

The reception and the party after: how vascular endothelial growth factor receptor 2 explores cytoplasmic space

Philipp Berger, Kurt Ballmer-Hofer

Paul Scherrer Institute, Biomolecular Research, Molecular Cell Biology, Villigen, Switzerland

Summary

Vascular endothelial growth factors (VEGFs) regulate blood and lymph vessel formation through activation of the type V receptor tyrosine kinases VEGFR-1, -2 and -3. In addition, VEGFs interact with co-receptors such as neuropilins, integrins, semaphorins or heparansulfate glycosaminoglycans. Ligand binding dimerises the receptors and activates their intracellular tyrosine kinase domains, resulting in phosphorylation of tyrosine residues acting as docking sites for intracellular signalling molecules. Ligand-induced receptor is internalised and then transported through early, late, and recycling endosomes, and finally degraded by proteasomal or lysosomal pathways. Biological output by VEGF is mediated through distinct receptor/co-receptor complexes and generates signals in all cellular compartments triggering cellular responses such as cell migration, cell proliferation, vessel formation and maturation, as well as changes in vessel fenestration, constriction and permeability. Here we review recent experiments showing how VEGFR-2 is transported through intracellular vesicular compartments specified by Rab family GTPases, and discuss how different VEGF-A isoforms specify intracellular receptor trafficking. We also discuss how the biological consequences of aberrant receptor trafficking bear on the development of vascular disease.

Key words: VEGFR-2; VEGF; cancer; neuropilin; trafficking; signalling; endocytosis

Introduction to VEGF receptors

Signalling by receptor tyrosine kinases (RTKs) requires dimerisation with precise positioning of receptor subunits initiated and controlled by ligand binding. Dimeric ligand/receptor complexes subsequently initiate transmembrane signalling which results in activation of the intracellular tyrosine kinase domain [1, 2]. Vascular endothelial growth factors (collectively abbreviated here as ‘VEGF’) constitute a large family of angiogenic and lymphangiogenic polypeptides, VEGF-A, -B, -C, -D, -E, and -F, and placenta growth factor (PlGF) [3]. These ligands bind to specific RTKs, called VEGF receptors (VEGFR), and interact in

an isoform-specific manner with additional cell surface-exposed proteins acting as co-receptors in angiogenic signalling. The biological functions of VEGF polypeptides predominantly arise from binding to the type V RTKs VEGFR-1 (Flt-1), VEGFR-2 (KDR/Flk-1), and VEGFR-3 (Flt-4) [4–6]. Neuropilin-1 and -2 (NRP-1, -2) [7], integrins [8], ephrin-B2 [9] and heparan sulfate proteoglycans (HSPG) [10] are at present the best characterised co-receptors. Some VEGFs interact with multiple receptors while others show very specific receptor binding properties. So, for instance, VEGF-A binds VEGFR-1 and -2, PlGF and VEGF-B are specific for VEGFR-1 [11, 12], while VEGF-E and most VEGF-F variants exclusively bind VEGFR-2 [13–15], and VEGF-C and -D bind VEGFR-2 and -3 as well as NRP-2 [16–18] (summarised in fig. 1). The complexity of VEGF signalling is further increased by the fact that some of the family members are processed posttranscriptionally and posttranslationally, giving rise to a bewildering number of isoforms with distinct receptor and ex-

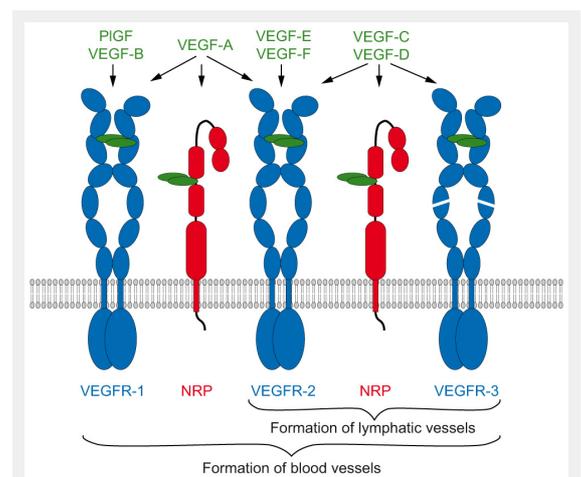


Figure 1

VEGFs and their interactions with VEGFRs and NRPs. The human genome encodes five VEGF genes (A, B, C, D, and PlGF). Two VEGFs are encoded by viruses (E) and snakes (F), respectively. They all exist as dimers and induce dimerisation of the VEGFRs upon binding. Their binding specificity to the three VEGFRs and NRPs is indicated by arrows.

tracellular matrix binding properties (reviewed in [3, 19]). VEGF-A, for instance, exists in more than 20 isoforms and we have shown recently that different splice variants of exon 8 alter co-receptor recruitment and thus processing of VEGFR-2 [20].

Ligand binding instigates transmembrane signalling and thereby generates distinct cellular output (reviewed in [21]). VEGFR-2 is the major receptor through which VEGFs regulate angiogenesis and vasculogenesis, and this receptor is essential for both blood and lymph vessel development and homeostasis. Distinct receptor/co-receptor complexes are formed upon activation with specific VEGF-A splice variants. The core domain of all VEGF-A variants encoded by exons 2-5 interacts with VEGFR-1 or -2, while sequences encoded by exons 6 and/or 7 and 8 determine co-receptor binding [22, 23]. Some VEGF variants bind simultaneously to two receptors such as VEGFR-2 and NRP-1 even when these are expressed separately on adjacent cells [24]. This might be required in order to promote endothelial cell migration and cell guidance, e.g. when vessels form along tracks defined by neural cells [25, 26] or during endothelial tip cell guidance [27, 28].

VEGFR-2 is internalised and transported to specific intracellular vesicular compartments upon ligand binding

Activation of VEGFRs initiates cell signalling at multiple steps of receptor processing in many distinct cellular compartments to promote endothelial cell survival, migration and proliferation as well as vessel fenestration and permeabilisation. Ligand-bound, activated receptors are transferred from the cell surface to intracellular vesicles and subsequently shuttled through early, late, and recycling endosomes. Activated receptors are destined for degradation in lysosomes or proteasomes, but evidence is emerging that subpopulations are recycled through the Golgi or directly back to the plasma membrane. Activated receptors initiate signalling in all cellular compartments during intracellular trafficking [29]. This documents that the cellular signalling machinery is compartmentalised to ensure proper spatio-temporal signal processing and integration.

Contrary to other RTKs, unstimulated VEGFR-2 is only partially localised at the plasma membrane with a significant fraction of the receptor present in internal vesicles [30, 31]. Inactive, unphosphorylated VEGFR-2 is present in resting cells in perinuclear caveolae which carry the early endosomal marker EEA-1 and dynamin [32]. Ligand-activated VEGFR-2 is rapidly internalised into early endosomes via clathrin coated vesicles. An indispensable step in receptor activation seems to be the release of receptors from adherens junctions [33] and caveolae [34]. More specifically, it was shown that VEGFR-2 is released from a lipid raft/caveolae membrane fraction and accumulates in focal adhesion contacts, where it becomes associated with a small subpopulation of caveolin phosphorylated at specific tyrosine residues following receptor activation [35]. This process is mediated by small G proteins of the Arf family. Resting endothelial cells (EC) are organised in tightly associated cell monolayers held together by adherens junc-

tions. Activation and release of VEGFR-2 from these structures and subsequent transfer to late endosomes, multivesicular bodies and finally lysosomes or proteasomes is achieved within minutes after ligand binding and leads to reorganisation of the cellular cytoskeleton and thus of EC monolayer morphology. This highly regulated process requires VEGFR-2 to interact with and activate a set of downstream signalling molecules which constitute the multiple molecular interactions regulating receptor trafficking to specific cellular compartments where biological signal output is generated. Phosphorylation of tyrosine residues 1054 and 1059 in the kinase activation loop stabilises receptor activity and is required for receptor internalisation [36]. Phosphorylation of tyrosine 951, 1175 and 1214 recruits and subsequently activates specific downstream signalling molecules mediating biological output [37]. Finally, VEGFR-2 is inactivated by dephosphorylation and recycled back to the plasma membrane or is degraded. Both proteasomal and lysosomal degradation have been described [38, 39]. A recent study showed that serine phosphorylation of a PEST motif in VEGFR-2 is essential for ubiquitination by the β -Trop1 ubiquitin ligase and triggers proteasomal degradation [40]. The data describing the role in degradation of the classical E3 ligase c-Cbl, which regulates localisation and degradation of several RTKs, are conflicting [41]. VEGFR-2 is apparently directly ubiquitinated, but it was also shown that ubiquitination of phospholipase C- γ 1, one of the major targets of activated VEGFR-2, attenuates receptor signalling [41–43]. VEGF-A mediated activation of VEGFR-2 is also regulated by specific cleavage of the cytoplasmic domain [44]. The rate at which VEGFR-2 is degraded thus depends on several cellular parameters such as the status of adhesion junction complexes [45] and the association with co-receptors such as neuropilins [46], as discussed in more detail below.

Intracellular trafficking of VEGFR-2 and NRP-1, a closer look at the role of Rab GTPases

VEGFR-2 and NRP-1 remain membrane-bound on intracellular vesicles even after internalisation exposing their carboxyterminal domains to the cytoplasm. These receptors are then shuttled and sorted among the various intracellular membrane compartments of the cell. SNARE proteins are the major mediators of vesicle fusion and Rab GTPases (reviewed in [47]) are, together with phosphoinositides (reviewed in [48]), the coordinators of this membrane sorting process. Rab GTPases act as molecular switches recruiting distinct effector molecules in their active (GTP-bound) state [49–53]. These protein complexes then orchestrate the correct transfer of vesicles and their associated cargo among the different intracellular compartments in a unidirectional manner. Mutant forms of Rab GTPases have become popular tools for monitoring and manipulation of membrane trafficking of RTKs [54].

It was shown for EGFR that kinase activation results in conversion of Rab5 to its active form at the plasma membrane, a step that is essential for receptor internalisation [55]. Jopling et al. [56] were the first to show that VEGFR-2 co-localises with Rab5 and Rab7. They also

showed that inactivation of Rab GTPases blocked receptor trafficking. Blocking Rab7 with a dominant negative mutant or with siRNA reduced phosphorylation of VEGFR-2 at tyrosine 1175 and resulted in increased p42/p44 MAPK signalling [56]. We recently showed that two different exon 8 splice variants of VEGF-A₁₆₅ promote specific VEGFR-2 trafficking [20]. The NRP1-binding isoform VEGF-A_{165a} led to receptor recycling to the plasma membrane through Rab11, while an isoform unable to bind NRP-1, VEGF-A_{165b}, failed to do so. Interestingly, VEGFR-2 present in Rab 11 vesicles was not phosphorylated, showing that a so far undefined phosphatase regulates recycling of VEGFR-2 to the plasma membrane. Candidate phosphatases are DEP-1, PTP1B, SHP1, SHP2, and HCPTA (see below).

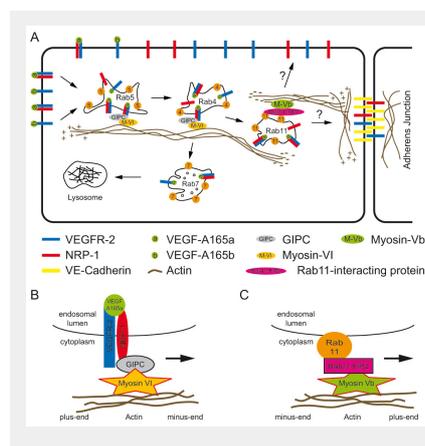
The function of NRP-1 and GIPC/synectin in VEGFR-2 trafficking

Recruitment of NRP-1 into the VEGFR-2 complex by VEGF-A_{165a} has significant implications for receptor recycling and phosphorylation as described above, but it is also relevant for signalling *in vivo*. It was previously shown that the NRP-1-binding ligand VEGF-A_{165a} activates the p38 MAP kinase and promotes sprouting of intersegmental blood vessels in developing zebrafish *in vivo*. VEGF-A₁₂₁, which has reduced affinity for NRP-1 and is unable to induce co-receptor complex formation, was unable to mediate these effects [22]. This was in agreement with the phenotype of NRP-1 null mice displaying severely impaired blood vessel formation in the developing embryo [25]. Similar defects were observed in zebrafish lacking NRP-1 [57]. Apparently the three carboxyterminal amino acids of NRP-1 constitute the PDZ domain binding motif interacting with GIPC, an adaptor molecule also known as syndectin [58]. Ablation of GIPC in mice or zebrafish led to similar vascular defects as NRP-1 knockdown, establishing that these two genes functionally interact *in vivo* [59, 60]. Myosin VI is a well characterised interaction partner of GIPC and its function in endocytosis is well documented [61, 62]. Experiments with myosin VI null mice and knockdown experiments in zebrafish confirmed that this cytoskeletal protein plays a role in vessel development [63]. This suggests that myosin VI, together with NRP-1 and GIPC, are organised in a complex essential for angiogen-

esis by mediating internalisation of VEGFR-2 (fig. 2). Our data clearly show that the PDZ binding motif of NRP-1 is necessary for the Rab4 to Rab11 transition, and it was also shown that GIPC is present on Rab5 vesicles [20, 61]. We thus propose that the attachment of an NRP-1/GIPC/myosin VI complex to VEGFR-2 by VEGF A_{165a} leads to association with the actin cytoskeleton soon after internalisation. It is unclear whether intact vesicles are then transported along the actin cytoskeleton or are disassembled by tubulation upon interaction with actin and myosin on endosomes [64]. It is unlikely that myosin VI is also responsible for the transport of VEGFR-2 back to the plasma membrane, since it is a minus-end-directed actin motor. Myosin VI and GIPC are presumably released from Rab11 vesicles and the residues are subsequently linked to a plus-end-directed myosin such as myosin Vb. In fact, it was shown that myosin Vb binds to Rab11 family-interacting protein-2 (Rab11-FIP2), an effector of Rab11 (fig. 2C). This ternary complex consisting of myosin Vb, Rab11-FIP2 and Rab11 could then initiate membrane recycling to the plasma membrane. The role of myosin Vb in angiogenesis has, however, not been determined so far [65].

Signalling during intracellular receptor trafficking

Binding of VEGF to VEGFR-2 results in receptor phosphorylation at several tyrosine residues located in the cytoplasmic receptor domain. To ensure proper receptor regulation and to prevent aberrant signalling, tyrosine phosphorylation of RTKs must be tightly regulated. The signal output also depends on the cellular context. Cadherins not only mediate cell-cell contacts, they also influence signalling [66]. VEGFR-2 co-localises with either caveolin-1 [34] or VE-cadherin at the plasma membrane in specific cellular contact sites called adherens junctions [33]. Endothelial adherens junctions contain catenins and the density-enhanced phosphatase-1 (DEP-1/CD148) as well as VEGFR-2 and VE-cadherin. VE-cadherin is an important modulator of VEGF signalling *in vivo* and was shown to negatively regulate VEGFR-2 activity [33, 67]. Silencing of DEP-1 increases VEGFR-2 internalisation and signalling, indicating that downregulation of receptor activity in the presence of VE-cadherin in resting EC monolayers is mediated by DEP-1. However, VEGFR-2 and VE-cadher-



in do not co-internalise and therefore DEP-1 may dephosphorylate VEGFR-2 exclusively at the plasma membrane. T-cell protein tyrosine phosphatase, TCPTP, also known as PTPN2, is a non-receptor tyrosine phosphatase broadly expressed in most tissues. TCPTP is a negative regulator of many cancer-relevant signalling pathways and dephosphorylates RTKs such as PDGFR- β , EGFR, or VEGFR-2. It is activated by the cytoplasmic domain of integrin α 1, indicating that TCPTP also acts at the plasma membrane, similarly to DEP-1. In focal adhesions, TCPTP dephosphorylates VEGFR-2 but does not dephosphorylate tyrosine 1175, suggesting that it differentially influences downstream signalling [68]. In endothelial cell monolayers held together by adherens junctions or integrin α 1 β 1 basement membrane, VEGFR-2 is inactivated by DEP-1 and TCPTP. During angiogenesis, the basement membrane and cell-cell junctions are disrupted and activation of VEGFR-2 is no longer blocked by these phosphatases.

Overexpression of another protein tyrosine phosphatase, PTP1B dephosphorylating VEGFR-2 and VE-cadherin, results in reduced receptor phosphorylation and attenuation of ERK1/2 activity. As expected, knockdown of PTP1B by siRNA has the opposite effect. Interestingly, p38 activation is not affected under these conditions [69]. We assume that PTP1B acts early after internalisation and interfering with GIPC-myosin VI trafficking promotes prolonged exposure to PTP1B and thus reduces phosphorylation at tyrosine 1175, as shown by blockage of arteriogenesis. This is confirmed by the fact that PTP1B siRNA restores arterial morphogenesis [63].

Src-homology-2 domain-containing protein tyrosine phosphatase 2 (SHP-2, also known as PTPN11) is another non-receptor type tyrosine phosphatase involved in downregulation of VEGFR-2 signalling [70]. Sinah et al. [71] showed that activation of the dopamine receptor leads to activation of SHP-2, promoting dephosphorylation of VEGFR-2 at tyrosine Y951, Y996, and Y1059, but not at tyrosine Y1175, required for endothelial migration. The close homologue SHP-1 (also known as PTPN6) also negatively regulates VEGFR-2 phosphorylation, but with slightly different specificity [72]. Finally, HCPTPA is another low molecular weight tyrosine phosphatase involved in downregulating VEGFR-2 signalling [73] while VE-PTP dephosphorylates Tie-2 [74, 75].

Future directions and medical applications

Besides Rab GTPases a particular type of lipids, phosphoinositides, which exist in cells in multiply-phosphorylated species localised in distinct subcellular membrane compartments, regulate vesicular protein transport. In addition, the late stage of protein trafficking is regulated by ESCRT proteins, which are involved in transferring proteins from late endosomes into multivesicular bodies and lysosomes [76]. Spatio-temporal regulation of cell signalling is the consequence of receptors being targeted to specific cellular compartments that carry specific signalling molecules. From what was presented here it is obvious that interfering with intracellular protein trafficking

may represent a promising means of modifying signal output.

Pathological angiogenesis is a hallmark of many diseases and plays a role in tumour vascularisation, atherosclerosis [77], wound healing [78], cardiovascular disease [79], in diabetes [80] or in ocular retinopathies [81–83]. The idea of blocking the formation of new blood and lymphatic vessels to prevent tumour growth and metastasis was proposed many decades ago by the late Judah Folkman [84, 85]. Understanding the process of angiogenesis and vasculogenesis in molecular terms sets the stage for the development of new drugs aiming at modulating these processes, either positively in ischaemic tissues, e.g. in diabetic patients, or negatively to block excess vessel growth, such as in attempts to halt or reverse macular degeneration. Treatment of retinopathy patients with inhibitors of VEGF signalling emerged as a highly successful strategy while the original promises to block tumour vascularisation to prevent tumour progression and metastasis have not yet been fulfilled. The limited success of VEGF inhibition in tumour therapy was in the meantime attributed to upregulation of c-Met under hypoxic conditions favouring invasive growth [86]. Clinical trials with combined inhibition of VEGFR-2 and c-Met signalling are currently ongoing. In the future it will be important to improve anti-angiogenic drugs by making them more specific, and to allow for a more targeted approach, in particular to ensure that normal vessels are not affected and thereby avoid serious side effects. Along this line a promising approach may also be to deplete only specific VEGF isoforms such as the pro-angiogenic VEGF A_{165a}, without affecting VEGF A_{165b} levels that may be required to maintain the existing vasculature. This review of VEGFR signalling and trafficking will hopefully arouse new enthusiasm for the development of drugs interfering with intracellular receptor trafficking.

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Correspondence: Philipp Berger, PhD, Paul Scherrer Institute, Molecular Cell Biology, OFLC 101, CH-5232 Villigen, Switzerland, [philipp.berger\[at\]psi.ch](mailto:philipp.berger[at]psi.ch)

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Figures (large format)

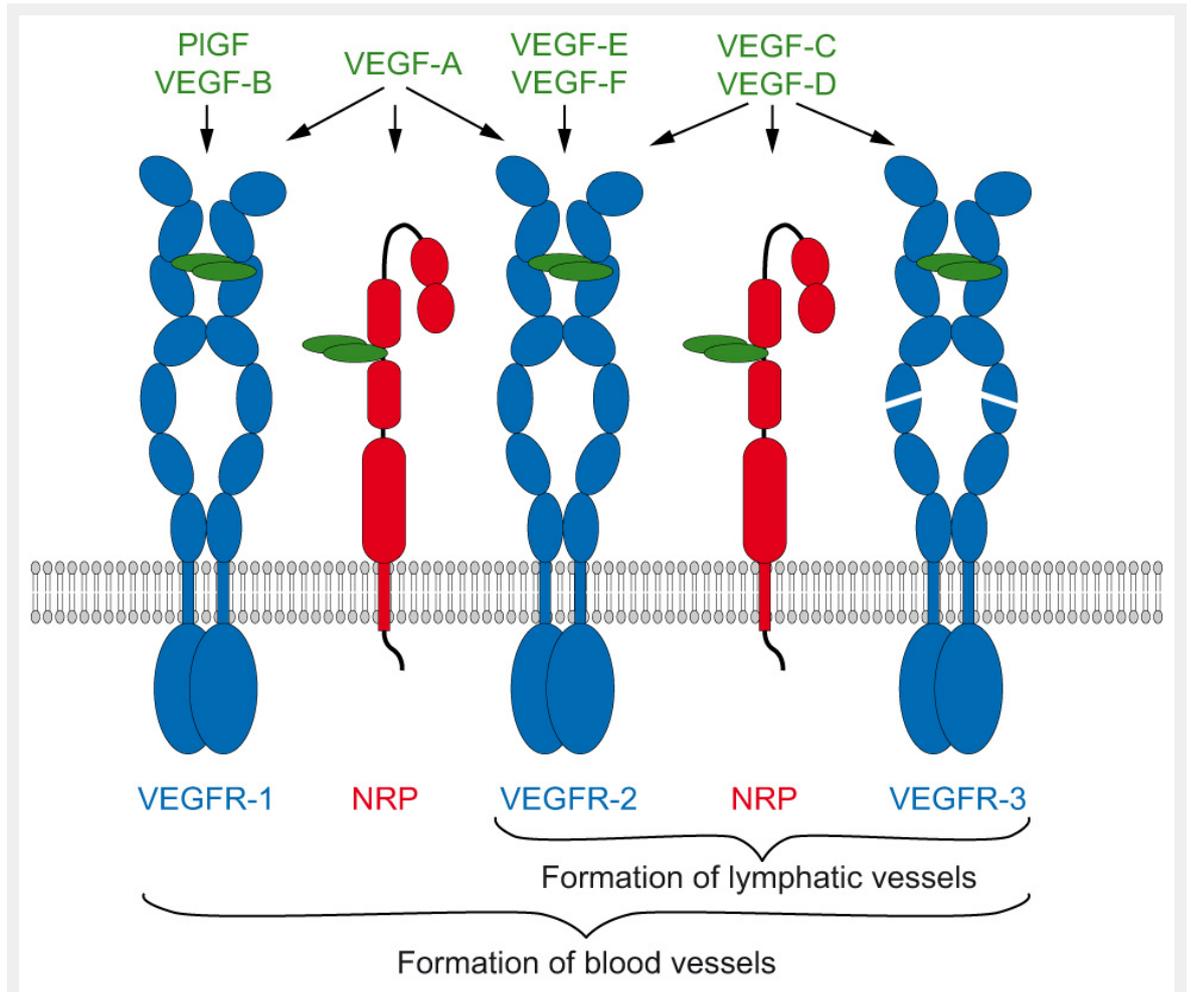


Figure 1

VEGFs and their interactions with VEGFRs and NRPs.

The human genome encodes five VEGF genes (A, B, C, D, and PIGF). Two VEGFs are encoded by viruses (E) and snakes (F), respectively. They all exist as dimers and induce dimerisation of the VEGFRs upon binding. Their binding specificity to the three VEGFRs and NRP-1 is indicated by arrows.

