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# **VEGFR-3 and Tie pathways in vascular network formation**

**Tuomas Tammela**

**Molecular/Cancer Biology Laboratory  
Haartman Institute and Biomedicum Helsinki  
&  
Helsinki Biomedical Graduate School**

**Faculty of Medicine  
University of Helsinki**

*Academic dissertation*

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**Supervisor:**

Kari Alitalo, M.D., Ph.D.  
Research Professor of the Finnish Academy of Sciences  
Molecular/Cancer Biology Laboratory  
Haartman Institute and Biomedicum Helsinki  
University of Helsinki  
Finland

**Reviewers appointed by the Faculty:**

Sirpa Jalkanen, M.D., Ph.D.  
Professor  
MediCity Research Laboratory  
University of Turku  
Finland

and

Tomi Mäkelä, M.D., Ph.D.  
Professor  
Department of Biomedicine  
University of Helsinki  
Finland

**Opponent appointed by the Faculty:**

Douglas Hanahan, Ph.D.  
Professor  
University of California San Francisco  
USA

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## ORIGINAL PUBLICATIONS

The thesis is based on the following original publications, which have been assigned the following roman numerals:

- I **Tammela T**, Saaristo, AS, Lohela M, Morisada T, Tornberg J, Norrmén C, Pajusola K, Thurston G, Suda T, Ylä-Herttuala S, and Alitalo K. Angiopoietin-1 induces lymphatic sprouting and hyperplasia.  
*Blood* 105:4642-4648 (2005)
- II **Tammela T**, Saaristo A, Holopainen T, Lyytikä J, Pitkonen M, Abo-Ramadan U, Ylä-Herttuala S, Petrova T and Alitalo K. Therapeutic differentiation and maturation of collecting lymphatic vessels after lymph node dissection and transplantation.  
*Nature Medicine* 13:1458-1466. (2007)
- III **Tammela T\***, He Y\*, Lyytikä J, Jeltsch M, Markkanen J, Ylä-Herttuala S, Pajusola K, and Alitalo K. Distinct architecture of lymphatic vessels induced by a chimeric VEGF-C/VEGF heparin-binding domain fusion protein.  
*Circulation Research* 100:1460-147 (2007)
- IV **Tammela T**, Zarkada G, Murtomäki A, Wallgard E, Suchting S, Wirzenius M, Waltari M, Hellström M, Schomber T, Peltonen R, Freitas C, Duarte A, Isoniemi H, Laakkonen P, Christofori G, Ylä-Herttuala S, Eichmann A, Betsholtz C, and Alitalo K. Inhibiting VEGFR-3 suppresses angiogenic sprouting and vascular network formation.  
*Nature, in press*

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\* The authors contributed equally to the study.

## ABBREVIATIONS

AAV	adeno-associated virus
Ad	adenovirus
Akt	V-akt murine thymoma viral oncogene homolog-1
Alk	activin receptor-like kinase
AMD	age-related macular degeneration
Ang	angiopoietin
<i>Angpt1</i>	mouse angiopoietin-1 gene
Bcr-Abl	breakpoint cluster region – Abelson leukemia virus homologue
bHLH	basic helix-loop-helix
BM	basement membrane
CA65	VEGF-C/VEGF-exon 7-8 chimera
CA89	VEGF-C/VEGF-exon 6a-8 chimera
CCL	cysteine-cysteine chemokine ligand
CD	cluster of differentiation
COUP-TFII	chicken ovalbumin upstream promoter transcription factor II
CSL	CBF-1/Suppressor of hairless/Lag-1
C-terminal	carboxyterminal
CXCL	cysteine-X-cysteine chemokine ligand
CXCR	CXCL-receptor
Dll	delta-like ligand
DNA	deoxyribonucleic acid
E	embryonic day ... of mouse development (here)
EC	endothelial cell
ECM	extracellular matrix
EDG	endothelial differentiation gene
<i>Efb4</i>	zebrafish EphB4 gene (here)
EGF	epidermal growth factor
EGFR	EGF-receptor
<i>Eng</i>	mouse endoglin gene
eNOS	endothelial nitric oxide synthase
EPC	endothelial progenitor cell
Eph	erythropoietin-producing hepatocellular carcinoma tyrosine kinase
ErbB	erythroblastic leukemia viral oncogene homolog B
FGF	fibroblast growth factor
Flk	fetal liver kinase
Flt	fms-like tyrosine kinase
FN	fibronectin
FoxC2	forkhead box C2
HBD	heparin-binding domain
HB-EGF	heparin-binding EGF
Hes	Hairy/Enhancer of Split-1
Hey	Hes-related (Hesr) with YRPW
HGF	hepatocyte growth factor
HIF-1 $\alpha$	hypoxia-inducible factor-1 $\alpha$
HLTS	hypotrichosis-lymphedema-teleangiectasia syndrome
HSPG	heparan sulfate proteoglycan
Ig	immunoglobulin
IGF	insulin-like growth factor
IL-7R $\alpha$	interleukin-7-receptor- $\alpha$
K14	keratin-14
kDa	kilodalton
KDR	kinase-insert domain receptor
LD	lymphedema distichiasis



LEC	lymphatic endothelial cell
LT	lymphotoxin
LT $\beta$ R	LT $\beta$ -receptor
LTi	lymphoid tissue inducer
LYVE-1	lymphatic vessel hyaluronan receptor-1
MAML-1	mastermind-like-1
MAPK	mitogen-activated protein kinase
mRNA	messenger-RNA
MT1-MMP	membrane-type-1 matrix metalloproteinase (MMP-14)
N-cadherin	neural cadherin
NF- $\kappa$ B	nuclear factor kappa-B
NICD	Notch intracellular domain
NP	neuropilin
N-terminal	aminoterminal
OL-EDA-ID	anhidrotic ectodermal dysplasia with immunodeficiency, osteopetrosis, and lymphedema
OMIM	online Mendelian inheritance of man
PC	proprotein convertase
PCR	polymerase chain reaction
PDGF	platelet-derived growth factor
PDGFR	PDGF-receptor
PDZ	post synaptic density protein (PSD95), <i>Drosophila</i> disc large tumor suppressor (DlgA), and zonula occludens-1 protein (ZO-1) homology domain
PIGF	placenta growth factor
PGC-1 $\alpha$	peroxisome-proliferator-activated receptor-gamma coactivator-1 $\alpha$
Prox1	prospero-related homeobox-1
Rac	Ras-related C3 botulinum toxin substrate
RBP-J	recombination signal binding protein for immunoglobulin kappa J region
Rbpsuh	recombining binding protein – suppressor of hairless
RNA	ribonucleic acid
Robo	roundabout
S1K	sphingosine-1-kinase
S1P	sphingosine-1-phosphate
S1P1	S1P-receptor-1
SCD	superclustering domain
Slp76	SH2 domain containing leukocyte protein of 76 kDa
Smad5	smoothened mothers against decapentaplegly-5
SMC	smooth muscle cell
SOX18	SRY (sex determining region Y)-box 18
Src	sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog
Syk	spleen tyrosine kinase
<i>T<math>\beta</math>rII</i>	mouse TGF- $\beta$ -receptor II gene
TGF- $\beta$	transforming growth factor- $\beta$
<i>Tgfb1</i>	mouse TGF- $\beta$ 1 gene
Tie	tyrosine kinase with immunoglobulin and EGF homology domains
TKI	tyrosine kinase inhibitor
TNF- $\alpha$	tumor necrosis factor- $\alpha$
TRANCE	TNF-related activation induced cytokine
Unc5b	<i>C. elegans</i> unc-5 homolog B
VCAM-1	vascular-cell adhesion molecule-1
VE-cadherin	vascular endothelial cadherin
VEGF	vascular endothelial growth factor
VEGFR	VEGF-receptor
VHL	von Hippel-Lindau
VPF	vascular permeability factor

## ABSTRACT

Angiogenesis, the growth of new blood vessels from pre-existing vasculature, is uncontrolled in tumor growth and insufficient in tissue ischemia. Similarly, the growth of lymphatic vessels, or lymphangiogenesis, is involved in human disease. In particular, insufficient lymphatic vessel function is responsible for development of lymphedema, a debilitating condition characterized by chronic tissue edema and impaired immunity. Vascular endothelial growth factors (VEGFs) stimulate angiogenesis and lymphangiogenesis by activating VEGF receptor (VEGFR) tyrosine kinases in endothelial cells. VEGFR-3 is present on all endothelia during development, but in the adult its expression becomes restricted to the lymphatic endothelium. VEGF-C and VEGF-D are ligands for VEGFR-3, and primarily induce lymphangiogenesis in adult tissues.

The objective of this study was to evaluate the potential of natural and engineered growth factors in inducing therapeutic lymphatic vessel growth, as well as to elucidate the function of VEGFR-3 in angiogenesis in mouse models. Angiopoietin-1 (Ang1), a ligand for the endothelial receptor tyrosine kinases Tie1 and Tie2, induced growth of lymphatic vessels when overexpressed in the skin. A new mouse model of secondary lymphedema was established, which was used to show that collecting lymphatic vessels could be regenerated after lymph node removal using adenoviral gene transfer of VEGF-C or VEGF-D. Notably, the growth factor therapy greatly improved the outcome of lymph node transplantation, including functional reconstitution of the barrier function for tumor metastasis. In order to accelerate the process of lymphatic vessel maturation, novel heparin-binding forms of VEGF-C were engineered. These chimeric growth factors induced formation of lymphatic vessels directly along basement membranes that are rich in heparan sulfate, leading to formation of lumenized lymphatic vessels more efficiently than wild-type VEGF-C.

VEGFR-3 expression was observed specifically in blood vessels undergoing angiogenesis in adult tissues. Notably, VEGFR-3 was highly expressed in angiogenic sprouts, and blocking VEGFR-3 resulted in decreased blood vessel growth in a variety of physiological and pathological settings. Stimulation of VEGFR-3 augmented VEGF-induced angiogenesis and sustained angiogenesis even in the presence of VEGFR-2 inhibitors, whereas blocking both VEGFR-3 and VEGFR-2 in combination resulted in additive inhibition of angiogenesis and tumor growth. Furthermore, these studies indicated that the Notch signaling pathway down-regulates VEGFR-3 in blood vascular endothelial cells, rendering the cells less sensitive to angiogenic signals.

These results constitute the first report of growth factor-induced lymphatic vessel maturation in adults, as well as a novel strategy to accelerate the process by using engineered heparin-binding forms of VEGF-C. The approach of combining growth factor expression with lymph node transplantation provides a basis for future treatment of lymphedema, whereas VEGF/VEGF-C chimeras and angiopoietin-1 could be used to improve and augment VEGF-C/D therapy. Furthermore, these results implicate VEGFR-3 as a novel regulator of sprouting angiogenesis along with its role in regulating lymphatic vessel growth. Targeting VEGFR-3 may provide additional efficacy for anti-angiogenic therapies, especially towards vessels that are resistant to VEGF/VEGFR-2 inhibitors.

## REVIEW OF THE LITERATURE

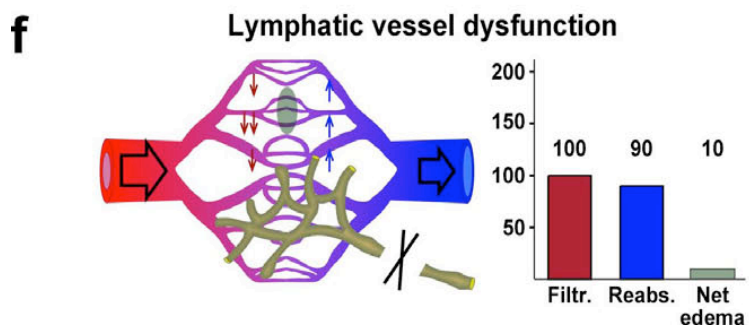
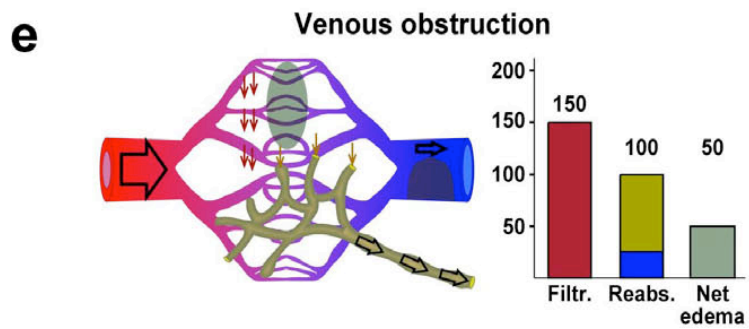
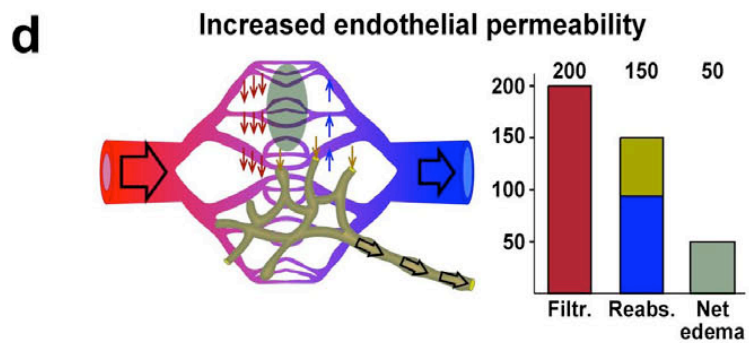
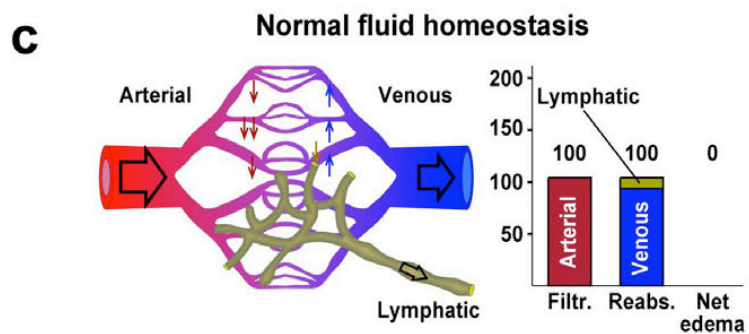
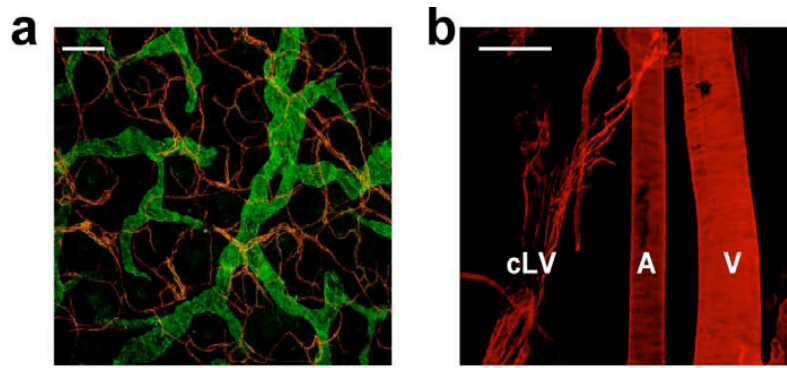
### 1. Development and function of the cardiovascular and lymphatic systems

Large multicellular organisms such as humans have developed a circulatory system, the blood vascular system, to distribute oxygen, nutrients, hormones and even cells to tissues, as well as to collect carbon dioxide and other metabolic waste products. The principal components of blood are red blood cells (erythrocytes), white blood cells (leukocytes), platelets (thrombocytes), immunoglobulins, as well as a variety of colloid proteins that help maintain the water content of blood higher than in the surrounding tissues. The heart pumps the blood through arteries into a fine network of blood vessel capillaries, 10-20  $\mu\text{m}$  in diameter, which connect with veins that return the blood back to the heart. The exchange of gases from the blood to surrounding tissues occurs through the capillaries, which are found within 200  $\mu\text{m}$  of any cell, with the exception avascular tissues such as cartilage, as well as the lens and cornea of the eye (Ambati et al., 2006). Blood pressure causes plasma proteins accompanied by water molecules to filtrate continuously from the arterial side of the capillary bed into the interstitial space. Approximately 90% of the extravasated water is reabsorbed at the venous side of the capillary bed, where the colloid osmotic pressure of the blood exceeds blood pressure, but the remaining 10% results in a net excess of protein-rich fluid in the interstitial space (**Figure 1**).

The main function of the lymphatic vasculature is to return this excess fluid back to the blood circulation system. Fluid, macromolecules, and cells enter blind-ended lymphatic capillaries in tissues. The lymph is further transported towards collecting lymphatic vessels and is returned to the blood circulation through the lymphatico-venous junctions at the subclavian veins. The collecting lymphatic vessels connect with chains of lymph nodes. Therefore the lymphatic vascular system also plays an important role in immune responses by serving as a conduit for extravasated leukocytes and activated antigen-presenting cells. In the small intestine, lacteal lymphatic vessels inside the intestinal villi absorb dietary lipids released by intestinal epithelial cells in the form of chylomicrons. Lymphatic vessels are typically found in all vascularized tissues, with the notable exception of bone marrow and the

central nervous system, although some connections between the lymphatic vascular and cerebrospinal fluid systems exist (Johnston et al., 2004). Besides the fat-adsorbing small intestine, tissues that frequently become in contact with foreign antigens, such as the skin and mucous membranes, are particularly rich in lymphatic vessels. The lymphatic vascular system is found at least in vertebrates such as teleost fish, amphibians, reptiles and mammals (Ny et al., 2005; Kuchler et al., 2006; Yaniv et al., 2006; reviewed in Jeltsch et al., 2003; and in Ny et al., 2006), whose complex cardiovascular system and relatively large body size require the presence of a secondary vascular system for the maintenance of fluid balance (Figure 1).

**Figure 1. Contributions of the blood and lymphatic vascular systems to tissue fluid homeostasis.** (a) Blood vessels (red) and lymphatic vessels (green) in the mouse ear skin visualized by PECAM-1 and LYVE-1 immunostaining, respectively. Note that here the intense LYVE-1 staining overlies weak PECAM-1 staining in the lymphatic vessels. (b) An artery (A), a vein (V), and a collecting lymphatic vessel (cLV) in the mouse ear. Smooth muscle cells are visualized by staining for smooth muscle  $\alpha$ -actin (red). (c-f) Mechanisms leading to tissue edema. Normal fluid homeostasis in tissues is shown in (c): Colloid proteins and associated water are constantly filtrated from the arterial side of the capillary bed into the interstitial space (red arrows). 90% of the filtrate is reabsorbed into the capillaries on the venous side of the capillary bed (blue arrows), whereas 10% is collected by the lymphatic vessels (brown arrows). (d) In conditions of increased blood vascular permeability, such as in inflammation, the amount of filtrate is dramatically increased. Although the lymphatic vessels have a remarkable capacity to increase their drainage, net edema remains. (e) Obstruction of the veins, e.g. due to venous thrombosis, will impair reabsorption and increase blood pressure within the capillary bed, leading to increased filtration. Again, the lymphatic vessels are capable of increasing drainage, yet net edema is generated. (f) Inherited or acquired damage to the lymphatic vessels, such as surgery or radiation therapy, block lymphatic drainage. This will lead to gradual accumulation of edematous fluid in tissues. Reabs: reabsorption; Filtr: filtration. The units in the bar graphs are arbitrary. Note: Only the underlying reasons for edema formation are given in each figure, and secondary effects due to e.g. increased interstitial fluid pressure in edematous conditions are not accounted for. Scalebars: 100  $\mu$ m.



## The blood vascular system

The luminal surface of blood vessels is lined by a monolayer of endothelial cells (ECs), which are adjoined by tight junctions and the more plastic adherens junctions (reviewed in Risau, 1998). Far from being passive bystanders, ECs have multiple functions: They regulate blood flow by releasing nitric oxide to relax smooth muscle that constricts vessels; act as gatekeepers for cells and macromolecules in between the blood and the interstitium; and respond to growth factors that stimulate the formation of new blood vessels. Besides adopting arterial or venous identity in their gene expression pattern (reviewed in Hirashima and Suda, 2006), ECs exhibit a wide range of functional and morphological differences. For example, the capillary endothelium of endocrine organs, such as the thyroid and adrenal glands, and the  $\beta$ -islets of the pancreas, is fenestrated, allowing a high rate of transport across the EC monolayer (reviewed in Risau, 1998). On the other hand, ECs of the central nervous system form part of the blood-brain barrier, which allows only very selective passage of molecules and cells. The high-endothelial venules found in secondary lymphoid organs (with the exception of the spleen) are specialized for cell transmigration, allowing entry of lymphocytes into the lymphoid tissues. Furthermore, even ECs that appear ultrastructurally similar have unique tissue-specific molecular fingerprints, which has facilitated the discovery of tissue-specific vascular targets (reviewed in Ruoslahti and Rajotte, 2000; and in Trepel et al., 2002).

The basolateral side of the blood vascular EC monolayer, with the exception of blood vessels with a discontinuous endothelium found in the liver, spleen and bone marrow, is lined with a basement membrane (BM), an approximately 50-100 nm thick sheet of extracellular matrix (ECM). The EC monolayer is also supported by mesenchymal mural cells called pericytes, which share the BM with the ECs. The pericytes become in contact with the ECs at focal points called peg-socket contacts, conferring survival and stability signals to the endothelium, and providing physical support against hemodynamic stress (reviewed in Armulik et al., 2005; and in von Tell et al., 2006). Arteries are also surrounded by a tunica media composed of a concentric ring of contractile smooth muscle cells (SMCs), which regulate blood pressure and flow, and an outer connective tissue layer, the tunica adventitia. The return of the blood to the heart via the veins is powered by contractions of the

surrounding skeletal muscle and venous SMCs, as well as by arterial pulsations, whereas intraluminal valves positioned at intervals help to prevent venous backflow.

During embryogenesis, the cardiovascular system is the first organ system to develop. The hematopoietic and EC lineages differentiate from a common precursor, the hemangioblast. The early blood vessels of the embryo and yolk sac in mammals develop by aggregation of EC precursors, or angioblasts, which are derived from hemangioblasts, into a primitive vascular plexus (reviewed in Coultas et al., 2005). This assembly of a vascular network by ECs that have differentiated *de novo* from stem cells is termed vasculogenesis. The early vascular plexus undergoes a complex expansion process that is characterized by migration, sprouting and proliferation of ECs. This formation of new blood vessels by sprouting from pre-existing vasculature is denoted angiogenesis. Angiogenic sprouting involves specification of subpopulations of ECs into tip cells, that respond to guidance cues in the surrounding microenvironment, and stalk cells that follow the tip cells and proliferate to form a lumenized vascular network (Gerhardt et al., 2003).

The ECs of the newly formed blood vessels adopt an arterial, venous, or capillary identity, while the nascent vascular network is remodeled by pruning of excess vessels and by the recruitment of pericytes. Interestingly, angiogenesis and organogenesis are closely linked processes, as evidenced by the crucial role of ECs in the induction of e.g. the liver and the pancreas (Lammert et al., 2001; Matsumoto et al., 2001; LeCouter et al., 2003; Yoshitomi and Zaret, 2004; reviewed in Lammert et al., 2003). During pre- and postnatal development after organogenesis, the blood vessel networks meet the requirements of growing organs by expanding within the tissues by angiogenic sprouting as well as by splitting, intussusception, and circumferential enlargement, which are processes that remain poorly understood (Djonov et al., 2000).

Physiological neovascularization is uncommon in stable adult tissues. However, new blood vessels form in response to tissue hypertrophy in e.g. skeletal muscle or fat, during wound healing, and during the estrus cycle in fertile females both in developing ovarian follicles as well as in the uterine endometrium (Zimmermann et al., 2003; reviewed in Carmeliet, 2005). The neovascularization of adult tissues is thought to occur primarily by angiogenesis, but the possibility of adult vasculogenesis by bone-marrow derived endothelial precursor cells (EPCs) has also been suggested in the literature (reviewed in Aicher et al., 2005; and in Kopp et al., 2006). Pathological angiogenesis occurs in a variety of conditions,

such as in tumors and in proliferative retinal vasculopathies, like age-related macular degeneration (AMD) and in late-stage diabetic retinopathy (reviewed in Gariano and Gardner, 2005). Conversely, angiogenesis is frequently insufficient in ischemic tissues e.g. following arterial occlusion in the heart or the lower limb.

Arteriogenesis, or remodeling of angiogenic blood vascular capillaries or small arterioles into larger caliber vessels that acquire a thick SMC coating, is known to occur in ischemic conditions (reviewed in Schaper and Scholz, 2003). Circumferentially directed stress and shear stress acting on the endothelium are key forces that drive arteriogenesis, and changes in fluid flow have been shown to regulate gene expression in both blood and lymphatic vascular ECs (Garcia-Cardena et al., 2001; Ng et al., 2004; reviewed in Schaper and Scholz, 2003). Furthermore, reactive inflammation of the vessel wall and recruitment of monocytes/macrophages are important for arteriogenesis (Ito et al., 1997; Arras et al., 1998; Pipp et al., 2003)

### The lymphatic vascular system

The lymphatic capillaries are thin-walled vessels of approximately 30-80  $\mu\text{m}$  in diameter, and composed of a single layer of non-fenestrated lymphatic endothelial cells (LECs), which are not ensheathed by pericytes or SMCs, and have little or no BM (Leak and Burke, 1966; Leak and Burke, 1968; Leak, 1970). The LEC-LEC junctions in lymphatic capillaries are discontinuous, and the interjunctional gaps act as sites of leukocyte entry into the vessels (Baluk et al., 2007). Collecting lymphatic vessels are characterized by the presence of a SMC layer, a basement membrane, continuous interendothelial junctions, and valves (reviewed in Alitalo et al., 2005). The intrinsic contractility of SMCs, as well as the contraction of surrounding skeletal muscles and arterial pulsations are necessary for lymph propulsion, whereas valves prevent lymph backflow, implying an analogous structure-function relationship between collecting lymphatic vessels and veins. The LECs are terminally differentiated cells distinct from blood vascular ECs. Both cell types remain distinct also in culture conditions (Kriehuber et al., 2001; Mäkinen et al., 2001; Wick et al., 2007), which has facilitated the discovery of lymphatic vascular specific molecular targets that are used for identification of lymphatic vessels in tissues, as well as for finding targets



for the specific induction or inhibition of lymphatic vessel growth in pathological conditions (reviewed in Saharinen et al., 2004). The most commonly used lymphatic vessel markers are the prospero-related homeodomain transcription factor Prox1, the membrane glycoprotein podoplanin, vascular endothelial growth factor receptor-3 (VEGFR-3), and lymphatic vessel hyaluronan receptor-1 (LYVE-1) (reviewed in Saharinen et al., 2004). Notably, LYVE-1 expression is restricted to the lymphatic capillaries and it is not found in the collecting vessels (Makinen et al., 2005).

Genetic experiments in mice have validated that mammalian lymphatic vessels originate from embryonic veins (Wigle and Oliver, 1999; Wigle et al., 2002; Kärkkäinen et al., 2004; Srinivasan et al., 2007), as postulated by the American immunologist Florence Sabin already in 1902 (Sabin, 1902). Several timely papers utilizing dynamic imaging in developing zebrafish embryos have elegantly demonstrated that this process is conserved in evolution (Kuchler et al., 2006; Yaniv et al., 2006). According to this model of lymphatic vessel development, a subset of ECs in the large central veins of the embryo begin to express Prox1, signifying commitment to the LEC lineage, and sprout laterally to form primordial lymphatic vascular structures, the lymph sacs, which expand by sprouting to form the lymphatic vascular network (Wigle and Oliver, 1999; Petrova et al., 2002; reviewed in Oliver, 2004). Compared to the emergence of blood vessels, lymphatic vessels develop considerably later, at around embryonic weeks 6-7 in humans and at embryonic day (E) 10.5 in mice. However, it is not known whether lymphatic endothelium can differentiate in the embryonic mesenchyme in mammals, as has been suggested by experiments in chicks (Wilting et al., 2000; Wilting et al., 2006).

During the course of development, connections between the lymphatics and veins are lost, except the sites where lymph enters the blood in the subclavian veins, although additional lymphatico-venous communications may exist in other peripheral locations (reviewed in Jeltsch et al., 2003). Mice with homozygous mutations in either the tyrosine kinase Syk or the adaptor protein Slp76 display arterio-venous shunts and abnormal lymphatico-venous communications (Abtahian et al., 2003). Syk and Slp76 are expressed almost exclusively in hematopoietic cells, suggesting that these cells contribute to the separation of the two vascular systems (Abtahian et al., 2003; Sebzda et al., 2006).

In adults, lymphangiogenesis occurs physiologically during inflammation, ovarian growth, and wound healing (Pullinger and Florey, 1937; Otsuki et al., 1986; Paavonen et al.,

2000; Baluk et al., 2005). Lymphatic vessel growth is also associated with a number of pathological conditions, including tumor metastasis and transplant rejection (Cursiefen et al., 2004; Kerjaschki et al., 2004; reviewed in Stacker et al., 2002; and in Alitalo et al., 2005). Adult lymphangiogenesis occurs primarily by sprouting from pre-existing vessels (Saaristo et al., 2002a; He et al., 2004; He et al., 2005), although bone-marrow derived cells, such as macrophages, have been suggested to transdifferentiate into lymphatic endothelium at least in human kidney transplants (Kerjaschki et al., 2006), and in a mouse model of corneal injury (Maruyama et al., 2005).

Remodeling of the blood vasculature into arteries, capillaries, and veins is known to play a critical role in the development of a functional blood vessel network. Although the lymphatic vasculature also undergoes significant remodeling after its initial establishment, the molecular mechanisms involved in these processes are largely unknown. Developmental remodeling of the lymphatic vasculature includes sprouting of lymphatic capillaries from the primary lymphatic plexus, while deeper lymphatic vessels recruit SMCs and develop lymphatic valves, acquiring a collecting vessel phenotype (reviewed in Kärpanen and Alitalo, 2007). The ephrins and their Eph receptors have been implicated in repulsive axon guidance in the nervous system, and in controlling blood vessel remodeling (reviewed in Adams, 2002; and in Coultas et al., 2005). Mutant mice lacking the PDZ domain of ephrinB2 develop normal blood vasculature, but display hyperplasia of the collecting lymphatic vessels, lack of luminal valve formation, and failure to remodel the primary lymphatic capillary plexus (Makinen et al., 2005). The forkhead transcription factor FoxC2 is highly expressed in the developing lymphatic vessels as well as in lymphatic valves in adults (Dagenais et al., 2004; Petrova et al., 2004). The early development of lymphatic vessels proceeds normally in the absence of *Foxc2*, but the collecting lymphatic vessels in *Foxc2*<sup>-/-</sup> mice lack valves, whereas the lymphatic capillaries acquire an ectopic coverage by BM components and SMCs, indicating that FoxC2 controls the specification of the lymphatic capillary versus collecting lymphatic vessel phenotype (Petrova et al., 2004).

## Lymph nodes

The first lymph nodes begin to develop as protrusions of connective tissue into the lymph sacs at around E12.5. Lymph node induction is initiated by lymphoid tissue inducer (LTi) cells of hematopoietic origin, which express interleukin-7-receptor- $\alpha$  (IL-7R $\alpha$ ), CD45, and CD4, but lack CD3 (Mebius et al., 1997; reviewed in Mebius, 2003). These cells differentiate from CD45-/CD4-/CD3- precursor cells in response to tumor necrosis factor(TNF)-related activation induced cytokine (TRANCE) (Kim et al., 2000a). Signaling via IL-7R $\alpha$  induces the LTi cells to produce lymphotoxin- $\alpha$ 1 $\beta$ 2 (LT $\alpha$ 1 $\beta$ 2), a member of the TNF family, and associate with stromal cells expressing vascular-cell adhesion molecule-1 (VCAM-1) and the LT $\beta$ -receptor (LT $\beta$ R) (Yoshida et al., 2002). Both LT $\alpha$ 1 $\beta$ 2 and LT $\beta$ R are absolutely required for lymph node development, which highlights the importance of this signaling pathway in lymphoid organogenesis (De Togni et al., 1994; Rennert et al., 1998).

The lymphoid chemokine CXCL13 activates CXCR5 in the LTi cells, leading to increased CXCL13 production from the surrounding cells in a positive feedback loop, as well as expression of activated  $\alpha$ 4 $\beta$ 1 integrin, a cell-ECM adhesion molecule, in the LTi cells (Ansel et al., 2000; Finke et al., 2002). The stromal cell VCAM-1 activates integrin  $\alpha$ 4 $\beta$ 1, resulting in increased expression of adhesion molecules and secreted chemokines, such as CCL19, CCL21, CXCL12, and CXCL13 (Finke et al., 2002). This will lead to the amplification of both the LTi and the stromal cell populations, and presumably also to the differentiation of resident blood vessels into high-endothelial venules (reviewed in Mebius, 2003). The emergence of these vessels allows T- and B-cells, attracted by CCL 19, CCL21, CXCL12, and CXCL13 signals, to enter the lymph node from the bloodstream (Cyster, 1999; Okada et al., 2002). These chemokines are also required for the organization of the lymph node into B-cell follicles, which become surrounded by T-cell areas (Forster et al., 1996; Forster et al., 1999; Gunn et al., 1999; Ansel et al., 2000; Luther et al., 2000)

Continuous influx of antigen-presenting cells through the afferent lymphatics is required for the maintenance of organized lymph nodes (Mebius et al., 1991). Although lymph nodes are highly plastic organs in adults, it is not known whether lymph nodes can form spontaneously after embryogenesis. Interestingly, artificial lymph nodes composed of collagen scaffolds have been shown to attract lymphocytes, which elicit immune responses in mouse models, suggesting an approach for the replacement of damaged lymph nodes or for

the augmentation of regional immune responses (Okamoto et al., 2007). So-called tertiary lymphoid organs consisting of clonally expanding B-cell follicles and T-cells are commonly found at sites of chronic inflammation. The organization of these structures may involve many of the same chemokines involved in lymph node development (reviewed in Mebius, 2003; and in Drayton et al., 2006).

## 2. Molecular mechanisms of angiogenesis and lymphangiogenesis

### Vascular endothelial growth factors and their receptors

The mammalian vascular endothelial growth factor (VEGF) gene family comprises five dimeric glycoproteins: VEGF, VEGF-B, VEGF-C, VEGF-D and placenta growth factor (PlGF). VEGFs bind and activate their cognate high-affinity VEGF-receptor (VEGFR) tyrosine kinases (**Figure 2**), but also interact with neuropilins (NPs) and several integrin class cell adhesion molecules (reviewed in Ferrara et al., 2003; and in Tammela et al., 2005a).

VEGFRs are composed of seven extracellular immunoglobulin (Ig) homology domains, a single transmembrane region, and a C-terminal intracellular tyrosine kinase domain that is interrupted by a kinase-insert domain (Figure 2). Binding of the VEGF ligand induces receptor dimerization and autophosphorylation, as well as C-terminal phosphorylation of the receptors by intracellular tyrosine kinases. This is followed by the docking and subsequent activation of various intracellular downstream signaling molecules. The signals from tyrosine kinase receptors such as VEGFRs typically converge at mitogen-activated protein kinases (MAPKs), actin cytoskeleton-activating proteins and the serine/threonine kinase Akt, which promote cell proliferation, migration, and survival, respectively (reviewed in Olsson et al., 2006). The outcome of VEGFR signals is context-dependent, i.e. determined by the gene expression profile and the activity of other signaling pathways within the cell, as well as by the surrounding microenvironment (reviewed in Olsson et al., 2006).

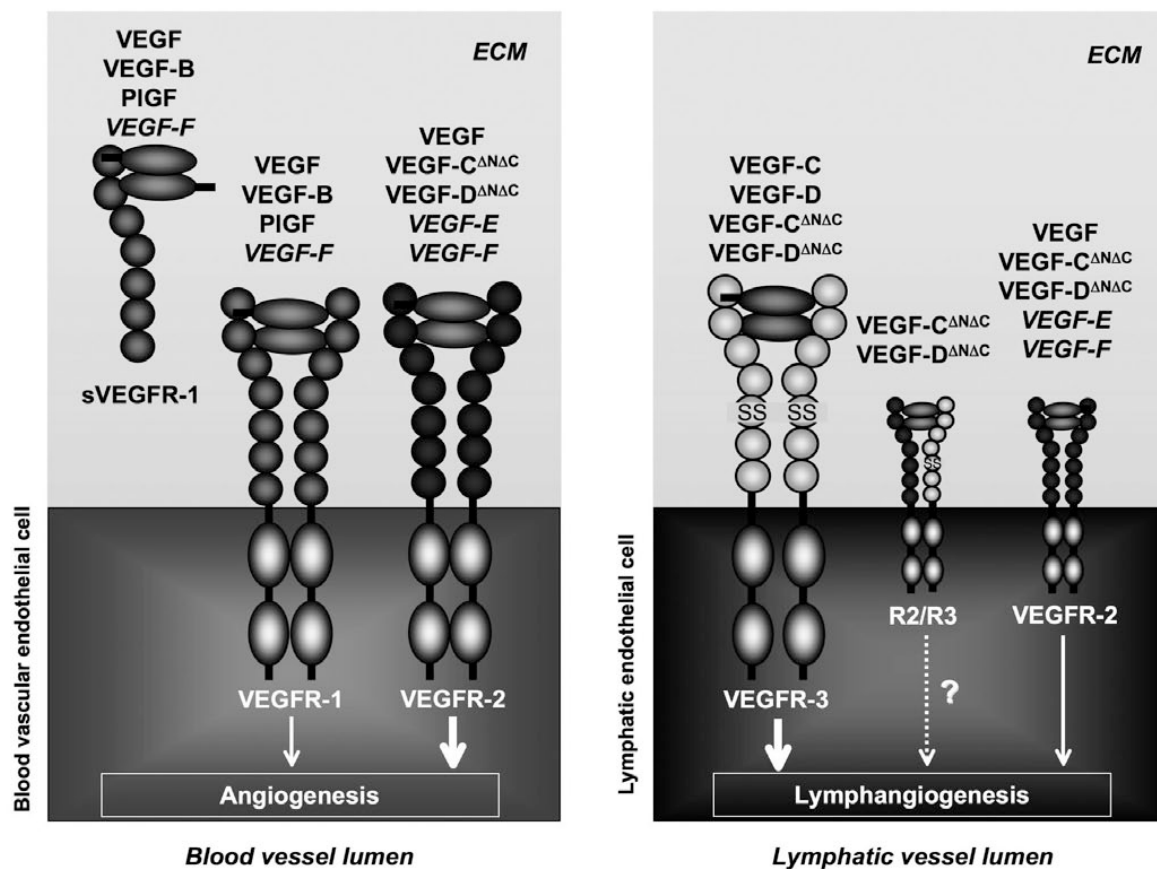
Over the past two decades, the VEGFs and their receptors have been shown to be essential regulators of vasculogenesis, angiogenesis and lymphangiogenesis (reviewed in Ferrara, 2005; and in Tammela et al., 2005a). This signaling system also plays a role in immune function, and recent evidence indicates that it may also regulate neurogenesis and motoneuron survival (Oosthuysen et al., 2001; reviewed in Carmeliet and Tessier-Lavigne, 2005; Greenberg and Jin, 2005; and in Carvalho et al., 2007).

## *VEGF*

VEGF (also known as VEGF-A) was the first member of the *VEGF* gene family to be discovered (Senger et al., 1983; Ferrara and Henzel, 1989; Leung et al., 1989). Later studies demonstrated that VEGF is a ligand for VEGFR-1 and VEGFR-2 (De Vries et al., 1992; Quinn et al., 1993), as well as for NP-1 and NP-2 (Soker et al., 1998; Gluzman-Poltorak et al., 2000), and that it induces EC proliferation, sprouting, migration and tube formation (reviewed in Ferrara, 2005; and in Olsson et al., 2006). VEGF is also a survival factor for ECs during physiological and tumor angiogenesis, as it induces the expression of anti-apoptotic proteins (Benjamin and Keshet, 1997; Gerber et al., 1998). VEGF was originally denoted vascular permeability factor (VPF), as it potently increases blood vascular permeability via VEGFR-2 and Src-mediated phosphorylation of VE-cadherin, and subsequent disintegration of endothelial adherens junction complexes (Senger et al., 1983; reviewed in Bazzoni and Dejana, 2004; and in Gavard and Gutkind, 2006). VEGF also causes vasodilation through the induction of the endothelial nitric oxide synthase (eNOS) and subsequent increase in nitric oxide production, which leads to the relaxation of vascular SMCs (Hood et al., 1998; Kroll and Waltenberger, 1999).

Although VEGF is ubiquitously expressed during embryonic development, the expression is more pronounced at sites of active vasculogenesis and angiogenesis (reviewed in Weinstein, 1999). Mice lacking even a single VEGF allele die by E12.5 from defects in blood island formation, EC development, and vascular assembly, which highlights the central role of VEGF in angiogenesis (Carmeliet et al., 1996; Ferrara et al., 1996). VEGF is strongly induced in hypoxic conditions via hypoxia-inducible factor (HIF)-regulated elements of the VEGF gene promoter (reviewed in Pugh and Ratcliffe, 2003). In hypoxic conditions, the constitutive degradation of HIF-1 $\alpha$  is blocked by the inactivation of oxygen-dependent prolyl hydroxylases, followed by stabilization of HIF-1 $\alpha$ , its binding to hypoxia-responsive elements in the promoters of hypoxia-inducible genes involved in glucose transport, glycolysis, erythropoiesis and angiogenesis (reviewed in Pugh and Ratcliffe, 2003). Interestingly, VEGF was recently shown to also be induced independently of HIF-1 $\alpha$  by the lack of nutrients via induction of the transcriptional coactivator PGC-1 $\alpha$  (peroxisome-proliferator-activated receptor-gamma coactivator-1 $\alpha$ ), a potent metabolic sensor and regulator (Arany et al., 2008).

Overexpression of VEGF or application of recombinant VEGF leads to robust angiogenesis in a multitude of biological model systems (reviewed in Tammela et al., 2005a). Interestingly, adenoviral or transgenic overexpression of VEGF in the skin was shown to induce lymphatic vessel enlargement, but not lymphatic vessel sprouting (Nagy et al., 2002; Saaristo et al., 2002a; Wirzenius et al., 2007). At least in midgestation mouse embryos, VEGF-C but not VEGF had the capacity to induce migration of ECs committed to the lymphatic endothelial lineage (Kärkkäinen et al., 2004).



**Figure 2. Vascular endothelial growth factors (VEGFs) and VEGF receptors (VEGFRs).** Schematic representation of the VEGF family growth factors (ovals), and the VEGFR tyrosine kinases. The VEGFs are antiparallel dimers, which induce dimerization and activation of their cognate receptors upon binding. VEGFRs are composed of seven immunoglobulin-like domains (spheres) and a split tyrosine kinase domain (double ovals). The fifth Ig-like domain of VEGFR-3 is proteolytically cleaved, leaving the fourth and sixth Ig-loops attached by a disulfide bond (SS). In adult tissues, VEGFR-1 and VEGFR-2 are predominantly expressed in blood vascular endothelial cells, whereas VEGFR-3 is expressed in lymphatic vascular endothelium. Low levels of VEGFR-2 are found in lymphatic endothelial cells, and therefore VEGFR-3/VEGFR-2 heterodimers may form in these cells. VEGF-E and VEGF-F (in italics) are not mammalian growth factors, being derived from Orf viruses and snake venoms, respectively. ECM: extracellular matrix; sVEGFR-1: soluble VEGFR-1; <sup>ΔNΔC</sup>: Fully processed forms of VEGF-C and VEGF-D lacking the N- and C-terminal propeptides.

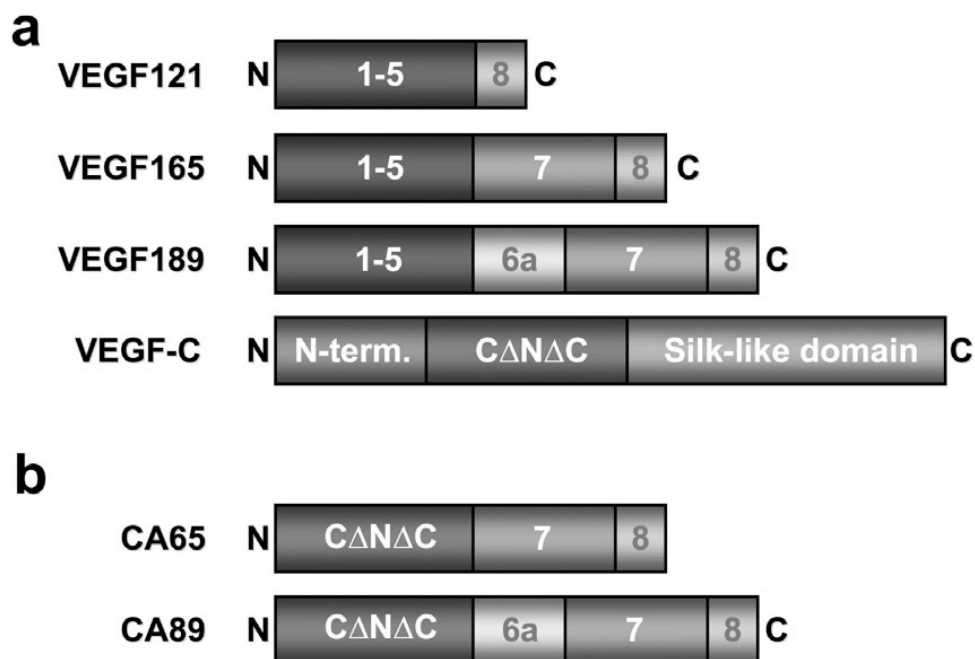
## *VEGF-C and VEGF-D*

VEGF, PlGF and VEGF-B isoforms are formed through alternative splicing, whereas different forms of VEGF-C and VEGF-D are the result of proteolytic processing. Both growth factors are produced as precursor proteins, which are activated by intracellular secretory proprotein convertases (PC) such as furin, PC5, and PC7 (Joukov et al., 1997; Siegfried et al., 2003; McColl et al., 2007). The secreted, disulphide-linked 31/29 kD VEGF-C subunits only bind VEGFR-3, but the factor is further proteolyzed in the extracellular environment by plasmin and other proteases to generate a 21 kD non-disulfide-linked homodimeric protein with high affinity for both VEGFR-2 and VEGFR-3 (Joukov et al., 1997) (**Figure 3a**). VEGF-C induces proliferation, migration, and survival of ECs (reviewed in Tammela et al., 2005b). During development, VEGF-C is expressed predominantly in regions where lymphatic vessels develop (Kukk et al., 1996; Kärkkäinen et al., 2004). In adults, VEGF-C expression remains high in the lymph nodes (Lymboussaki et al., 1999), arterial SMCs (Partanen et al., 2000), and cortical regions of the brain (P. Haiko and T. Tammela, unpublished). Overexpression of VEGF-C potently induces lymphangiogenesis with little angiogenesis as demonstrated by early experiments in the chick chorioallantoic membrane, and in transgenic mice overexpressing VEGF-C in the skin (Jeltsch et al., 1997; Oh et al., 1997). Adenoviral VEGF-C or VEGF-D gene transduction has been shown to induce growth of lymphatic capillaries in several animal models, although the mature form of human VEGF-D also potently promotes angiogenesis at least in rabbit skeletal muscle (Rissanen et al., 2003). Human VEGF-C and VEGF-D also increase blood vascular permeability by activating VEGFR-2 (Veikkola et al., 2001; Saaristo et al., 2002b). Specific activation of VEGFR-3 with a mutant form of VEGF-C (VEGF-C<sup>C156S</sup>) is sufficient to induce lymphangiogenesis *in vivo* without effects on blood vessels (Joukov et al., 1998; Veikkola et al., 2001; Saaristo et al., 2002b; Wirzenius et al., 2007). Mouse VEGF-D binds only VEGFR-3, suggesting a more limited function for VEGF-D in mice when compared to humans (Baldwin et al., 2001).

Homozygous deletion of *Vegfc* leads to the complete absence of a lymphatic vascular system in mouse embryos, whereas *Vegfc*<sup>+/-</sup> mice display severe lymphatic hypoplasia, indicating an analogous requirement of VEGF-C for lymphangiogenesis as has been described for VEGF in angiogenesis (Kärkkäinen et al., 2004). In mice, *Xenopus laevis*



tadpoles, and zebrafish where *Vegfc* has been inactivated, LECs initially differentiate in the embryonic cardinal veins, but fail to migrate and form the primary lymph sacs (Kärkkäinen et al., 2004; Ny et al., 2005; Kuchler et al., 2006). In contrast, deletion of *Vegfd* does not affect development of the lymphatic vasculature in mice, although exogenous VEGF-D protein rescues the impaired vessel sprouting in *Vegfc*<sup>-/-</sup> embryos (Kärkkäinen et al., 2004; Baldwin et al., 2005).



**Figure 3. The primary structure of VEGF, VEGF-C, and the VEGF-C/VEGF chimeras used in the study.** (a) The predominant human VEGF isoforms VEGF121, VEGF165, and VEGF189 are formed as a result of alternative splicing. The numbers refer to VEGF exons. VEGF165 and VEGF189 contain exon 7 with neuropilin and heparin-binding sequences. In addition, VEGF189 contains exon 6a, which increases the affinity of the growth factor towards heparin. VEGF-C is produced as a single prepropeptide, which is proteolytically cleaved in intracellular processing compartments to yield the secreted form that contains an aminoterminal propeptide (N-term.), as well as a carboxyterminal silk-like propeptide. The propeptides are cleaved in the extracellular environment by proteases to yield the mature growth factor, VEGF-CΔNΔC (CΔNΔC). (b) The chimeric growth factors have been generated by replacing the receptor-binding domains of VEGF165 and VEGF189 with VEGF-CΔNΔC to generate CA65 and CA89, respectively. These factors bind VEGFR-2 and VEGFR-3, like VEGF-CΔNΔC, but in addition have the capacity to bind heparin and neuropilins (III).

VEGF-C mRNA is induced in tumor cells by a variety of growth factors and oncogenes, but not hypoxia, indicating that VEGF-C does not collaborate with VEGF in the initiation of angiogenic responses (Enholm et al., 1997). On the other hand, VEGF-C is induced in ECs in response to pro-inflammatory cytokines (Ristimäki et al., 1998), suggesting that VEGF-C could regulate lymphatic vessel function during inflammation, possibly reflecting the role of the lymphatic vasculature in the control of immune function and leukocyte trafficking. Accordingly, both VEGF-C and VEGF-D are produced by leukocytes, particularly macrophages, at sites of inflammation (Baluk et al., 2005).

#### *Placenta growth factor and VEGF-B*

Placenta growth factor (PlGF) and VEGF-B homodimers bind VEGFR-1 and NP-1, and *Plgf* or *Vegfb* gene-targeted mice survive and lead apparently normal lives (Bellomo et al., 2000; Carmeliet et al., 2001a). However, *Plgf* null mice recover poorly from experimental myocardial infarction, and show impaired collateral formation in response to hind limb ischemia (Carmeliet et al., 2001a). Overexpression of PlGF in the skin of transgenic mice results in marked hyperplasia of cutaneous blood vessels with increased inflammatory and permeability responses, while local administration of PlGF potently promotes arteriogenesis (Luttun et al., 2002; Odorisio et al., 2002; Oura et al., 2003; Pipp et al., 2003). The effects of PlGF are thought to be mediated by displacement of VEGF from VEGFR-1, leading to more VEGF available for the activation of VEGFR-2, and by the recruitment of VEGFR-1 expressing monocytes/macrophages, which are also important for the development of tumor stroma (Carmeliet et al., 2001b; Pipp et al., 2003; Fischer et al., 2007). The biological role of VEGF-B is poorly characterized. Overexpression of VEGF-B does not lead to angiogenesis or to the recruitment of bone-marrow-derived cells. However, as VEGF-B is highly expressed in striated muscle, myocardial muscle, and brown fat, its function may be linked to high cellular energy metabolism (Enholm et al., 1997; Salven et al., 1998).

## *VEGFR-1*

VEGFR-1 (fms-like tyrosine kinase-1, Flt1) transmits weak mitogenic signals in ECs, but it can heterodimerize with VEGFR-2, forming a complex with altered signaling properties when compared to VEGFR-1 or VEGFR-2 homodimers (Fong et al., 1995; Carmeliet et al., 2001b; Huang et al., 2001). VEGFR-1 is expressed in ECs and in monocytes/macrophages (Zachary and Glick, 2001). In fact, VEGFR-1 mediated angiogenesis and arteriogenesis have been shown to be dependent on monocytes, and angiogenesis in experimental tumors is at least partially inhibited by anti-VEGFR-1 antibodies (Luttun et al., 2002; Pipp et al., 2003). *Vegfr1* gene targeted mice die between E8.5 and E9.5 due to disorganization of blood vessels and excessive commitment of mesenchymal stem cells to the hemangioblast lineage (Fong et al., 1995; Fong et al., 1999). Mice lacking only the intracellular tyrosine kinase domain of VEGFR-1 are normal except for impaired angiogenesis during pathological conditions, suggesting a VEGF-trapping function at least during the early stages of vascular development (Hiratsuka et al., 1998; Hiratsuka et al., 2001). The naturally occurring soluble VEGFR-1 ectodomain (sVEGFR-1) potently blocks VEGF-induced angiogenesis (Carmeliet et al., 2001b; Gerhardt et al., 2003). High levels of circulating sVEGFR-1 correlate with the incidence of pre-eclampsia, a syndrome where hypertension arises in pregnancy in association with significant proteinuria (Levine et al., 2004; Levine et al., 2006).

## *VEGFR-2*

VEGFR-2 is also known as fetal liver kinase-1 (Flk1) and kinase-insert domain receptor (KDR) (reviewed in Ferrara et al., 2003). The binding affinity of VEGF towards VEGFR-2 is approximately 10-fold lower than for VEGFR-1, yet VEGFR-2 is the primary receptor transducing VEGF signals in ECs, including the induction of vascular permeability responses (Meyer et al., 1999; Wise et al., 1999; Gille et al., 2001). VEGF-E (viral VEGF) is a VEGFR-2 specific ligand that is encoded by the parapoxviruses Orf-NZ2 and Orf-NZ7 (Ogawa et al., 1998; Meyer et al., 1999). Certain viper venoms contain VEGF-like proteins, collectively termed as VEGF-F, which bind both VEGFR-2 and VEGFR-1 (Suto et al., 2005;

Tokunaga et al., 2005; Yamazaki et al., 2005a; Yamazaki et al., 2005b). VEGF-E and VEGF-F lack the C-terminal heparin-binding domain found in other heparin-binding VEGFs, and differ in the structure of their receptor binding domain from other VEGFs (Ogawa et al., 1998; Meyer et al., 1999; Suto et al., 2005).

VEGFR-2 gene targeted mice die at E8.5-E9.5 due to lack of development of the blood islands, embryonic vasculature and hematopoietic cells (Shalaby et al., 1995; Gille et al., 2001). VEGFR-2 expression is downregulated in the adult blood vascular ECs, but low levels of VEGFR-2 and autocrine VEGF signaling are required for EC survival even in quiescent vessels (Partanen et al., 1999; Lee et al., 2007). Furthermore, constitutive VEGFR-2 expression maintains ECs responsive to angiogenic VEGF signals, which upregulate VEGFR-2 in the endothelium (Gerhardt et al., 2003; Suchting et al., 2007). During angiogenic sprouting, VEGFR-2 is particularly strongly expressed in the endothelial tip cells, rendering the tip cells most sensitive to VEGF signals (Gerhardt et al., 2003).

Low levels of VEGFR-2 are also found in lymphatic endothelium, but VEGFR-2 signals alone are not sufficient for inducing sprouting lymphangiogenesis (Nagy et al., 2002; Saaristo et al., 2002a; Wirzenius et al., 2007). In fact, careful dissection of the VEGFR-2 and VEGFR-3 pathways utilizing receptor-specific ligands and VEGFR-blocking antibodies demonstrated that VEGFR-3 signals are required for lymphatic vessel sprouting, whereas VEGFR-2 activation leads to circumferential enlargement of the vessels (Wirzenius et al., 2007).

### *VEGFR-3*

Following biosynthesis, VEGFR-3 (fms-like tyrosine kinase 4, Flt4) undergoes proteolytic cleavage of the fifth Ig-homology domain, and the resulting polypeptide chains remain linked via a disulfide bond (Figure 2) (Pajusola et al., 1994; Lee et al., 1996). VEGFR-3 can form heterodimers with VEGFR-2 upon stimulation with the mature forms of VEGF-C and VEGF-D, which may lead to unique downstream signals due to asymmetry between the intracellular domains of the two receptors (Dixelius et al., 2003; reviewed in Olsson et al., 2006). VEGFR-3 is present in all endothelia during development but in the adult it becomes restricted to LECs and fenestrated blood vessels in endocrine organs such as

the thyroid, the adrenal glands, and pancreas (Partanen et al., 2000). However, VEGFR-3 is upregulated in blood vascular ECs in pathological conditions such as in tumors and in wounds (Valtola et al., 1999; Paavonen et al., 2000; Bando et al., 2004; Grau et al., 2007). Interestingly, blood vascular VEGFR-3 expression has been demonstrated to positively correlate with a high tumor grade (Grau et al., 2007). *Vegfr3* gene-targeted mice exhibit embryonic lethality at E9.5 from defective arterio-venous remodeling of the primary vascular plexus and disturbed hematopoiesis (Dumont et al., 1998; Hamada et al., 2000). Correspondingly, knock-down of the VEGFR-3 homologue *Flt4* in zebrafish using morpholino oligonucleotides results in defective segmental artery morphogenesis (Covassin et al., 2006). Transgenic mice overexpressing a soluble VEGFR-3 immunoglobulin G VEGFR-3-Ig fusion protein in the skin from E14.5 onwards lack dermal lymphatic vessels and have hypoplastic deeper lymphatic vessels, but blood vessels in these mice appear normal (Makinen et al., 2001a), suggesting that VEGFR-3 signaling is not required for expansion of the blood vascular networks after organogenesis. Missense mutations in VEGFR-3 have been linked to hereditary lymphedema in humans, as well as in a mouse model of lymphedema (Irrthum et al., 2000; Kärkkäinen et al., 2000; Kärkkäinen et al., 2001).

VEGFR-3 is also expressed in a subpopulation of monocytes/macrophages, and VEGF-C has been shown to promote homing of these cells into tumors and wounds (Skobe et al., 2001b; Saaristo et al., 2006). Interestingly, VEGFR-3 is also expressed in antigen-presenting dendritic cells, and blocking VEGFR-3 suppresses the induction of corneal alloimmunity by inhibiting trafficking of these cells (Hamrah et al., 2003; Chen et al., 2004).

## Neuropilins

Neuropilins (NP-1 and NP-2) are transmembrane receptor glycoproteins that do not have enzymatic activities (Takagi et al., 1991; Kolodkin et al., 1997). Neuropilins bind class 3 semaphorins, which are secreted proteins that mediate repulsive signals during neuronal axon guidance, but they also function as receptors for certain VEGFs, and thereby play a role in angiogenesis as well as lymphangiogenesis (reviewed in Carmeliet and Tessier-Lavigne, 2005; and in Klagsbrun and Eichmann, 2005). NP-1 acts as a co-receptor enhancing VEGF-VEGFR-2 interactions, while it also forms complexes with VEGFR-1 (Soker et al., 2002). *Np1* gene-targeted mice die at E13.5 from vascular defects such as insufficient development of yolk sac vascular networks, deficient neural vascularization, and transposition of large vessels (Kawasaki et al., 1999). Interestingly, NP-1 is required for the guidance of angiogenic sprouts (Gerhardt et al., 2004), suggesting that maximal sensing of VEGF by the endothelial tip cells is crucial for the formation and patterning of vascular networks (Gluzman-Poltorak et al., 2000; Soker et al., 2002).

NP-2 is expressed in veins and lymphatic vessels, and *Np2* mutant mice exhibit lymphatic capillary hypoplasia (Yuan et al., 2002). Interestingly, both VEGF-C and VEGF-D bind to NP-2, which co-internalizes with VEGFR-3 upon ligand stimulation (Kärpänen et al., 2006a). This indicates an analogy between the VEGF/NP-1/VEGFR-2 and the VEGF-C/NP-2/VEGFR-3 signaling pathways in angiogenesis and lymphangiogenesis, respectively, and suggests that NP-2 may be important in lymphatic vessel sprouting.

## Notch signaling

The Notch signaling pathway regulates cell fate specification, growth, differentiation, and patterning processes in multicellular organisms. In mammals, four Notch receptors (Notch1–Notch4) interact with five membrane-bound ligands, Delta-like 1 (Dll1), Dll3, Dll4, Jagged1, and Jagged2 (reviewed in Roca and Adams, 2007). Both receptors and ligands are EGF repeat-containing transmembrane proteins (Weinmaster, 2000; Lai, 2004; Le Borgne et al., 2005; Bray, 2006; Hurlbut et al., 2007). In analogy with ephrins, the Notch ligands also contain an intracellular PDZ-binding domain that is conserved in evolution, suggesting the possibility of retrograde signaling.

Upon ligand binding, Notch becomes susceptible to processing by the intracellular protease  $\gamma$ -secretase (presenilin), which releases the Notch intracellular domain (NICD) (Weinmaster, 2000; Selkoe and Kopan, 2003; Schweisguth, 2004; reviewed in Nichols et al., 2007). Following translocation of the NICD into the nucleus, its interaction with the DNA-binding protein CSL (RBP-J) and the coactivator MAML-1 leads to the displacement of corepressor proteins and associated chromatin-modifying factors from CSL, which triggers the transcription of Notch target genes such as the basic helix–loop–helix (bHLH) proteins Hes1, Hey1 (Hesr1), and Hey2 (Hesr2), which typically act as repressors of downstream genes (Lai, 2002; Fischer and Gessler, 2003; Iso et al., 2003; reviewed in Ehebauer et al., 2006).

Notch signaling plays a role in arterial specification, and several Notch receptors and ligands are expressed specifically in arteries in mice and in zebrafish (Shutter et al., 2000; Mailhos et al., 2001; Lawson et al., 2001; Leslie et al., 2007; Siekmann and Lawson, 2007). Furthermore, Notch1 signaling activated by Dll1 is critical for postnatal arteriogenesis (Limboung et al., 2007; Takeshita et al., 2007). In contrast, the orphan nuclear receptor COUP-TFII promotes venous EC differentiation by suppressing Notch signaling during development (You et al., 2005). Disruption of Notch signaling in zebrafish leads to loss of arterial markers such as ephrinB2, and ectopic expression of EphB4, an ephrinB2 receptor that is prominently expressed in veins (Lawson et al., 2001). Conversely, ectopic activation of the Notch pathway represses expression of *Efb4* (EphB4) and *Flt4* (VEGFR-3) and thereby imposes a more artery-like gene expression profile on veins (Lawson et al., 2001), although

NICD was recently shown to bind to the *VEGFR3* promoter and induce VEGFR-3 expression in mammals (Shawber et al., 2007).

The formation of the tracheal system in *Drosophila melanogaster* embryos by growth factor-induced guided migration and self-limiting branching of the tracheal epithelial cells has served as a model for the formation of vascular networks in higher organisms (Zelzer and Shilo, 2000; Ghabrial and Krasnow, 2006). In *Notch* mutant *Drosophila* embryos, an excess of cells attempt to lead the tracheal branches and compete for the lead position, whereas expression of constitutively active Notch prevents outgrowth due to the lack of leading tip cells (Ikeya and Hayashi, 1999; Llimargas, 1999). The Dll–Notch signal also prevents the stalk epithelium from becoming terminal or fusion cells (Steneberg et al., 1999; Zelzer and Shilo, 2000).

Notch signals play a strikingly similar role in the specification of endothelial tip cells, which express the Notch ligand Dll4, and stalk cells, in which Notch signaling becomes activated (Hellstrom et al., 2007; Roca and Adams, 2007). *Dll4* gene-targeted mouse embryos die by E10.5 due to severe defects in arterial-venous remodeling of the embryonic vasculature, whereas the *Dll4* heterozygous embryos have a similar, but attenuated phenotype, and a small proportion survive to adulthood (Duarte et al., 2004; Gale et al., 2004; Krebs et al., 2004). The *Dll4* heterozygous mice and mice treated with Dll4-blocking antibodies or small-molecular  $\gamma$ -secretase inhibitors exhibit excessive numbers of tip cells (Noguera-Troise et al., 2006; Ridgway et al., 2006; Hellstrom et al., 2007; Lobov et al., 2007; Siekmann and Lawson, 2007; Suchting et al., 2007). Furthermore, disruption of the Notch downstream signaling component *Rbpsuh* in zebrafish results in increased sprouting and high *Flt4* expression (Siekmann and Lawson, 2007). These studies indicate that Dll4 is the key Notch ligand in the process, and Dll4/Notch appears to limit tip cell behavior in the stalk cells by suppressing VEGFR-2 and inducing VEGFR-1, rendering the stalk cells less responsive to VEGF than the tip cells, which express low levels of VEGFR-1 and high levels of VEGFR-2 (Ridgway et al., 2006; Hellstrom et al., 2007; Lobov et al., 2007; Suchting et al., 2007). Befitting this role, VEGF has been shown to induce Dll4 in ECs (Liu et al., 2003).



## The angiopoietin/Tie system

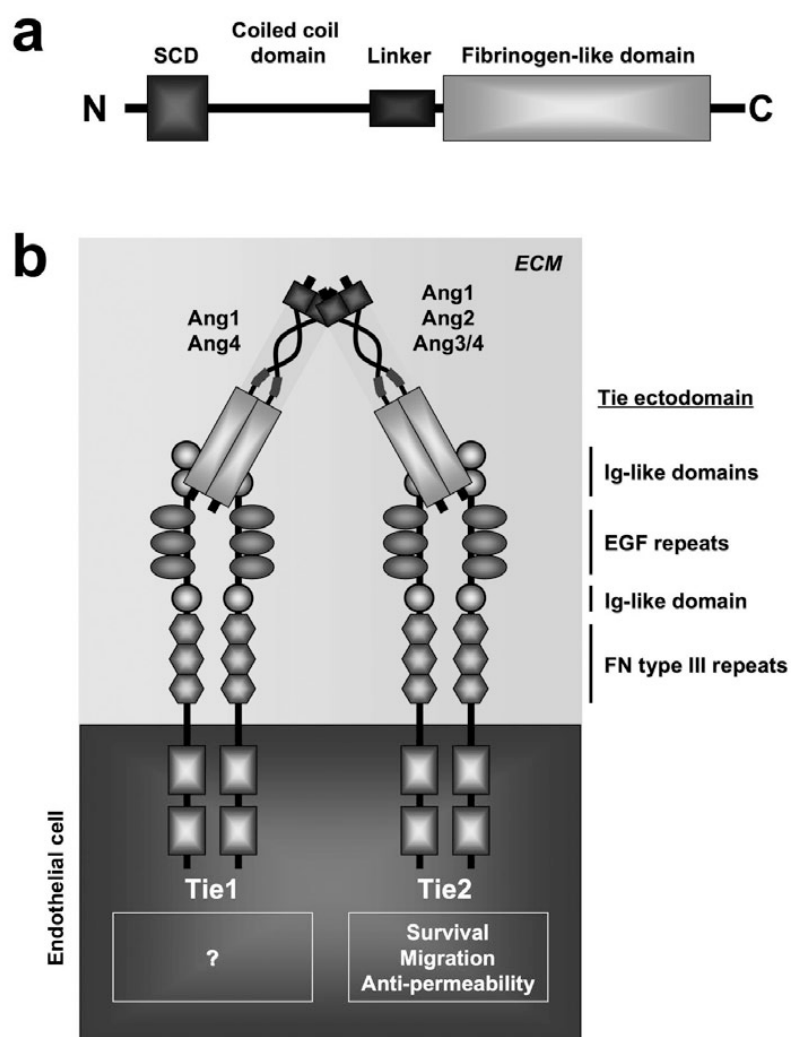
The angiopoietin (Ang) family of growth factors includes Ang1 and Ang2, as well as Ang3 and Ang4, which are mouse and human orthologues, respectively (Suri et al., 1996; Maisonpierre et al., 1997; Valenzuela et al., 1999). The angiopoietins bind to the Tie2 receptor tyrosine kinase, expressed almost exclusively in ECs, and regulate interactions between ECs and pericytes (reviewed in Thurston, 2003; Brindle et al., 2006; and in Shim et al., 2007). The Tie receptors (Tie1 and Tie2) are composed of an extracellular domain containing three immunoglobulin homology domains, three EGF-like repeats, three fibronectin-type III-like repeats, a transmembrane domain, and a split tyrosine kinase domain (**Figure 4**) (Partanen et al., 1992; Dumont et al., 1993; Ziegler et al., 1993). Ang1 and Ang3/Ang4 are obligate agonists of Tie2, whereas Ang2 can act either as an agonist or an antagonist, depending on the cell type and the surrounding microenvironment (Davis et al., 1997; Maisonpierre et al., 1997; Teichert-Kuliszewska et al., 2001). Tie2 activation promotes EC survival and migration (reviewed in Thurston, 2003; Brindle et al., 2006; and in Shim et al., 2007). Ang1 and Ang4 were shown to stimulate the activation of Tie1, a Tie2 homologue with a highly similar expression pattern, although the presence of Tie2 is required for maximal Tie1 phosphorylation (Saharinen et al., 2005).

All angiopoietins share a similar overall structure with a short amino-terminal motif followed by a coiled-coil domain and carboxyterminal fibrinogen-like domain (Figure 4) (Suri et al., 1996; Maisonpierre et al., 1997; Valenzuela et al., 1999). Tie2 binding is mediated by the fibrinogen-like domain, while the short supercoiling domain (SCD) within the coiled-coil domain is responsible for the formation of angiopoietin homodimers and higher order homo-oligomers (Procopio et al., 1999; Barton et al., 2005; Barton et al., 2006). The linker peptide between the two major domains of Ang1 has been shown to associate Ang1 with the extracellular matrix, rendering Ang1 less soluble in tissues when compared to Ang2 (Thurston et al., 2000; Xu and Yu, 2001).

Ang1 expression in the mouse embryo occurs first in the myocardium, and later in a more widespread manner around the developing vessels (Davis et al., 1997). Ang2 is expressed in the embryonic dorsal aorta and the major aortic branches, and in adults in tissues that are undergoing vascular remodeling (Maisonpierre et al., 1997; Gale et al., 2002). Gene targeting experiments have indicated that Ang1 is necessary for maintaining maximal

interactions between ECs and pericytes and the ECM (Suri et al., 1996). Loss of *Tie2* recapitulates the *Angpt1* null phenotype, with embryonic lethality at E12.5 due to vessel rupture and lack of periendothelial support, whereas *Tie1* gene-targeted mice succumb to similar defects by E14.5 (Puri et al., 1995; Sato et al., 1995; Partanen et al., 1996). Ang1 promotes the integrity of EC monolayers in culture (Wang et al., 2004; Gavard et al., 2008), and exogenously provided Ang1 prevents leakage of plasma components into the interstitium caused by potent vascular permeability agents, such as VEGF, in adult tissues (Thurston et al., 2000). A recent report has indicated that this activity occurs through the suppression of Src activation (Gavard et al., 2008). Conversely, release of Ang2 from Weibel-Palade bodies in ECs upon stimulation with proinflammatory cytokines leads to rapid destabilization of the endothelium and extravasation of plasma components (Fiedler et al., 2004; Fiedler et al., 2006b).

**Figure 4. The angiopoietins and the Tie receptors.** (a) The domain structure of angiopoietin-1 (Ang1). Ang1 migrates at 70 kDa. The N-terminal part of the coiled-coil domain contains the superclustering domain (SCD) responsible for formation of Ang homodimers and higher order oligomers. Ang1 must form at least tetramers in order to cluster and activate Tie receptors. The linker domain associates Ang1 with the extracellular matrix. The C-terminal fibrinogen-like domain is required for the activation of Tie receptors. (b) Tie1 and Tie2 are composed of two Ig-loops, followed by three EGF-like repeats, an Ig-loop, three fibronectin (FN) type III repeats, a single transmembrane domain and an intracellular tyrosine kinase domain (double rectangles) that is interrupted by a kinase-insert. Tie2 signals mediate endothelial cell survival and migration, as well as counteract vascular permeability responses. ECM: extracellular matrix.



Abundant evidence suggests that members of the angiopoietin and VEGF families collaborate during different stages of angiogenesis. Ang2 is expressed at sites of pericyte detachment and blood vessel remodeling in conjunction with VEGF, whereas in the absence of VEGF, Ang2 activity leads to EC apoptosis (Maisonpierre et al., 1997; Goede et al., 1998; Holash et al., 1999). In addition, factors that induce angiogenesis *in vivo*, such as hypoxia and VEGF, have been shown to upregulate Ang2 in ECs (Mandriota and Pepper, 1998).

The role of angiopoietins in lymphangiogenesis has remained unclear, although Tie2 and Tie1 mRNA and protein have been detected at least in cultured LECs (Kriehuber et al., 2001; Makinen et al., 2001b). Ang2 knockout mice have defects in regression of hyaloid blood vessels as well as lymphatic vessel maturation, suggesting that Ang2 may be needed for lymphatic vessel stabilization (Gale et al., 2002). Notably, replacement of the Ang2 gene with a cDNA encoding Ang1 was sufficient to rescue the lymphatic phenotype but not the blood vascular phenotype (Gale et al., 2002).

#### Endothelial cell – pericyte interactions

Stabilization of the endothelium requires pericyte recruitment, and the lack of pericytes leads to EC hyperplasia, formation of aberrant EC-EC junctions, vessel rupture and embryonic lethality (reviewed in Armulik et al., 2005; and in von Tell et al., 2006). The *de novo* induction of vascular SMCs around the first blood vessels is stimulated by transforming growth factor- $\beta$  (TGF- $\beta$ ) and possibly other factors that remain to be characterized. Genetic inactivation of *Tgfb1* in mice and genes encoding its receptors, activin-receptor-like kinase-1 (*Alk1*), *Alk5*, TGF- $\beta$  receptor II (*t $\beta$ rII*), and *Eng* (endoglin, a TGF- $\beta$  co-receptor), as well as its downstream effector *Smad5* all lead to comparable cardiovascular defects and embryonic lethality (Dickson et al., 1995; Oshima et al., 1996; Li et al., 1999; Yang et al., 1999; Oh et al., 2000; Urness et al., 2000; Larsson et al., 2001). TGF- $\beta$  has context-dependent effects on ECs, as signaling through ALK1/Smad1/5 promotes EC proliferation, whereas ALK5/Smad2/3 stimulates differentiation (Goumans et al., 2002). TGF- $\beta$  signaling in ECs promotes TGF- $\beta$  expression, synthesis, and release by these cells, which, in turn, induces differentiation of SMCs from surrounding mesenchymal cells, but also auto-induces TGF- $\beta$  expression in the ECs themselves (Carvalho et al., 2004). The role of TGF- $\beta$  signaling in

lymphangiogenesis and lymphatic vessel maturation is not known, although it is conceivable that this pathway is involved in the differentiation of the SMCs surrounding the collecting vessels.

Platelet-derived growth factor-B (PDGF-B) signaling via PDGF-receptor- $\beta$  (PDGFR- $\beta$ ) plays a critical role in the recruitment of pericytes to newly formed vessels (reviewed in Hoch and Soriano, 2003; and in Betsholtz, 2004). During angiogenesis, sprouting ECs secrete PDGF-B, which signals through PDGFR- $\beta$  expressed by pericytes, resulting in proliferation and migration of pericytes during vessel maturation (reviewed in Armulik et al., 2005). Loss of *Pdgfb* or *Pdgfrb* leads to similar phenotypes and perinatal death caused by vascular dysfunction due to the lack of pericytes (Leveen et al., 1994; Lindahl et al., 1997; Crosby et al., 1998; Hellstrom et al., 1999). Gene-targeting studies have demonstrated that PDGF-B/PDGFR- $\beta$  signaling is not required for the induction of pericytes, but it is crucial for the expansion of the pericyte population (Hellstrom et al., 1999). The ectopic SMC coverage observed in lymphatic capillaries of *Foxc2* null mice is presumably due to failure in suppression of *Pdgfb* transcription in LECs (Petrova et al., 2004).

Sphingosine-1-phosphate (S1P) is a secreted sphingolipid synthesized by sphingosine-1-kinase (S1K) in ECs, and involved in cell-cell communication through five G-protein coupled receptors (S1P<sub>1</sub>-S1P<sub>5</sub>, also known as EDG1-EDG5) (Shu et al., 2002; Limaye et al., 2005). S1P<sub>1</sub>, S1P<sub>2</sub> and S1P<sub>3</sub> are expressed in SMCs/pericytes, and single or compound inactivation of these genes leads to embryonic lethality with severe defects in vascular pericyte investment (Liu et al., 2000b; Kono et al., 2004). S1P1 signaling through the small G-protein Rac promotes trafficking of N-cadherin to polarized plasma membrane domains in ECs, which enforces contacts with mural cells (Paik et al., 2004). N-cadherin-based adherence junctions are located at peg–socket contacts between ECs and pericytes (Gerhardt et al., 2000; reviewed in Armulik et al., 2005; and in von Tell et al., 2006), and N-cadherin is functionally important for the maintenance of these junctions (Gerhardt et al., 2000; Paik et al., 2004). Interestingly, Ang1 was recently shown to activate S1K and stimulate S1P production, suggesting that Ang1 produced by the pericytes can enhance EC-pericyte interactions via this pathway along with having direct effects on ECs (Li et al., 2008). Furthermore, Ang1 has been reported to stimulate pericyte recruitment by inducing heparin-binding epidermal growth factor (HB-EGF) in ECs, although *Hb-egf/Egfr* gene-targeted mice do not display pericyte defects (Iivanainen et al., 2003; Iwamoto et al., 2003).

## The extracellular matrix

ECs in quiescent blood vessels are insulated from the surrounding tissue environment by a basement membrane (BM), which is composed of type IV and XVIII collagens, laminin, fibronectin, nidogen (entactin), and heparan sulfate proteoglycans (HSPGs) (reviewed in Davis and Senger, 2005). The BM is required for the stability of blood vessels (Thyboll et al., 2002), as well as for the polarization of ECs (Drake et al., 1995; reviewed in Davis and Senger, 2005). Interestingly, lymphatic capillary ECs express a truncated laminin- $\alpha$  chain that is unable to assemble into networks, which may explain the very sparse BM surrounding lymphatic capillaries (Vainionpää et al., 2007).

At the onset of angiogenic sprouting, ECs utilize a number of proteases to invade through the BM (Pepper, 2001; Davis et al., 2002; Heissig et al., 2003), and become exposed to type I collagen, which stimulates tube formation and vessel morphogenesis (reviewed in Davis and Senger, 2005). The ECM acts as a reservoir for HSPG-binding growth factors, which can be released by proteolysis (reviewed in Lundkvist et al., 2007). PDGF-B produced by sprouting ECs is bound to HSPGs at the EC surface, which provides a high local growth factor concentration for optimal pericyte guidance (reviewed in Armulik et al., 2005; and in von Tell et al., 2006). In fact, loss of the HSPG retention motif in PDGF-B, or defective N-sulfation of HSPGs leads to impaired pericyte recruitment, which highlights the importance of the ECM in generating growth factor gradients and limiting their effects to the local microenvironment (Lindblom et al., 2003; Nystrom et al., 2006; Abramsson et al., 2007; reviewed in Lundkvist et al., 2007).

Three predominant VEGF isoforms of variable amino acid number, VEGF<sub>121</sub>, VEGF<sub>165</sub>, and VEGF<sub>189</sub>, are produced through alternative splicing (reviewed in Robinson and Stringer, 2001; and in Ferrara et al., 2003). After secretion, VEGF<sub>121</sub> is freely diffusible in tissues, and does not bind to the neuropilins, while larger forms of VEGF retain the ability to bind NP-1 and NP-2, and are progressively less diffusible as their molecular weight increases (Soker et al., 1998; Gluzman-Poltorak et al., 2000). Except for VEGF<sub>121</sub>, all the larger forms of VEGF contain a heparin-binding domain (HBD) encoded by exon 6a and/or exon 7, and remain bound to the cell surface and the ECM (Gitay-Goren et al., 1996). The heparin-binding capacity in VEGF exon 7 is conveyed by a cationic polypeptide sequence (44 amino acids) (Poltorak et al., 1997), whereas other parts of the domain enable its binding

to NP-1 (Soker et al., 1996). VEGF165 contains the exon 7-encoded domain, and binds to cell surface HSPGs with intermediate affinity, while VEGF189 contains both exon 6a- and exon7-encoded domains, remaining almost completely sequestered by HSPGs in the ECM (Figure 3a) (reviewed in Lundkvist et al., 2007). Other members of the VEGF family that contain a HBD include VEGF-B167 and PlGF-2 (Hauser and Weich, 1993; Maglione et al., 1993; Mäkinen et al., 1999).

Optimal three-dimensional distribution of VEGF isoforms is required for the guided migration of endothelial tip cells, which lead the outgrowth of blood vessel sprouts during angiogenesis (Ruhrberg et al., 2002; Gerhardt et al., 2003). Expression of a protease-resistant mutant form of VEGF in tissues was shown to result in excessive vascular sprouting, indicating that, besides mRNA splicing, post-translational modifications of VEGF in the extracellular environment are important for regulating its activity and bioavailability (Houck et al., 1992; Lee et al., 2005). Interestingly, HSPGs provided by pericytes *in trans* prolong VEGF-mediated activation of VEGFR-2, and suffice for normal VEGF signaling in ECs (Jakobsson et al., 2006). VEGF-C and VEGF-D do not bind heparan-sulfate (Joukov et al., 1996; Achen et al., 1998). However, the C-terminal domains of these factors are homologous to silk proteins, and thus may aggregate into stable fibrils in the extracellular environment (Figure 3a) (reviewed in Dicko et al., 2006).

Integrins are dimeric membrane-bound adhesion molecules composed of  $\alpha$  and  $\beta$  subunits, which attach cells to the ECM via focal-adhesion complexes that are active in cell survival and motility signaling (reviewed in Schlaepfer and Mitra, 2004; Mitra and Schlaepfer, 2006; and in Romer et al., 2006). Interestingly, integrins physically interact with several growth factors and receptors that stimulate angiogenesis and lymphangiogenesis (reviewed in Davis and Senger, 2005; Brindle et al., 2006; and in Kärpänen and Alitalo, 2007). *In vitro* studies show that VEGFR-2 may be involved in integrin-dependent migration of ECs, as it forms a complex with integrin  $\alpha\beta 3$  upon binding VEGF (Soldi et al., 1999; Hutchings et al., 2003). Furthermore, upon binding to matrix fibronectin,  $\beta 1$  integrin interacts with VEGFR-3 and induces weak activation of its tyrosine kinase, whereas integrin  $\alpha 5\beta 1$  potentiates VEGFR-3 activation in the presence of VEGF-C (Wang et al., 2001; Zhang et al., 2005a). Integrin  $\alpha 9$  binds VEGF-C and inactivation of *Itga9* in mice results in accumulation of lymphatic fluid in the thoracic cavity (chylothorax), although the mechanism remains unresolved (Huang et al., 2000; Vlahakis et al., 2005). Furthermore, Kaposi sarcoma herpes

virus envelope glycoprotein gB can activate both VEGFR-3 and  $\alpha 3\beta 1$  integrin, which results in increased EC proliferation and migration (Zhang et al., 2005b). In addition, Ang1 can bind several different integrins, including  $\alpha 2\beta 1$ ,  $\alpha 5\beta 1$ ,  $\alpha v\beta 3$ , and  $\alpha v\beta 5$  (Carlson et al., 2001; Cascone et al., 2005; Dallabrida et al., 2005; Weber et al., 2005). The abundance of interactions between integrins and endothelial-specific tyrosine kinase receptors indicate that integrin function is required for EC migration and adhesion during ligand-activated angiogenesis.

### 3. Angiogenesis and lymphangiogenesis in human disease - the therapeutic horizon

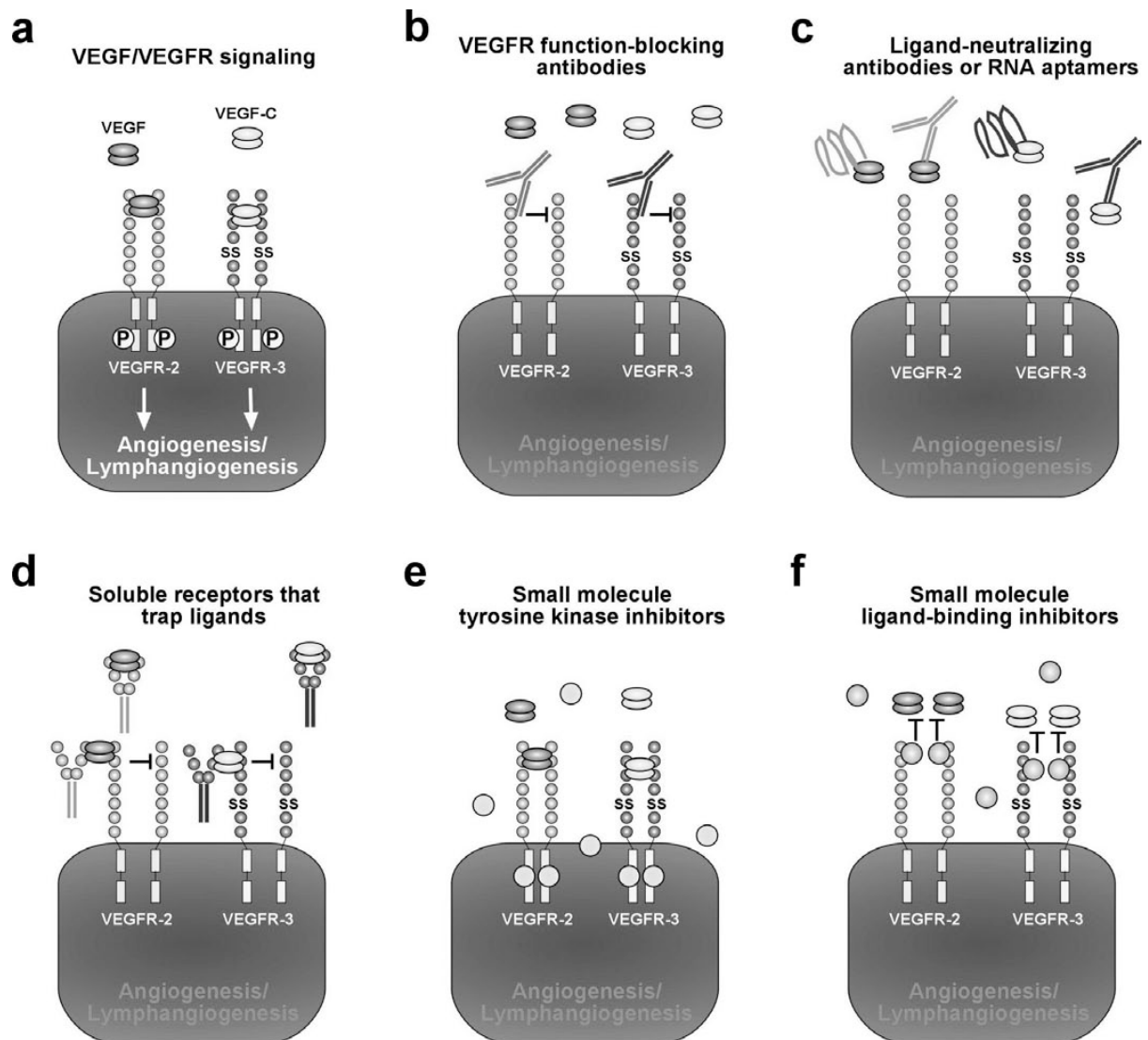
Insufficient or undesired angiogenesis is involved in a plethora of human diseases, and future pro- or anti-angiogenic therapies are estimated to benefit approximately 500 million people worldwide (reviewed in Carmeliet, 2005). Awareness on the role of the lymphatic vascular system in human disease is growing, as connections between the lymphatics and tumor metastasis, edema formation, transplant rejection, fat metabolism, and wound healing continue to be made (Paavonen et al., 2000; Kerjaschki et al., 2004; Alitalo et al., 2005; Harvey et al., 2005; Saaristo et al., 2006). Angiogenesis and lymphangiogenesis are particularly important for tumor growth and metastasis, respectively. An overview of the strategies available for blocking the function of angiogenic/lymphangiogenic molecules is given in **Figure 5**.

#### Tumor progression

##### *Tumor angiogenesis*

Growing tumors rely on sustained angiogenesis for the delivery of oxygen and nutrients (reviewed in Folkman, 1971; and in Hanahan and Weinberg, 2000). Neoplastic lesions are unable to grow beyond a small size without engaging a gene expression program that initiates angiogenesis, termed “the angiogenic switch” (Folkman et al., 1989; reviewed in Ferrara and Kerbel, 2005). Blood vessels in tumors lack hierarchical organization and are leaky, leading to sluggish blood flow and high interstitial fluid pressure within the tumor (reviewed in Jain, 2003; McDonald and Choyke, 2003; and in Jain, 2005). Hypoperfusion within the tumor perpetuates hypoxia and VEGF production, while high intratumoral fluid pressure hampers the delivery of therapeutic agents (reviewed in Jain, 2003; and in Jain, 2005). As tumor growth is dependent on angiogenesis, and as vascular cells, unlike tumor cells, are less likely to become resistant to therapeutics, targeting the tumor vasculature is an attractive strategy to treat cancer patients (reviewed in Folkman, 1971; and in Hanahan and Weinberg, 2000). On the other hand, it is conceivable that anti-angiogenic therapies promote the dedifferentiation of tumor cells by increasing hypoxic stress (reviewed in Axelson et al., 2005).





**Figure 5. Strategies to inhibit VEGF/VEGFR signaling.** (a) Ligand-activated VEGFR signaling. (b) VEGFR activation can be inhibited by monoclonal antibodies that prevent receptor dimerization and/or the ligand from binding the receptor. (c) VEGF ligands can be specifically neutralized using monoclonal antibodies or RNA aptamers. (d) Soluble decoy receptors containing the ligand-binding domain(s) of a given VEGFR, typically fused to the Fc domain of immunoglobulin G, trap ligands and may also interfere with receptor dimerization. (b) and (c) are the most specific means available, while (d) offers relatively specific blocking. All of these inhibitors must be administered parenterally, and are expensive to produce with current methods. (e) VEGFR tyrosine kinase activation can be blocked with small molecules that bind the intracellular kinase domain either at the ATP-binding site or at an allosteric site. (f) Small molecules can also be designed to block ligand-binding to the receptor ectodomain. Small molecule inhibitors are less specific, as they typically block multiple tyrosine kinases. However, these compounds may be administered orally and are inexpensive to synthesize.

Interestingly, many of the genes that are required for the development of the blood vascular system re-adopt their developmental function during tumor angiogenesis, which has led to the discovery of tumor-specific, and therefore potentially safe, vascular targets. Furthermore, tumor cell interactions with ECs promote the expression of surface proteins unique for the tumor endothelium, which may be utilized for specific therapeutic targeting (Arap et al., 1998; Joyce et al., 2003; reviewed in Ruoslahti and Rajotte, 2000).

Reflecting its paramount role in developmental angiogenesis, the VEGF/VEGFR-2 system appears to be the most important regulator of blood vessel growth in tumors (reviewed in Ferrara et al., 2007), and elevated levels of VEGF mRNA are found in most human tumors (reviewed in Dvorak, 2002). Besides hypoxia, a number of oncogenes are associated with VEGF production, including k-Ras, ErbB2, activated ErbB1, VHL, and Bcr-Abl (Rak et al., 1995; reviewed in Kerbel and Folkman, 2002). Blocking VEGF/VEGFR-2 signaling inhibits angiogenesis and growth of tumors, and even premalignant lesions, in experimental models without direct effects on tumor cells *in vitro* (Kim et al., 1993; Millauer et al., 1994; Prewett et al., 1999; Holash et al., 2002; Inoue et al., 2002; Korsisaari et al., 2007). Long-term experiments have shown that adult mice are highly resistant to the adverse effects of VEGF/VEGFR-2 inhibitors, unlike neonatal or adolescent mice (Kitamoto et al., 1997; Gerber et al., 1999; Eremina et al., 2003; Baffert et al., 2004). Nevertheless, the administration of VEGF axis inhibitors leads to apoptotic death of a small number of ECs, loss of EC fenestrations, resulting in subclinical hypothyroidism, and proteinuria even in adult mice (Baffert et al., 2004; Inai et al., 2004; Kamba et al., 2006; Lee et al., 2007; reviewed in Kamba and McDonald, 2007).

In 2004 the monoclonal VEGF-neutralizing antibody bevacizumab became the first anti-angiogenic agent to be approved for use in patients (Kabbinavar et al., 2003; Hurwitz et al., 2004). Bevacizumab combined to the standard chemotherapy regimen has shown marked clinical benefit in the treatment of metastatic colorectal cancer, non-small cell lung cancer, and breast cancer (Hurwitz et al., 2004; Miller et al., 2005; Sandler et al., 2006; Miller et al., 2007), and a positive result was obtained in a recent phase III trial in renal cell cancer (Escudier et al., 2007b). Further examples of specific VEGF axis inhibitors that are currently evaluated in phase II/III trials include the soluble VEGFR-1/VEGFR-2/immunoglobulin G fusion protein aflibercept (VEGF-Trap), and VEGFR-2 neutralizing antibodies (Lau et al., 2005; Baka et al., 2006; Youssoufian et al., 2007). Two small-molecular tyrosine kinase

inhibitors, sunitinib and sorafenib, which potently block the activation of VEGFRs and other tyrosine kinases, have recently been shown to be effective in the treatment of renal cell cancer and other malignancies (Demetri et al., 2006; Escudier et al., 2007a; Llovet et al., 2007; Motzer et al., 2007). Besides inhibiting angiogenesis and further tumor growth, VEGF/VEGFR-2 inhibitors are thought to improve tumor microcirculation by pruning excess vessels and reducing vascular leakage, facilitating the delivery of chemotherapeutics (reviewed in Jain, 2003; and in Jain, 2005). VEGF axis inhibitors are generally well tolerated in patients, although the combined use of chemotherapeutics often accentuates the adverse effects, which include hypertension, proteinuria, hemorrhage, gastrointestinal perforations, thromboembolism, and delayed wound healing (reviewed in Kamba and McDonald, 2007).

The fact that VEGF/VEGFR-2 inhibitors are not effective in all tumor types has suggested the existence of overlapping signaling pathways that drive tumor angiogenesis. Antibodies that block PlGF inhibit tumor growth and neovascularization synergistically with VEGFR-2 antibodies by suppressing macrophage recruitment leading to a poorly developed tumor stroma (Fischer et al., 2007). Interestingly, VEGFR-3 neutralizing antibodies also reduce tumor angiogenesis and growth (Roberts et al., 2006; Laakkonen et al., 2007). NP-1 function-blocking antibodies suppress the growth and angiogenesis of experimental tumors, and, interestingly, synergized with VEGF antibodies, which may indicate that other NP-1 ligands are important for tumor angiogenesis (Liang et al., 2007; Pan et al., 2007). Other neural guidance ligand/receptor systems that have been implicated in the growth and angiogenesis of experimental tumors include Robo1/Slit-2, netrin-1/Unc5b, and ephrinB2/EphB4 (Wang et al., 2003; Lu et al., 2004; Martiny-Baron et al., 2004; Larrivee et al., 2007; reviewed in Carmeliet and Tessier-Lavigne, 2005; and Klagsbrun and Eichmann, 2005).

Interestingly, Dll4 inhibitors were recently shown to promote excessive but non-productive tumor angiogenesis that impaired tumor perfusion and suppressed tumor growth, which has led to the emergence of a novel concept in anti-angiogenesis biology (Noguera-Troise et al., 2006; Ridgway et al., 2006; reviewed in Thurston et al., 2007).

In analogy with embryonic vascular development, blood vessels in tumors also recruit pericytes, which have been shown to protect tumor ECs from VEGF withdrawal (Liu et al., 2000a; Bergers et al., 2003; reviewed in von Tell et al., 2006). Therapeutic targeting of the PDGF-B/PDGFR- $\beta$  signaling pathway results in a decreased number of pericytes and in

reduced tumor vascularity, whereas targeting both PDGFRs and VEGFRs with kinase inhibitors leads to synergistic anti-angiogenic and anti-tumor activity (Bergers et al., 2003; Pietras and Hanahan, 2005; Sennino et al., 2007; Pietras et al., 2008). Blocking Tie2 has also been shown to reduce the growth of tumor xenografts, which may be due to endothelial destabilization (Lin et al., 1997; Lin et al., 1998; Popkov et al., 2005). On the other hand, specific neutralization of Ang2 reduces tumor vascularization and growth via a poorly understood mechanism (Oliner et al., 2004).

### *Lymphatic metastasis*

Metastatic spread of tumor cells via blood or lymphatic vessels occurs in many forms of human cancer, and patients with lymph node metastases have a radically less favorable prognosis when compared to patients with local disease (reviewed in Stacker et al., 2002). The first regional lymph node to be colonized by metastatic tumor cells is denoted a sentinel lymph node, and further dissemination may occur to other nodes and distant organs from this location.

Lymphangiogenesis has been observed in a variety of human tumors, as well as in experimental tumors (reviewed in Stacker et al., 2002). At least in animal models intratumoral lymphatic vessels may not be completely functional, because they collapse in conditions of high intratumoral pressure (Padera et al., 2002). Peritumoral lymphatics were recently shown to originate from the preexisting lymphatic vasculature without any detectable contribution from circulating lymphatic EPCs (He et al., 2004; He et al., 2005). The lymphatic vessels of tumors, and even premalignant lesions, express specific markers, which represent potential targets of anti-metastatic therapeutics (Laakkonen et al., 2002; Laakkonen et al., 2004; Fiedler et al., 2006a; Zhang et al., 2006).

Interestingly, several clinical studies have shown a positive correlation between VEGF-C or VEGF-D expression and vascular invasion, lymphatic vessel and lymph node involvement, distant metastasis, and, in some instances, poor clinical outcomes (reviewed in Stacker et al., 2002). VEGF-C expression in tumor cells may be induced by oncogenes, growth factors or proinflammatory cytokines, whereas some of the VEGF-C may be derived from stromal inflammatory cells (reviewed in Alitalo et al., 2005). Forced expression of

VEGF-C or VEGF-D in tumor cells enhances lymphatic metastasis in various experimental models, which applies even to tumors that normally do not have this propensity (Skobe et al., 2001a; Stacker et al., 2001; Kärpänen et al., 2001; Mandriota et al., 2001; He et al., 2002). Conversely, inhibition of lymphangiogenesis with a soluble form of VEGFR-3 or monoclonal antibodies that neutralize this receptor have been shown to inhibit lymphatic metastasis by 50-70% in preclinical animal models (He et al., 2002; Lin et al., 2005; Roberts et al., 2006). Importantly, although the lymphatic vessels are dependent on VEGFR-3 signaling during the first two postnatal weeks, blocking VEGFR-3 has no effects on normal lymphatic vessels in adult mice (Lin et al., 2005; Kärpänen et al., 2006b).

Interestingly, primary tumors were shown to elicit lymphangiogenesis in the sentinel lymph nodes already before the arrival of the first metastatic tumor cells (Hirakawa et al., 2005). A similar response occurs following immunization, and this promotes trafficking of antigen-presenting dendritic cells, suggesting that tumor cells utilize similar mechanisms as the immune cells to reach the lymph nodes (Angeli et al., 2006). In both cases VEGF was implicated as the key growth factor, although further studies have shown that tumors that produce VEGF-C can also initiate lymph node lymphangiogenesis (Hirakawa et al., 2005; Angeli et al., 2006; Hirakawa et al., 2007). Fibroblast growth factor(FGF)-2, insulin-like growth factor(IGF)-1, IGF-2, hepatocyte growth factor (HGF), and PDGF-B also induce lymphangiogenesis, and at least PDGF-B promotes lymph node metastasis of experimental tumors, but most of these effects may be secondary to the induction of VEGF-C and VEGF-D in a variety of cell types (Kubo et al., 2002; Tang et al., 2003; Cao et al., 2004; Chang et al., 2004; Bjorndahl et al., 2005; Kajiya et al., 2005; Cao et al., 2006).

### Lymphedema

Impairment of lymphatic transport capacity due to abnormal vessel development or obstruction or obliteration of the lymphatic vessels causes stagnation of proteins and associated water in the interstitium, resulting in lymphedema, usually a progressive and lifelong condition for which curative treatments are at present not available (Figure 1f). The protein-rich interstitial fluid initiates an inflammatory reaction, leading to fibrosis, impaired

immune responses, and accumulation of subcutaneous fat. Lymphedema is classified into primary (hereditary) lymphedema, and secondary (acquired) lymphedema, based on the mechanism of pathogenesis (reviewed in Rockson, 2001; and in Warren et al., 2007).

Although primary lymphedema is a rare condition, identification of the underlying genetic causes has provided valuable insight into the molecular mechanisms regulating the development and function of the lymphatic vasculature. Heterozygous tyrosine kinase-inactivating point mutations of the *VEGFR3* gene have been identified as a major cause of Milroy disease (OMIM #153100), a form of lymphedema due to hypoplasia of lymphatic capillaries, and typically present at birth (Irrthum et al., 2000; Kärkkäinen et al., 2000; Kärkkäinen et al., 2001). Mutations in the transcription factor *FOXC2* have been linked to lymphedema-distichiasis (LD, OMIM #153400), characterized by late-onset lymphedema, a double row of eyelashes, and varicose veins (Fang et al., 2000; Bell et al., 2001; Finegold et al., 2001; Mellor et al., 2007). Analysis of *Foxc2* mutant mice revealed that LD is due to ectopic SMC coverage of the lymphatic capillaries and loss of valves in the collecting vessels, and similar defects were also observed in samples obtained from LD patients (Petrova et al., 2004).

Dominant-negative mutations of the homeobox transcription factor *SOX18* have been linked with hypotrichosis-lymphedema-telangiectasia syndrome (HLTS, OMIM #607823) (Irrthum et al., 2003). Although the precise molecular mechanisms leading to the phenotype have not been discovered, a mouse model that recapitulates most hallmarks of the syndrome is available for the elucidation of the molecular pathogenesis (Pennisi et al., 2000; James et al., 2003). Lymphatic vessels express constitutively high levels of nuclear factor kappa-B (NF- $\kappa$ B), and mutations in the NF- $\kappa$ B regulatory protein *NEMO* associate with a rare and complex syndrome involving lymphedema (anhidrotic ectodermal dysplasia with immunodeficiency, osteopetrosis, and lymphedema, OL-EDA-ID, OMIM #300301) (Döffinger et al., 2001; Saban et al., 2004).

Over 99% of lymphedema cases worldwide are secondary to acquired damage to the lymphatic vessels (reviewed in Rockson, 2001; and in Warren et al., 2007). Filariasis (elephantiasis) is an infection of the lymphatics by the parasitic worms *Wuchereria bancrofti* or *Brugia malayi*, which leads to obstruction and scarring of lymphatic vessels, and chronic lymphedema of the lower limbs or genital organs. Filariasis is the principal cause of lymphedema worldwide, affecting approximately 100 million people, whereas breast cancer

surgery is the leading cause for secondary lymphedema in industrialized countries (reviewed in Rockson, 2001; and in Alitalo et al., 2005). Metastatic tumor cells frequently spread to the lymph nodes, necessitating radical surgery and radiotherapy, which destroy the lymphatic vessel network and lead to impairment of afferent lymphatic flow (reviewed in Rockson, 2001; and in Alitalo et al., 2005). For example, approximately 20-30% of patients that have undergone radical axillary lymph node dissection develop lymphedema of the upper limb later on (Mortimer et al., 1996; reviewed in Clark et al., 2005; and in Warren et al., 2007). Damage to the lymphatics may also result from bacterial infections of the skin (e.g. erysipelas) or the lymphatic vessels (lymphangitis) (reviewed in Rockson, 2001; and in Warren et al., 2007).

Unlike primary lymphedema, secondary lymphedema is typically due to damage to the collecting lymphatic vessels. Spontaneous recanalization of collecting vessels may occur in minimal lesions, but formation of new lymphatic vessels is typically not observed in lymphedema patients, although pre-existing vessels dilate to accommodate the increased fluid (Ikomi et al., 2006; Tabibiazar et al., 2006). Hypoxia is a ubiquitous stimulus for the initiation of angiogenesis, but it is not known whether intrinsic edema-induced mechanisms for engaging lymphangiogenic gene expression programs exist. The treatment of lymphedema is currently based on physiotherapy, compression garments, liposuction, and occasionally surgery (reviewed in Rockson, 2001; Warren et al., 2007), but means to reconstitute the collecting lymphatic vessels and cure the condition are rarely successful (Baumeister et al., 1981; Olszewski, 1988; Becker et al., 2006). VEGF-C gene transfer via adenoviruses (Ad), adeno-associated viruses (AAV), or naked plasmids, as well as the application of recombinant VEGF-C protein have been shown to stimulate the formation of new lymphatic capillaries and alleviate edema in preclinical animal models of lymphedema (Kärkkäinen et al., 2001; Szuba et al., 2002; Yoon et al., 2003; Saaristo et al., 2004), pointing to a promising means to restore lymphatic vessels in lymphedema patients.

## **AIMS OF THE STUDY**

This study was undertaken to study the potential of Ang1, VEGF-C, VEGF-D, and chimeric heparin-binding forms of VEGF-C in inducing therapeutic lymphatic vessel growth, as well as to elucidate the function of VEGFR-3 in angiogenesis under normal and pathological conditions.

The specific aims were to elucidate:

- I The role of angiopoietin-1 in lymphatic vessel sprouting and growth in adult tissues.
- II The potential of VEGF-C and VEGF-D to regenerate collecting lymphatic vessels and improve the outcome of lymph node transplantation in a mouse model of secondary lymphedema.
- III The analysis of the biological activity and vascular patterns induced by heparin-binding chimeric VEGF/VEGF-C fusion proteins *in vitro* and *in vivo*.
- IV The function of VEGFR-3 in angiogenesis in developmental, physiological, and pathological settings.



## MATERIALS AND METHODS

The materials and methods are described in detail in the original publications. A list of the most relevant materials and methods used in the studies is provided below.

### 1. Materials

Mouse line	Description	Source or reference	Used in
<i>Dll4</i> <sup>+LacZ</sup>	The <i>LacZ</i> gene has been inserted into the <i>Dll4</i> locus resulting in <i>Dll4</i> inactivation	(Duarte et al., 2004)	IV
DsRed	Expresses the <i>Discosoma</i> coral red fluorescent protein DsRed in all cells under the control of the chicken $\beta$ -actin promoter	(Vintersten et al., 2004)	II
K14-Ang1	Overexpresses Ang1 in basal epidermal keratinocytes	(Thurston et al., 1999)	I
K14-VEGF-E	Overexpresses VEGF-E in basal epidermal keratinocytes	(Kiba et al., 2003)	IV
K14-VEGF165	Overexpresses VEGF165 in basal epidermal keratinocytes	(Zheng et al., 2006)	IV
K14-VEGFR-3-Ig	Overexpresses the VEGFR-3-Ig fusion protein in basal epidermal keratinocytes	(Makinen et al., 2001a)	IV
Nu/nu	Immunodeficient athymic nude mice	Taconic	I, II, III, IV
Rip1Tag2	Expresses the oncogenic simian virus 40 large T antigen in pancreatic $\beta$ -cells under the control of the rat insulin promoter	(Hanahan, 1985)	IV
<i>Vegfc</i> <sup>+LacZ</sup>	The <i>LacZ</i> gene has been inserted into the <i>Vegfc</i> locus resulting in <i>Vegfc</i> inactivation	(Kärkkäinen et al., 2004)	IV
<i>Vegfr3</i> <sup>LacZ/LacZ</sup> , <i>Vegfr3</i> <sup>+LacZ</sup>	The <i>LacZ</i> gene has been inserted into the <i>Vegfr3</i> locus resulting in <i>Vegfr3</i> inactivation	(Dumont et al., 1998)	IV
Recombinant AAV	Description	Source or reference	Used in
AAV-Ang1	Encodes human Ang1	I	I
AAV-CA65	Encodes the chimeric VEGF-C $\Delta$ N $\Delta$ C-VEGF(exons 7-8) fusion protein	III	III
AAV-CA89	Encodes the chimeric VEGF-C $\Delta$ N $\Delta$ C-VEGF(exons 6a-8) fusion protein	III	III
AAV-EGFP	Encodes the green fluorescent protein from the jellyfish <i>Aequorea victoria</i>	(Kärkkäinen et al., 2001)	I, III
AAV-VEGF-B167	Encodes the human VEGF-B167 isoform	III	III
AAV-VEGF-C	Encodes human full-length VEGF-C	(Kärkkäinen et al., 2001)	I, III
AAV- VEGF-C $\Delta$ N $\Delta$ C	Encodes the mature form of human VEGF-C	III	III

<b>Recombinant adenovirus</b>	<b>Description</b>	<b>Source or reference</b>	<b>Used in</b>
AdAng1	Encodes human Ang1	I	I
AdCA65	Encodes the chimeric VEGF-C $\Delta$ N $\Delta$ C-VEGF(exons 7-8) fusion protein	III	III
AdCA89	Encodes the chimeric VEGF-C $\Delta$ N $\Delta$ C-VEGF(exons 6a-8) fusion protein	III	III
AdLacZ	Encodes <i>E. coli</i> $\beta$ -galactosidase	(Laitinen et al., 1997)	I, II, III, IV
AdmVEGF-D	Encodes mouse full-length VEGF-D	IV	IV
AdPDGF-B	Encodes human PDGF-B	From Dr P. Korpisalo and Dr. S. Ylä-Herttuala	II
AdVEGF165	Encodes the human VEGF165 isoform	(Enholm et al., 2001)	IV
AdVEGF-B186	Encodes the human VEGF-B186 isoform	II	II
AdVEGF-C	Encodes human full-length VEGF-C	(Enholm et al., 2001)	I, II, III, IV
AdVEGF-C $\Delta$ N $\Delta$ C-5'UTR	Encodes the mature form of human VEGF-C (contains the 5' untranslated region of <i>VEGFC</i> )	III	III
AdVEGF-D $\Delta$ N $\Delta$ C	Encodes the mature form of human VEGF-D	(Rissanen et al., 2003)	II
AdVEGF-E	Encodes the VEGF homologue VEGF-E originating from the Orf-NZ7 virus	(Wirzenius et al., 2007)	IV
AdVEGFR-3-Ig	Encodes the VEGFR-3-Ig fusion protein	(Kärpänen et al., 2001)	I, IV

<b>Cell line</b>	<b>Description</b>	<b>Source or reference</b>	<b>Used in</b>
B16	Murine skin melanoma line derived from the inbred C57/black/6 mouse strain	(Riley, 1963)	IV
G401	Human renal cancer cell line	American Type Culture Collection (ATCC)	IV
HDMEC	Primary human dermal microvascular endothelial cells	Promo Cell	I, II
HEK-293T	Human embryonic kidney fibroblast line expressing the simian virus 40 large T antigen	ATCC	I, III, IV
HeLa	Human cervical cancer line	ATCC	I, II, III, IV
MKN45	Human gastric carcinoma cell line	(Sakai et al., 1987)	IV
NCI-H460-LNM35-Luciferase	Subline of NCI-H460-N15, a human large-cell lung carcinoma. Selected <i>in vivo</i> for the propensity for lymph node metastasis. Tagged with <i>Photinus pyralis</i> (firefly) luciferase.	(Kozaki et al., 2000) (He et al., 2005)	II, IV
LLC	Murine lung carcinoma, derived from the inbred C57/black/6 mouse strain	ATCC	IV

<b>Recombinant protein</b>	<b>Description</b>	<b>Source or reference</b>	<b>Used in</b>
Jag1	A 17mer peptide consisting of the receptor-activating motif of the Notch-ligand Jagged1	(Weijzen et al., 2002)	IV
NP-1-Ig	Human NP-1 extracellular domain and immunoglobulin G1 fusion protein	(Kärkkäinen et al., 2001)	III
NP-2-Ig	Human NP-2 extracellular domain and immunoglobulin G1 fusion protein	(Kärkkäinen et al., 2001)	III
PDGFR- $\beta$ -Ig	Human PDGFR- $\beta$ - extracellular domain and immunoglobulin G1 fusion protein	R&D Systems	II
Tie2-Ig	Human Tie2- extracellular domain and immunoglobulin G1 fusion protein	R&D Systems	I
SC-Jag1	A scrambled 17mer peptide consisting of the same amino acids as Jag1	(Weijzen et al., 2002)	IV
VEGF165	Human VEGF165	R&D Systems	IV
VEGF-C $\Delta$ N $\Delta$ C	Human VEGF-C consisting of amino acids 103-215 and a H6 tag	(Kärpänen et al., 2006a)	III, IV
VEGFR-1-Ig	Consists of the first five Ig homology domains of human VEGFR-1 fused to the Fc region of human IgG1	(Makinen et al., 2001a)	III
VEGFR-2-Ig	Consists of the first three Ig homology domains of human VEGFR-2 fused to the Fc region of human IgG1	(Uutela et al., 2004)	III
VEGFR-3-Ig	Consists of the first three Ig homology domains of human VEGFR-3 fused to the Fc region of human IgG1	(Makinen et al., 2001a)	III

<b>Antigen</b>	<b>Antibody</b>	<b>Source or reference</b>	<b>Used in</b>
Ang1 C-terminus (human)	Goat polyclonal	Santa Cruz Biotech.	I
Ang1 N-terminus (human)	Goat polyclonal	Santa Cruz Biotech.	I
Bromodeoxyuridine	Mouse monoclonal-Alexa 594	Molecular Probes/ Invitrogen	IV
CD11b (mouse)	Rat monoclonal (clone M1/70)	BD Biosciences	IV
Cytokeratin 7 (human)	Rabbit polyclonal	AbCam	II
Dll4 (mouse)	Goat polyclonal	R&D Systems	IV
F4/80 (mouse)	Rat monoclonal (clone BM8)	Acris antibodies	III, IV
FITC	Rabbit polyclonal	Zymed/Invitrogen	IV
GFAP (cow)	Rabbit polyclonal	DAKO	IV
LYVE-1 (mouse)	Rabbit polyclonal	(Petrova et al., 2004)	I, II, III, IV
LYVE-1 (mouse)	Rat monoclonal (clone ALY7)	(Morisada et al., 2005)	I
MECA-32 (mouse endothelial cell antigen)	Rat monoclonal (clone MECA-32)	BD Biosciences	IV

<b>Antigen</b>	<b>Antibody</b>	<b>Source or reference</b>	<b>Used in</b>
N-cadherin (mouse)	Rabbit polyclonal	From Dr. M. Takeichi and Dr. H. Semb	II
NG2 (mouse)	Rabbit polyclonal	Chemicon/Millipore	IV
PCNA (human)	Mouse monoclonal-biotin	Zymed/Invitrogen	I
PDGFR- $\alpha$ (mouse)	Goat polyclonal	R&D Systems	IV
PDGFR- $\beta$ (mouse)	Rat monoclonal (clone APB5)	eBioscience	IV
PECAM-1 (mouse)	Hamster monoclonal (clone 2H8)	Chemicon/Millipore	II, III, IV
PECAM-1 (mouse)	Rat monoclonal (clone MEC 13.3)	BD Biosciences	II, III, IV
Phosphohistone H3 (mouse)	Rabbit polyclonal	Upstate/Millipore	I, III
Pimonidazole adducts	Mouse monoclonal-FITC	Chemicon/Millipore	IV
Podoplanin (human)	Rabbit polyclonal	(Kriehuber et al., 2001)	II, IV
Prox1 (mouse)	Rabbit polyclonal	(Kärkkäinen et al., 2004)	II
SMA (human)	Mouse monoclonal-Cy3 (clone 1A4)	Sigma	II, IV
Tie2 (mouse)	Rat monoclonal (clone TEK4)	eBioscience	I
VE-cadherin (mouse)	Rat monoclonal (clone 11D4.1)	BD Biosciences	II, IV
VEGF-C (human)	Rabbit polyclonal (#6)	(Baluk et al., 2005)	I, IV
VEGF-C $\Delta$ NAC (human)	Rabbit polyclonal (#3 and #4)	III	III
VEGFR-1 (mouse)	Rat monoclonal (clone 5B12)	ImClone	IV
VEGFR-2 (mouse)	Goat polyclonal	R&D Systems	IV
VEGFR-2 (mouse)	Rat monoclonal (clone AVAS-12 $\alpha$ 1)	BD Biosciences	IV
VEGFR-2 (mouse)	Rat monoclonal (DC101)	(Prewett et al., 1999)	IV
VEGFR-3 (mouse)	Goat polyclonal	R&D Systems	I, II, III, IV
VEGFR-3 (mouse)	Rat monoclonal (clone AFL4)	eBioscience	IV
VEGFR-3 (mouse)	Rat monoclonal (clone mF4-31C1)	(Pytowski et al., 2005)	IV
VEGFR-3 (human)	Mouse monoclonal (clone 9D9)	(Jussila et al., 1998)	IV
von Willebrand factor (human)	Rabbit polyclonal	DAKO	IV
ZO-1 (mouse)	Rat monoclonal	Chemicon/Millipore	II

## 2. Methods

<b>Method</b>	<b>Used in</b>
AAV transduction of cells or mice	I, III
Adenoviral transduction of cells or mice	I, II, III, IV
Bioassay for growth factor–mediated cell survival	III
Bioluminescence imaging	II, IV
Cell culture	I, II, III, IV
Confocal microscopy	I, II, III, IV
Dissection and transplantation of mouse lymph nodes	II
DNA subcloning	I, II, III, IV
Immunofluorescence	I, II, III, IV
Immunohistochemistry	I, II, III, IV
Immunoprecipitation	I, III, IV
Implantation of tumors into mice	II, IV
Mating and screening of genetically modified mice	II, IV
Metabolic labeling	I, III, IV
Microlymphangiography (tomato lectin, dextran, Evans blue)	II
Northern blotting	I
Polymerase chain reaction (PCR)	I, III, IV
Preparation of human tissues	II, IV
Preparation of mouse tissues	I, II, III, IV
Quantitative analysis and vessel morphometry	I, II, III, IV
RNA extraction	I, IV
Real-time quantitative PCR	IV
Superovulation of mice	IV
Stimulation of mouse embryos with recombinant growth factors	IV
Transduction of cells	I, III, IV
Transfection of cells	III
Transmission electron microscopy	IV
Western blotting	IV
X-gal staining of tissues	IV

## RESULTS AND DISCUSSION

### 1. Angiopoietin-1 induces lymphangiogenesis in adult tissues (I)

Analysis of gene-targeted mice has shown that Ang2 is essential for the proper patterning of lymphatic vessels, while Ang1 is able to rescue the lymphatic phenotype in Ang2 gene-targeted mice, suggesting that either ligand acts as a receptor agonist in LECs (Gale et al., 2002). In order to expand the repertoire of available pro-lymphangiogenic growth factors, it was rational to study whether Ang1 could induce lymphangiogenesis in adult tissues. For this purpose, adenoviral and adeno-associated virus (AAV) vectors encoding human Ang1 were transduced into the skin of adult mice, as this tissue is rich in lymphatic vessels. Ang1 induced lymphatic endothelial proliferation, vessel enlargement and formation of long LEC filopodia that eventually fused, leading to new sprouts over a period of four days. At two weeks, new lymphatic vessels were observed. Lymphatic capillary hyperplasia was also detected in the skin of K14-Ang1 transgenic mice, which express human Ang1 in the basal epidermal keratinocytes under the control of the keratin-14 promoter. Later studies have corroborated these findings, as Ang1, Ang2, and Ang3/Ang4 have now been shown to promote lymphangiogenic sprouting, with Ang1 being the most potent lymphangiogenic factor (Kim et al., 2007). Furthermore, an engineered Ang1 with enhanced biological activity and solubility was shown to promote wound healing through enhanced angiogenesis, lymphangiogenesis, and blood flow in a diabetic mouse model (Cho et al., 2006).

The Ang1 receptor Tie2 is expressed in cultured LECs (Kriehuber et al., 2001; Makinen et al., 2001b; Morisada et al., 2005), and Tie2 expression was observed also in cutaneous lymphatic vessels *in vivo*. Interestingly, stimulation of LECs with Ang1 resulted in upregulation of VEGFR-3 *in vivo* and *in vitro*. Furthermore, the lymphatic vascular effects of Ang1 were blocked by a soluble VEGFR-3-Ig fusion protein *in vivo*, suggesting that the Ang1/Tie2 and VEGF-C/VEGFR-3 pathways interact in the molecular regulation of lymphatic vessel growth and survival. It is possible that by upregulating VEGFR-3, Ang1 sensitizes the lymphatic vessels to VEGF-C and VEGF-D signals emanating from e.g. vascular SMCs, which have been shown to express both VEGF-C and VEGF-D (Partanen et al., 2000; Achen et al., 2001).

The upregulation of VEGFR-3 in response to Tie2 activation in the LECs could account for at least part of the observed increase in the rate of LEC proliferation, as VEGFR-3 signals have been shown to be sufficient for lymphatic vessel growth *in vivo* (Veikkola et al., 2003; Wirzenius et al., 2007). Ang1 may also exert direct effects promoting LEC proliferation and sprouting, as it has been reported to promote the survival and migration of blood vascular ECs (Koblizek et al., 1998; Hayes et al., 1999; Papapetropoulos et al., 2000; Kim et al., 2000b; Cho et al., 2004). Furthermore, Ang1 may also play a role in early lymphatic vessel development, as it was shown to expand colonies of LECs isolated from developing mouse embryos (Morisada et al., 2005). However, biochemical evidence for the cooperation of the Tie2 and VEGFR-3 signaling systems in lymphangiogenesis is lacking. Interestingly, Ang1 has been reported to bind to integrin  $\beta$ 1, even in the absence of Tie2, and to stimulate cell adhesion to fibronectin via  $\beta$ 1 integrin (Takakura et al., 1998; Carlson et al., 2001). On the other hand, VEGFR-3 has been shown to form a ligand-independent signaling complex with integrin  $\beta$ 1 (Wang et al., 2001). It is thus possible that Ang1 complexes with integrin  $\beta$ 1 - VEGFR-3 clusters, in addition to activating of Tie2, suggesting the possibility of a VEGF-C/VEGF-D-independent mechanism. Finally, Ang1 and Ang4 have also been shown to activate Tie1 in cultured LECs, which may be an additional explanation for the lymphangiogenic activity of Ang1 (Saharinen et al., 2005).

Ang1 is an important regulator of vascular permeability, being capable of preventing plasma leakage even after stimulation of blood vessels with highly potent permeabilizing agents, such as VEGF (Thurston et al., 2000; Thurston, 2002). These findings show that Ang1 can also be implicated as a lymphangiogenic factor, and further promote the utility of this factor in the management of tissue edema. Ang1 therapy could be applied in settings of edema, provoked by e.g. inflammation or allergens (Figure 1 d), in order to restore the integrity of EC monolayers in blood vessels, but also to promote the activation of lymphangiogenesis in response to VEGF-C and VEGF-D, which are produced by leukocytes in inflammatory infiltrates (Baluk et al., 2005). Ang1 therapy could also be applied in patients at a risk of secondary lymphedema in order to decrease the volume of extravasated fluid, thus reducing the drainage requirement of the lymphatic vessels that are still functional. Furthermore, Ang1 has been shown to protect ECs from radiation-induced injury, and it could also support LEC survival under stress (Cho et al., 2004b). Ang1 could be applied in patients suffering from reduced activity of the VEGFR-3 signaling pathway, such as Milroy

patients, although this would require evidence of VEGFR-3-independent lymphangiogenic activity of Ang1.

The low solubility of native Ang1 allows for localized treatment in order to minimize adverse effects, and to generate growth factor gradients. However, Ang1 is constantly produced by pericytes, and it is thus unlikely that even intravascularly administered Ang1 would lead to dramatic adverse effects. Systemic administration of Ang1 could be achieved with variants that have been engineered to form predominantly tetramers or pentamers instead of the highly insoluble aggregates formed by native Ang1 (Thurston et al., 2000; Cho et al., 2004a). Further solubility may be achieved by deletion of the linker peptide (Xu and Yu, 2001). Prolonged stimulation with such soluble forms of Ang1 has been reported to induce dilation of postcapillary venules, and to promote blood flow in these vessels, but other systemic effects have not been reported (Baffert et al., 2004; Cho et al., 2005).

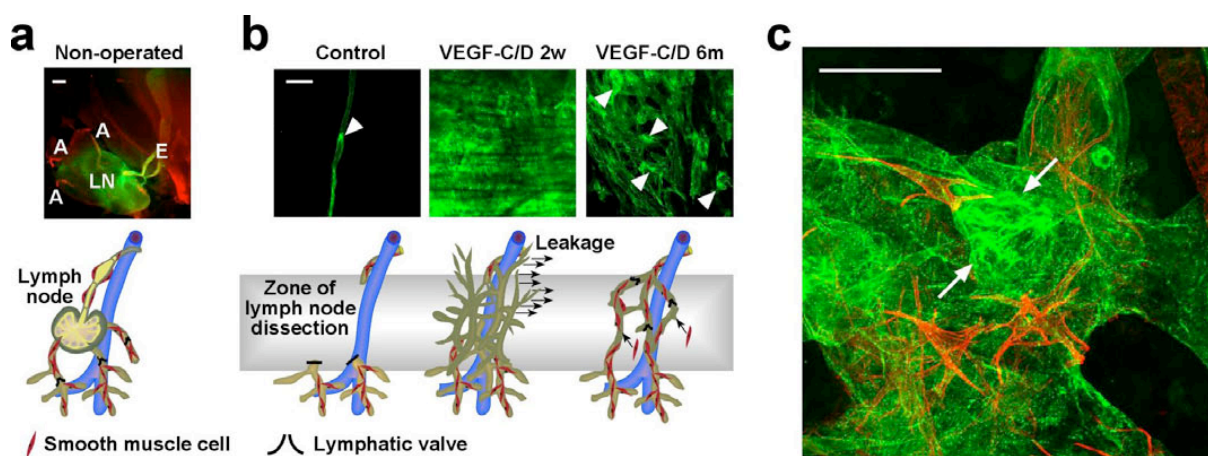
## **2. VEGF-C/VEGF-D therapy restores collecting lymphatic vessels and improves the outcome of lymph node transplantation (II)**

Surgery or radiation therapy of metastatic cancer often damages lymph nodes, leading to secondary lymphedema, a highly prevalent and debilitating condition (Figure 1f). Previous studies have demonstrated that VEGF-C and VEGF-D stimulate lymphangiogenesis in adult tissues, but they have been limited to analysis of lymphatic capillaries identified by markers such as LYVE-1 and VEGFR-3, while a comprehensive molecular analysis of the lymphatic vessel phenotype and especially the collecting lymphatic vessels, most commonly damaged in secondary lymphedema, has been lacking. (Jeltsch et al., 1997; Enholm et al., 2001; Kärkkäinen et al., 2001; Veikkola et al., 2001; Saaristo et al., 2002b; Yoon et al., 2003; Rissanen et al., 2003; Saaristo et al., 2004; Kärpänen et al., 2006b).

In order to study secondary lymphedema in a clinically relevant setting, a mouse model involving the dissection of all axillary lymph nodes and collecting vessels, frequently damaged in humans by breast cancer treatments, was established. This was followed by administration of adenoviral vectors into the surrounding tissues. Mice treated with control adenoviruses developed lymphedema of the paws, and demonstrated impaired return of lymph from the paw to the bloodstream. In contrast, mice treated with AdVEGF-C or AdVEGF-D $\Delta$ N $\Delta$ C displayed decreased edema and restoration of lymphatic drainage, which



continued to improve over time. Histological analysis of axillas treated with adenoviral VEGF-C or VEGF-D demonstrated robust growth of the lymphatic capillaries, which gradually underwent an intrinsic remodeling, differentiation, and maturation program into functional collecting lymphatic vessels. These vessels acquired all hallmarks of collecting vessels, including formation of uniform endothelial cell-cell junctions and intraluminal valves, although the vessels remained smaller in diameter than in normal non-operated axillas even at 6 months (**Figure 6**). Importantly, the vessels also acquired a coating of SMCs, which coincided with the formation of N-cadherin-mediated junctions and down-regulation of the lymphatic capillary marker LYVE-1. Conversely, the data indicated that the detachment of SMCs upon PDGF-B stimulation re-induced LYVE-1 in the collecting lymphatic vessels, indicating that SMC contact is required for maintenance of the collecting vessel phenotype. Besides N-cadherin, LEC-SMC signaling may be regulated by the ephrinB2/EphB4, Ang/Tie, S1P/S1P receptor, and TGF- $\beta$ /TGF- $\beta$ R pathways, as in blood vessels during development (Gale et al., 2002; Makinen et al., 2005; reviewed in Armulik et al., 2005).



**Figure 6. Maturation of the lymphatic vessels formed in response to VEGF-C/D therapy.** (a) In a normal non-operated mouse axilla the lymph nodes (LN) take up fluorescent dextran (green), which is transported to the lymph node via the afferent lymphatic vessels (A) after injection to the footpad of the mouse. The efferent lymphatic vessel (E) transports the tracer onwards from the lymph node. SMCs are stained with smooth muscle  $\alpha$ -actin (red). (b) In mice that underwent lymph node dissection only a few collecting lymphatic vessels remain (Control). Abundant leaky lymphatic vessels are observed at two weeks (2 w) following adenoviral gene transduction of VEGF-C or VEGF-D to the axillary tissues, while functional collecting lymphatics containing intraluminal valves (arrowheads) are seen at 6 months (6 m). (c) A magnified image of the lymphatic vascular plexus at 6 months. The vessel is in contact with SMCs (red), and contains an intraluminal valve (arrows). *Lycopersicon esculentum* lectin lymphangiography (green) was used to visualize lymphatic vessels in (b-c). Scalebars: 100  $\mu$ m.

According to these results, the process of lymphatic vessel maturation is analogous to arteriogenesis, which can be induced by prolonged stimulation with VEGF or PlGF, and by shear stress due to increased flow in the vessels (Garcia-Cardena et al., 2001; Dor et al., 2002; Pipp et al., 2003; reviewed in Schaper and Scholz, 2003). Interestingly, VEGF-C is a chemoattractant for monocytes/macrophages, which are important for arteriogenesis, and these cells may also play a role in lymphatic vessel maturation (Ito et al., 1997; Arras et al., 1998; Skobe et al., 2001b; Pipp et al., 2003; Saaristo et al., 2006). Prolonged VEGF-C stimulation may also directly promote LEC differentiation. In fact, the lymphatic vessels formed in response to VEGF-C stimulation resemble the lymphatic vascular plexus that forms early on during development, and it is likely that the intrinsic developmental mechanisms governing lymphatic vessel maturation are reactivated in these vessels. The molecular players regulating this process are poorly known, but it is likely that flow of the lymph in the nascent vessels contributes to the remodeling (Ng et al., 2004). The transcription factor FoxC2 is likely to be involved in the maturation process, as it regulates the formation of lymphatic and venous valves, as well as other characteristics of collecting lymphatic vessels during development (Petrova et al., 2004; Mellor et al., 2007).

In order to comprehensively restore the anatomy of the axilla following surgery, combined AdVEGF-C therapy with lymph node transplantation was applied. Such an approach has been previously undertaken without growth factor therapy, but in these experiments the autologously transplanted lymph nodes incorporated into existing lymphatic vasculature at a low frequency (Rabson et al., 1982; Becker et al., 2006). The lymph nodes transduced with AdVEGF-C survived, formed connections with the pre-existing lymphatic vessel network, and could even trap metastatic tumor cells, whereas the majority of control-treated nodes regressed, indicating that VEGF-C therapy can improve the success rate of lymph node transplantation (**Figure 7a**). These findings demonstrate for the first time that growth factor therapy can be used to generate functional and mature collecting lymphatic vessels. VEGF-C combined with lymph node transplantation allows for complete restoration of the lymphatic system in damaged tissues, and provides a model for future treatment of lymphedema in patients.

These findings are based on a mouse model, which has several limitations when considering direct extrapolation to the human patient setting. Firstly, the hydrostatic conditions are dramatically different in mice, as humans are considerably larger. This also

means that the absolute area damaged by axillary lymph node dissection in humans is greater in size, and the regenerating lymphatic vessels must span a longer distance in order to form anastomoses with both the distal and the proximal ends of the lymphatic vascular tree. However, this gap could be bridged by the transplantation of chains of lymph nodes from another location in the patient, whereas VEGF-C could be used to form the microvascular anastomoses. On the other hand, maturation of the lymphatic vessel plexus induced by VEGF-C therapy could be more complete in humans due to a longer life span.

VEGF-C has been shown to accelerate wound healing by promoting lymphangiogenesis, angiogenesis, and macrophage recruitment (Saaristo et al., 2004; Saaristo et al., 2006). Furthermore, VEGF-C could be used to augment immune responses by promoting antigen-presenting cell migration (Chen et al., 2004), as well as by increasing the number of lymphatic vessel routes available for these cells. On the other hand, VEGF-C has been shown to promote lymphatic metastasis of tumor cells (reviewed in Alitalo et al., 2005), to increase blood vascular permeability (Saaristo et al., 2002), as well as to stimulate extravasation of lymph from the lymphatic vessels (II). In light of these findings, patient safety is an important issue, which must be considered when identifying patients for future clinical trials.

### **3. Altered tissue distribution of VEGF-C by fusion to heparin-binding domains of VEGF produces distinct lymphatic vascular patterns**

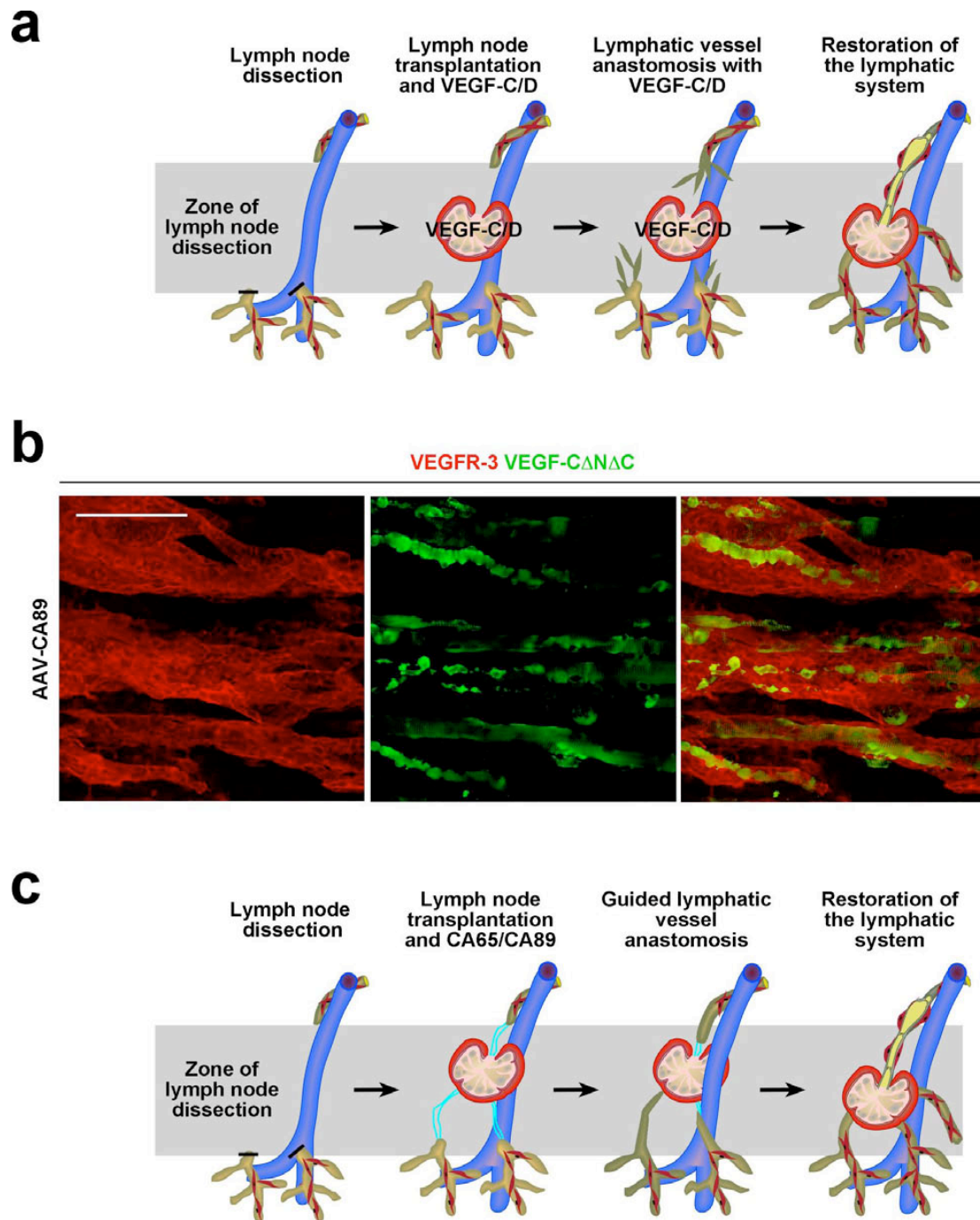
VEGF-C and VEGF-D have an N-terminal propeptide, as well as a C-terminal domain homologous to certain silk proteins. VEGF-C does not contain heparin-binding motifs, and it is unknown how, if at all, VEGF-C associates with the ECM (Joukov et al., 1996; Joukov et al., 1997). In order to study the effects of altered distribution of VEGF-C in tissues, a gain-of-function approach was adopted, comprising fusion of the exon 6a-8 or exon 7-8 encoded domains from VEGF to the C-terminus of the fully processed VEGF-C $\Delta$ N $\Delta$ C, denoted CA89 and CA65, respectively (Figure 3b). The VEGF-C/VEGF-HBD chimeras were produced, and shown to activate VEGF-C receptors, as well as to bind to NP-1 and NP-2. Both CA65 and CA89 stimulated lymphangiogenesis *in vivo* when expressed in tissues via adenovirus or AAV vectors. However, both chimeras induced a distinctly different pattern of lymphatic vessels when compared with the wild type VEGF-C. The tropism of the AAV serotype 2 vectors towards skeletal muscle was utilized to target expression into this tissue. The vessels induced by VEGF-C were initially a thick network of small diameter vessels that reorganized and matured slowly, but the lymphatic vessels induced by the chimeric growth factors were wider, less complex, and tended to form directly along tissue borders, along basement membranes that are rich in heparan sulfate (Figure 7b).

The altered biological activity of CA89 and CA65 in comparison to VEGF-C likely results from redistribution of the growth factors by binding of the HBD to pericellular matrix structures that are rich in HSPGs, which are typically present in basal laminae and on the surface of certain cells. Mice lacking the VEGF isoforms corresponding to VEGF165 and VEGF189 display disturbed vascular patterning, with a dramatic reduction in the number of vascular sprouts and branching points, highlighting the importance of the exon 6a- and 7-encoded sequences for normal VEGF function (Carmeliet et al., 1999; Ruhrberg et al., 2002). Conversely, protease-resistant large molecular-weight forms of VEGF produce abnormal vascular patterns characterized by excessive sprouting and branching (Lee et al., 2005). Consistent with the capacity of VEGF-C $\Delta$ N $\Delta$ C to activate VEGFR-2, both chimeras and VEGF-C $\Delta$ N $\Delta$ C induced angiogenesis, although the effects on blood vessels were not pronounced. Importantly, changes in lymphatic vessels were not observed after gene transfer of VEGF-B167, which contains similar high-affinity heparin- and neuropilin-binding

domains as VEGF189 and CA89 (Mäkinen et al., 1999), indicating that heparin and neuropilin binding capacities alone are not sufficient to stimulate either angiogenesis or lymphangiogenesis unless the factor is able to activate VEGFR-2 or VEGFR-3, respectively.

An inverse chimeric protein was generated, consisting of the minimal receptor-activating domain of VEGF flanked by the N- and C-terminal propeptides of VEGF-C. Interestingly, overexpression of this factor primarily stimulated the formation of very thin blood vessel capillaries, which was not observed by overexpressing VEGF165 or the minimal receptor-activating domain alone, suggesting a unique tissue distribution pattern for VEGF-C when compared to heparin-binding species of the VEGF family (Keskitalo et al., 2007).

These findings indicate that the heparin-binding forms of VEGF-C can be immobilized in a given tissue, and therefore the danger of obtaining aberrant side effects at distant sites is minimized. The matrix-binding domain of VEGF can target VEGF-C activity to heparin-rich basement membrane structures, which may prove useful in guiding the growth of lymphatic vessels into desired locations, such as transplanted lymph nodes (II), as well as in accelerating the formation of lymphatic vessel anastomoses. (Figure 7c).



**Figure 7. The therapeutic application of engineered heparin-binding and wild type forms of VEGF-C.** (a) A schematic representation of lymph node transplantation combined to VEGF-C therapy. Lymph node transplants transduced with AdVEGF-C attract lymphatic vessels to form anastomoses with the lymph node (a summary of the findings reported in II). (b) Skeletal muscle transduced with AAV2 vectors encoding CA89, a chimera consisting of VEGF- $\Delta$ N $\Delta$ C and exons 6a-8 of VEGF, in the mouse ear. Muscle fibers transduced with the vector are visualized by antibodies that recognize VEGF- $\Delta$ N $\Delta$ C (green). Note that CA89 (green) is immobilized to the muscle fibers. Lymphatic vessels, visualized by LYVE-1 immunostaining (red) have formed longitudinally alongside the transduced muscle fibers. (c) Growth of the lymphatic vessels towards the transplanted lymph node could possibly be accelerated by heparin-containing filaments (light blue) coated with CA65 and/or CA89. Scalebar: 100  $\mu$ m.

#### 4. Blocking VEGF-3 suppresses angiogenic sprouting, vascular network formation and tumor growth (IV)

Angiogenesis is a key process in several pathological conditions, including tumor growth and AMD (reviewed in Carmeliet, 2005). VEGF potently promotes angiogenesis and is indispensable for vascular development (Carmeliet et al., 1996; Ferrara et al., 1996), while VEGFR-2 is the primary receptor transmitting VEGF signals in ECs (Shalaby et al., 1995; Gille et al., 2001). VEGFR-3 is present in all endothelia during development, but in the adult it becomes restricted to the lymphatic endothelium (Kaipainen et al., 1995). However, VEGFR-3 is upregulated in the microvasculature of tumors and wounds (Valtola et al., 1999; Paavonen et al., 2000). The fact that *Vegfr3/Flt4* gene-targeted mice and zebrafish exhibit severe blood vascular defects, and that VEGFR-3 function-blocking antibodies suppress tumor angiogenesis (Dumont et al., 1998; Covassin et al., 2006; Laakkonen et al., 2007), prompted an investigation into the mechanisms of how VEGFR-3 contributes to angiogenesis.

During late embryogenesis and in the adult, blood vessels form primarily by angiogenesis, i.e. sprouting from pre-existing vessels. Angiogenic sprouting involves EC specification into leading tip cells, which respond to VEGF guidance cues, and stalk cells that follow the tip cells (Gerhardt et al., 2003). The findings presented here demonstrated that VEGFR-3 is highly expressed in the tip cells of angiogenic sprouts, and genetic deletion of VEGFR-3 or blocking VEGFR-3 signaling with monoclonal antibodies results in decreased sprouting, vascular density, vessel branching, and EC proliferation *in vivo*. On the other hand, stimulation of VEGFR-3 augmented VEGF-induced angiogenesis and sustained angiogenesis even in the presence of VEGFR-2 inhibitors, whereas antibodies against VEGFR-3 and VEGFR-2 in combination resulted in additive inhibition of angiogenesis and tumor growth.

Expression of the VEGFR-3 ligand VEGF-C was detected in ECs of the developing intersomitic vessels and in retinal leukocytes. In addition, many tumors are known to produce VEGF-C, and this has been correlated with increased propensity for lymphatic metastasis (Stacker et al., 2002). The VEGF-C signal is therefore present for the activation of VEGFR-3 in all angiogenic settings studied (**Figure 8**). However, VEGF-C was not expressed in a gradient, which is typically thought to be required for the guided migration of cells (reviewed in Lundkvist et al., 2007). It is therefore possible that VEGF-C/VEGFR-3 signaling regulates

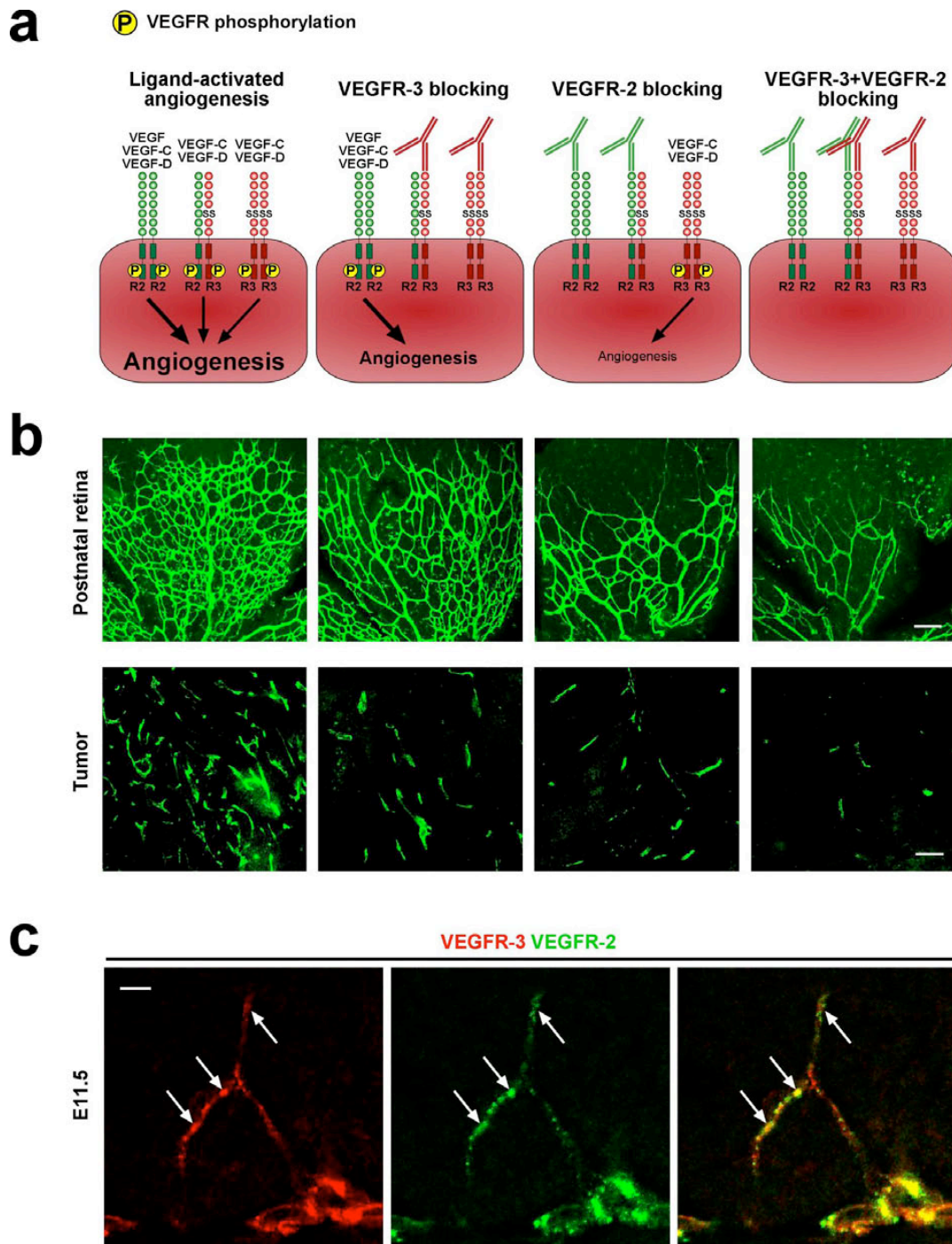
other aspects of vascular network formation, such as sprout fusion, or provides autocrine survival signals to the ECs, as has been described for VEGF (Lee et al., 2007).

Due to its silk-like domain, VEGF-C may aggregate into filaments with a long half-life in tissues (reviewed in Dicko et al., 2006). On the other hand, the endothelial tip cells express a variety of proteases, such as membrane-type-1 matrix metalloproteinase (MT1-MMP), to invade through the ECM (Yana et al., 2007). One possibility is that VEGF-C is a substrate of such proteases, leading to the release of mature VEGF-C, which potently activates both VEGFR-2 and VEGFR-3 homodimers, as well as VEGFR-2/VEGFR-3 heterodimers in the tip cells (Figure 8). This would indicate that the tip cells are capable of generating VEGF-C gradients by proteolysis. In analogy, certain tumor cells have been shown to generate chemotactic gradients by autocrine release of cytokines, which direct cell migration along lines of interstitial fluid flow (Shields et al., 2007).

However, the final explanation may not involve the canonical VEGFR-3 ligands at all: *Vegfc*<sup>-/-</sup>;*Vegfd*<sup>-/-</sup> double null embryos do not recapitulate the *Vegfr3*<sup>-/-</sup> null phenotype, and rather resemble *Vegfc*<sup>-/-</sup> single knock-outs, suggesting that alternative ligands for VEGFR-3 exist at least during early embryonic development (Haiko et al., 2008). It is possible that other VEGFs, such as VEGF, can promote endogenous activation of the VEGFR-3 signaling pathway in analogy to EGF-like growth factors that activate ErbB receptors by promoting receptor-mediated homodimerization or, alternatively, by the formation of heterodimers with the orphan receptor ErbB2 (reviewed in Olayioye et al., 2000). Furthermore, VEGF is present at very high concentrations in hypoxic tissue microenvironments (reviewed in Lundkvist et al., 2007), which may provide a stoichiometrically favorable ratio for VEGF-VEGFR-3 interactions that may previously have been overlooked *in vitro*.

Recent evidence indicates that VEGF induces Dll4 in the tip cells, which leads to suppression of excess sprouts in adjacent ECs (Noguera-Troise et al., 2006; Ridgway et al., 2006; Hellstrom et al., 2007; Lobov et al., 2007; Siekmann and Lawson, 2007; Suchting et al., 2007; reviewed in Roca and Adams, 2007). The data presented here indicate that VEGF signaling via VEGFR-2 also induces VEGFR-3 in the blood vascular endothelium. Furthermore, VEGFR-2 signals have been shown to be required for the maintenance of VEGFR-3 expression in the fenestrated endothelium under normal conditions (Kamba et al., 2006).





**Figure 8. The role of VEGFR-3 in angiogenesis.** (a) VEGFR-3 is not expressed in quiescent blood vascular endothelial cells. However, VEGFR-2 activation will induce VEGFR-3 in the blood vascular endothelium. Specific blocking of VEGFR-3 with monoclonal antibodies will attenuate angiogenic signaling in the endothelial cells, whereas blocking VEGFR-2 is more effective in blocking angiogenic signals. Blocking both VEGFR-2 and VEGFR-3 leads to additive inhibition of angiogenesis. (b) Angiogenesis in the mouse retina on postnatal day 5, and pathological angiogenesis in human tumor xenografts were studied (IV). Blood vessels were visualized by isolectin B4 staining and PECAM-1 immunostaining, respectively. (c) Arrows indicate co-localization of VEGFR-3 (red) and VEGFR-2 (green) in filopodial extensions of intersomitic vessel sprouts at E11.5. Scalebars: 100  $\mu$ m (b); 10  $\mu$ m (c).

A further objective of this study was to determine whether Dll4/Notch regulates VEGFR-3 expression in the angiogenic ECs. The data indicated that genetic or pharmacological disruption of the Notch signaling pathway led to widespread endothelial VEGFR-3 expression and excessive sprouting, which was inhibited by blocking VEGFR-3 signals. According to the results of this study, at the onset of angiogenesis VEGFR-3 becomes upregulated in the tip cells (by VEGF) and suppressed in the stalk cells (by Notch), indicating that VEGFR-3 functions as a positive regulator of endothelial sprouting and tip cell guidance. Interestingly, VEGFR-2 appears to be regulated in much the same way during angiogenesis (Gerhardt et al., 2003; Ridgway et al., 2006; Suchting et al., 2007; Lobov et al., 2007), suggesting that these two receptors collaborate, possibly via VEGFR-2/VEGFR-3 heterodimer signaling, in the tip cells (Figure 8c). The Notch signal is known to be high in the arteries during development, and these results may help explain why VEGFR-3 first becomes downregulated in arterial ECs during embryonic development (Dumont et al., 1998; Shutter et al., 2000; Lawson et al., 2001; Mailhos et al., 2001; Leslie et al., 2007; Siekmann and Lawson, 2007). A previous study has reported that NICD is capable of inducing *VEGFR3* transcription (Shawber et al., 2007), suggesting that *Vegfr3* repression by Notch is not direct and rather occurs via downstream effectors, such as the Hes and Hey transcription factors. A further mechanism downregulating VEGFR-3 in the nascent vessels may involve EC-pericyte interactions (Veikkola et al., 2003).

In addition to mature lymphatic vessels that do not require VEGFR-3 signals for survival (Makinen et al., 2001a), VEGFR-3 is only present in a few fenestrated endothelia and in angiogenic endothelium in adults (Kaipainen et al., 1995; Valtola et al., 1999; Paavonen et al., 2000; Partanen et al., 2000). As VEGF/VEGFR-2 pathway inhibitors have been shown to cause nephrosis and proteinuria in both humans and in animal models, the effects of VEGFR-3 blockers on kidney function and histology were thoroughly analyzed. Ultrastructural analysis of kidneys of all antibody-treated mice, as well as the K14-VEGFR-3-Ig transgenic mice by transmission electron microscopy did not reveal any hallmarks of glomerular damage, when compared to several examples in the literature (Gerber et al., 1999; Cingel-Ristic et al., 2005; Elliot et al., 2007). Furthermore, nephrosis or pathological albuminuria was not observed in mice that were treated with VEGFR-3 or VEGFR-2 antibodies, or both in combination, indicating normal kidney function (Sugimoto et al., 2003). These findings suggest that VEGFR-3 could be safely targeted in patients.

Surprisingly, even VEGFR-2 function-blocking antibodies did not induce kidney damage in our experiments. These data are in line with the literature showing that adult mice are more resistant to the adverse effects of VEGF/VEGFR-2 inhibitors (Baffert et al., 2004), unlike neonatal or adolescent mice (Kitamoto et al., 1997; Gerber et al., 1999; Eremina et al., 2003).

These results implicate VEGFR-3 as a novel regulator of angiogenic sprouting and vascular network formation, and suggest that VEGFR-3 can be safely targeted in adult patients to provide additional efficacy for anti-angiogenic therapies, especially towards vessels that are resistant to VEGF/VEGFR-2 inhibitors.

## CONCLUSIONS

The blood and lymphatic vascular systems are essential for life, but they may become harnessed for sinister purposes in pathological conditions. For example, tumors learn to grow a network of blood vessels, securing a source of oxygen and nutrients for sustained growth. On the other hand, damage to the lymph nodes and the collecting lymphatic vessels may lead to lymphedema.

The Ang1/Tie2 pathway has previously been implicated in promoting endothelial stability and integrity of EC monolayers. The studies presented here elucidate a novel function for Ang1 as a lymphangiogenic factor. Ang1 is known to decrease the permeability of blood vessels, and could thus act as a more global antagonist of plasma leakage and tissue edema by promoting growth of lymphatic vessels and thereby facilitating removal of excess fluid and other plasma components from the interstitium. These findings reinforce the idea that Ang1 may have therapeutic value in conditions of tissue edema.

VEGF-C and VEGF-D are potent lymphangiogenic factors, with direct and remarkably specific effects on the lymphatic endothelium in adult tissues. VEGF-C and VEGF-D therapy restored the collecting lymphatic vessels in a novel orthotopic mouse model of breast cancer-related lymphedema. These results introduce a novel approach to improve VEGF-C/VEGF-D therapy by using engineered heparin-binding forms of VEGF-C, which induced the rapid formation of organized lymphatic vessels. Importantly, VEGF-C therapy also greatly improved the survival and integration of lymph node transplants. The combination of lymph node transplantation and VEGF-C therapy provides a basis for future therapy of lymphedema.

In adults, VEGFR-3 expression is restricted to the lymphatic endothelium and the fenestrated endothelia of certain endocrine organs. However, these results show that VEGFR-3 is induced in the leading endothelial tip cells at the onset of angiogenesis, providing a tumor-specific vascular target. VEGFR-3 acts downstream of VEGF/VEGFR-2 signals, but, once induced, can sustain angiogenesis when VEGFR-2 signaling is inhibited. The data presented here implicate VEGFR-3 as a novel regulator of sprouting angiogenesis along with its role in regulating lymphatic vessel growth. Targeting VEGFR-3 may provide added efficacy to currently available anti-angiogenic therapies, which typically target the VEGF/VEGFR-2 pathway.

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