Cell, Vol. 92, 735–745, March 20, 1998, Copyright ©1998 by Cell Press

Neuropilin-1 Is Expressed by Endothelial and Tumor Cells as an Isoform-Specific Receptor for Vascular Endothelial Growth Factor

Shay Soker,*‖ Seiji Takashima,*# Hua Quan Miao,* Gera Neufeld,‡ and Michael Klagsbrun*†§
*Department of Surgery
†Department of Pathology
Children's Hospital
Harvard Medical School
Boston, Massachusetts 02115
‡Department of Biology
Technion
Israel Institute of Technology
Haifa 32000
Israel

Summary

Vascular endothelial growth factor (VEGF), a major regulator of angiogenesis, binds to two receptor tyrosine kinases, KDR/Flk-1 and Flt-1. We now describe the purification and the expression cloning from tumor cells of a third VEGF receptor, one that binds $VEGF_{165}$ but not $VEGF_{121}$. This isoform-specific VEGF receptor ($VEGF_{165}R$) is identical to human neuropilin-1, a receptor for the collapsin/semaphorin family that mediates neuronal cell guidance. When coexpressed in cells with KDR, neuropilin-1 enhances the binding of $VEGF_{165}$ to KDR and $VEGF_{165}$-mediated chemotaxis. Conversely, inhibition of $VEGF_{165}$ binding to neuropilin-1 inhibits its binding to KDR and its mitogenic activity for endothelial cells. We propose that neuropilin-1 is a novel VEGF receptor that modulates VEGF binding to KDR and subsequent bioactivity and therefore may regulate VEGF-induced angiogenesis.

Introduction

Vascular endothelial growth factor (VEGF), also known as vascular permeability factor, is a prime regulator of angiogenesis, vasculogenesis, and vascular permeability (reviewed in Klagsbrun and Soker, 1993; Dvorak et al., 1995; Ferrara and Davis-Smith, 1997). The increased expression of VEGF has been correlated with vascularization of tissues, for example, during embryogenesis (Breier et al., 1992; Millauer et al., 1993; Flamme et al., 1995) and during the female reproductive cycle (Shweiki et al., 1993). Targeted disruption of even one allele of the *VEGF* gene results in impaired blood vessel formation, growth retardation, and death by day 10.5 (Carmeliet et al., 1996; Ferrara et al., 1996). An important role for VEGF as a mediator of tumor angiogenesis is suggested by observations that high levels of VEGF are produced by various types of tumors (Dvorak et al., 1991; Plate et al., 1992), capillaries are clustered along VEGF-producing tumor cells (Plate et al., 1992), and tumor angiogenesis and subsequent tumor growth are inhibited in vivo by antibodies directed against VEGF (Kim et al., 1993) by soluble VEGF receptors (Kendall and Thomas, 1993) and by expression of dominant-negative VEGF receptors (Millauer et al., 1994). These properties have made the study of VEGF function relevant and significant for the study of normal physiological angiogenesis and of angiogenesis associated with abnormal cellular growth such as occurs in cancer.

Structurally, VEGF is a 40–45K homodimer with limited sequence homology to the platelet-derived growth factor (Keck et al., 1989; Tischer et al., 1989). Recently, a number of structurally homologous VEGF family members have been identified, including placenta-derived growth factor (PlGF), VEGF-B, VEGF-C, and VEGF-related protein (reviewed in Klagsbrun and D'Amore, 1996). Human VEGF monomers exist as five different isoforms of 121, 145, 165, 189, and 206 amino acids that are produced by alternative splicing from a single gene containing eight exons (Tischer et al., 1991; Poltorak et al., 1997). $VEGF_{121}$ and $VEGF_{165}$ appear to be the most abundant of the isoforms. These two VEGF isoforms differ somewhat in their biological properties. For example, $VEGF_{165}$ but not $VEGF_{121}$ binds to cell surface heparan sulfate proteoglycan (HSPG), with the result that $VEGF_{165}$ is partially retained by cells while $VEGF_{121}$ is totally released (Houck et al., 1992). In addition, $VEGF_{165}$ is a more potent endothelial cell mitogen than $VEGF_{121}$ (Keyt et al., 1996b; Soker et al., 1997).

VEGF activities are mediated by high affinity tyrosine kinase receptors associated with endothelial cells (EC). Two such VEGF receptors have been identified: the 180 kDa fms-like tyrosine kinase (Flt-1) (Shibuya et al., 1990; de Vries et al., 1992) and the 200 kDa kinase insert domain–containing receptor (KDR) (Terman et al., 1992) and its murine homolog, Flk-1 (Millauer et al., 1993). KDR binds VEGF and VEGF-C, whereas Flt-1 binds VEGF and PlGF. A third structurally related tyrosine kinase receptor, 180 kDa Flt-4, binds VEGF-C but not VEGF (Joukov et al., 1996). KDR appears to be the major transducer of VEGF signals in EC that result in chemotaxis, mitogenicity, actin reorganization, and gross morphological changes in target cells (Waltenberger et al., 1994; Yoshida et al., 1996; Ferrara and Davis-Smith, 1997). Targeted disruption of the *KDR/Flk-1* gene in mice results in a defect in the development of EC and embryonic death by day 9.5 (Shalaby et al., 1995). Although Flt-1 has a higher affinity for VEGF than KDR and is phosphorylated in response to VEGF, no mitogenic response is generated (Waltenberger et al., 1994). Nevertheless, Flt-1 appears to be an important mediator of angiogenesis. It is localized to the endothelium in adult tissue (Peters et al., 1993), and targeted disruption of this receptor gene, while showing normal EC formation, results in impaired EC assembly into blood vessels and embryonic lethality (Fong et al., 1995).

VEGF has been typically considered to be an EC-specific growth factor (Keck et al., 1989; Leung et al., 1989; Plouet et al., 1989). However, there have been several reports showing VEGF interactions with non-EC.

§ To whom correspondence should be addressed.
‖ Present address: Department of Urology, Children's Hospital, Harvard Medical School, Boston, MA 02115.
Present address: The First Department of Medicine, Osaka University School of Medicine, Osaka, 565, Japan.

For example, VEGF binds to Balb/C 3T3, HeLa, and melanoma cells (Gitay-Goren et al., 1992; Enomoto et al., 1994; Soker et al., 1996). It also stimulates the migration of monocytes and osteoblasts (Midy and Plouet, 1994; Barleon et al., 1996). Cell surface receptor cross-linking experiments with ^{125}I-VEGF have suggested that additional VEGF receptors might exist that are neither KDR nor Flt-1 (Gitay-Goren et al., 1996; Soker et al., 1996; Omura et al., 1997). Recently, we identified and characterized a 130–135 kDa VEGF receptor that is different from KDR or Flt-1 (Soker et al., 1996). Interestingly, this VEGF receptor is not only associated with EC but with the cell surface of tumor cells as well, e.g., breast carcinoma, prostate carcinoma, and melanoma. It has a K_d of about 2–3 $\times$ 10^{-10} M and is expressed in relatively high copy number, 2.5 $\times$ 10^4 receptors/cell for EC and 1–2 $\times$ 10^5 receptors/cell for MDA-MB-231 (231) breast carcinoma cells (Soker et al., 1996). A striking feature of this receptor is that it binds $VEGF_{165}$ but not $VEGF_{121}$, making it isoform-specific, and we thus named it $VEGF_{165}$ receptor ($VEGF_{165}R$). The structural difference between $VEGF_{165}$ and $VEGF_{121}$ is the 44 amino acids encoded by VEGF exon 7. Recently, we demonstrated that a fusion protein containing the exon 7–encoded domain of $VEGF_{165}$ bound $VEGF_{165}R$ directly and, furthermore, that it inhibited ^{125}I-$VEGF_{165}$ binding to $VEGF_{165}R$ on EC and 231 cells (Soker et al., 1996, 1997). Thus, the binding of $VEGF_{165}$ to $VEGF_{165}R$ occurrs via VEGF exon 7 in contrast to KDR and Flt-1, which bind $VEGF_{165}$ via VEGF exons 4 and 3, respectively (Keyt et al., 1996a). The fusion protein also inhibited $VEGF_{165}$-mediated EC proliferation (Soker et al., 1997).

Given these results, we set out to purify and clone $VEGF_{165}R$. In this report, we demonstrate by protein purification and concomitant expression cloning that 231 cell–derived $VEGF_{165}R$ is identical to human neuropilin-1, a cell surface glycoprotein that has been previously associated with axonal guidance in the developing nervous system (Kawakami et al., 1995; Takagi et al., 1995) and that recently has been demonstrated to be the receptor for the collapsin/semaphorin family of proteins (He and Tessier-Lavigne, 1997; Kolodkin et al., 1997). A second cDNA with 47% homology to *neuropilin-1* (*neuropilin-2*) was also discovered by expression cloning. Transfection of *neuropilin-1* cDNA into cells lacking endogenous VEGF receptors resulted in expression of a 130–140 kDa receptor that binds $VEGF_{165}$ but not $VEGF_{121}$. Furthermore, neuropilin-1 appears to act as a coreceptor that enhances $VEGF_{165}$ binding to KDR and $VEGF_{165}$ chemotactic and mitogenic activity. We conclude that $VEGF_{165}R$ is neuropilin-1 and that this receptor may have a novel role in VEGF-associated EC and tumor biology.

Results

Purification of $VEGF_{165}R$

Cross-linking of ^{125}I-$VEGF_{165}$ to cell surface receptors of 231 breast carcinoma cells results in formation of a single 165–175 kDa labeled complex with $VEGF_{165}R$ (Figure 1A, lane 1) (Soker et al., 1996). These cells have about 1–2 $\times$ 10^5 $VEGF_{165}$-binding sites/cell. In contrast to $VEGF_{165}$, $VEGF_{121}$ does not bind to the 231 cells and does not form a ligand-receptor complex (Soker et al., 1996). The relatively high $VEGF_{165}R$ number and the lack of any detectable KDR or Flt-1 mRNA in 231 cells (data not shown) suggested that these cells would be useful for $VEGF_{165}R$ purification. Preliminary characterization indicated that $VEGF_{165}R$ was a glycoprotein. A combination of Con A Sepharose and $VEGF_{165}$-Sepharose affinity chromatography was used for the purification of $VEGF_{165}R$ as described in Experimental Procedures. A prominent doublet with a molecular mass of about 130–135 kDa was detected by SDS-PAGE and silver stain (Figure 1A, lane 2). This size is consistent with the formation of a 165–175 kDa complex of 40–45 kDa $VEGF_{165}$ bound to receptors approximately 130–135 kDa in size (Figure 1A, lane 1). The two bands were excised separately and N-terminal amino acid sequencing was carried out (Figure 1A, right). Both the upper and lower bands had similar N-terminal amino acid sequences and showed high degrees of sequence homology to the predicted amino acid sequences in the N-terminal regions of

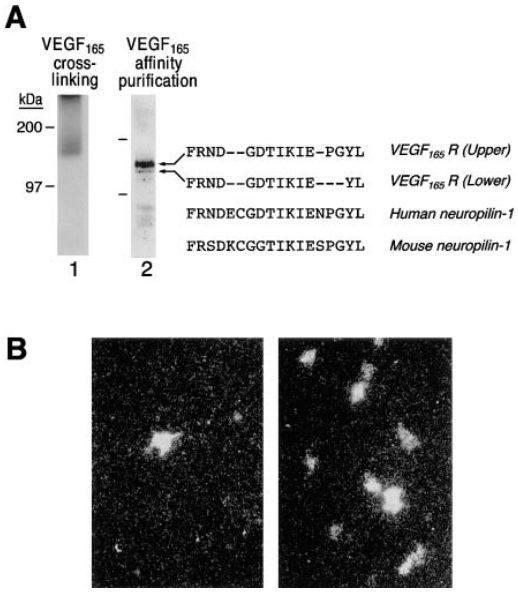

Figure 1. Purification and Expression Cloning of $VEGF_{165}R$ from 231 Cells

(A) Purification. ^{125}I-$VEGF_{165}$ (5 ng/ml) was bound and cross-linked to receptors on 231 cells and analyzed by SDS-PAGE and autoradiography (lane 1). $VEGF_{165}R$ was purified by Con A and $VEGF_{165}$ affinity chromatography and analyzed by SDS-PAGE and silver stain (lane 2). Two prominent bands were detected (arrows) and N-terminally sequenced separately. Their N-terminal 18–amino acid sequences are shown to the right of the arrows. The published N-terminal sequences of human and mouse neuropilin (Kawakami et al., 1995; He and Tessier-Lavigne, 1997) are shown below the $VEGF_{165}R$ sequences.

(B) Expression Cloning. Photomicrographs (dark-field illumination) of COS 7 cells binding ^{125}I-$VEGF_{165}$. ^{125}I-$VEGF_{165}$ was bound to transfected COS 7 cells, which were then washed, fixed, and overlayed with photographic emulsion that was developed as described in Experimental Procedures. Left, COS 7 cells were transfected with a primary plasmid pool (number 55 of the 231 cell library) representing approximately 3 $\times$ 10^3 clones, and one COS 7 cell binding ^{125}I-$VEGF_{165}$ in the first round of screening is shown. Right, several COS 7 cells transfected with a single-positive cDNA clone (A2) binding ^{125}I-$VEGF_{165}$ after the third round of screening.

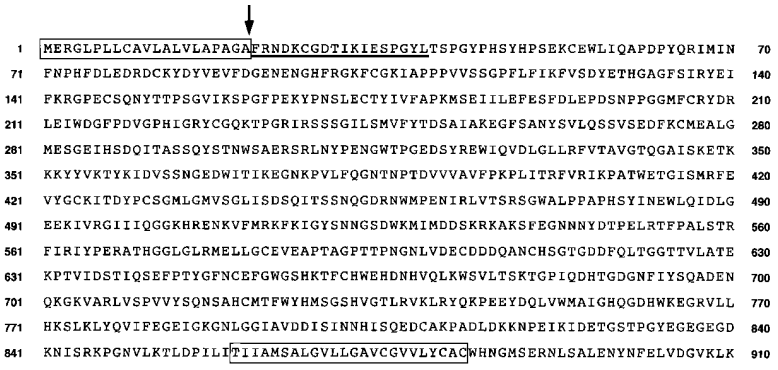

Figure 2. The Deduced Amino Acid Sequence of Human *neuropilin-1*

The deduced 923–amino acid sequence of the ORF of *neuropilin-1* clone A2 (full insert size of 6.5 kb) is shown. The putative signal peptide sequence (amino acids 1–21) and the putative transmembrane region (amino acids 860–883) are in boxes. The amino acid sequence obtained by N-terminal amino acid sequencing (Figure 1A, amino acids 22–39) is underlined. The arrow indicates where the signal peptide has been cleaved and removed based on comparison of the N-terminal sequence of purified neuropilin-1 and the cDNA sequence. The sequence of human *neuropilin-1* reported here differs from that reported by He and Tessier-Lavigne (1997) in that we find Lys26 rather than Glu26 and Asp855 rather than Glu855. Lys26 and Asp855 are found, however, in mouse and rat *neuropilin-1* (Kawakami et al., 1995; He and Tessier-Lavigne, 1997).

mouse (Kawakami et al., 1995) and human (He and Tessier-Lavigne, 1997) neuroplilin-1.

Expression Cloning of $VEGF_{165}R$ from 231 Cell-Derived mRNA

Concomitant with the purification, expression cloning was used to clone $VEGF_{165}R$. The details of these experiments are described in Experimental Procedures. For expression cloning, 231 cell mRNA was used to prepare a cDNA library of approximately 10^7 clones in a eukaryotic expression plasmid. Pools of this library were transfected into COS-7 cells in separate wells, and individual cells were screened for the ability to bind ^{125}I-$VEGF_{165}$ as detected by autoradiography of monolayers overlayed with photographic emulsion (Figure 1B, left). After three rounds of subpooling and screening, seven single-positive cDNA clones were obtained. Figure 1B (right) shows binding of ^{125}I-$VEGF_{165}$ to COS-7 cells transfected with one of these single-positive clones (clone A2).

Restriction enzyme analysis revealed that six of the seven single-positive clones had identical restriction digestion patterns, but one clone had a pattern that was different (data not shown). Sequencing of one of the identical cDNA clones, clone A2 (Figure 2), showed it to be identical to a sequence derived from a human-expressed sequence tag data bank (dbEST). This sequence also showed a high percentage of homology to the sequence of mouse *neuropilin-1* (Kawakami et al., 1995). After we had cloned human *$VEGF_{165}R$*, two groups reported the cloning of rat and human receptors for semaphorin III and identified them to be *neuropilin-1* (He and Tessier-Lavigne, 1997; Kolodkin et al., 1997). The 231 cell–derived $VEGF_{165}R$ cDNA sequence is virtually identical (see the Figure 2 legend for exceptions) to the human *neuropilin-1* sequence (He and Tessier-Lavigne, 1997). Significantly, the predicted amino acid sequence obtained by expression cloning (Figure 2) confirmed that *$VEGF_{165}R$* was *neuropilin-1* as was determined by N-terminal sequencing of purified receptor (Figure 1A). The human *neuropilin-1* cDNA sequence predicts an open reading frame (ORF) of 923 amino acids with two hydrophobic regions representing putative signal peptide and transmembrane domains. Overall, the sequence predicts ectodomain, transmembrane, and cytoplasmic domains consistent with the structure of a cell surface receptor. The N-terminal sequence obtained via protein purification as shown in Figure 1A is downstream of a 21–amino acid putative hydrophobic signal peptide domain, thereby indicating directly where the signal peptide domain is cleaved and removed.

Sequence analysis of the one clone obtained by expression cloning that had a different restriction enzyme profile predicted an ORF of 931 amino acids with about a 47% homology to *neuropilin-1* (data not shown). This human cDNA has a 93% sequence homology with rat *neuropilin-2* and is identical to the recently cloned human *neuropilin-2* (Chen et al., 1997).

Expression of Neuropilin-1 in Adult Cell Lines and Tissues

Reports of *neuropilin-1* gene expression have been limited so far predominantly to the nervous system of the developing embryo (Takagi et al., 1987, 1995; Kawakami et al., 1995). Cell surface $VEGF_{165}R$, however, is associated with nonneuronal adult cell types such as EC and a variety of tumor-derived cells (Soker et al., 1996). Northern blot analysis was carried out to determine whether cells that bind ^{125}I-$VEGF_{165}$ also synthesized *neuropilin-1* mRNA (Figure 3). *neuropilin-1* mRNA transcripts were expressed in human umbilical vein EC (HUVEC) (Figure 3A, lane 1). In tumor cell lines (Figure 3A, lanes 2–8), *neuropilin-1* mRNA levels were highest in 231 and PC3 cells and to a lesser degree in LNCaP, EP-mel, and RU-mel cells. There was little if any expression in MDA-MB-453 and WK-mel cells. The *neuropilin-1* gene expression patterns were consistent with our previous results showing that HUVEC, 231, PC3, LNCaP, EP-mel, and RU-mel cells bind ^{125}I-$VEGF_{165}$ to cell surface $VEGF_{165}R$ but that MDA-MB-453 and WK-mel cells do not (Soker et al., 1996).

neuropilin-1 gene expression was analyzed also by Northern blot in a variety of adult tissues in comparison to *KDR* gene expression (Figure 3B). *neuropilin-1* mRNA

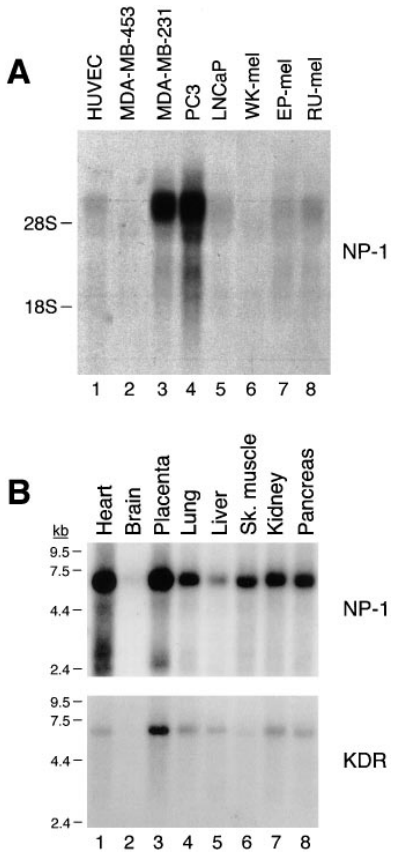

Figure 3. Northern Blot Analysis of *neuropilin-1* Expression

(A) Human EC and tumor-derived cell lines. Total RNA samples prepared from HUVEC and tumor-derived breast carcinoma, prostate carcinoma, and melanoma cell lines as indicated were resolved on a 1% agarose gel and blotted onto a GeneScreen nylon membrane. The membrane was probed with ^{32}P-labeled neuropilin-1 cDNA and exposed to X-ray film. Equal RNA loading was demonstrated by ethydium bromide staining of the gel prior to blotting. A major species of *neuropilin-1* mRNA of approximately 7 kb was detected in several cell lines.

(B) Adult human tissues. A premade Northern blot membrane containing multiple samples of human mRNA (Clontech) was probed with ^{32}P-labeled *neuropilin-1* cDNA (top) and then stripped and reprobed with ^{32}P-labeled *KDR* cDNA (bottom).

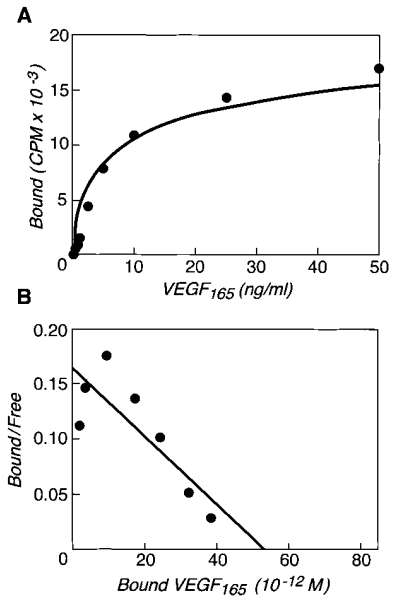

Figure 4. Scatchard Analysis of $VEGF_{165}$ Binding to Neuropilin-1

(A) Increasing amounts of ^{125}I-$VEGF_{165}$ (0.1–50 ng/ml) were added to subconfluent cultures of PAE cells transfected with human *neuropilin-1* cDNA (PAE/NP-1 cells) in 48-well dishes. No exogenous heparin was added. After binding the cells were washed, lysed, and the cell-associated radioactivity was determined using a γ counter. Nonspecific binding was determined by competition with a 200-fold excess of unlabeled $VEGF_{165}$.

(B) The binding data shown in (A) were analyzed by the method of Scatchard, and a best fit plot was obtained with the Ligand program (Munson and Rodbard, 1980). PAE/NP-1 cells express approximately 4.5×10^4 $VEGF_{165}$-binding sites per cell and bind ^{125}I-$VEGF_{165}$ with a K_d of 3×10^{-10} M.

levels were relatively high in heart and placenta; more moderate in lung, liver, skeletal muscle, kidney, and pancreas; and relatively low in adult brain. Interestingly, previous analysis of *neuropilin-1* gene expression in mouse and chicken brain suggested that this gene was expressed primarily during embryonic development and was greatly diminished after birth (Takagi et al., 1995; Kawakami et al., 1995). The tissue distribution of *KDR* mRNA was similar to that of *neuropilin-1*, with the exception that it was not expressed as highly in the heart. These results indicate that *neuropilin-1* is expressed widely in adult nonneuronal tissue, including tissues in which angiogenesis occurs such as heart and placenta.

Characterization of $VEGF_{165}$ Binding to Neuropilin-1

In order to characterize the binding properties of neuropilin-1, porcine aortic endothelial (PAE) cells were transfected with *neuropilin-1* cDNA. The PAE cells were chosen for these expression studies because they express neither KDR, Flt-1, (Waltenberger et al., 1994), nor $VEGF_{165}$R. Stable cell lines synthesizing neuropilin-1 (PAE/NP-1) were established, and ^{125}I-$VEGF_{165}$ binding experiments were carried out (Figure 4). ^{125}I-$VEGF_{165}$ binding to PAE/NP-1 cells increased in a dose-dependent manner and reached saturation at approximately 30 ng/ml (Figure 4A). Scatchard analysis of $VEGF_{165}$ binding revealed a single class of $VEGF_{165}$-binding sites with a K_d of approximately 3.2×10^{-10} M and approximately 4.5×10^4 binding sites per cell (Figure 4B). Similar K_d values were obtained for several PAE/NP-1 clones generated independently, although the receptor number varied from clone to clone (data not shown). The K_d of 3.2×10^{-10} M for the PAE/NP-1 cell lines is consistent with the $2–2.8 \times 10^{-10}$ M K_d values obtained for $VEGF_{165}$R expressed naturally by HUVEC and 231 cells (Soker et al., 1996). The binding of ^{125}I-$VEGF_{165}$ to PAE/NP-1 cells was enhanced by 1 μg/ml heparin (data not shown), consistent with previous studies showing that heparin enhances ^{125}I-$VEGF_{165}$ binding to $VEGF_{165}$R on HUVEC and 231 cells (Gitay-Goren et al., 1992; Soker et al., 1996).

Isoform-Specific Binding of VEGF to Cells Expressing Neuropilin-1

$VEGF_{165}$, but not $VEGF_{121}$, binds to $VEGF_{165}$R on HUVEC and 231 cells (Gitay-Goren et al., 1996; Soker et al., 1996).

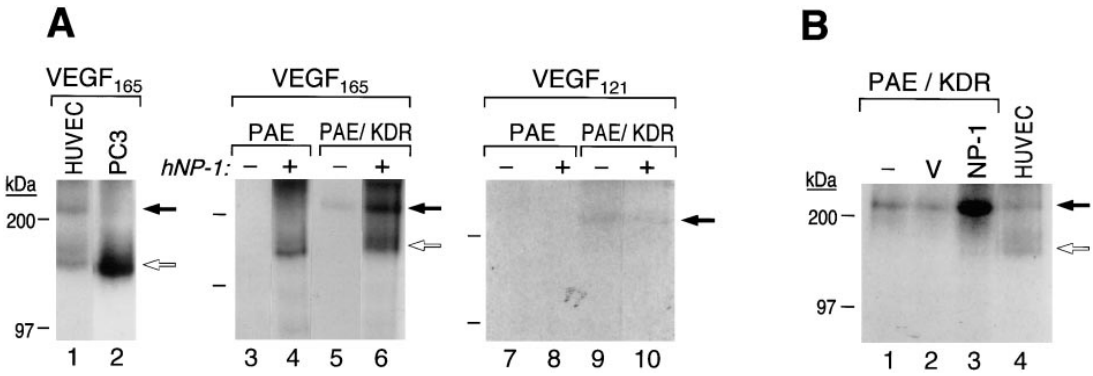

Figure 5. Cross-linking of VEGF Isoforms to PAE Cells Expressing Neuropilin-1, KDR, or Both Receptors

Stable transfections. ^{125}I-VEGF$_{165}$ (5 ng/ml) (lanes 1–6) or ^{125}I-VEGF$_{121}$ (10 ng/ml) (lanes 7–10) were bound to subconfluent cultures of HUVEC (lane 1), PC3 cells (lane 2), PAE cells (lanes 3 and 7), PAE cells transfected with human *neuropilin-1* cDNA (PAE/NP-1) (lanes 4 and 8), PAE cells transfected with *KDR* cDNA (PAE/KDR) (lanes 5 and 9), and PAE/KDR cells transfected with human *neuropilin-1* cDNA (PAE/KDR/NP-1) (lanes 6 and 10). At the end of a 2 hr incubation, each ^{125}I-VEGF isoform was chemically cross-linked to the cell surface. The cells were lysed and proteins were resolved by 6% SDS-PAGE. The polyacrylamide gel was dried and exposed to X-ray film. Solid arrows denote radiolabeled complexes containing ^{125}I-VEGF and KDR; open arrows denote radiolabeled complexes containing ^{125}I-VEGF$_{165}$ and neuropilin-1.

(B) Transient transfections. PAE/KDR cells were transfected with pCPhygro or pCPhyg-NP-1 plasmids as described in Experimental Procedures and grown for 3 days in 6 cm dishes. ^{125}I-VEGF$_{165}$ (5 ng/ml) was bound and cross-linked to parental PAE/KDR cells (lane 1), PAE/KDR cells transfected with vector control (V) (lane 2), PAE/KDR cells transfected with pCPhyg-NP-1 plasmids (NP-1) (lane 3), and HUVEC (lane 4). The cells were lysed and proteins were resolved by 6% SDS-PAGE as (A). Solid and open arrows denote labeled complexes as in (A).

To ascertain whether cells transfected with *neuropilin-1* had the same isoform binding specificity, PAE/NP-1 cells were incubated with ^{125}I-VEGF$_{165}$ or ^{125}I-VEGF$_{121}$ followed by cross-linking (Figure 5A). ^{125}I-VEGF$_{165}$ did not bind to parental PAE cells (Figure 5A, lane 3) but did bind to PAE/NP-1 cells via neuropilin-1 (Figure 5A, lane 4). The radiolabeled complexes formed with neuropilin-1 were similar in size to those formed in PC3 cells (Figure 5A, lane 2). On the other hand, ^{125}I-VEGF$_{121}$ did not bind to parental PAE (Figure 5A, lane 7) or to PAE/NP-1 cells (Figure 5A, lane 8). These results demonstrate that the VEGF isoform–specific binding that occurs with cells expressing endogenous neuropilin-1 (VEGF$_{165}$R) such as HUVEC, 231, and PC3 cells can be replicated in cells transfected with *neuropilin-1* cDNA and support the finding that VEGF$_{165}$R and neuropilin-1 are identical.

Coexpression of Neuropilin-1 and KDR Modulates VEGF$_{165}$ Binding to KDR

To determine whether expression of neuropilin-1 had any effect on VEGF$_{165}$ interactions with KDR, PAE cells that were previously transfected with *KDR* cDNA to produce stable clones of PAE/KDR cells (Waltenberger et al., 1994) were transfected with *neuropilin-1* cDNA, and stable clones expressing both receptors (PAE/KDR/NP-1) were obtained. These cells bound ^{125}I-VEGF$_{165}$ to KDR (Figure 5A, lane 6, upper complex) and to neuropilin-1 (Figure 5A, lane 6, lower complex) to yield a cross-linking profile similar to HUVEC (Figure 5A, lane 1). On the other hand, PAE/KDR/NP-1 cells bound ^{125}I-VEGF$_{121}$ to form a complex only with KDR (Figure 5A, lane 10), consistent with the inability of VEGF$_{121}$ to bind to neuropilin-1.

It appeared that in cells coexpressing KDR and neuropilin-1 (Figure 5A, lane 6) the degree of ^{125}I-VEGF$_{165}$-KDR 240 kDa complex formation was enhanced about 4-fold compared to the parental PAE/KDR cells (Figure 5A, lane 5). These results were reproducible, and the degree of 240 kDa complex formation in different PAE/KDR/NP-1 clones correlated positively with the levels of neuropilin-1 expressed. Binding experiments were carried out to quantitate these results (data not shown). Increasing concentrations of ^{125}I-VEGF$_{165}$ were added to PAE/KDR and PAE/KDR/NP-1 cells. At 30 ng/ml, the levels of ^{125}I-VEGF$_{165}$ bound to PAE/KDR/NP-1 cells were about 6-fold higher than to PAE/KDR cells, consistent with the cross-linking data shown in Figure 5. However, accurate measurement of the individual affinities (K_ds) of VEGF$_{165}$ binding to KDR and neuropilin-1 when they were coexpressed in PAE cells was difficult because the K_ds of KDR (Waltenberger et al., 1994; our results) and neuropilin-1 (Figure 4), when expressed independently in PAE cells, are fairly similar.

It could not be ruled out definitively that the enhanced binding to KDR was possibly due to clonal selection posttransfection. Therefore, parental PAE/KDR cells were transfected with *neuropilin-1* cDNA and ^{125}I-VEGF$_{165}$ was bound and cross-linked to the cells 3 days later in order to avoid selecting clones that might have shown diversity in KDR expression (Figure 5B). A labeled 240 kDa complex containing KDR was formed in parental PAE/KDR cells (Figure 5B, lane 1) and in PAE/KDR cells transfected with the expression vector alone (Figure 5B, lane 2). However, when ^{125}I-VEGF$_{165}$ was cross-linked to PAE/KDR cells expressing neuropilin-1 transiently, a more intensely labeled 240 kDa complex, about four times greater, was observed (Figure 5B, lane 3), compared to parental PAE/KDR cells (Figure 5B, lane 1) and PAE/KDR cells transfected with expression vector (Figure 5B, lane 2). Taken together, the results shown in Figures 5A and 5B suggest that coexpression of *KDR* and *neuropilin-1* genes in the same cell enhances the ability of VEGF$_{165}$ to bind to KDR.

Coexpression of Neuropilin-1 and KDR Enhances VEGF$_{165}$ Chemotactic Activity

To determine whether neuropilin-1 expression modulated VEGF$_{165}$ bioactivity, PAE, PAE/NP-1, PAE/KDR,

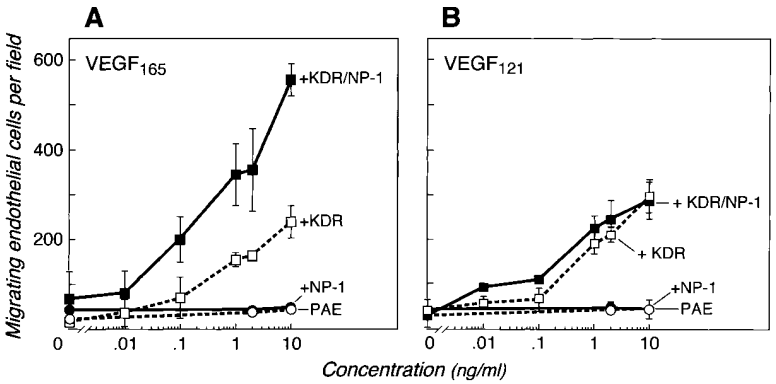

Figure 6. VEGF-Induced Chemotaxis in PAE Cells Expressing Neuropilin-1, KDR, or Both Receptors

Chemotaxis of PAE cells (open circles), PAE cells expressing neuropilin-1 (closed circles), PAE cells expressing KDR (open boxes), and PAE cells expressing both neuropilin-1 and KDR (closed boxes) toward increasing concentrations of $VEGF_{165}$ (A) or $VEGF_{121}$ (B) was measured in a Boyden chamber as described in Experimental Procedures. Each point represents the mean cell number and standard deviations of four independent wells.

and PAE/KDR/NP-1 cells were analyzed for their chemotaxis toward gradients of $VEGF_{165}$ or $VEGF_{121}$ in a Boyden chamber assay (Figure 6). There was no chemotaxis of parental PAE or PAE-NP-1 toward either VEGF isoform. Both these cell types were viable, however, and migrated well toward 10% serum (data not shown). Both $VEGF_{165}$ (Figure 6A) and $VEGF_{121}$ (Figure 6B) stimulated PAE/KDR cell migration in a dose-response manner and, to a similar extent, about 8-fold above control at 10 ng/ml VEGF. However, when PAE/KDR/NP-1 cells were examined, a notable difference in chemotaxis was observed. $VEGF_{165}$ at 10 ng/ml stimulated a 2.5-fold greater migration of PAE/KDR/NP-1 cells compared to PAE/KDR cells, while $VEGF_{121}$ did not induce any enhanced migration. Checkerboard analysis (Yoshida et al., 1996; Elenius et al., 1997) confirmed that the motility of the cell types was due to chemotaxis (data not shown). It was concluded that coexpression of neuropilin-1 with KDR not only results in increased $VEGF_{165}$ binding to KDR but in increased chemotaxis as well.

A GST-VEGF Exon 7+8 Fusion Protein Inhibits EGF_{165} Binding to VEGF Receptors and Mitogenicity for HUVEC

We have previously shown that ^{125}I-$VEGF_{165}$ binds to $VEGF_{165}$R through its exon 7–encoded domain and that a GST fusion protein containing the peptide encoded by VEGF exon 7+8 (GST-Ex 7 + 8) inhibits completely the binding of ^{125}I-$VEGF_{165}$ to $VEGF_{165}$R associated with 231 cells and HUVEC (Soker et al., 1996, 1997). When added to PAE/NP-1 cells, the fusion protein completely inhibited binding to neuropilin-1 (Figure 7A, lane 2 compared to lane 1). On the other hand, it did not inhibit ^{125}I-$VEGF_{165}$ binding to KDR (Figure 7A, lane 4 compared to lane 3). Thus, these results demonstrate that GST-Ex 7+8 binds to neuropilin-1 but not to KDR. The effects of GST-Ex 7+8 were different, however, in cells coexpressing both neuropilin-1 and KDR. The degree of ^{125}I-$VEGF_{165}$ binding to KDR in PAE/KDR/NP-1 cells (Figure 7A, lane 5) was greater than to the parental PAE/KDR cells (Figure 7A, lane 3), consistent with the results in Figure 5. In PAE/KDR/NP-1 cells, GST-Ex 7+8 inhibited not only ^{125}I-$VEGF_{165}$ binding to neuropilin-1 completely, but, unexpectedly, it also inhibited binding to KDR substantially (Figure 7A, lane 6 compared to lane 5). In fact, in the presence of GST-Ex 7+8, binding of ^{125}I-$VEGF_{165}$ to KDR in PAE/KDR/NP-1 cells was reduced to the levels seen in parental PAE/KDR cells not expressing neuropilin-1 (Figure 7A, lane 6 compared to lane 4). Similar inhibition of ^{125}I-$VEGF_{165}$ binding and cross-linking to KDR by GST-Ex 7+8 was observed in HUVEC, which express both KDR and neuropilin-1 (Soker et al., 1997). Since the fusion protein does not bind to KDR, these results suggest that inhibiting the binding of ^{125}I-$VEGF_{165}$ to neuropilin-1 directly inhibits its binding to KDR indirectly.

To determine whether the inhibitory effects of GST-Ex 7+8 on $VEGF_{165}$ binding also affected VEGF-induced mitogenicity, HUVEC were incubated with $VEGF_{165}$ in the presence or absence of GST-Ex 7+8 (Figure 7B). GST-Ex 7+8 inhibited $VEGF_{165}$-induced DNA synthesis by about 2- to 3-fold, confirming previous results (Soker et al., 1997). GST alone did not affect HUVEC proliferation. These results suggest that blocking $VEGF_{165}$ access to neuropilin-1 inhibits $VEGF_{165}$ mitogenic activity.

Discussion

Neuropilin-1, a Mediator of Neuronal Guidance, Is an Isoform-Specific $VEGF_{165}$ Receptor

Recently, we described a novel 130–135 kDa VEGF cell surface receptor that binds $VEGF_{165}$ but not $VEGF_{121}$ and that we named, accordingly, $VEGF_{165}$R (Soker et al., 1996). We have now purified $VEGF_{165}$R, expression cloned its cDNA, and shown it to be identical to human neuropilin-1 (He and Tessier-Lavigne, 1997), a 130–140 kDa cell surface glycoprotein first identified in *Xenopus* tadpole nervous tissue (Takagi et al., 1987). The evidence that $VEGF_{165}$R is identical to neuropilin-1 and that neuropilin-1 serves as a receptor for $VEGF_{165}$ is as follows: (i) Purification of $VEGF_{165}$R protein from human MDA-MB-231 (231) cells using VEGF affinity yielded a 130–140 kDa doublet upon SDS-PAGE and silver stain. N-terminal sequencing of both proteins yielded the same N-terminal sequence of 18 amino acids that demonstrated a high degree of homology to mouse and human neuropilin-1 (Kawakami et al., 1995; He and Tessier-Lavigne, 1997). The molecular mass of $VEGF_{165}$R is about 130–140 kDa, consistent with the size of neuropilin-1. (ii) Expression cloning using a 231 cell cDNA library resulted in isolation of several cDNA clones whose sequences were identical to that of human *neuropilin-1* cDNA (He and Tessier-Lavigne, 1997). The combination of purification and expression cloning has the advantage

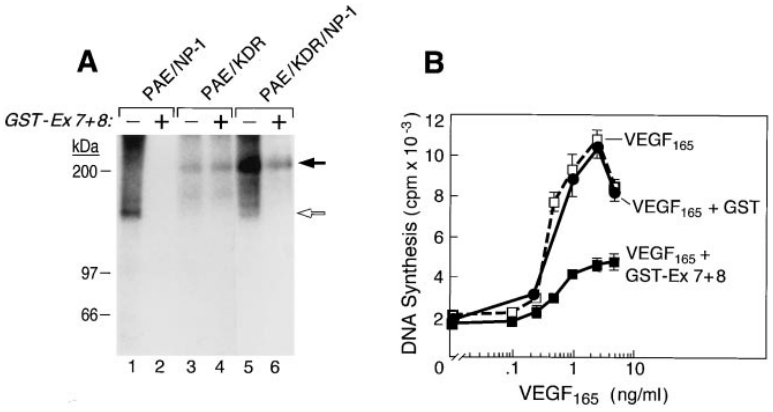

Figure 7. Inhibition of ^{125}I-VEGF$_{165}$ Binding to Neuropilin-1 Interferes with Its Binding to KDR and Its Mitogenic Activity for HUVEC

(A) Inhibition of binding. ^{125}I-VEGF$_{165}$ (5 ng/ml) was bound to subconfluent cultures of PAE transfected with *neuropilin-1* cDNA (PAE/NP-1) (lanes 1 and 2), PAE cells transfected with KDR (PAE/KDR) (lanes 3 and 4), and PAE/KDR cells transfected with *neuropilin-1* cDNA (PAE/KDR/NP-1) (lanes 5 and 6) in 35 mm dishes. The binding was carried out in the presence (lanes 2, 4, and 6) or absence (lanes 1, 3, and 5) of 25 μg/ml GST-Ex 7+8. ^{125}I-VEGF$_{165}$ was chemically cross-linked to the cell surface. Cells were lysed and labeled proteins were resolved by SDS-PAGE as in Figure 5. Solid and open arrows denote radiolabeled complexes as in Figure 5.

(B) Inhibition of proliferation. HUVEC were cultured in 96-well dishes (5000 cells/well) with increasing concentrations of VEGF$_{165}$ (open squares), VEGF$_{165}$ + 25 μg/ml of GST-Ex 7+8 (closed squares), or VEGF$_{165}$ + 30 μg/ml GST alone (closed circles). After a 4 day incubation, incorporation of ^{3}H-thymidine into HUVEC was measured. The results represent the average count of three wells, and the standard deviations were determined.

of allowing unambiguous identification of the neuropilin-1 protein N terminus. (iii) Northern blot analysis of *neuropilin-1* gene expression was consistent with previous ^{125}I-VEGF$_{165}$ cross-linking experiments (Soker et al., 1996). (iv) When neuropilin-1 was expressed in PAE cells, the transfected cells were able to bind VEGF$_{165}$ but not VEGF$_{121}$, consistent with the isoform specificity of binding previously shown for HUVEC and 231 cells (Soker et al., 1996). Furthermore, the K_d of ^{125}I-VEGF$_{165}$ binding to PAE expressing neuropilin-1 was about 3×10^{-10} M, consistent with previous VEGF$_{165}$R K_d binding values of 2 and 2.8×10^{-10} M for HUVEC and 231 cells, respectively (Soker et al., 1996). Taken together, these results show that VEGF$_{165}$R is identical to neuropilin-1.

In addition to the expression cloning of *neuropilin-1* cDNA, another human cDNA clone was isolated whose predicted amino acid sequence was 47% homologous to that of *neuropilin-1* and over 90% homologous to rat *neuropilin-2*, which was recently cloned (Kolodkin et al., 1997). Neuropilin-2 binds members of the collapsin/semaphorin family selectively (Chen et al., 1997). Whether this type of selectivity occurs for members of the VEGF family is under investigation.

The discovery that neuropilin-1 serves as a receptor for VEGF$_{165}$, an angiogenesis factor, is surprising since, to date, neuropilin-1 has been considered to be essentially a neuronal cell surface protein that plays a role in axon growth and guidance in the developing embryo (Fujisawa et al., 1995; Kawakami et al., 1995). Our results are novel in showing that *neuropilin-1* is also expressed widely in human adult tissues. Northern blot analysis demonstrates relatively high levels of *neuropilin-1* mRNA transcripts in nonneuronal human tissues such as heart, placenta, lung, liver, skeletal muscle, kidney, and pancreas. Interestingly, there is very little relative *neuropilin-1* expression in adult brain, consistent with previous studies in the mouse nervous system showing greatly diminished *neuropilin-1* expression after birth (Kawakami et al., 1995). *neuropilin-1* is also expressed in a number of cultured nonneuronal cell lines including a variety of tumor-derived cells and EC. Expression of *neuropilin-1* by cultured EC is consistent with previous studies demonstrating *neuropilin-1* expression in capillary EC in vivo in the embryonic mouse cardiovascular system (Kitsukawa et al., 1995).

Neuropilin-1 has been identified recently as a receptor that mediates the chemorepulsant activity of the collapsin/semaphorins (collapsin-1/Sema III/Sem D), a large family of transmembrane and secreted glycoproteins that function in repulsive growth cone and axon guidance (Kolodkin et al., 1993, 1997; He and Tessier-Lavigne, 1997). The K_d of Sema III binding to neuropilin-1, 0.15–3.25×10^{-10} M (He and Tessier-Lavigne, 1997; Kolodkin et al., 1997) is similar to that of VEGF$_{165}$ binding to neuropilin-1, which is about 2–3 $\times$ 10^{-10} M. These results indicate that two structurally different ligands with markedly different biological activities, stimulation of angiogenesis by VEGF and chemorepulsion of neuronal cells by Sema III, bind to the same receptor and with similar affinity. An interesting question is whether the two ligands bind to the same site on neuropilin-1 or to different sites. Neuropilin-1 has five discrete domains in its ectodomain, and it has been suggested that this diversity of protein modules in neuropilin-1 is consistent with the possibility of multiple binding ligands for neuropilin-1 (Takagi et al., 1991; Feiner et al., 1997; He and Tessier-Lavigne, 1997). Preliminary analysis does not indicate any large degree of sequence homology between Sema III and VEGF exon 7, which is responsible for VEGF binding to neuropilin-1. However, there may be some three-dimensional structural similarities between the two ligands. Since both neurons and blood vessels display branching and directional migration, it would be interesting to determine whether VEGF$_{165}$ displays any neuronal guidance activity and whether Sema III has any EC chemorepulsant activity.

A Role for Neuropilin-1 in Mediating VEGF$_{165}$ Activity and Angiogenesis

An important question is whether neuropilin-1 mediates VEGF$_{165}$ activity and, by extension, angiogenesis. Several pieces of evidence presented here suggest that neuropilin-1 regulates VEGF$_{165}$/KDR interactions and VEGF$_{165}$ activity as follows: (i) Neuropilin-1 enhances the binding

of $VEGF_{165}$ to KDR. When neuropilin-1 and KDR are coexpressed in EC, cross-linking and quantitative binding studies demonstrate that the binding of ^{125}I-$VEGF_{165}$ to KDR in cells coexpressing neuropilin-1 is enhanced by 4- to 6-fold compared to cells expressing KDR alone. It was not possible, however, to determine accurately the effect of neuropilin-1 on KDR binding affinity due to the similarities of the individual K_ds of neuropilin-1 and KDR in these cells. Enhanced binding can be demonstrated in stable clones coexpressing neuropilin-1 and KDR and also in PAE/KDR cells transfected transiently with *neuropilin-1* cDNA where clonal selection does not take place. (ii) The chemotaxis of PAE coexpressing neuropilin-1 and KDR toward a gradient of $VEGF_{165}$ is enhanced about 2.5-fold compared to PAE expressing KDR alone. On the other hand, there is no enhancement in the chemotaxis of cells coexpressing the two receptors toward $VEGF_{121}$, consistent with the isoform-specific binding of VEGF to neuropilin-1. PAE cells expressing neuropilin-1 alone do not migrate in response to gradients of $VEGF_{165}$, suggesting that this receptor does not function by itself in mediating cell motility but acts rather as a coreceptor. (iii) Conversely, blocking $VEGF_{165}$ access to neuropilin-1 substantially inhibits $VEGF_{165}$ binding to KDR and its mitogenic activity for HUVEC. This result was achieved using a GST fusion protein containing the 44–amino acid exon 7 of VEGF, the domain responsible for $VEGF_{165}$ binding to neuropilin-1, and the 6 amino acid exon 8, which facilitates production of the fusion protein (Soker et al., 1996, 1997). GST-Ex 7+8 is not only a direct and complete inhibitor of $VEGF_{165}$ binding to neuropilin-1 in PAE/KDR/NP-1 cells, but it is also inhibits indirectly $VEGF_{165}$ binding to KDR down to the levels observed in cells expressing KDR alone. The GST-Ex 7+8 protein also inhibits $VEGF_{165}$ mitogenic activity for HUVEC by 2- to 3-fold, confirming previous studies which showed that $VEGF_{165}$-induced HUVEC proliferation was inhibited down to the level induced by $VEGF_{121}$ (Soker et al., 1997). The combination of experiments in which neuropilin-1 is either overexpressed or is inhibited suggest strongly that neuropilin-1 is functional in EC by serving as a coreceptor that enhances $VEGF_{165}$ but not $VEGF_{121}$ binding to KDR and subsequent bioactivity. The concept that dual receptors regulate growth factor binding and activity has been previously demonstrated for TGF-β, bFGF, and NGF (Yayon et al., 1991; Lopez-Casillas et al., 1993; Barbacid, 1995). Expression of betaglycan in particular has been shown to increase TGF-β binding to its signaling receptor and to enhance cell responsiveness to TGF-β (Lopez-Casillas et al., 1993). At this point, the possible effects of neuropilin-1 on mediating KDR signaling have not been determined.

Compelling evidence suggesting that neuropilin-1 is involved in mediating angiogenesis comes from previous studies in other laboratories using transgenic mice (Kitsukawa et al., 1995). In the normal mouse embryo, neuropilin-1 is expressed in EC and in mesenchymal cells surrounding the EC. However, overexpression of neuropilin-1 ectopically in transgenic mice resulted in embryonic lethality, and the mice died in utero no later than on embryonic day 17.5. In these mice, the embryos possessed excess capillaries and blood vessels that were abnormal compared to normal counterparts. Dilated blood vessels were also observed and some of the chimeric mice showed hemorrhaging, mainly in the head and neck. These results are consistent with the possibility that ectopic overexpression of neuropilin-1 results in inappropriate $VEGF_{165}$ activity, thereby leading to aberrant angiogenesis. Furthermore, in a recent study the embryos of transgenic mice targeted for disruption of the *neuropilin-1* gene had severe abnormalities in the peripheral nervous system, but their death in utero at day 10.5–12.5 appeared to be due to anomalies in the cardiovascular system (Kitsukawa et al., 1997).

Neuropilin-1 Is Associated with Tumor-Derived Cells

The greatest degree of neuropilin-1 expression that we have detected so far occurs in tumor-derived cells such as 231 breast carcinoma cells and PC3 prostate carcinoma cells, far more than occurs in HUVEC. The tumor cells express abundant levels of *neuropilin-1* mRNA and about 200,000 $VEGF_{165}$ receptors/cell (Soker et al., 1996). On the other hand, these tumor cells do not express KDR or Flt-1, so neuropilin-1 is the only VEGF receptor associated with these cells. The role of neuropilin-1 in tumors in the absence of high affinity receptors is unknown. It may be that, besides the documented paracrine effects of tumor cell-derived VEGF on stimulating EC, $VEGF_{165}$ can affect tumor cells directly in an autocrine manner. To date, we have not been able to show $VEGF_{165}$-induced phosphorylation of neuropilin-1 in tumor-derived cells, consistent with the lack of a consensus tyrosine kinase domain. Nevertheless, many other cellular signaling mechanisms exist, and $VEGF_{165}$ might have an effect on tumor cells by inducing some as yet undetermined activity such as enhanced survival, differentiation, or motility. Another possibility is that tumor cell neuropilin-1 has a storage and sequestration function for $VEGF_{165}$. The ability of $VEGF_{165}$ but not $VEGF_{121}$ to bind to tumor cells via neuropilin-1 suggests that $VEGF_{165}$ might have a broader spectrum of interaction and activities than does $VEGF_{121}$, for example, with nonendothelial cells.

A recent report has demonstrated that glioma cells express a 190 kDa protein that binds $VEGF_{165}$ efficiently but not $VEGF_{121}$ (Omura et al., 1997). No stimulation of tyrosine phosphorylation of this receptor could be demonstrated upon binding of $VEGF_{165}$. Whether the 190 kDa receptor is related to neuropilin-1 is not known presently.

In summary, we have demonstrated by independent purification and expression cloning methods that the VEGF isoform–specific receptor $VEGF_{165}R$ is identical to neuropilin-1, a neuronal cell surface protein previously identified as a receptor for the collapsin/semaphorin family. Furthermore, expression of neuropilin-1 enhances the binding of $VEGF_{165}$ to KDR and $VEGF_{165}$ bioactivity. Future studies are aimed at elucidating the mechanisms by which neuropilin-1 mediates $VEGF_{165}$ bioactivity.

Experimental Procedures

Materials

Cell culture media, lipofectin, and lipofectamin were purchased from Life Technologies. Human recombinant $VEGF_{165}$ and $VEGF_{121}$ were produced in Sf-21 insect cells infected with recombinant baculovirus

vectors as previously described (Cohen et al., 1992). GST VEGF exons 7+8 fusion protein was prepared in *E. coli* and purified as previously described (Soker et al., 1996). Heparin, hygromycin B, and protease inhibitors were purchased from Sigma (St. Louis, MO). ^{3}H-thymidine, ^{125}I-Sodium, ^{32}P-dCTP, and GeneScreen-Plus hybridization transfer membrane were purchased from DuPont NEN (Boston, MA). Disuccinimidyl suberate (DSS) and IODO-BEADS were purchased from Pierce Chemical (Rockford, IL). Con A Sepharose was purchased from Pharmacia LKB Biotechnology (Piscataway, NJ). RNAzol-B was purchased from TEL-TEST (Friendswood, TX). Silver Stain kit and Trans-Blot PVDF membranes were purchased from Bio-Rad Laboratories (Hercules, CA). Multiple-tissue Northern blot membranes were purchased from Clontech (Palo Alto, CA). PolyATract mRNA isolation kits were purchased from Promega (Madison, WI). DNA-labeling kits and molecular weight markers were purchased from Amersham (Arlington Heights, IL). pcDNA3.1 plasmid was purchased from Invitrogen (Carlsbad, CA), and pCPhygro plasmid, containing the CMV promoter and encoding hygromycin B phosphorylase, was kindly provided by Dr. Urban Deutsch (Max Planck Institute, Bad Nauheim, Germany). Restriction endonucleases and Ligase were purchased from New England Biolabs (Beverly, MA). NT-B2 photographic emulsion and X-ray film were purchased from the Eastman Kodak company (Rochester, NY).

Cell Culture

HUVEC were obtained from American Type Culture Collection (ATCC) (Rockville, MD) and grown on gelatin-coated dishes in M-199 medium containing 20% fetal calf serum (FCS) and glutamine, penicillin, and streptomycin (GPS). Basic fibroblast growth factor (2 ng/ml) was added to the culture medium every other day. Parental PAE cells and PAE cells expressing KDR (PAE/KDR) (Waltenberger et al., 1994) were kindly provided by Dr. Lena Claesson-Welsh and were grown in F12 medium containing 10% FCS and GPS. MDA-MB-231 cells and MDA-MB-453 cells were obtained from ATCC and grown in DMEM containing 10% FCS and GPS. The human melanoma cell lines RU-mel, EP-mel, and WK-mel were kindly provided by Dr. Randolf Byer (Boston University Medical School, Boston, MA), and grown in DMEM containing 2% FCS, 8% calf serum, and GPS. Human metastatic prostate adenocarcinoma (LNCaP) and prostate carcinoma (PC3) cells were kindly provided by Dr. Michael Freeman (Children's Hospital, Boston, MA) and grown in RPMI 1640 containing 5% FCS and GPS.

Purification and Protein Sequencing

Approximately 5×10^8 MDA-MB-231 cells grown in 150 cm dishes were washed with PBS containing 5 mM EDTA, scraped, and centrifuged for 5 min at 500 $\times$ g. The cell pellet was lysed with 150 ml of 20 mM HEPES (pH 8.0), 0.5% Triton X-100, and protease inhibitors including 1 mM AEBSF, 5 μg/ml leupeptin, and 5 μg/ml aprotinin for 30 min on ice, and the lysate was centrifuged at 30,000 $\times$ g for 30 min. $MnCl_2$ and $CaCl_2$ were added to the supernatant to obtain a final concentration of 1 mM each. The lysate was absorbed onto a Con A Sepharose column (7 ml), and bound proteins were eluted with 15 ml 20 mM HEPES (pH 8.0), 0.2 M NaCl, 0.1% Triton X-100, and 1 M methyl-α-D-mannopyranoside at 0.2 ml/min. The elution was repeated twice more at 30 min intervals. The Con A column eluates were pooled and incubated for 12 hr at 4°C with 0.5 ml of $VEGF_{165}$-Sepharose beads containing about 150 μg $VEGF_{165}$. $VEGF_{165}$ was immobilized as described previously (Wilchek and Miron, 1982). The $VEGF_{165}$-Sepharose beads were washed with 50 ml of 20 mM HEPES (pH 8.0), 0.2 M NaCl, and 0.1% Triton X-100 and then with 25 ml of 20 mM HEPES (pH 8.0). The beads were boiled in SDS-PAGE buffer, and bound proteins were separated by 6% SDS-PAGE. Proteins were transferred to a TransBlot PVDF membrane using a semi-dry electric blotter (Hoefer Scientific), and the PVDF membrane was stained with 0.1% Coomassie brilliant blue in 40% methanol. The two prominent proteins in a 130–140 kDa doublet were cut out separately and N-terminally sequenced using an Applied Biosystems model 477A microsequenator, a service provided by Dr. William Lane of the Harvard Microchemistry Facility (Cambridge, MA).

Expression Cloning and DNA Sequencing

Complementary DNA (cDNA) was synthesized from 5 μg 231 cell mRNA. Double-stranded cDNA was ligated to EcoRI adaptors and size-fractionated on a 5%–20% potassium acetate gradient. DNA fragments larger than 2 kb were ligated to an eukaryotic expression plasmid, pcDNA3.1. The plasmid library was transfected into *E. coli* to yield a primary library of approximately 1×10^7 individual clones. A portion of the transformed bacteria was divided into 240 pools, each representing approximately 3×10^3 individual clones. DNA prepared from each pool was used to transfect COS-7 cells seeded in 12-well dishes using the Lipofectin reagent according to the manufacturer's instructions. Three days after transfection, the cells were incubated on ice for 2 hr with ^{125}I-$VEGF_{165}$ (10 ng/ml) in the presence of 1 μg/ml heparin, washed, and fixed with 4% paraformaldehyde in PBS. ^{125}I-$VEGF_{165}$ binding to individual cells was detected by overlaying the monolayers with a photographic emulsion, NT-B2, and developing the emulsion after 2 days as described (Gearing et al., 1989). Seven positive DNA pools were identified, and DNA from one of the positive pools was used to transform *E. coli*. The *E. coli* were subdivided into 50 separate pools and plated onto 50 LB ampicillin dishes, with each pool representing approximately 100 clones. DNA made from these pools was transfected into COS-7 cells, which were screened for ^{125}I-$VEGF_{165}$ binding as described above. Twenty positive pools were detected at this step, and their corresponding DNAs were used to transform *E. coli*. Each pool was plated onto separate LB ampicillin dishes, and DNA was prepared from 96 individual colonies and screened in a 96-well two-dimensional grid for ^{125}I-$VEGF_{165}$ binding to tranfected COS-7 cells as described above. Seven single clones were identified as being positive at this step. The seven positive plasmid clones were amplified, and their DNA was analyzed by restriction enzyme digestion. Six clones showed an identical digestion pattern of digest, and one was different. One clone from each group was submitted for automated DNA sequencing.

Northern Analysis

Total RNA was prepared from cells in culture using RNAzol according to the manufacturer's instructions. Samples of 20 μg RNA were separated on a 1% formaldehyde-agarose gel and transferred to a GeneScreen-Plus membrane. The membrane was hybridized with a ^{32}P-labeled fragment of human *neuropilin-1* cDNA corresponding to nucleotides 63–454 in the ORF at 63°C for 18 hr. The membrane was washed and exposed to X-ray film for 18 hr. A commercially obtained multiple human adult tissue mRNA blot (Clontech, 2 μg/lane) was probed for human *neuropilin-1* in a similar manner. The multiple tissue blot was stripped by boiling in the presence of 0.5% SDS and reprobed with a ^{32}P-labeled fragment of *KDR* cDNA corresponding to nucleotides 2841–3251 of the ORF (Terman et al., 1992).

Transfection of PAE Cells

Human *neuropilin-1* cDNA was digested with XhoI and XbaI restriction enzymes and subcloned into the corresponding sites of pCPhygro to yield pCPhyg-NP-1. PAE and PAE/KDR cells were grown in 6 cm dishes and transfected with 5 μg of pCPhyg-NP-1 using Lipofectamine according to the manufacturer's instructions. Cells were allowed to grow for an additional 48 hr, and the medium was replaced with fresh medium containing 200 μg/ml hygromycin B. After 2 weeks, isolated colonies (5–10 $\times$ 10^3 cell/colony) were transferred to separate wells of a 48-well dish and grown in the presence of 200 μg/ml hygromycin B. Stable PAE cell clones expressing neuropilin-1 (PAE/NP-1) or coexpressing neuropilin-1 and KDR (PAE/KDR/NP-1) were screened for $VEGF_{165}$ receptor expression by binding and cross-linking of ^{125}I-$VEGF_{165}$. For transient transfection, PAE/KDR cells were transfected with *neuropilin-1* as described above, and after 3 days ^{125}I-$VEGF_{165}$ cross-linking analysis was carried out.

Radioiodination of VEGF, Binding, and Chemical Cross-linking

The radioiodination of $VEGF_{165}$ and $VEGF_{121}$ using IODO-BEADS was carried out as previously described (Soker et al., 1997). The specific activity ranged from 40,000–100,000 cpm/ng protein. Binding and cross-linking experiments using ^{125}I-$VEGF_{165}$ and ^{125}I-$VEGF_{121}$ were performed as previously described in the presence of 1 μg/ml heparin (Gitay-Goren et al., 1992; Soker et al., 1996). VEGF binding was quantitated by measuring the cell-associated radioactivity in a

γ-counter (Beckman, Gamma 5500). The counts represent the average of three wells. All experiments were repeated at least three times and similar results were obtained. The results of the binding experiments were analyzed by the method of Scatchard using the LIGAND program (Munson and Rodbard, 1980). ^{125}I-VEGF$_{165}$ and ^{125}I-VEGF$_{121}$ cross-linked complexes were resolved by 6% SDS/PAGE, and the gels were exposed to X-ray films that were subsequently scanned by using an IS-1000 digital imaging system (Alpha Innotech Corporation).

Proliferation and Chemotaxis Assays

VEGF-induced proliferation was measured by adding increasing amounts of VEGF to HUVEC in gelatin-coated 96-well dishes, and DNA synthesis was measured as described previously (Soker et al., 1997). The preparation of the GST exon 7+8 fusion proteins and their use in HUVEC proliferation assays have been previously described (Soker et al., 1996, 1997). VEGF-induced chemotaxis was measured in a Boyden chamber as described previously (Yoshida et al., 1996; Elenius et al., 1997). Briefly, PAE, PAE/NP-1, PAE/KDR, and PAE/KDR/NP-1 cells were added to wells in the upper chamber and increasing amounts of VEGF isoforms were added to wells in the lower chamber. After a 4 hr incubation, the number of cells migrating through the filter were counted. A checkerboard analysis was used to ascertain that the migration was due to chemotaxis.

Acknowledgments

This work was supported by National Institutes of Health grants CA37392 (M. K.) and CA45548 (M. K.), a research award from the Association for the Cure of Cancer of the Prostate (CaPCURE) (M. K.), and an Angiogenesis Research Center grant from the Israeli Academy of Sciences (G. N.). We thank Drs. Gerhard Raab and Michael Freeman for thoughtful discussions and reading of the manuscript. We thank Drs. Makoto Seki and Takaaki Abe for help in expression cloning. We thank Mrs. Stela Gengrinovitch for providing the VEGF$_{165}$-Sepharose beads.

Received December 12, 1997; revised February 4, 1998.

References

Barbacid, M. (1995). Neurotrophic factors and their receptors. Curr. Opin. Cell Biol. *7*, 148–155.

Barleon, B., Sozzani, S., Zhou, D., Weich, H.A., Mantovani, A., and Marme, D. (1996). Migration of human monocytes in response to vascular endothelial growth factor (VEGF) is mediated via the VEGF receptor flt-1. Blood *87*, 3336–3343.

Breier, G., Albrecht, U., Sterrer, S., and Risau, W. (1992). Expression of vascular endothelial growth factor during embryonic angiogenesis and endothelial cell differentiation. Development *114*, 521–532.

Carmeliet, P., Ferreira, V., Breier, G., Pollefeyt, S., Kieckens, L., Gertsenstein, M., Fahrig, M., Vandenhoeck, A., Harpal, K., Eberhardt, C., et al. (1996). Abnormal blood vessel development and lethality in embryos lacking a single VEGF allele. Nature *380*, 435–439.

Chen, H., Chedotal, A., He, Z., Goodman, C.S., and Tessier-Lavigne, M. (1997). Neuropilin-2, a novel member of the neuropilin family, is a high affinity receptor for the semaphorins Sema E and Sema IV but not Sema III. Neuron *19*, 547–559.

Cohen, T., Gitay, G.H., Neufeld, G., and Levi, B.Z. (1992). High levels of biologically active vascular endothelial growth factor (VEGF) are produced by the baculovirus expression system. Growth Factors *7*, 131–138.

de Vries, C., Escobedo, J.A., Ueno, H., Houck, K., Ferrara, N., and Williams, L.T. (1992). The fms-like tyrosine kinase, a receptor for vascular endothelial growth factor. Science *255*, 989–991.

Dvorak, H.F., Sioussat, T.M., Brown, L.F., Berse, B., Nagy, J.A., Sotrel, A., Manseau, E.J., Van de Water, L., and Senger, D.R. (1991). Distribution of vascular permeability factor (vascular endothelial growth factor) in tumors: concentration in tumor blood vessels. J. Exp. Med. *174*, 1275–1278.

Dvorak, H.F., Brown, L.F., Detmar, M., and Dvorak, A.M. (1995). Vascular permeability factor/vascular endothelial growth factor, microvascular hyperpermeability, and angiogenesis. Am. J. Path. *146*, 1029–1039.

Elenius, K., Paul, S., Allison, G., Sun, J., and Klagsbrun, M. (1997). Activation of HER4 by heparin-binding EGF-like growth factor stimulates chemotaxis but not proliferation. EMBO J. *16*, 1268–1278.

Enomoto, T., Okamoto, T., and Sato, J.D. (1994). Vascular endothelial growth factor induces the disorganization of actin stress fibers accompanied by protein tyrosine phosphorylation and morphological change in Balb/C3T3 cells. Biochem. Biophys. Res. Commun. *202*, 1716–1723.

Feiner, L., Koppel, A.M., Kobayashi, H., and Raper, J.A. (1997). Secreted chick semaphorins bind recombinant neuropilin with similar affinities but bind different subsets of neurons in situ. Neuron *19*, 539–545.

Ferrara, N., and Davis-Smith, T. (1997). The biology of vascular endothelial growth factor. Endocrine Rev. *18*, 4–25.

Ferrara, N., Carver-Moore, K., Chen, H., Dowd, M., Lu, L., O'Shea, K.S., Powell-Braxton, L., Hillan, K.J., and Moore, M.W. (1996). Heterozygous embryonic lethality induced by targeted inactivation of the VEGF gene. Nature *380*, 439–442.

Flamme, I., Breier, G., and Risau, W. (1995). Vascular endothelial growth factor (VEGF) and VEGF receptor 2 (flk-1) are expressed during vasculogenesis and vascular differentiation in the quail embryo. Dev. Biol. *169*, 699–712.

Fong, G.H., Rossant, J., Gertsenstein, M., and Breitman, M.L. (1995). Role of the Flt-1 receptor tyrosine kinase in regulating the assembly of vascular endothelium. Nature *376*, 66–70.

Fujisawa, H., Takagi, S., and Hirata, T. (1995). Growth-associated expression of a membrane protein, neuropilin, in *Xenopus* optic nerve fibers. Dev. Neurosci. *17*, 343–349.

Gearing, D.P., King, J.A., Gough, N.M., and Nicola, N.A. (1989). Expression cloning of a receptor for human granulocyte-macrophage colony-stimulating factor. EMBO J. *8*, 3667–3676.

Gitay-Goren, H., Soker, S., Vlodavsky, I., and Neufeld, G. (1992). The binding of vascular endothelial growth factor to its receptors is dependent on cell surface–associated heparin-like molecules. J. Biol. Chem. *267*, 6093–6098

Gitay-Goren, H., Cohen, T., Tessler, S., Soker, S., Gengrinovitch, S., Rockwell, P., Klagsbrun, M., Levi, B.-Z., and Neufeld, G. (1996). Selective binding of VEGF$_{121}$ to one of the three VEGF receptors of vascular endothelial cells. J. Biol. Chem. *267*, 6093–6098.

He, Z., and Tessier-Lavigne, M. (1997). Neuropilin is a receptor for the axonal chemorepellent Semaphorin III. Cell *90*, 739–751.

Houck, K.A., Leung, D.W., Rowland, A.M., Winer, J., and Ferrara, N. (1992). Dual regulation of vascular endothelial growth factor bioavailability by genetic and proteolytic mechanisms. J. Biol. Chem. *267*, 26031–26037.

Joukov, V., Pajusola, K., Kaipainen, A., Chilov, D., Lahtinen, I., Kukk, E., Saksela, O., Kalkkinen, N., and Alitalo, K. (1996). A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases. EMBO J. *15*, 1751.

Kawakami, A., Kitsukawa, T., Takagi, S., and Fujisawa, H. (1995). Developmentally regulated expression of a cell surface protein, neuropilin, in the mouse nervous system. J. Neurobiol. *29*, 1–17.

Keck, P.J., Hauser, S.D., Krivi, G., Sanzo, K., Warren, T., Feder, J., and Connolly, D.T. (1989). Vascular permeability factor, an endothelial cell mitogen related to PDGF. Science *246*, 1309–1312.

Kendall, R.L., and Thomas, K.A. (1993). Inhibition of vascular endothelial growth factor activity by endogenously encoded soluble receptor. Proc. Natl. Acad. Sci. USA *90*, 10705–10709.

Keyt, B.A., Nguyen, H.V., Berleau, L.T., Duarte, C.M., Park, J., Chen, H., and Ferrara, N. (1996a). Identification of vascular endothelial growth factor determinants for binding KDR and FLT-1 receptors. Generation of receptor-selective VEGF variants by site-directed mutagenesis. J. Biol. Chem. *271*, 5638–5646.

Keyt, B.A., Berleau, L.T., Nguyen, H.V., Chen, H., Heinsohn, H., Vandlen, R., and Ferrara, N. (1996b). The carboxyl-terminal domain (111–165) of vascular endothelial growth factor is critical for its mitogenic potency. J. Biol. Chem. *271*, 7788–7795.

Kim, K.J., Li, B., Winer, J., Armanini, M., Gillett, N., Phillips, H.S., and Ferrara, N. (1993). Inhibition of vascular endothelial growth factor–induced angiogenesis suppresses tumor growth in vivo. Nature *362*, 841–844.

Kitsukawa, T., Shimono, A., Kawakami, A., Kondoh, H., and Fujisawa, H. (1995). Overexpression of a membrane protein, neuropilin, in chimeric mice causes anomalies in the cardiovascular system, nervous system and limbs. Development *121*, 4309–4318.

Kitsukawa, T., Shimizu, M., Sanbo, M., Hirata, T., Taniguchi, M., Bekku, Y., Yagi, T., and Fujisawa, H. (1997). Neuropilin-semaphorin III/D-mediated chemorepulsive signals play a crucial role in peripheral nerve projection in mice. Neuron *19*, 995–1005.

Klagsbrun, M., and Soker, S. (1993). VEGF/VPF: the angiogenic factor found? Curr. Biol. *3*, 699–702.

Klagsbrun, M., and D'Amore, P.A. (1996). Vascular endothelial growth factor and its receptors. Cytokine Growth Factor Rev. *7*, 259–270.

Kolodkin, A.L., Matthes, D.J., and Goodman, C.S. (1993). The *semaphorin* genes encode a family of transmembrane and secreted growth cone guidance molecules. Cell *75*, 1389–1399.

Kolodkin, A.L., Levengood, D.V., Rowe, E.G., Tai, Y.-T., Giger, R.J., and Ginty, D.D. (1997). Neuropilin is a Semaphorin III receptor. Cell *90*, 753–762.

Leung, D.L., Cachianes, G., Kuang, W.-J., Goeddel, D.V., and Ferrara, N. (1989). Vascular endothelial growth factor is a secreted angiogenic mitogen. Science *246*, 1306–1309.

Lopez-Casillas, F., Wrana, J.L., and Massague, J. (1993). Betaglycan presents ligand to the TGFβ signaling receptor. Cell *73*, 1435–1444.

Midy, V., and Plouet, J. (1994). Vasculotropin/vascular endothelial growth factor induces differentiation in cultured osteoblasts. Biochem. Biophys. Res. Commun. *199*, 380–386.

Millauer, B., Wizigmann-Voos, S., Schnurch, H., Martinez, R., Moller, N.P., Risau, W., and Ullrich, A. (1993). High affinity VEGF binding and developmental expression suggest Flk-1 as a major regulator of vasculogenesis and angiogenesis. Cell *72*, 835–846.

Millauer, B., Shawver, L.K., Plate, K.H., Risau, W., and Ullrich, A. (1994). Glioblastoma growth inhibited in vivo by a dominant-negative Flk-1 mutant. Nature *367*, 576–579.

Munson, P.J., and Rodbard, D. (1980). Ligand: a versatile computerized approach for characterization of ligand-binding systems. Anal. Biochem. *107*, 220–239.

Omura, T., Miyazawa, K., Ostman, A., and Heldin, C.-H. (1997). Identification of a 190-kDa vascular endothelial growth factor165 cell surface binding protein on human glioma cell line. J. Biol. Chem. *272*, 23317–23322.

Peters, K.G., DeVries C., and Williams L.T. (1993). Vascular endothelial growth factor expression during embryogenesis and tissue repair suggests a role in endothelial differentiation and blood vessel growth. Proc. Natl. Acad. Sci. USA *90*, 8915–8919.

Plate, K.H., Breier, G., Weich, H.A., and Risau, W. (1992). Vascular endothelial growth factor is a potential tumour angiogenesis factor in human gliomas in vivo. Nature *359*, 845–848.

Plouet, J., Schilling, J., and Gospodarowicz, D. (1989). Isolation and characterization of newly identified endothelial cell mitogen produced by AtT-20 cells. EMBO J. *8*, 3801–3806.

Poltorak, Z., Cohen, T., Sivan, R., Kandelis, Y., Spira, G., Vlodavsky, I., Keshet, E., and Neufeld, G. (1997). $VEGF_{145}$, a secreted vascular endothelial growth factor isoform that binds to extracellular matrix. J. Biol. Chem. *272*, 7151–7158.

Shalaby, F., Rossant, J., Yamaguchi, T.P., Gertsenstein, M., Wu, X.F., Breitman, M.L., and Schuh, A.C. (1995). Failure of blood-island formation and vasculogenesis in Flk-1-deficient mice. Nature *376*, 62–66.

Shibuya, M., Yamaguchi, S., Yamane, A., Ikeda, T., Tojo, A., Matsushime, H., and Sato, M. (1990). Nucleotide sequence and expression of a novel human receptor-type tyrosine kinase gene (flt) closely related to the fms family. Oncogene *5*, 519–524.

Shweiki, D., Itin, A., Neufeld, G., Gitay-Goren, H., and Keshet, E. (1993). Patterns of expression of vascular endothelial growth factor (VEGF) and VEGF receptors in mice suggest a role in hormonally regulated angiogenesis. J. Clin. Invest. *91*, 2235–2243.

Soker, S., Fidder, H., Neufeld, G., and Klagsbrun, M. (1996). Characterization of novel vascular endothelial growth factor (VEGF) receptors on tumor cells that bind $VEGF_{165}$ via its exon 7-encoded domain. J. Biol. Chem. *271*, 5761–5767.

Soker, S., Gollamudi-Payne, S., Fidder, H., Charmahelli, H., and Klagsbrun, M. (1997). Inhibition of vascular endothelial growth factor (VEGF)-induced endothelial cell proliferation by a peptide corresponding to the exon 7-encoded domain of $VEGF_{165}$. J. Biol. Chem. *272*, 31582–31588.

Takagi, S., Tsuji, T., Amagai, T., Takamatsu, T., and Fujisawa, H. (1987). Specific cell surface labels in the visual centers of *Xenopus laevis* tadpole identified using monoclonal antibodies. Dev. Biol. *122*, 90–100.

Takagi, S., Hirata, T., Agata, K., Mochii, M., Eguchi, G., and Fujisawa, H. (1991). The A5 antigen, a candidate for the neural recognition molecule, has homologies to complement components and coagulation factors. Neuron *7*, 295–307.

Takagi, S., Kasuya, Y., Shimizu, M., Matsuura, T., Tsuboi, M., Kawakami, A., and Fujisawa, H. (1995). Expression of a cell adhesion molecule, neuropilin, in the developing chick nervous system. Dev. Biol. *170*, 207–222.

Terman, B.I., Dougher-Vermazen, M., Carrion, M.E., Dimitrov, D., Armellino, D.C., Gospodarowicz, D., and Bohlen, P. (1992). Identification of the KDR tyrosine kinase as a receptor for vascular endothelial cell growth factor. Biochem. Biophys. Res. Commun. *187*, 1579–1586.

Tischer, E., Gospodarowicz, D., Mitchell, R., Silva, M., Schilling, J., Lau, K., Crisp, T., Fiddes, J.C., and Abraham, J.A. (1989). Vascular endothelial growth factor: a new member of the platelet-derived growth factor gene family. Biochem. Biophys. Res. Commun. *165*, 1198–1206.

Tischer, E., Mitchell, R., Hartman, T., Silva, M., Gospodarowicz, D., Fiddes, J.C., and Abraham, J.A. (1991). The human gene for vascular endothelial growth factor. Multiple protein forms are encoded through alternative exon splicing. J. Biol. Chem. *266*, 11947–11954.

Waltenberger, J., Claesson-Welsh, L., Siegbahn, A., Shibuya, M., and Heldin, C.-H. (1994). Different signal transduction properties of KDR and Flt1, two receptors for vascular endothelial growth factor. J. Biol. Chem. *269*, 26988–26995.

Wilchek, M., and Miron, T. (1982). Immobilization of enzymes and affinity ligands onto agarose via stable and uncharged carbamate linkages. Biochem. Int. *4*, 629–635.

Yayon, A., Klagsbrun, M., Esko, J.D., Leder, P., and Ornitz, D.M. (1991). Cell surface, heparin-like molecules are required for binding basic fibroblast growth factor to its high affinity receptors. Cell *64*, 841–848.

Yoshida, A., Anand-Apte, B., and Zetter, B.R. (1996). Differential endothelial migration and proliferation to basic fibroblast growth factor and vascular endothelial growth factor. Growth Factors *13*, 57–64.

GenBank Accession Numbers

Accession numbers for human *neuropilin-1* and human *neuropilin-2* are AF016050 and AF016098, respectively.