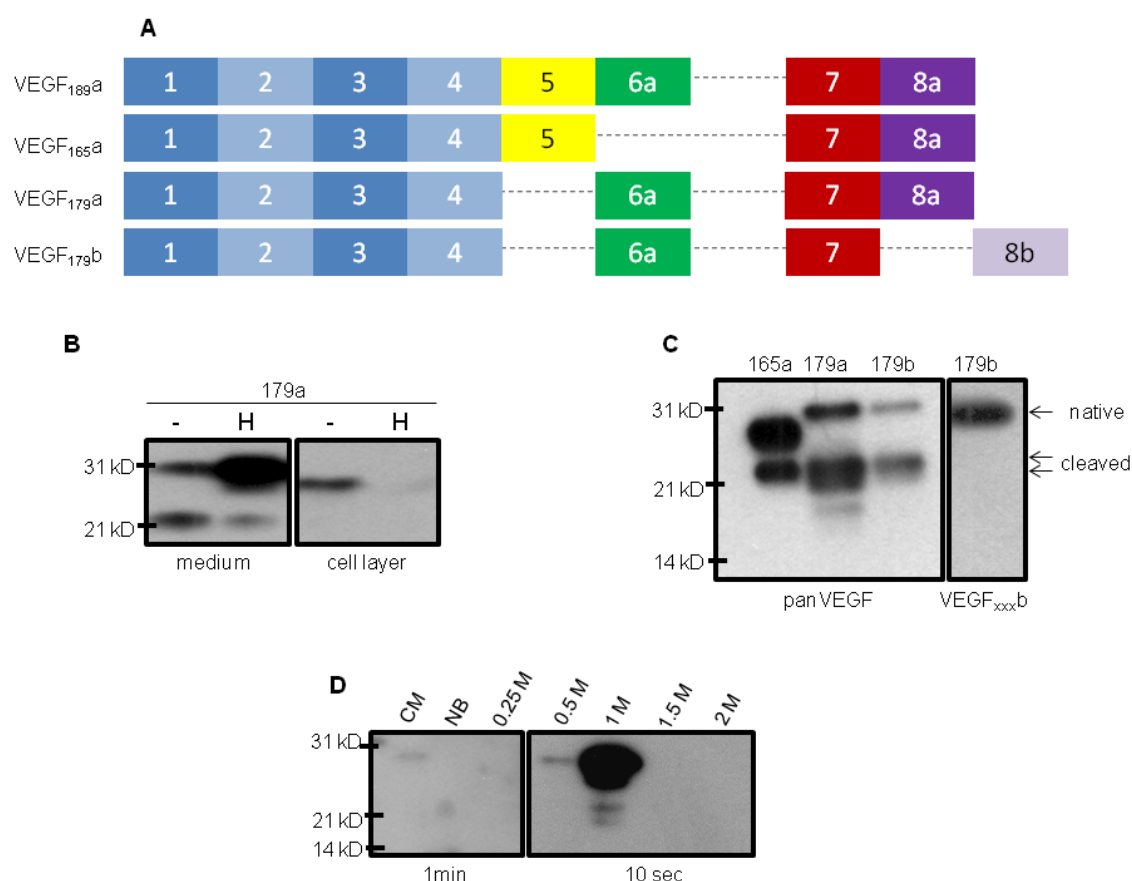


Figure 50 : Production and purification of VEGF_{179a} and VEGF_{179b}

(A) VEGF_{179a} and VEGF_{179b} can be considered as VEGF₁₈₉ variants lacking the E5-encoded sequence. (B) Western blot analyses (panVEGF antibody) of conditioned medium (left panel) and cell layer (right panel) of HEK cells expressing VEGF_{179a} cultured in presence (H) or absence (-) of heparin (50µg/ml). (C) Western blot analyses of conditioned medium of HEK cells expressing VEGF_{165a}, VEGF_{179a} or VEGF_{179b} using panVEGF antibody (left panel) and VEGF_{xxx}b antibody (right panel). VEGF_{179a} and VEGF_{179b} are both detected as a full size glycosylated product (≈30 kD) and smaller products probably resulting from proteolytic cleavage in the E6a-encoded domain (≈22 kD and 20 kD). (D) Western-blot (panVEGF antibody) of the different fractions collected during a Heparin Sepharose Chromatography of the conditioned medium from HEK293 expressing VEGF_{179a}. Two exposures times (10 sec and 1 min) are shown. The cleaved products did not bind while the full size VEGF_{179a} was eluted at 1 M NaCl. 165a: VEGF_{165a}, 179a: VEGF_{179a}, 179b: VEGF_{179b}, CM: Conditioned Medium, NB: Not Bound fraction.

Effect of VEGF_{179a} and VEGF_{179b} *in vivo*

Besides the still ongoing *in vitro* characterizations of VEGF_{179a} and VEGF_{179b}, they were also used *in vivo* in the model of HEK293 cells implanted in nude mice. After 3 weeks, tumours expressing VEGF_{179a} or VEGF_{179b} had the same general appearance as tumours expressing VEGF_{165a} and VEGF_{165b}, respectively (Fig 51A). Immunostaining of endothelial cells (CD31, Fig 51B) or smooth muscle cells /pericytes (α-SMA, Fig 51C) was in agreement with the macroscopic observations. The vascular network consisted in enlarged vessels

covered by α -SMA positive cells for VEGF_{179a} and VEGF_{165a} while vessels were much smaller and immature for VEGF_{179b} as also observed for VEGF_{165b}.

Altogether these data show that the presence of the E6a-encoded domain does not modify the VEGF-induced angiogenesis, at least in this model.

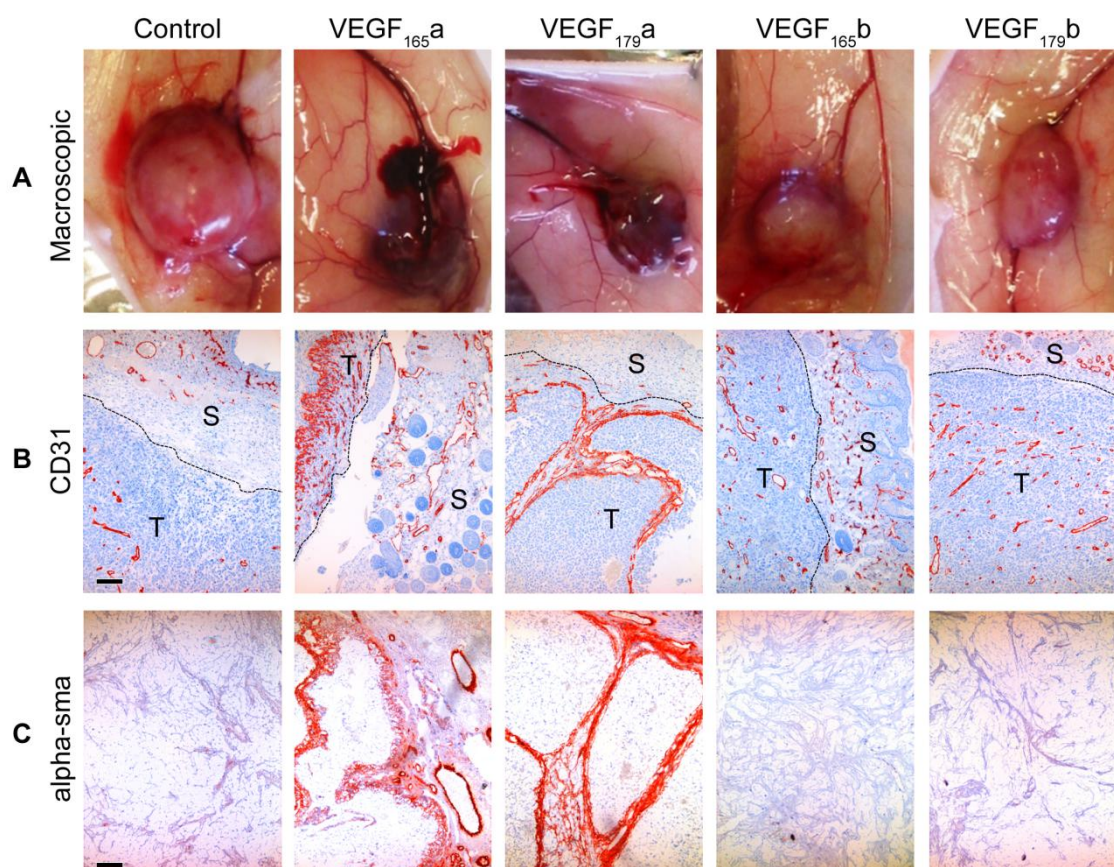


Figure 51 : *In vivo* tumour angiogenesis induced by VEGF_{179a} and VEGF_{179b}

Two millions HEK293 cells, transfected with the empty vector (control) or expressing different VEGF variants, were mixed with Matrigel and injected in the flanks of nude mice. In this experiment, tumours expressing VEGF_{165a} or VEGF_{165b} were used as reference controls for VEGF_{179a} and VEGF_{179b}, respectively **(A)** Macroscopic view of the tumours obtained in each group. Control (n=5), VEGF_{165a} (n=6), VEGF_{165b} (n=6), VEGF_{179a} (n=4), and VEGF_{179b} (n=6). **(B)** CD31 immunostaining showing the presence of blood vessels in the tumour (T) and the adjacent skin (S). **(C)** α -SMA immunostaining showing the presence of pericytes (scale bar = 100 μ m).

IX-2 VEGF_{111a}-R1m

As VEGF-R1 is considered as a decoy receptor for VEGF at endothelial cell surface and, consequently, as an inhibitor of VEGF signalling in angiogenesis, we designed, produced and purified VEGF_{111a}-R1m, a VEGF_{111a} mutated at the three critical sites for VEGF-R1 binding (Asp⁶³ mutated in Ala, Glu⁶⁴ in Ala and Glu⁶⁷ in Ala). In a preliminary experiment, VEGF_{111a}-R1m significantly triggered VEGF-R2 and ERK1/2 phosphorylation as compared

to a negative control (not illustrated). This showed that the variant was active on angiogenesis at least *in vitro*. The effects of VEGF₁₁₁a-R1m and VEGF₁₁₁a were also compared in the HEK293 tumour model. VEGF₁₁₁a-R1m displayed the same pattern of vascularization as the native VEGF₁₁₁a with the formation in the adjacent skin of the tumour of a dense network of small blood vessels (Fig 52), not covered by pericytes as highlighted by an absence of staining with an anti- α -SMA immunostaining (not illustrated).

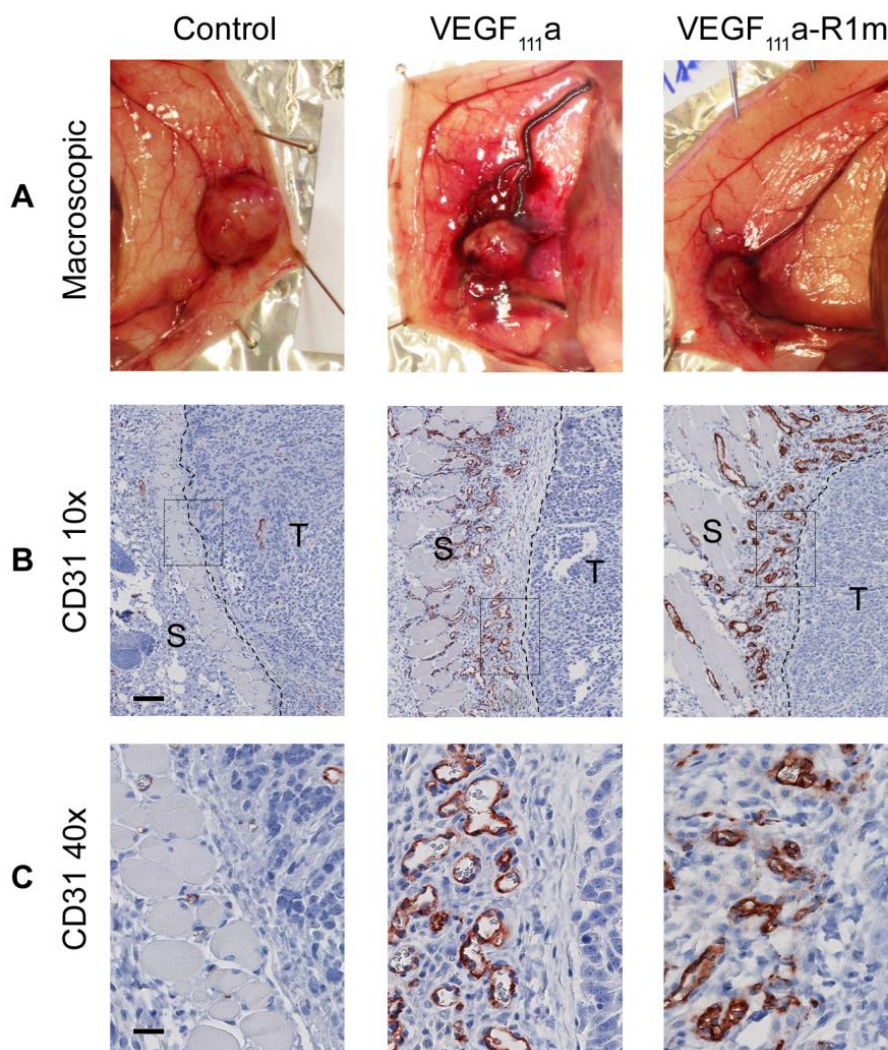


Figure 52 : *In vivo* tumour angiogenesis induced by VEGF₁₁₁a-R1m

Two millions HEK293 cells, transfected with the empty vector (control) or expressing the VEGF variants, were mixed with Matrigel and injected in the flanks of nude mice. **(A)** Macroscopic views of the tumours obtained in each group. Control (n=4), VEGF₁₁₁a (n=4), VEGF₁₁₁a-R1m (n=6). **(B)** CD31 immunostaining in the tumour (T) and the adjacent skin (S) (scale bar = 100 μ m). Black lined rectangles delineate the areas of the sections represented in **(C)** at higher magnification (scale bar = 25 μ m).

XI- Endocan as a marker of the activity of the VEGF variants

Although the VEGF variants display specific effects *in vitro* and *in vivo*, it is not clear yet how regulations operating through a single receptor (VEGF-R2) can be responsible for such diverse responses. Endocan is a dermatan sulphate proteoglycan that promotes the activity of HGF (Sarrazin et al., 2006). It has been reported to be induced by VEGF in endothelial cells (Rennel et al., 2007). As a proteoglycan, endocan could also influence the cell response to VEGF by functioning as a co-receptor displaying preferential affinities for some specific VEGF variants. We therefore evaluated the induction of endocan secretion by our variants as an additional tool for comparing their biological activity. Its affinity towards VEGF receptors and co-receptors is currently under investigation.

XI-1 Stimulation of endocan synthesis by VEGF

HUVEC were treated with 1nM of VEGF variants for 24h or 48h. Endocan concentrations in the conditioned medium were quantified by ELISA (Fig 53). VEGF_{165b} did not stimulate endocan secretion while VEGF_{165a} was the most active (2.6-fold stimulation). Lower but still significant stimulations were observed for other variants (2-fold stimulation). Similar trends were observed after 48 hours (not shown) and were in good correlation with the proliferation assay data (Fig 38).

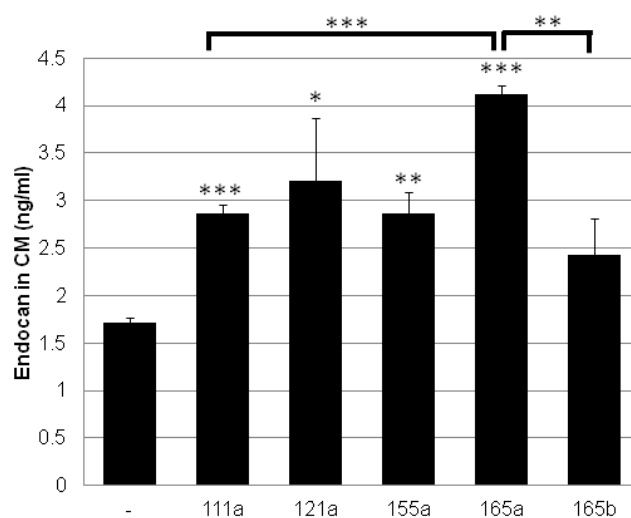


Figure 53 : Secretion of endocan from endothelial cells treated with VEGF variants

HUVEC were treated for 24h with 1nM of VEGF variants. Endocan secreted in the conditioned medium (CM) was quantified by ELISA. 111a: VEGF_{111a}, 121a: VEGF_{121a}, 155a: VEGF_{155a}, 165a: VEGF_{165a}, 165b: VEGF_{165b}. * $p < 0.05$, ** $p < 0.01$ and *** $p < 0.001$ (t-test of Student).

XI-2 Binding of Endocan to VEGF-receptors and co-receptors

By SPR analyses, endocan was found to bind with high affinity to heparin (Fig 54) but not to VEGF-R2 or NRP1 (not illustrated). Binding was never observed when the two constituents of endocan, the protein core and the dermatan sulphate side chain, were injected separately. Future studies will evaluate the binding of VEGF variants on endocan and the effect of endocan on the formation of large complexes involving heparin, VEGF-R2 and NRP1.

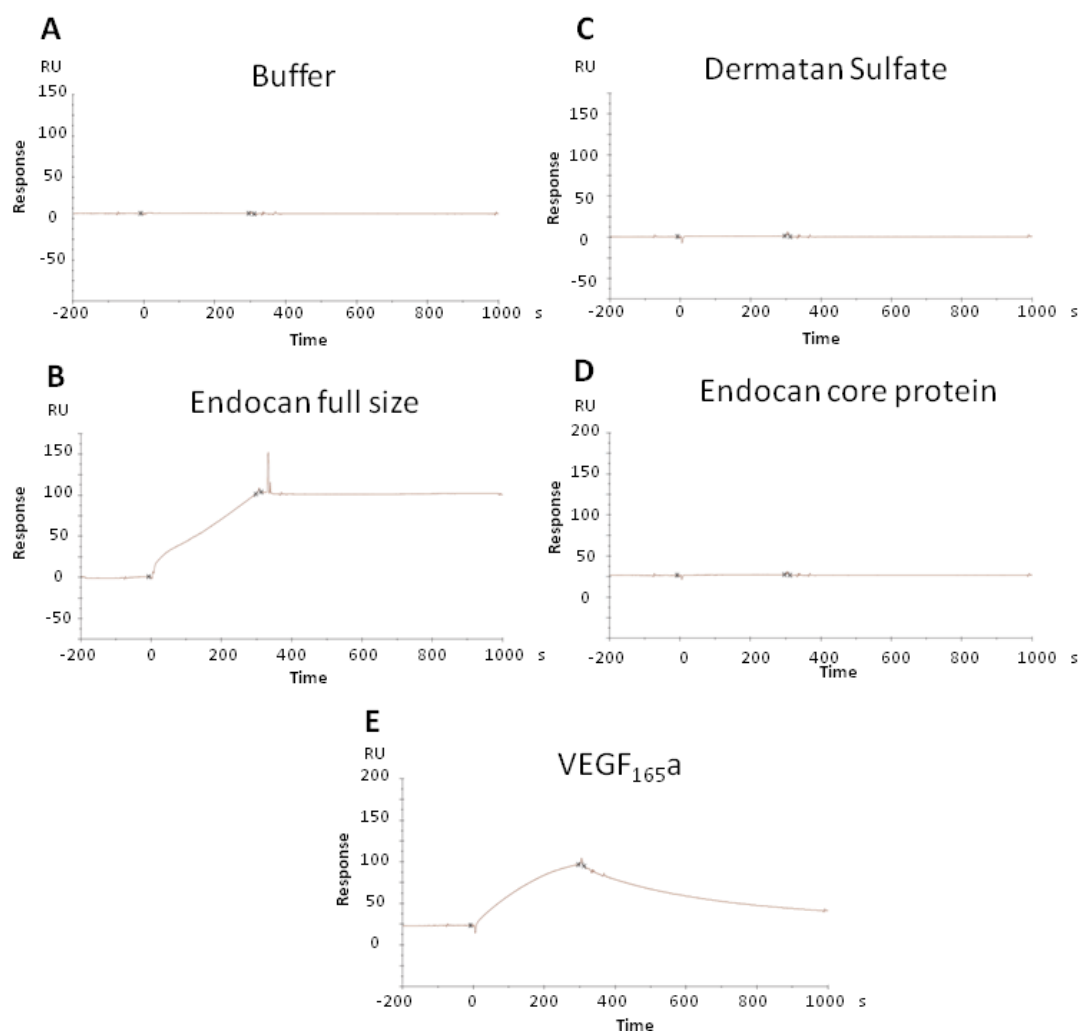


Figure 54 : Binding of endocan to heparin

Binding of endocan (40 nM) to heparin was measured by Surface Plasmon Resonance. **(A)** HBS-EP buffer, **(B)** Endocan full size, **(C)** dermatan sulfate side chain alone, **(D)** endocan core protein alone **(E)** or VEGF_{165a} (40nM), used as a positive control, were injected for ~250 seconds followed by injection of HBS-EP buffer in order to visualize the dissociation rate. RU: Response in arbitrary units.

GENERAL DISCUSSION

VEGF is considered as a promising molecule for treating ischemic diseases whereas inhibiting its activity has found beneficial therapeutic applications in ocular diseases and cancers. VEGF is produced as several different isoforms resulting from a dynamic mechanism of alternative splicing of the primary transcript. The roles of the amino-terminal domains encoded by the exons 1 to 4 are well-established. They contain the signal peptide, dimerization and glycosylation sites as well as the binding domains to VEGF-R1 and VEGF-R2. The functions of the C-terminal domains are also becoming more characterized. For example, a limited proteolytic processing (mainly in the E5-encoded sequence) is required for the release and the bioavailability of the VEGF variants firmly immobilized in the ECM by their E6a-encoded domain (Keyt et al., 1996a; Lee et al., 2005; Plouet et al., 1997). The C-terminal part of VEGF is also required for interactions with NRP1. A role for the 6 amino acids encoded by E8a has been demonstrated but potential participation of other domains are still controversial (Cebe-Suarez et al., 2008; Cebe Suarez et al., 2006). An additional, but possibly related, controversy concerns the activity of the VEGF isoforms produced by differential splicing of E8 into E8a or E8b, the latter resulting in a VEGF subfamily referred to as VEGF_{xxx}b (Bates et al., 2002; Harper and Bates, 2008). Although these variants were largely reported as anti-angiogenic (Bates et al., 2002; Hua et al., 2010; Rennel et al., 2009b; Woolard et al., 2004), a recent publication reports a weak pro-angiogenic effect of VEGF₁₂₁b and VEGF₁₆₅b (Catena et al., 2010).

To explore the functions of the C-terminal part of the VEGF-A protein, we generated and characterized the properties of a set of variants translated from mRNA containing exons 1-4, a combination of exons 5 to 7 and exon 8a or exon 8b: VEGF₁₁₁a, VEGF₁₁₁b, VEGF₁₂₁a, VEGF₁₂₁b, VEGF₁₅₅a, VEGF₁₅₅b, VEGF₁₆₅a, VEGF₁₆₅b, VEGF₁₇₉a and VEGF₁₇₉b. VEGF₁₆₅a and VEGF₁₂₁a are the two most abundant pro-angiogenic isoforms (Ferrara, 2010) while VEGF₁₆₅b and VEGF₁₂₁b are the two most largely described endogenous VEGF_{xxx}b isoforms. VEGF₁₁₁a is the shortest isoform produced by alternative splicing that still contains the binding sites for VEGF-R1 and VEGF-R2 (Mineur et al., 2007). The other variants (VEGF₁₁₁b, VEGF₁₅₅a, VEGF₁₅₅b, VEGF₁₇₉a and VEGF₁₇₉b) have not been observed endogenously but were designed here as tools to investigate the functions of the different domains and to evaluate their potential therapeutic interest. All these variants possess the Cys residues required for the dimerization of VEGF and the Cystine knots that participate in the correct folding of the protein (Iyer and Acharya, 2011; Muller et al., 2002). To reduce the possibility of inappropriate folding and/or glycosylation, two features that could alter the properties of our recombinant growth factors, the different VEGF isoforms were produced in human cells. The data obtained during this work have been summarized (table 8) for

facilitating the understanding of the following discussion. VEGF_{111a}, VEGF_{111b}, VEGF_{121a}, VEGF_{121b}, VEGF_{155a}, VEGF_{155b}, VEGF_{165a} and VEGF_{165b} were systematically compared for their physical interactions with receptors and co-receptors and their biological effect, in cell culture and *in vivo*. VEGF_{179a} and VEGF_{179b} were produced more recently, which explain why their characterization is only partial. The discussion will address more specifically new insights provided by our work concerning the function of the C-terminal domain of VEGF-A isoforms.

I- The domain encoded by E8a cooperates with upstream sequences for NRP1 and heparin binding

NRP1 is a co-receptor for several factors, including VEGF. The formation of a complex between VEGF-R2, VEGF and NRP1 strengthens VEGF-R2 phosphorylation, downstream signalling pathways and angiogenesis (Soker et al., 2002). Amongst the most abundant isoforms, VEGF_{165a} (E1-4, 5, 7, 8a) has been reproducibly shown to bind to NRP1 while VEGF_{121a} (E1-4, 5, 8a) was initially described as unable to stably interact (Herve et al., 2008). This apparent lack of high affinity binding has been later attributed to partial degradation of the E8a-encoded 6 amino acids sequence (CDKPRR:Cys-Asp-Lys-Pro-Arg-Arg) (Cebe-Suarez et al., 2008; Pan et al., 2007a; Parker et al., 2012).

By Surface Plasmon Resonance (SPR) we showed here a binding of VEGF_{165a} (E1-5, 7, 8a), VEGF_{121a} (E1-5, 8a) and VEGF_{155a} (E1-4, 7, 8a) on NRP1 and the absence of affinity of all the VEGF_{xxx}b isoforms. As the synthetic VEGF₁₅₉ variant (exons 1-5, 7) is also unable to bind (Cebe Suarez et al., 2006), it strongly suggests that the absence of affinity of the VEGF_{xxx}b isoforms for NRP1 is due to the absence of the CDKPRR sequence (E8a) and not caused by the presence of the E8b-encoded SLTRKD (Ser-Leu-Thr-Arg-Lys-Asp) sequence. Interestingly, VEGF_{111a} (E1-4, 8a) has no affinity for NRP1, although it possess the CDKPRR terminal sequence, demonstrating that the E8a-encoded sequence alone is not sufficient and must cooperate with another domain for efficient binding. The E5-encoded sequence is probably involved as this 10 amino acids domain represents the only difference between VEGF_{111a} and VEGF_{121a}. In support of this hypothesis, we demonstrated that a peptide mimicking the E5-encoded sequence (R8R) blocks the binding of VEGF_{165a} to NRP1, reduces the activation of VEGFR2-ERK1/2 pathway in PAEC-R2-NRP1 to a level similar to that observed in PAEC-R2 and partly inhibits the VEGF_{165a}-induced proliferation of HUVEC. By contrast, VEGF_{155a} does not possess this domain but can bind NRP1, although with a slower association rate as compared to VEGF_{165a} and VEGF_{121a}, suggesting a further cooperation between E8a and E7-encoded sequences.

Table 6 : Summary of the properties of the different VEGF isoforms

	Exons	Binding to			Formation of complex	Resistance to plasmin	Signaling			Proliferation	In vivo angiogenesis		Vessel permeability	
		VEGF-R2	NRP1	Heparin			PAEC-R2	PAEC-R2-NRP1	HUVEC		HUVEC	Intra-tumoral	Extra-tumoral	Local
VEGF_{111a}	E1-4; E8a	Yes	-	-	-	Yes	+++	+++	++	++	-	+++	+++	+++
VEGF_{111b}	E1-4; E8b	Yes	-	-	-	Yes	+++	+++	++	++	-	+++	+++	+++
VEGF_{121a}	E1-4; E5; E8a	Yes	Yes	-	-	-	+++	+++	++	++	+++	++	+++	-
VEGF_{121b}	E1-4; E5; E8b	Yes	-	-	-	Yes	+++	+++	++	++	-	-	-	-
VEGF_{155a}	E1-4; E7-8a	Yes	Yes	Yes	Yes	-	+/-	+	+	++	++	+/-	++	-
VEGF_{155b}	E1-4; E7-8b	Yes	-	-	-	-	+/-	+/-	+/-	-	+	+	-	-
VEGF_{165a}	E1-4; E5; E7-8a	Yes	Yes	Yes	Yes	-	++	+++	+++	+++	+++	+	+++	-
VEGF_{165b}	E1-4; E5; E7-8b	Yes	-	-	-	-	+/-	+/-	+/-	-	+	+	-	-
VEGF_{179a}	E1-4; E6a; E7-8a	nd	nd	Yes	nd	nd	nd	nd	nd	nd	+++	+	nd	nd
VEGF_{179a}	E1-4; E6a; E7-8b	nd	nd	nd	nd	nd	nd	nd	nd	nd	+	+	nd	nd

E: Exon ; - : Negative ; +/- : Low ; + : Medium ; ++ : High ; +++ : Very High; nd: not determined

NMR studies have shown that an intramolecular disulfide bridge is formed between Cys¹⁶⁰ (encoded by E8a) and Cys¹⁴⁶ (encoded by E7) in VEGF_{165a}, causing a specific folding that brings the KPRR basic C-terminal sequence close to other basic residues encoded by E7 (Grunewald et al., 2010). A recent publication (Parker et al., 2012) reports that the E8a encoded C-terminal R is crucial for NRP1 binding and that the E7-derived sequence allows additional interactions that are however not essential since VEGF_{121a} can bind NRP1. In the light of our results, we suggest that the maximal direct interaction between VEGF and NRP1 involves three domains. The E8a-encoded 6 amino acids are crucial but need to cooperate with the E5 and/or the E7 sequences (Fig 52) to adopt an optimal 3D-structure. Such cooperation between these three domains are likely to participate in the specificity of the effects induced by the different VEGF isoforms.

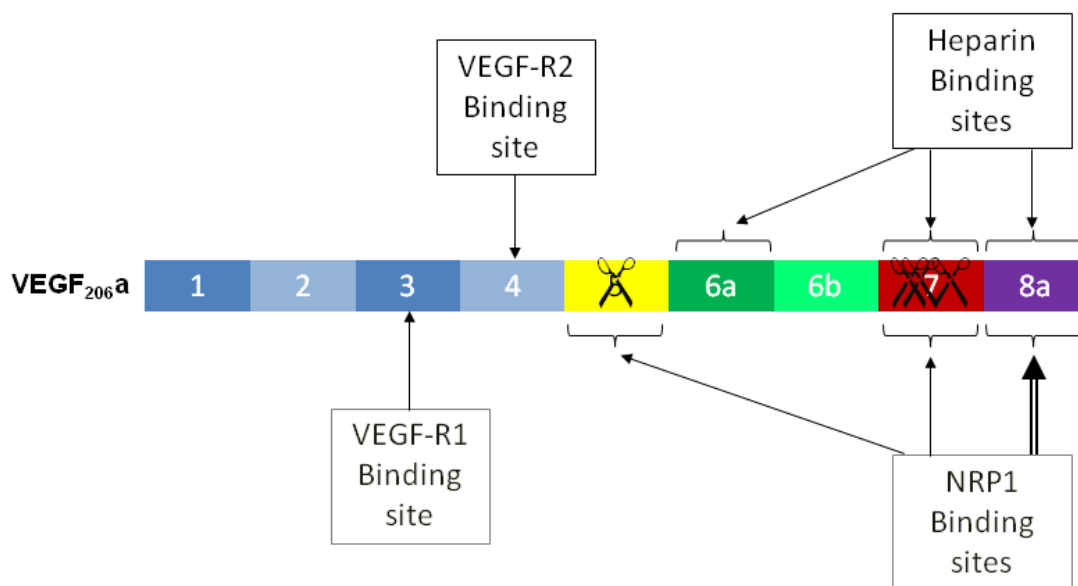


Figure 55 : Roles of the exon-encoded domains of VEGF for (co-)receptors binding and susceptibility to cleavage by plasmin

This drawing is based on previous publications and on SPR studies performed during this work. More specifically, we have demonstrated that the E5-encoded sequence is crucial for efficient binding to NRP1 and that maximal interactions require the presence of the domains encoded by E5, E7 and E8a. Similar cooperation have been demonstrated for efficient heparin binding. It also shows preferential sites of proteolytic degradation (black scissors). This work confirmed that plasmin cleaves VEGF in E5-encoded domain and highlights that in absence of this sequence, additional sites of cleavage can be found in E7 encoded sequence.

The use of heparin *in vitro* allows mimicking the effect of HSPG found in the extracellular matrix. A strong binding of VEGF_{189a} and VEGF_{206a} to heparin and HSPG occurs through the highly basic E6a-encoded domain (Houck et al., 1991). Such strong affinity was also observed here for VEGF_{179a} for example. As this domain is not present in the 8 variants extensively characterized in this work, this gave us the opportunity to investigate the potential role of domains with lower affinities. We showed that only variants possessing the E7+E8a domains (VEGF_{165a} and VEGF_{155a}) are able to bind to heparin (Fig 52). This is in agreement with a lack of retention of VEGF_{165b} on heparin-Sepharose (Cebe Suarez et al., 2006) or on HSPG coated nitrocellulose filters (Kawamura et al., 2008b). These data indicate that E7 and E8a both contribute to heparin binding of VEGF. A possible explanation relies on the formation of the disulfide bridge between Cys¹⁴⁶ and Cys¹⁶⁰ and on the proper positioning of basic residues present in E7 and E8a. Alternatively, the SLTRKD sequence from E8b, especially the acidic aspartic acid terminal residue, might prevent the interaction between heparin and the basic residues oriented at the surface of the E7 encoded domain.

In the SPR assays, injection of VEGF_{165a} in presence of heparin drastically increased the binding to NRP1 as compared to injection of VEGF_{165a} alone. Conversely injection of VEGF_{165a} in presence of soluble NRP1 drastically enhanced the binding to heparin as compared to injection of VEGF_{165a} alone. These results are in agreement with a model describing two types of VEGF_{165a}-NRP1 interaction, one being direct and the other bridged by heparin (Vander Kooi et al., 2007). Both of them implicate the E7-E8a domain and may synergize. Since the effect of heparin on the binding of VEGF_{155a} to NRP1 is much more modest than the effect observed for VEGF_{165a}, it strongly suggests that the highly basic E5-derived domain is also involved. It remains to determine however whether this domain interacts with NRP1 independently or in synergy with the E7/E8a encoded sequence for forming a large negatively charged pocket.

II- VEGF variants display diverse relative activities in different models due to dynamic interactions with receptors and co-receptors

The specific effects of the different VEGF variants were extensively explored at a cellular level in HUVEC and Porcine Aortic Endothelial Cells (PAEC) expressing VEGF-R1 only (PAEC-R1), VEGF-R2 only (PAEC-R2), NRP1 only (PAEC-NR1) or both VEGF-R2 and NRP1 (PAEC-R2-NRP1). PAEC-R1 and PAEC-NRP1 do not respond significantly to VEGF. When only VEGF-R2 is expressed (PAEC-R2), short variants (VEGF_{111a/b} and VEGF_{121a/b})

are systematically and significantly more active than VEGF_{165a}. This difference no longer exists in PAEC-R2-NRP1, illustrating the importance of NRP1 in the full activity of VEGF_{165a}. In HUVEC, VEGF_{165a} is the most active in terms of intracellular signalling and cell proliferation.

These apparently surprising observations can be explained by considering the dynamic interactions between the VEGF variants and their receptors and co-receptors. For clarity reasons, VEGF_{111a} and VEGF_{165a} will be only considered here although the described mechanisms would affect similarly the activity of the other VEGF variants. As predicted by computational models (Mac Gabhann et al., 2006; Mac Gabhann and Popel, 2005, 2007a, b), the overexpression of recombinant VEGF receptors at the PAEC membrane induces a “Dynamic Pre-Dimerization” process in absence of any ligand (Fig 53A), while in more physiological situations most of these receptors are monomeric (Mac Gabhann and Popel, 2007a).

In PAEC-R2 (Fig 53A), the higher activity of VEGF_{111a} as compared to VEGF_{165a} probably results from two different features. In absence of the E5-E7 encoded regions, VEGF_{111a} has no affinity for the ECM, which explains higher diffusibility and bioavailability. Moreover, its small size should improve its accessibility in the binding pockets present in the pre-dimerized receptors. This is supported by SPR data evaluating the binding of VEGF variants on VEGF-R2. In this model where VEGF-R2 are pre-dimerized because of the Fc fragments, VEGF_{111a} has a higher association rate as compared to VEGF_{165a} while the K_d are similar. This strongly suggests that a limiting step is accessibility to the binding pocket within the dimer.

In PAEC-R2-NRP1 (Fig 53B), VEGF-R2 is expected to be also pre-dimerized as in PAEC-R2. However the presence of NRP1 increases the relative activity of VEGF_{165a} by acting as a co-receptor (Becker et al., 2005; Soker et al., 2002) while it does not affect the signals triggered by VEGF_{111a}, explaining why the signalling by both variants is now similar.

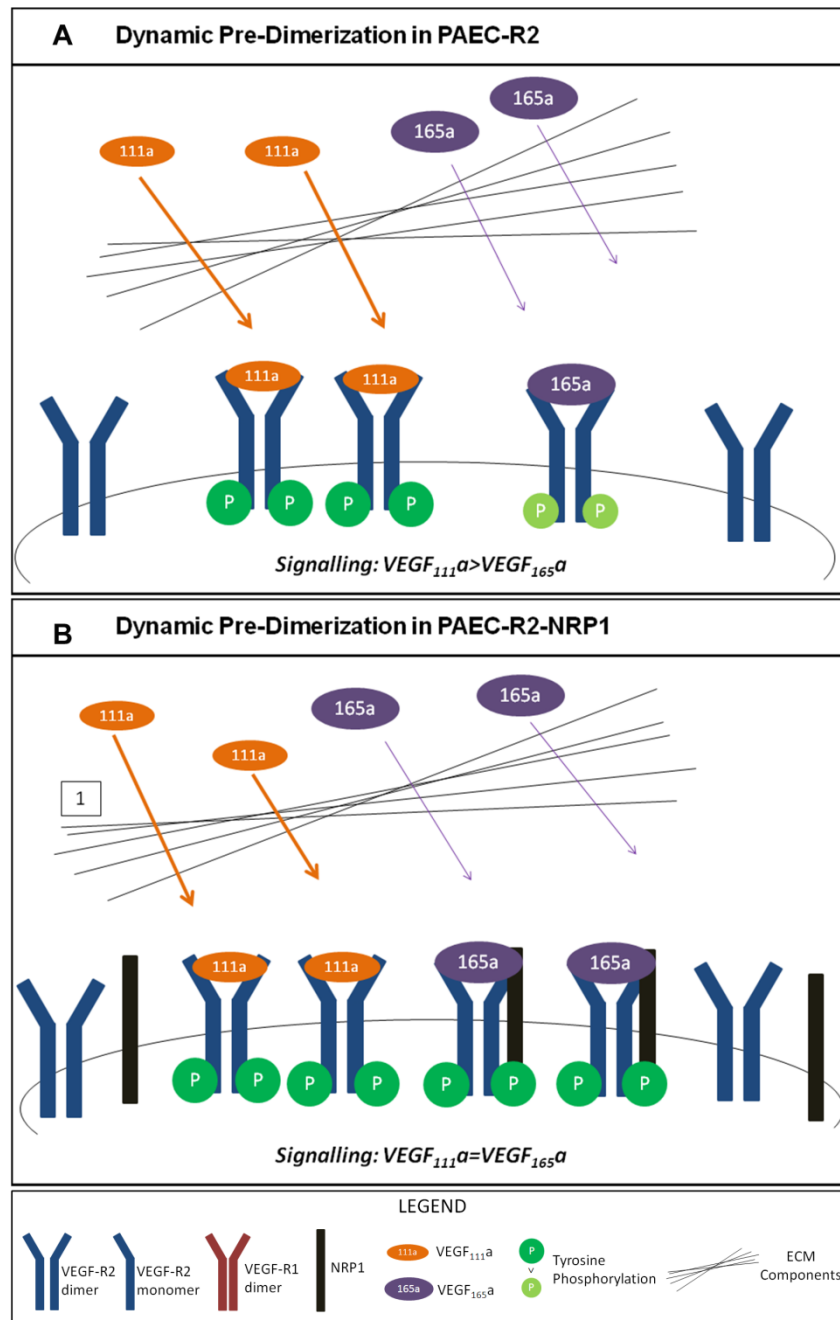


Figure 56 : Modelisation of VEGF-R2 activation by VEGF_{111a} and VEGF_{165a} in PAEC-R2 (A) and PAEC-R2-NRP1 (B)

According to *in silico* models, a high number of VEGF-R2, as found at the surface of PAEC-R2 and PAEC-R2-NRP1, should result in a “Dynamic Pre-Dimerization” process. As VEGF_{111a} has much more limited interactions with the ECM or the cell surface components than VEGF_{165a}, it can bind more rapidly to pre-dimerized VEGF-R2. Its small size could also favour its interactions with the pre-dimerized binding pockets. These two features would explain the high activity of VEGF_{111a} in PAEC-R2. **(B)** The additional presence of NRP1 is not expected to modify the pre-dimerized process. However, it should favour the “presentation” of VEGF_{165a}, but not of VEGF_{111a}, to VEGF-R2, explaining the increased activity of VEGF_{165a} only.

The situation is completely different in HUVEC (Fig 54) because several receptors and co-receptors (VEGF-R1, VEGF-R2, NRP1, NRP2 and HSPG) are expressed at the cell surface, all of them at more physiological levels than when expressed as recombinant proteins (Herve et al., 2008). In these cells, VEGF-R1 and VEGF-R2 are not pre-dimerized, which should strongly reduce problems related to accessibility, mainly for the longer isoforms. The presence of NRP1, and potentially NRP2, at the cell surface has several consequences, either clearly demonstrated or suggested by our data and other publications (Favier et al., 2006; Soker et al., 1998). NRP1 favours the binding of VEGF_{165a} on VEGF-R2 monomers, which induces dimer formation and downstream signalling (Fig 54A). Such mechanism is not possible for VEGF variants that do not bind NRP1, such as VEGF_{111a}. As another potential mechanism, it was also reported that VEGFR2-VEGF_{165a}-NRP1 complexes are internalized in specific endosomes (characterized by the presence of Rab 11) where they continue to activate downstream pathways (Ballmer-Hofer et al., 2011). In absence of NRP1, the endosomal trafficking is modified and degradation occurs more rapidly, which suppresses the VEGF-induced signalling.

The presence of VEGF-R1 might have also important consequences (Fig 54B). Although it has high affinity for all the tested VEGF variants (SPR data) it does not induce a significant downstream signalling upon VEGF binding (PAEC-R1 in culture). At the surface of HUVEC, it sequesters VEGF isoforms, reducing their bioavailability for VEGF-R2. While it should affect similarly the effect of the different VEGF variants, this is not the case because of the presence of NRP1. It has been shown indeed that NRP1 can decrease the binding to VEGF-R1 of VEGF_{165a} but not of VEGF_{121a} and probably not of VEGF_{111a} (Fuh et al., 2000). It could also favour the release of VEGF_{165a} already bound to VEGF-R1, which would increase its availability for VEGF-R2. Although not tested specifically here, it is most likely that the release from VEGF-R1 by NRP1 is directly related to the affinity of VEGF variants for NRP1. These dynamic and finely tuned interactions involving several molecules would explain some apparent discrepancies between data obtained in different types of models, such as short term VEGF-R2 phosphorylation and cell proliferation for example. For *in vivo* analyses, especially regarding clinical applications, it underlines also the critical need of studying the expression and the effect of individual variants rather than considering them globally as VEGF-A factors having identical properties.

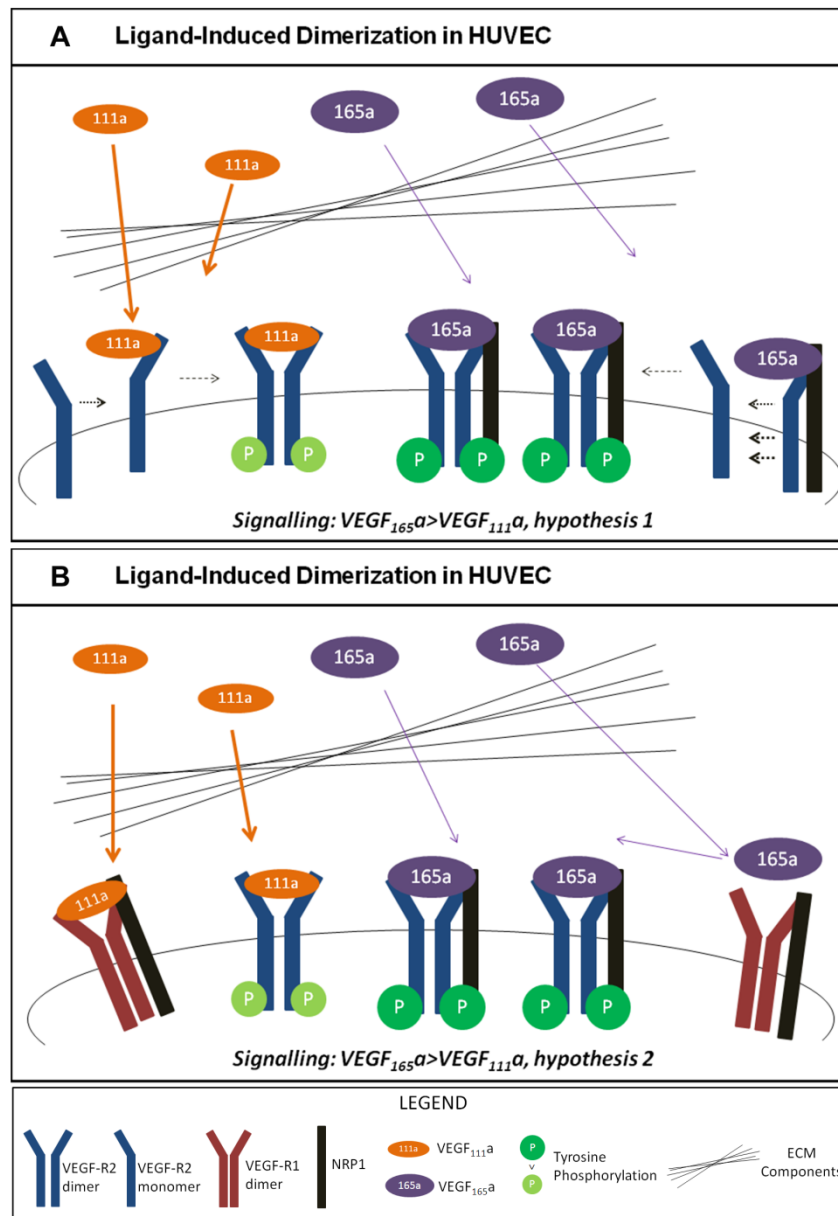


Figure 57 : Modelisation of VEGF-R2 activation by VEGF_{111a} and VEGF_{165a} in HUVEC

As compared to the different PAEC models, HUVEC express at their surface a more physiological number of VEGF-R1, VEGF-R2 or NRP1. The expression of NRP2 and of endothelial cell specific proteoglycans is not illustrated here although it is expected to fine tune the response of HUVEC to VEGF. Several non mutually exclusive mechanisms could explain the stronger effects of VEGF_{165a} in these cells as compared to other isoforms, including VEGF_{111a}. Two are illustrated here. **(A)** As VEGF-R2 is monomeric, the small size of VEGF_{111a} is no longer an advantage for binding. Moreover, the presence of NRP1 should favour the binding of VEGF_{165a} on VEGF-R2, which should stimulate its dimerization and trans-phosphorylation, and finally downstream signalling pathway. **(B)** It has been reported that NRP1 could reduce interactions between VEGF-R1 and VEGF_{165a}, making it more available for VEGF-R2 binding and signalling. This mechanism is unlikely for VEGF_{111a} as it does not bind to NRP1.

III- The E8b-encoded sequence is not sufficient to determine the anti-angiogenic activity of VEGF_{xxx}b variants

The effect of substituting the E8a-encoded sequence by its corresponding E8b counterpart was carefully investigated. The activity of the longest isoforms (VEGF₁₅₅b and VEGF₁₆₅b) was strongly affected by the substitution, whatever the cell model and independently of the presence of NRP1. These two VEGF variants were also able to prevent the VEGF₁₆₅a-induced proliferation of HUVEC, probably by a competition for VEGF-R2 as suggested by SPR data. It has been suggested that VEGF₁₆₅b induces an incorrect relative positioning/orientation of the two VEGF-R2 molecules to form a functional dimer, which would prevent their efficient transphosphorylation (Kawamura et al., 2008b). This hypothesis is confirmed here since VEGF₁₆₅b binds to VEGF-R2 (SPR) but is unable to induce a robust phosphorylation of the VEGF-R2 and the downstream intracellular signalling factors.

In sharp contrast, VEGF₁₂₁b and VEGF₁₁₁b were pro-angiogenic *in vitro*, demonstrating that the presence of the E8b domain alone is not sufficient to convert an endothelial activating VEGF variant into an inhibitory factor. This observation does not correlate with previous data describing the anti-angiogenic properties of VEGF₁₂₁b (Rennel et al., 2009b), but it is worth mentioning that these experiments were essentially performed in other models, including cell migration or tumour formation by cells expressing VEGF₁₂₁b. Our *in vitro* data were validated *in vivo* in the two models of induced pathological angiogenesis in the eye that were previously used for the demonstration of the anti-angiogenic properties of VEGF₁₆₅b (Hua et al., 2010; Magnussen et al., 2010). In contrast to VEGF₁₆₅b, injection of VEGF₁₁₁b did not inhibit, and even slightly stimulated, ocular angiogenesis, confirming our *in vitro* data. It is therefore unlikely that the SLTRKD sequence encoded by E8b is by itself sufficient for the specific properties of VEGF₁₆₅b. This hypothesis is further strengthened by data showing that soluble SLTRKD peptide is not anti-angiogenic (unpublished observations, Rennel and Bates). Our data showing that VEGF₁₅₅b and VEGF₁₆₅b (and potentially VEGF₁₇₉b, as described below) have the same properties suggest that the folding of the domain formed by the E7 and E8b-encoded sequences would induce steric hindrance and lead to modification of the conformation of the VEGF dimer, which would ultimately prevent perfect VEGF-R2 dimerization and autophosphorylation (Harper and Bates, 2008). This might also explain why VEGF₁₁₁b, although possessing the SLTRKD terminal sequence, is pro-angiogenic due to the lack of the E7-derived sequence and because its size is not sufficient to interfere with receptor dimerization.

IV- Combinations of the E5, E7 and E8a/E8b-encoded domains determine vessel density and patterning *in vivo*

Subcutaneous injection of HEK293 cells provides an attractive model to evaluate the long term effects of the continuous expression of specific VEGF variants on angiogenesis (Mineur et al., 2007). Indeed, these cells express low levels of endogenous VEGF and form a tumour-like mass containing few blood vessels and growing independently of VEGF expression, which facilitates data analyses by dissociating vascularization from other features. The expression of VEGF_{165a}, VEGF_{155a} or VEGF_{121a} induced a dense vascularization of the tumor and led to the formation of enlarged blood vessels while VEGF_{111a} or VEGF_{111b} resulted in the presence of hundreds of small vessels but only in the adjacent dermis. Reasons for such differences remain to be firmly identified. It is not related to variability in protein production and receptor binding as all the variants were expressed in the tumour at similar levels and had comparable affinity for VEGF-R2. Different retention times in the Matrigel plug embedding the cells were also considered as potentially regulating the available VEGF concentration. This was evaluated *in vitro* by measuring the release of purified VEGF from a Matrigel plug immersed in culture medium. Diffusion rate was maximal for VEGF_{111a}, the equilibrium between plug and medium concentrations being observed after 2 to 4 hours. All the other tested isoforms reached equilibrium within 8-20 hours. Although the differences are significant, they are not expected to play a major role in our model of tumour angiogenesis as the duration of the entire experiment is much longer (3 weeks) and because the Matrigel plug is rapidly degraded in growing tumours. These data suggest however that VEGF_{111a} and VEGF_{111b} are able to diffuse more freely than the other isoforms and therefore to induce angiogenesis at longer distance from their site of production. This hypothesis was further evaluated *in vivo* in complementary models.

In the Miles and Miles' modified assay VEGF_{165a}, VEGF_{111a} and VEGF_{111b} induce a similar vascular permeability close to the site of injection. However the total surface of affected skin was much larger for VEGF_{111a} and VEGF_{111b} which demonstrates their capacity to diffuse at long distance in tissues *in vivo*. In another model, VEGF variants were injected intraperitoneously and subcutaneously and their blood concentrations were evaluated as a function of time. VEGF_{111a} was found at higher concentration and with a longer half-life as compared to VEGF_{165a} for example, which again illustrates its high capacity to diffuse and its reduced interactions with the extracellular environment.

The similar properties of VEGF_{111a} and VEGF_{111b} *in vivo* were expected from *in vitro* data. They further confirmed that the E8b domain alone is not sufficient to repress angiogenesis. By contrast, the weak pro-angiogenic activities of VEGF_{155b} and VEGF_{165b} in the tumoural

model were surprising as they were inactive or even inhibitors in other models. Proteolytic processing in the particular tumour environment, which is usually not observed in culture medium and in the eye (Fig 46A) (Magnussen et al., 2010), could account for this apparent discrepancy. The cleavage in the E5/E7 domains would shorten VEGF_{165b}, prevent the steric hindrance induced by the substitution of E8a by the E8b sequence and thus convert an anti-angiogenic variant into moderately pro-angiogenic processed forms (Fig 55B). The strongly limited effect of VEGF_{121b} *in vivo*, while it was pro-angiogenic in cell culture is not yet understood. Dose-response and time-course experiments performed *in vitro* do not show marked differences between VEGF_{121b} and VEGF_{121a}, VEGF_{111a} or VEGF_{111b}. Its remarkable resistance to degradation could potentially be implicated but the involved mechanisms still remain elusive.

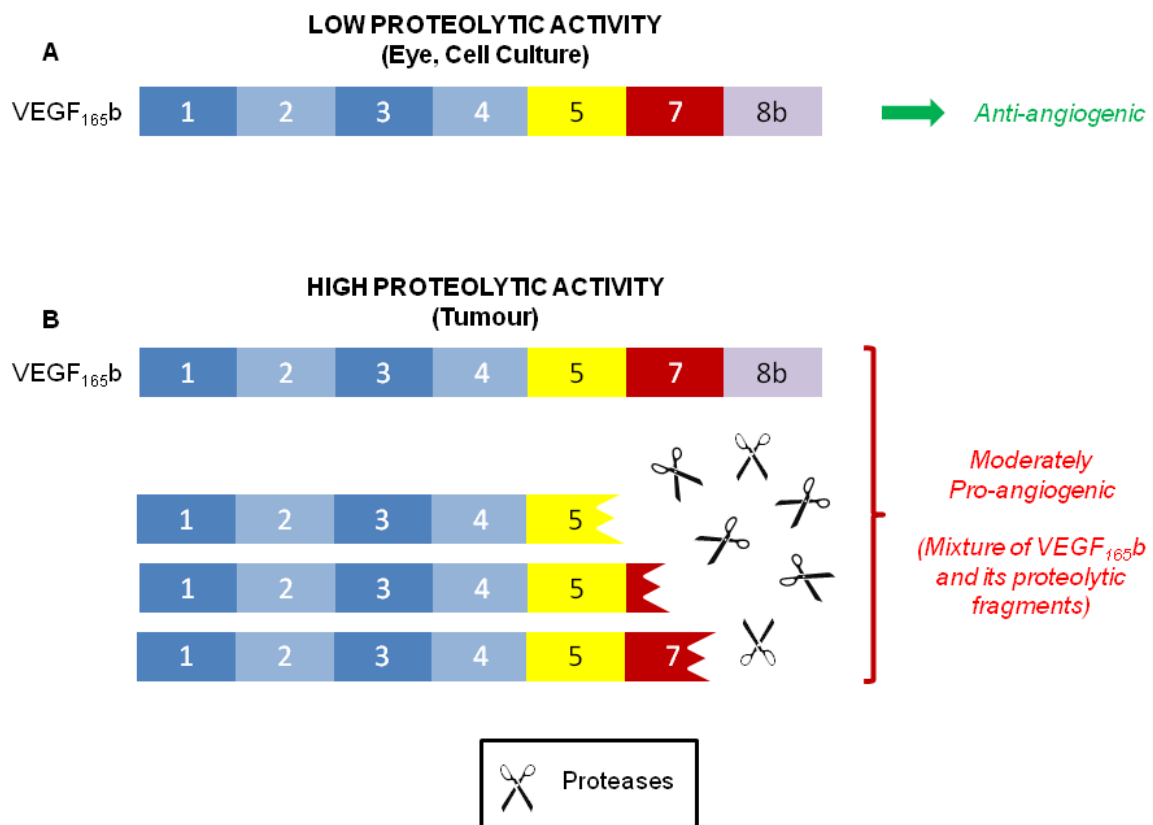


Figure 58 : The activity of VEGF_{165b} may be regulated by proteolytic processing

(A) In environments characterized by low protease activity, VEGF_{165b} is not cleaved, which preserved its anti-angiogenic function. **(B)** In presence of active proteases, such as plasmin or MMP, most of the VEGF_{165b} is processed (in the E5- and E7- derived domains) into smaller moderately pro-angiogenic fragments.

In all the experimental conditions, the blood vessels formed in or close to the tumours were lined by a continuous basement membrane and were functional as evidenced by the presence of red blood cells. However, only VEGF_{165a} and, to a much lesser extent, VEGF_{121a} and VEGF_{155a} promoted the recruitment of pericytes/alpha-SMA positive cells around the vessels. These three variants are able to bind NRP1, suggesting a differential and more sustained regulation of endothelial cells that would subsequently recruit pericytes likely by secreting PDGF-B (Hellstrom et al., 1999; Lindahl et al., 1997). It would be interesting to evaluate the PDGF-B secretion by HUVEC treated by our VEGF variants. Alternatively, a direct recruitment of pericytes by some VEGF variants might be hypothesized since these cells have been suggested to respond to VEGF_{165a} by a NRP1-VEGFR2 axis (Liu et al., 2005) and/or by a NRP1-VEGFR1-PI3K axis (Banerjee et al., 2008).

CONCLUSIONS AND PERSPECTIVES

Our work aimed at a better understanding of the functions and cooperation between the C-terminal domains of VEGF-A. Here, we provide new data demonstrating that the E5-encoded domain regulates the VEGF properties by modifying its resistance to degradation, its capacity to diffuse and its binding to NRP1. We confirmed some previously reported effects of VEGF_{xxx}b isoforms but we further showed that their anti-angiogenic properties strongly depend upon the domain organization of the VEGF molecule itself and upon the cell and tissue environment. The therapeutic use of VEGF_{xxx}b isoforms in clinic as anti-angiogenic molecules should therefore be considered in the context of isoforms resistant to degradation which could improve their effect. We have demonstrated that some VEGF variants induce the formation of small and poorly matured vessels at distance of their site of secretion while other isoforms trigger locally the formation of large vessels covered by pericytes. According to these data, we suggest also that the treatment of ischemic diseases by VEGF should probably benefit from using a combination of different isoforms synergizing for inducing a more robust angiogenesis. Among the different perspectives resulting from this work, some related fields of research seem more promising and would merit further studies.

I- Regulation of “tip”/“stalk” cells phenotype by VEGF variants

The specific vascular patterns observed *in vivo* during our work demonstrate that different VEGF variants affect differentially sprouting angiogenesis and blood vessel maturation. Today the Notch receptor/ Notch ligand pathway is identified as one of the most critical cascade regulating the “tip”/ “stalk” fate during angiogenesis.

In a preliminary experiment, we observed that VEGF_{165a}, but not VEGF_{111a}, stimulates the expression of Dll4 (a notch ligand). This could explain why VEGF_{165a} favours the formation of mature and enlarged vessels (“stalk” cell phenotype) and why VEGF_{111a} induces only poorly the Notch pathway which would shift the balance to “tips” cell phenotype and abundant sprouting. These observations should be confirmed and strengthened in other models. All the members of this regulating cascade (Notch 1 and 2; Jagged 1 and 2; Dll1 and 4) should be also evaluated simultaneously as some of them have opposing effects on angiogenesis and compete for an identical receptor, as shown for Jagged 1 and Dll4 for example (Kume, 2012). Identifying the entire regulatory pathway, from VEGF binding at the cell surface to transcriptomic modifications, responsible for such marked differences in the regulation of endothelial cell fate would be most interesting for future clinical applications. In the same context, endocan could be used as a helpful marker, as it has been reported to be more specifically produced by tip cells (Abid et al., 2006; Recchia et al., 2010; Sarrazin et al.,

2006; Strasser et al., 2010) and to be induced more efficiently by VEGF_{165a} than by the other isoforms.

II- Regulation of VSMC/pericytes by VEGF variants

In our work we have shown that maturation of blood vessels by recruitment of smooth muscle cells/pericytes is much faster and efficient with VEGF_{165a}. Several hypotheses could explain this specific effect and should be verified. As a first example, endothelial cells treated with VEGF_{165a} could express a specific pattern of growth factors (as PDGF-B) and cytokines that would, in a second step, influence the phenotype of the pericytes. As a second example, VEGF_{165a} could have a more direct effect on pericytes, either by direct signalling through NRP1 or by facilitating the formation of large complexes containing VEGF-R1 and NRP1 for instance. These hypotheses could be first evaluated by transcriptomic analyses of endothelial cells and pericytes, cultured alone or in co-culture models and treated with different VEGF variants. Production and evaluation of the effects of VEGF_{165a} mutated at the binding site for VEGF-R2 would also be useful for better defining VEGF functions related to the unique binding to NRP1, both in endothelial cells and VSMC/Pericytes.

III- Development of new VEGF variants for future clinical applications

Based on our data new types of variants with specific or improved properties could be envisaged. As a first example, modified versions of VEGF_{165b} that would be more resistant to proteolysis and/or that would possess a C-terminal domain of increasing length for interfering with VEGF-R2 dimerization would be worth to be evaluated as anti-angiogenic factors.

We have shown that VEGF_{111a} and VEGF_{111b} are pro-angiogenic and resistant to proteolysis. They are also freely diffusible which is an advantage for systemic or long distance effects. It limits however their use for local applications. Replacement of the E8a- or E8b-derived sequence by a short domain possessing affinity for cell surface or ECM components could help to solve this problem.

Besides the development of new molecules, the effects of the association of already available variants should be more extensively characterized as their complementary properties could possibly improve the treatment of ischemic diseases. Experiment using VEGF_{111a} only have been performed in several models including skin wound healing, heart infarction (in collaboration with FATH and CARD, Université Catholique de Louvain) and

ovary fragments grafting (Labied et al., 2013) (see annex 2). Some of these studies could be repeated for evaluating the benefits of using simultaneously several VEGF isoforms.

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ANNEX 1

ANNEX 2