

## CHAPTER 2

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# VEGF Receptor Signalling in Vertebrate Development

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### Abstract

The secreted glycoprotein vascular endothelial growth factor A (VEGF or VEGFA) affects many different cell types and modifies a wide spectrum of cellular behaviours in tissue culture models, including proliferation, migration, differentiation and survival. The versatility of VEGF signalling is reflected in the complex composition of its cell surface receptors and their ability to activate a variety of different downstream signalling molecules. A major challenge for VEGF research is to determine which of the specific signalling pathways identified *in vitro* control development and homeostasis of tissues containing VEGF-responsive cell types *in vivo*.

### Key Messages

- VEGF is expressed in different isoforms
- VEGF isoforms bind different subsets of cell surface receptors
- VEGF receptors activate a plethora of downstream signalling pathways
- VEGF receptors mediate different cellular effects

### Introduction

Vascular Endothelial Growth Factor A (VEGF or VEGFA) is a critical organiser of vascular development due to its ability to regulate proliferation, migration, specialisation and survival of endothelial cells (reviewed in ref. 1). VEGF also affects many other cell types in tissue culture models. For example, it is mitogenic for lymphocytes, retinal pigment epithelium and Schwann cells.<sup>2-4</sup> It also stimulates the migration of haematopoietic precursors, monocytes/macrophages, neurons and vascular smooth muscle cells,<sup>5-11</sup> and it promotes the survival of developing and mature neurons<sup>12</sup> as well as chondrocytes.<sup>13,14</sup>

Differential splicing of the eight exons comprising the VEGF gene (*Vegfa*) gives rise to three main isoforms, termed VEGF121, VEGF165 and VEGF189 in humans and VEGF120, VEGF164 and VEGF188 in mice (see Chapter 1 by Y.-S. Ng). All VEGF isoforms bind to two type III receptor tyrosine kinases, FLT1 (*fms*-related tyrosine kinase 1, also denominated VEGFR1) and KDR (kinase insert domain containing receptor, also known as FLK1 or VEGFR2) (Fig. 1A). In contrast, heparan sulphate proteoglycans (HSPGs) and the nontyrosine kinase receptors neuropilin 1 (NRP1) and neuropilin 2 (NRP2) preferentially bind the VEGF isoforms containing the heparin-binding domains, encoded by exons 6 and 7 (Fig. 1B). In addition to the versatility provided by the existence of several different VEGF isoforms and VEGF receptors, VEGF signalling attains further plasticity from the association of VEGF receptors with other transmembrane

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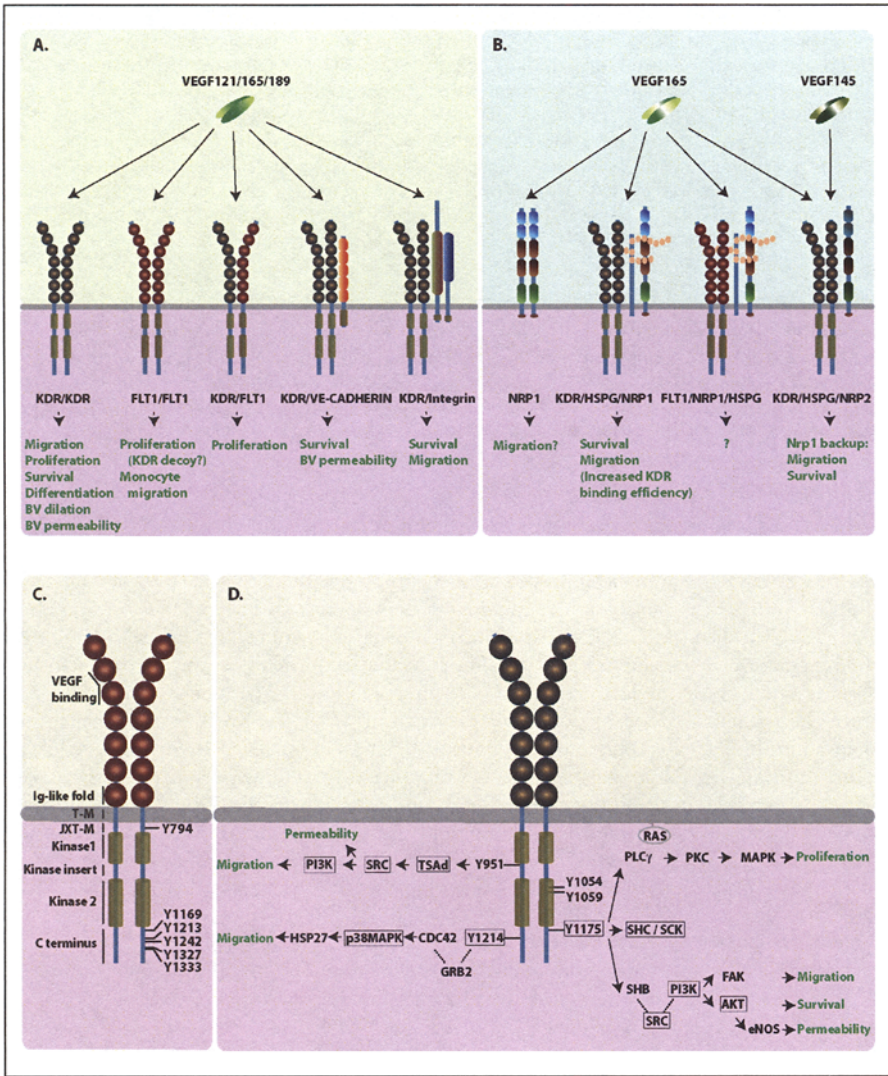


Figure 1. Working models for VEGF receptor signalling. (A-D) Schematic illustration of the different human VEGF receptors and their predicted physiological roles in endothelial cells, blood vessels and macrophages. (A) VEGF tyrosine kinase receptors: All VEGF isoforms (VEGF121, VEGF165, VEGF189) bind to homo- or heterodimers of KDR and FLT1. KDR can form higher order complexes with VE-cadherin or integrins. (B) Isoform-specific VEGF receptors: VEGF165, but not VEGF121, binds receptor complexes containing NRP1 and HSPGs, or higher order complexes containing additionally FLT1 or KDR. VEGF165 and VEGF145 bind NRP2. The neuropilin CUB domains (a1 and a2) are shown in blue, the coagulation factor V/VIII homology domains (b1 and b2) are highlighted red, and the MAM domain is coloured green. (C) FLT1 domain structure: The extracellular region consists of 7 Ig-like folds (shown as spheres); they bind ligands and mediate receptor dimerisation; the cytoplasmic domain contains two kinase domains (light brown cylinders) interrupted by a kinase insert domain; a juxtamembrane domain is thought to inhibit autophosphorylation. Legend continued on following page.

Figure 1, continued from previous page. FLT1 contains at least 7 known tyrosine phosphorylation sites (indicated by numbers that correspond to the position in the linear protein sequence); presently, *in vivo* data are lacking that demonstrate which of these tyrosine residues are essential for VEGF signalling in macrophages or other cell types. (D) KDR domain structure: The KDR structure is similar to that of FLT1, but KDR lacks a juxtamembrane inhibitory domain. The 7 known tyrosine phosphorylation sites are numbered according to their position in the linear protein sequence. The phosphorylated tyrosine residues are thought to interact with a collection of different proteins; experimentally confirmed interactions are represented by solid arrows, putative interactions with a dashed line. Interacting proteins that have been disrupted by gene targeting in the mouse are boxed. Abbreviation: BV, blood vessel.

proteins to form higher order signalling complexes (Fig. 1A). For example, KDR and FLT1 interact with integrins and vascular endothelial cadherin (VE-cadherin). In this chapter, we critically review current knowledge of the different VEGF signalling pathways and their interplay during development to extend a more general recent review on VEGF receptors.<sup>15</sup>

## Tyrosine Kinase Receptors for VEGF: FLT1 and KDR

### *Structure of FLT1 and KDR*

FLT1 and KDR are transmembrane glycoproteins of 180 and 200 kDa, respectively. They are closely related to other type III receptor tyrosine kinases, including FMS, KIT and PDGFR, and contain an extracellular domain composed of seven immunoglobulin (Ig)-like folds, a single transmembrane domain, a regulatory juxtamembrane domain and an intracellular tyrosine kinase domain (Fig. 1). The intracellular tyrosine kinase domain is interrupted by a kinase insert domain and contains several tyrosine residues that mediate the recruitment of downstream signalling molecules upon phosphorylation (Figs. 1C,D). Both KDR and FLT1 bind VEGF with high affinity. Mutation analysis of the extracellular domains of FLT1 and KDR revealed that the second and third Ig-like folds contain the high-affinity ligand-binding domain for VEGF, while the first and fourth Ig-like folds regulate ligand-binding and receptor dimerisation, respectively (Figs. 1C,D).<sup>16-18</sup> In addition to binding VEGF, FLT1 also acts as a receptor for VEGFB and PGF (previously known as PlGF), whilst KDR also binds the VEGF homologs VEGFC and VEGFD and the viral VEGFE.<sup>19</sup> Binding of VEGF by tyrosine kinase receptors promotes their homophilic or heterophilic interaction to activate the kinase domain.<sup>20,21</sup>

### *Expression Pattern of FLT1 and KDR*

KDR and FLT1 are expressed in endothelial cells in most, if not all tissues in mouse and human embryos. The expression level of FLT1 in vascular endothelium varies with gestational age. Between embryonic days 8.5 and 14 (E8.5 - E14) in the mouse, the *Flt1* gene is expressed at high levels in endothelial cells, but expression decreases thereafter.<sup>22</sup> In newborn mice, *Flt1* expression increases again, and it continues to be expressed in adults,<sup>22</sup> consistent with the idea that it plays a role in the homeostasis of blood vessels. *Flt1* gene expression is regulated by hypoxia, and a binding site for hypoxia-inducible factor (HIF1A) has been identified in the *Flt1* promoter.<sup>23</sup> Thus, *Flt1* is upregulated in vascular smooth muscle cells experiencing hypoxic stress, perhaps to control vascular remodelling or tone.<sup>24</sup> However, further studies are required to fully understand the physiological significance of the transcriptional regulation of FLT1 by hypoxia, and how it may complement the regulation of VEGF by hypoxia (see Chapter 3 by M. Fruttiger). In contrast to *Vegfa* and *Flt1*, *Kdr* has no HIF1A binding sites in its promoter region and is therefore not regulated by hypoxia.<sup>23</sup> *Kdr* is already expressed in mesodermal progenitors of vascular endothelial cells in the yolk sac at E7 in the mouse, and its expression is often used as a marker for these progenitor cells.<sup>25-27</sup> *Kdr* expression remains high on vascular endothelial cells during development, but it declines towards the end of gestation.<sup>28</sup> Nonendothelial expression of KDR has been reported in neurons, osteoblasts, pancreatic ducts cells, retinal progenitor cells, platelets and megakaryocytes (for

example in refs. 29-32). Due to its expression by adult neurons after brain injury, it has been suggested that KDR has a physiological, possibly neuroprotective function (see Chapter 8 by J. Rosenstein, J. Krum and C. Ruhrberg). Like KDR, FLT1 is expressed in endothelial progenitor cells and osteoblasts, but additionally in haematopoietic stem cells, macrophages, osteoclasts, dendritic cells, pericytes, smooth muscle cells and placental trophoblasts.<sup>33-38</sup>

### **Functional Requirements for FLT1**

An essential role for FLT1 in development is highlighted by the fact that FLT1-deficient mice die in utero between E8 and E9, most likely due to a failure of endothelial cells to assemble into a vascular circuit. The primary defect underlying this phenotype appears to be an altered cell fate determination among mesenchymal cells, which increases haemangioblast numbers.<sup>39</sup> The defect has been attributed to VEGF hyperactivity subsequent to the loss of endothelial FLT1.<sup>40</sup> Two different hypotheses have been put forward to explain the negative role of FLT1 in developmental angiogenesis. The most widely accepted hypothesis suggests that FLT1 functions as a cell surface-bound "decoy receptor" to sequester excess extracellular VEGF. In support of this idea, the FLT1 kinase domain is not normally active in endothelial cells, even though FLT1 has a ten-fold higher affinity for VEGF compared to KDR; in fact, FLT1 activation in endothelial cells has only been achieved by overexpression of recombinant protein.<sup>41-43</sup> Moreover, mice expressing a mutant form of FLT1 with an inactive tyrosine kinase domain (*Flt1TK-/-*) have no discernable defects in blood vessel formation, branching or remodelling, even though these mice show deficiencies in VEGF-induced macrophage migration.<sup>44</sup> Finally, membrane tethering of FLT1 is essential for vascular development: 50% of mice expressing solely a soluble form of FLT1, which lacks the transmembrane and tyrosine kinase domains, died between E8.5 and E9.0 with a disorganized vascular network, similar to the full knockout.<sup>45</sup> However, whilst 50% of mice expressing only a soluble form of FLT1 die, the other 50% of mice making only soluble FLT1 survive. A soluble form of FLT1 is produced endogenously by alternative splicing (sFLT1), raising the possibility that the soluble isoform normally cooperates with the membrane-tethered isoform to control vascular development. For example, it is conceivable that membrane bound FLT1 functions as a decoy receptor to limit VEGF availability to KDR, whilst sFLT1 sequesters soluble VEGF in the endothelial environment to sharpen VEGF gradients<sup>46</sup> (see Chapter 6 by H. Gerhardt).

Even though the FLT1 tyrosine kinase domain is dispensable for vascular development, FLT1 tyrosine kinase signalling significantly promotes pathological angiogenesis.<sup>47,48</sup> Several different explanations have been put forward to explain this difference in developmental and pathological angiogenesis. Firstly, FLT1 upregulation might activate PGF- and VEGF-responsive monocytes, which then release pro-angiogenic factors; in agreement with this idea, FLT1 tyrosine kinase signalling mediates chemotactic macrophage migration in response to PGF and VEGF,<sup>34,35,44,49</sup> and PGF promotes macrophage survival during tumour angiogenesis.<sup>50</sup> Alternatively, PGF may occupy FLT1 binding sites on endothelial cells, allowing VEGF to bind to KDR rather than FLT1; consistent with this suggestion, PGF potentiates mitogenic VEGF activity in endothelial cells in vitro, and it promotes VEGF-induced vascular permeability in vivo.<sup>51</sup> It is also possible that PGF binding to FLT1 promotes the transphosphorylation of KDR by FLT1 in FLT1/KDR heterodimers to increase VEGF/KDR signalling.<sup>48</sup> Lastly, PGF activation of FLT1 may stimulate vessel formation and maturation indirectly by acting on nonendothelial cell types, for example smooth muscle cells<sup>24,52</sup> or bone-marrow derived cells that are recruited to sites of neovascularisation.<sup>25,53,54</sup> It is presently debated whether pro-angiogenic bone-marrow derived cells support tumour angiogenesis by differentiating into endothelial cells<sup>55</sup> or by providing perivascular support cells.<sup>58</sup> The recruited perivascular cells have monocyte/macrophage characteristics, such as expression of the integrin CD11b and the hematopoietic lineage marker CD45;<sup>54</sup> this observation provides a link to the initial suggestion that PGF supports pathological angiogenesis by acting on cells in the monocyte/macrophage

lineage. Importantly, the regulation of FLT1 by hypoxia (see above) might promote PGF responsiveness of both endothelial cells and macrophages during pathological angiogenesis.

### ***FLT1-Stimulated Signalling Pathways***

FLT1 contains several potential tyrosine autophosphorylation sites (Fig. 1C) (reviewed in ref. 56). Whereas a repressor element in the juxtamembrane domain of FLT1 inhibits auto-phosphorylation after VEGF binding,<sup>57</sup> this repression appears to be alleviated by an unknown mechanism in monocytes/macrophages. Biochemical assays suggest that the phosphorylated FLT1 can recruit several different proteins containing a SRC homology 2 (SH2)-domain; this domain was first identified in the SRC protein kinase. In endothelial cells, phosphorylated KDR preferentially binds to and activates SRC, whereas phosphorylated FLT1 preferentially binds two other protein kinases that are closely related to SRC, namely FYN and YES.<sup>58</sup> Mice lacking any one of the SRC family kinases do not suffer developmental defects, but the combined loss of SRC, FYN and YES results in embryonic lethality at E9.5.<sup>59</sup> Lethality may be due to vascular insufficiency downstream of KDR rather than FLT1 signalling in endothelial cells (see below). The physiological role of the different SRC family kinases in VEGF/PGF mediated macrophage migration has not yet been examined, and the identity of the FLT1 and KDR phosphotyrosines involved in SRC kinase recruitment are also still unknown.

In addition to SRC kinase recruitment, tyrosine phosphorylation of FLT1 promotes recruitment of several other SH2 proteins, including phospholipase C gamma (PLC $\gamma$ ), SH2-domain containing tyrosine phosphatase 2 (SHP2), the noncatalytic region of tyrosine kinase adaptor protein 1 (NCK1), the class IA phosphatidylinositol 3-kinase (PI3K) and the cellular homolog of the viral oncogene *v-crk* (Fig. 1C). Phosphorylated Y1213, Y1333, Y794 and Y1169 all recruit PLC $\gamma$  to activate protein kinase C (PKC). Phosphorylated Y1213 specifically binds SHP2 and NCK1. Phosphorylated Y1213 also activates PI3K, which then catalyses the production of the second messenger lipid PIP3 (Box 1). Y1333 binds CRK (the cellular homolog of *v-crk*) and NCK. Proteins that bind to phosphorylated Y1242 and Y1327 have so far remained elusive. Interestingly, VEGF and PGF appear to induce phosphorylation of a different subset of tyrosine residues.<sup>48</sup> For example, PGF, but not VEGF binding to FLT1 results in Y1309 phosphorylation and activation of the AKT cell survival pathway (see below).

**Box 1.** Role of class IA PI3 kinase in vascular growth. The lipid kinases of the PI3 kinase (PI3K) family produce the intracellular messenger PIP3 (phosphatidyl-inositol-3,4,5-triphosphate); one of the major functions of PIP3 is activation of the serine/threonine kinase AKT to stimulate proliferation and prevent apoptosis. The PI3Ks have been grouped into three classes, with the class I family being further subdivided into IA and IB kinases. The class IA PI3Ks signal downstream of receptor tyrosine kinases. A role for class IA PI3Ks in endothelial cells was initially demonstrated in tissue culture models, but has more recently been studied by genetic alteration of the genes encoding its different subunits. Interpretation of the null mutant phenotypes has, however, been complicated by the fact that ablation of any one of the PI3K subunits deregulates other subunits. For example, ablation of the regulatory subunits p85a, p55a or p50 also reduces expression of the p110 catalytic subunits. Conversely, ablation of the p110a subunit results in over-expression of the p85 regulatory subunit, which has a dominant negative effect on all class IA PI3K proteins. Perhaps the most resounding evidence so far in support of an essential role for class IA PI3Ks in vascular development comes from the endothelial cell-specific knockout of PTEN (phosphatase and tensin homolog), a lipid phosphatase that reverses PI3K signalling. In this mouse model, loss of PTEN results in an overstimulation of endothelial cell proliferation and migration, causing embryonic death at E11.5.<sup>141</sup>

Understanding the physiological significance of the different FLT1 signalling pathways has so far proven difficult. Firstly, SHP2, PI3K, NCK and PLC $\gamma$  all play roles downstream of a variety of tyrosine kinases, and the analysis of null mutants for these genes therefore cannot identify specific requirements for signalling downstream of FLT1 or KDR. Secondly, no appropriate tissue culture model with a relevant readout has been identified to evaluate the physiological importance of the different phosphorylated tyrosine residues in FLT1.<sup>60</sup> It would be particularly interesting to learn more about FLT1 signalling pathways in the monocyte/macrophage lineage.

### **Functional Requirements for KDR**

Consistent with its expression in the mesodermal progenitors of blood islands in the yolk sac, *Kdr* is required for endothelial and haematopoietic cell differentiation and therefore vasculogenesis and haematopoiesis; thus, loss of KDR function results in embryonic death between E8.5 and 9.5<sup>28</sup> (see Chapter 4 by L. Goldie, M. Nix and K. Hirschi). As KDR is tyrosine-phosphorylated more efficiently than FLT1 upon VEGF binding in endothelial cells (see above), KDR is thought to be principally responsible for VEGF signalling to stimulate the proliferation, chemotaxis, survival, and differentiation of endothelial cells and to alter their morphology; moreover, KDR signalling is thought to stimulate vessel permeability and vessel dilation.<sup>41,61-63</sup> However, owing to the early lethality of *Kdr* knockout mice, the requirement for KDR in specific stages of vascular development subsequent to vasculogenesis has not yet been formally demonstrated by knockout technology.

### **KDR-Stimulated Signalling Pathways**

KDR functions similarly to most tyrosine kinase receptors: it dimerises and is autophosphorylated on several cytoplasmic tyrosine residues upon ligand binding (Fig. 1D). Early experiments using recombinant KDR in bacteria and yeast demonstrated that several tyrosine residues are autophosphorylated upon VEGF binding to recruit SH2-domain containing proteins. The following autophosphorylated tyrosine residues were subsequently identified in human endothelial cells: in the kinase insert domain, Y951 (corresponding to Y949 in the mouse); in the tyrosine kinase domain, Y1054 and Y1059 (corresponding to Y1053 and Y1057 in the mouse); and in the C-terminal domain, Y1175 and Y1214 (corresponding to Y1173 and Y1212 in the mouse).<sup>64</sup> As observed in the case of FLT1, KDR phosphotyrosines are recognised by a number of different SH2-domain containing proteins. For example, SRC kinases have been implicated in signalling pathways downstream of Y951 and Y1175 (Fig. 1D), and SRC kinases modulate endothelial proliferation and migration in tissue culture models<sup>65</sup> and during neoangiogenesis in adults.<sup>66</sup> To clarify the relative contribution of the different KDR phosphotyrosines to vascular development, we will discuss the phenotypes of mice that either lack single KDR tyrosine residues or the proteins predicted to bind to them following phosphorylation.

Human Y951, Y1175 and Y1214 have all been implicated in the control of endothelial cell proliferation or migration in culture models. Y951 is selectively phosphorylated in a subset of endothelial cells during development and binds to the T cell-specific adapter molecule (TSAd), which is thought to act upstream of SRC and PI3K (Fig. 1D). Even though TSAd is critical for actin reorganization in cell culture models, it is not essential for mouse development.<sup>67</sup> No other protein has so far been identified that interacts functionally with Y951 in endothelial cells, and it is not known if Y951 is essential for vascular development.

Y1214 is embedded in a region of KDR that resembles the consensus binding sequence for the growth factor receptor bound protein 2 (GRB2) and has been implicated in the control of actin reorganisation and cell migration through the activation of CDC42 and the mitogen activated protein kinase (MAPK) cascade<sup>68</sup> (Fig. 1D). A mouse model for the tyrosine residues corresponding to human Y1214 has been created by replacing Y1212 with a phenylalanine residue; surprisingly, these mutants have no discernable defects.<sup>69</sup>

A mouse model for the tyrosine residue corresponding to human Y1175 has also been created by replacement of Y1173 with a phenylalanine residue. This mutation results in embryonic lethality between E8.5 and E9.5 with endothelial and haematopoietic defects, similar to those seen in complete KDR knockout mice.<sup>70</sup> The essential Y1175 residue, located in the KDR C-terminal domain, interacts with a number of SH2 domain-containing proteins that are expressed in endothelial cells, including PLC $\gamma$  and the adaptor proteins SHCA, SHCB (also called SCK) and SHB (Fig. 1D). Activation of PLC $\gamma$  leads to the activation of PKC to control endothelial cell proliferation via the MAPK pathway in cultured endothelial cells (Fig. 1D). Several different MAPK are essential for embryogenesis, with p38 and ERK5 being required for vascular development; however, it is not clear if the effects on blood vessel growth reflect a requirement in endothelial cells or occur subsequent to defective placentation<sup>71</sup>. SHCA KO mice suffer from embryonic lethality due to extensive vascular defects.<sup>72</sup> However, SHCA also interacts with other tyrosine kinase receptors that may be involved in vasculogenesis and may therefore not be a specific downstream effector of KDR. SHCB is expressed in developing blood vessels, but SHCB KO mice have no vascular defects, possibly because it acts redundantly with other SHC family members such as SHCA.<sup>73</sup> SHB controls endothelial cell migration through the focal adhesion kinase FAK in a pathway that involves PI3K activation (Fig. 1D). Even though SHB has not yet been knocked out in mice, it is essential for blood vessel growth in an embryonic stem cell model of angiogenesis.<sup>74</sup>

In addition to promoting the proliferation and migration of endothelial cells, VEGF also promotes their survival. Genetic mouse models suggest that VEGF supports endothelial cell survival *in vivo* by acting both in a paracrine fashion<sup>75</sup> and in an autocrine loop.<sup>76</sup> *In vitro* models have identified several different downstream signalling pathways that are activated by VEGF to promote endothelial survival. Paracrine survival signalling in cultured endothelial cells involves the interaction of KDR with cell adhesion molecules of the integrin family, which control cell survival in response to matrix signals in many cell types including endothelium,<sup>77</sup> and the interaction of KDR with VE-cadherin, a component of endothelial cell adherens junctions<sup>78</sup> (Fig. 1A). Mice lacking VE-cadherin die at 9.5 dpc due to vascular insufficiency, caused by defective blood vessel remodelling and maturation.<sup>79</sup> These defects may be due to reduced activation of anti-apoptotic protein kinases such as AKT1, a protein that promotes endothelial cell survival *in vitro* and *in vivo*.<sup>80</sup> AKT1 activation normally occurs downstream of VE-cadherin and VEGF/KDR in a process that requires SRC and PI3K<sup>66,81,82</sup> (Fig. 1D). However, AKT1 is not essential for vascular development, possibly because it signals redundantly with closely related AKT1 and AKT3 proteins. Alternatively, or additionally, VE-cadherin/KDR interaction may impact on endothelial cell survival by controlling cell surface retention of KDR.<sup>83</sup> It is not known which intracellular effectors play a role in autocrine VEGF survival signalling, as this pathway does not require VEGF secretion<sup>76</sup> and therefore is likely to bypass KDR/VE-cadherin complexes on the cell surface.

### ***Negative Regulation of KDR Signalling***

Whereas much effort has been directed at identifying the forward signalling pathways downstream of KDR, the molecular mechanisms that modulate KDR activity have received less attention. Presumably, KDR activation must be downregulated at some point to terminate signalling. The phosphatases SHP1 and SHP2 dephosphorylate the nonessential KDR Y1214 residue,<sup>84,85</sup> and human cellular protein tyrosine phosphatase A (HCPTPA) inhibits VEGF-signalling in tissue culture models, possibly by dephosphorylating KDR to inhibit MAPK activation.<sup>86</sup> Unfortunately, the physiological significance of this pathway is unknown.

## **VEGF Isoform-Specific Receptors: Neuropilins and HSPGs**

### ***Identification of the Neuropilins as VEGF Receptors***

An isoform specific VEGF receptor that binds VEGF165, but not VEGF121, was first described in human umbilical vein-derived endothelial cells<sup>87</sup> and subsequently in several

tumour-derived cell lines that lack the expression of other VEGF receptors.<sup>88</sup> This novel VEGF receptor was purified and identified as neuropilin 1 (NRP1), a 130-kDa type I transmembrane protein (Fig. 1B). NRP1 had previously been discovered as an axonal adhesion protein in the developing frog nervous system<sup>89,90</sup> and as a receptor for secreted guidance molecules of the class 3 semaphorin family.<sup>91,92</sup> Besides NRP1, the neuropilin family includes NRP2.<sup>93</sup> Even though NRP1 and NRP2 share only 44% homology at the amino acid level, each protein is highly conserved amongst different vertebrate species, including frog, chick, mouse and human. NRP1 and NRP2 bind a different subset of VEGF isoforms and semaphorins *in vitro*: whereas NRP1 preferentially binds VEGF165 and SEMA3A, NRP2 binds both VEGF165 and VEGF145 as well as SEMA3F.<sup>91-94</sup>

### ***Structure of Neuropilins***

NRP1 and NRP2 have an identical domain structure.<sup>93,95</sup> Both contain a large N-terminal extracellular domain of approximately 850 amino acids, a short membrane-spanning domain of approximately 24 amino acid residues and a small cytoplasmic domain of 40 residues. The extracellular domain contains two complement-binding (CUB) domains (termed a1 and a2), two coagulation factor V/VIII homology domains (termed b1 and b2) and a meprin (MAM) domain (Fig. 1B). The a- and b-domains are crucial for ligand binding, whilst the MAM domain promotes dimerisation and the interaction with other cell surface receptors.<sup>96</sup> The cytoplasmic domain is short and was originally thought to lack signalling motifs, because its deletion did not impair axonal growth cone collapse in response to SEMA3A.<sup>97</sup> Instead, neuropilins transduce semaphorin signals in neurons through a signalling coreceptor of the plexin family.<sup>98,99</sup> In analogy, it was inferred that neuropilins recruit a coreceptor such as FLT1 and KDR to transmit VEGF signals in endothelial cells. In agreement with this idea, NRP1 potentiates the signalling of coexpressed KDR in porcine aortic endothelial cells, which surprisingly lack endogenous KDR expression.<sup>100</sup> However, the relationship of NRP1 and KDR is different to that of NRP1 and plexins: whereas NRP1 is the compulsory ligand binding subunit in the semaphorin receptor, KDR does not require NRP1 to bind VEGF. *Vice versa*, recent evidence suggests that NRP1 can also signal independently of KDR in endothelial cells, suggesting that the cytoplasmic tail may have signalling activity after all (see below).

### ***Functional Requirements for Neuropilins in Vascular Development***

Neuropilins are expressed by several types of embryonic neurons, and their targeted inactivation in the mouse impairs axon guidance and neuronal migration in response to semaphorins.<sup>101-105</sup> In addition, loss of NRP1 disrupts neuronal migration in response to VEGF.<sup>11</sup>

In the vasculature, NRP1 is preferentially expressed on arterial and brain microvessel endothelium, whereas NRP2 is present on venous and lymphatic endothelium.<sup>106,107</sup> Consistent with a role for NRP1 in vascular growth, over-expression of NRP1 in mice deregulates angiogenesis, causing embryonic lethality at E17.5; the mutant embryos exhibit excess capillaries and blood vessels, dilation of blood vessels, severe haemorrhage and malformed hearts.<sup>107</sup> Mice lacking NRP1 die even earlier, at around E12.5, with impaired neural tube vascularisation, agenesis or transposition of the aortic arches, persistent truncus arteriosus and insufficient development of the yolk sac vasculature.<sup>108</sup> The physiological role of NRP1 during vascular development has also been addressed in zebrafish models. In this organism, knockdown of NRP1 impairs angiogenic sprouting from the major axial vessels and therefore formation of the intersomitic vessels.<sup>109</sup> Others have shown that the knockdown of NRP1 in zebrafish disrupts even earlier stages of vascular development, including the formation of the dorsal longitudinal anastomosing vessels and the subintestinal vein.<sup>110</sup>

Consistent with its expression pattern, mice lacking NRP2 are deficient in the formation of small lymphatics and capillaries, but they show no other obvious cardiovascular abnormalities.<sup>111</sup> Noteworthy, loss of both NRP1 and NRP2 in mice impairs vascular development more severely than loss of NRP1 alone, with death at E8.0 due to impaired yolk sac vascularisation;<sup>112</sup> these data suggest that both proteins can partially compensate for each other during the formation of



arterio-venous circuits. However, the reason why NRP2 is able to compensate for NRP1 during vascular development is presently unclear. The observation that both proteins are expressed in a reciprocal pattern during the segregation of arterio-venous circuit in the chick<sup>106</sup> raises the possibility that venous NRP2 function becomes essential only when arterial NRP1 expression is lost. Alternatively, NRP2 may be upregulated in NRP1-deficient vascular endothelial cells to compensate for NRP1. Consistent with this hypothesis, NRP2 is able to enhance KDR signalling in porcine aortic endothelial cells,<sup>113</sup> which lack NRP1.<sup>100</sup>

The requirement for NRP1 in vascular growth is generally considered to reflect its essential role in promoting VEGF165 signalling in endothelial cells. In agreement with this idea, mice lacking NRP1 specifically in vascular endothelium show impaired microvessel growth in the brain.<sup>114</sup> However, there are some striking differences in the vascular defects caused by loss of NRP1 or loss of its VEGF ligands in the developing trunk and central nervous system, with loss of NRP1 causing a more severe vascular deficiency particularly in the brain.<sup>108,115,116</sup> These observations suggest that loss of VEGF isoform signalling through NRP1 is not entirely responsible for the vascular deficiency of NRP1 null mutants, and that NRP1 ligands other than VEGF165 may contribute to vessel patterning. The finding that SEMA3A inhibits endothelial cell migration *in vitro* by competing with VEGF165 for binding to NRP1/KDR complexes made it a candidate modulator of neuropilin-mediated vessel patterning *in vivo*.<sup>117</sup> Yet, class 3 semaphorin-signalling through neuropilins is not required for embryonic vascular development.<sup>114,118</sup> Therefore, the nature of the hypothetical NRP1 ligand that cooperates with VEGF165 during vascular patterning remains elusive.

### **VEGF165/NRP1 Signalling**

In analogy to the compulsory recruitment of plexins to transmit semaphorin signals, NRP1 was initially proposed to recruit a coreceptor such as FLT1 and KDR to transmit VEGF165 signals.<sup>100,119,120</sup> In support of this idea, NRP1 does not promote the VEGF165-induced chemotaxis of KDR-negative cultured porcine aortic endothelial cells, but when coexpressed with KDR, it enhances chemotaxis more than KDR alone.<sup>100</sup> Two alternative hypotheses have been proposed to explain the beneficial effect of NRP1 on KDR signalling: Complexes containing both KDR and NRP1 may bind VEGF165 with higher affinity than KDR or NRP1 alone,<sup>121</sup> or NRP1 may promote KDR clustering to promote VEGF165 signalling.<sup>120</sup>

However, other tissue culture models suggest that NRP1 may also function in endothelial cells independently of its ability to enhance VEGF/KDR signalling. Firstly, when the extracellular domain of epidermal growth factor (EGF) receptor was fused to a NRP1 fragment comprised of its membrane-spanning and cytoplasmic domain, the chimeric receptor promoted endothelial cell migration in response to EGF.<sup>122</sup> Secondly, the last three amino acid residues of NRP1 (SEA-COOH) bind to the neuropilin-interacting protein NIP (also known as GIPC or synectin),<sup>123</sup> and this interaction contributes to vascular development in zebrafish and mice.<sup>115,124</sup> One zebrafish study demonstrated that disruption of trunk vessel development by NRP1 knock down could be rescued by delivery of full length human NRP1, but not by human NRP1 lacking the NIP-binding SEA motif.<sup>113</sup> Moreover, ectopic expression of NRP1 lacking the SEA motif or knockdown of NIP disrupted vessel growth in this study.<sup>113</sup> Another zebrafish study found that knockdown of NIP affected vascular development at an even earlier stage by impairing dorsal aorta formation.<sup>124</sup> In mice, loss of NIP leads to less severe cardiovascular defects than loss of NRP1.<sup>124</sup> NIP null mice are born at the expected Mendelian frequency; moreover, the brain and spinal chord are vascularised normally, even though these tissues are severely affected in NRP1 null mutants (J. M. V., C. R. and M. Simmons, unpublished observations). However, NIP-deficient mice show a specific defect in arterial development and adult arteriogenesis, with reduced arterial density and branching in the retina, heart and kidney.<sup>124</sup> These observations agree with those of other mouse studies, in which loss of VEGF165 signalling through NRP1 affected arterial patterning in the limb skin<sup>125</sup> and in the retina.<sup>126</sup>

In summary, NRP1 is likely to play a dual role in vascular growth by enhancing VEGF164 signalling through KDR and by promoting VEGF164 signalling through its own intracellular domain.

### ***Heparan Sulphate Proteoglycans***

Heparan sulphate proteoglycans (HSPGs) are abundant and highly conserved components of the cell surface and extracellular matrix. They play an important role in the formation and modulation of gradients of heparin-binding growth factors, morphogens and chemokines.<sup>127</sup> Several reports have implicated HSPGs as modulators of VEGF signalling. Firstly, VEGF164 and VEGF188 bind heparin *in vitro* with different degrees of affinity, depending on the presence/absence of the so-called heparin-binding domains; heparin-binding ability *in vitro* is thought to indicate HSPG binding *in vivo*.<sup>128</sup> In support of this idea, loss of the heparin-binding VEGF isoforms affects VEGF distribution in the extracellular matrix during angiogenic sprouting in the brain and retina.<sup>115,129</sup> Heparin also promotes VEGF165 binding to its receptors KDR<sup>130,131</sup> and NRP1.<sup>88,100</sup> Moreover, when heparan sulphate is enzymatically removed from endothelial cells, KDR phosphorylation is inhibited.<sup>132</sup> The beneficial effect of heparin or heparan sulphate on VEGF signalling may additionally stem from a direct interaction with the VEGF receptors. Consistent with this suggestion, HSPG expression by perivascular smooth muscle cells transactivates endothelial KDR in an embryonic stem cell model of angiogenesis, and possibly facilitates the cross talk between both cell types during blood vessel formation *in vivo*.<sup>133</sup> Finally, NRP1 may itself become a proteoglycan by post-transcriptional modification with glycosaminoglycan side chains of the heparan sulphate or the chondroitin sulphate type, and this modification may enhance VEGF binding.<sup>134</sup>

### **Conclusions and Future Perspectives**

Initially, VEGF signalling pathways were characterised in tissue culture models of endothelium. More recently, the physiological relevance of the different pathways has been addressed with mouse mutants that carry point mutations in single KDR tyrosine phosphorylation sites or harbour null mutations in proteins that interact with these tyrosines. A more complete understanding of KDR signalling will, however, depend on the creation of further mouse mutants lacking other KDR tyrosine residues implicated in intracellular signalling, as well as the design of a novel strategy to study FLT1 tyrosine kinase signalling *in vivo*.

Despite the progress made in identifying intracellular adaptor molecules for KDR and FLT1, we still know very little about the intracellular trafficking of VEGF and its receptor complexes. For example, in some endothelial culture models the phosphorylation of tyrosine residues Y1054 and Y1059 controls internalisation of the VEGF/KDR complex into clathrin-coated vesicles and endosomes prior to degradation,<sup>135</sup> and KDR may also signal from endosomes to promote endothelial cell proliferation.<sup>83</sup> In other endothelial tissue culture models, VEGF stimulates nuclear translocation of KDR.<sup>136-139</sup> In addition, circumstantial evidence is emerging that autocrine VEGF signalling may be based on intracrine signalling; for example, autocrine VEGF survival signalling in endothelial cells does not require VEGF secretion.<sup>76</sup> Further effort should therefore be directed at establishing the physiological significance of intracellular interactions between VEGF and its receptors during development or disease.

Owing to the absolute requirement for VEGF during embryogenesis, many previous studies focussed on elucidating the physiological requirement for VEGF signalling pathways in early vascular development. These studies also benefited from the fact that developmental angiogenesis produces a stereotypic pattern of hierarchical blood vessel networks in a well-defined tissue context. In contrast, adult angiogenesis occurs against a backdrop of environmental fluctuations and is influenced by the dynamic interaction of growing vessels with the immune system. Nevertheless, research into developmental VEGF signalling pathways has impacted on our understanding of neoangiogenesis in the adult, owing to the reactivation of VEGF signalling pathways in physiological processes such as wound healing and pathological conditions such as cancer, diabetic retinopathy and ischemic heart disease. Thus, the potential of novel

anti-angiogenic therapies can be evaluated in the perinatal rodent eye before being tested in a disease model, because the rodent retina is vascularised only after birth and the eye is easily accessible for drug delivery (e.g., ref. 140).

Finally, it will be necessary to extend the study of VEGF signalling pathways to include other VEGF-responsive cell types, most notably circulating progenitors cells (see Chapter 4 by L. C. Goldie, M. K. Nix and K. K. Hirschi), bone cell types (see Chapter 7 by C. Maes and G. Carmeliet) and neuronal progenitors (see Chapter 8 by J. M. Rosenstein, J. M. Krum and C. Ruhrberg). It will be particularly interesting to elucidate if different VEGF-responsive cell types that grow in close spatiotemporal proximity activate distinct VEGF signalling pathways to coordinate their behaviour. For example, VEGF signalling is likely to play a dual role in blood vessels and bone cell types during bone development (see Chapter 7 by C. Maes and G. Carmeliet), and it supports both blood vessel growth and neuronal growth in the angiogenic niche of neurogenesis (see Chapter 8 by J. Rosenstein, J. Krum and C. Ruhrberg). The identification of cell-type specific components in the VEGF signalling pathway might then provide the basis for the creation of selective tools to balance vascular effects of VEGF such as permeability against effects on nonendothelial cell types in novel pro- and anti-angiogenic therapies.

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