Discovery of pan-VEGF inhibitory peptides directed to the extracellular ligand-binding domains of the VEGF receptors

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Receptor tyrosine kinases (RTKs) are key molecules in numerous cellular processes, the inhibitors of which play an important role in the clinic. Among them are the vascular endothelial growth factor (VEGF) family members and their receptors (VEGFR), which are essential in the formation of new blood vessels by angiogenesis. Anti-VEGF therapy has already shown promising results in oncology and ophthalmology, but one of the challenges in the field is the design of specific small-molecule inhibitors for these receptors. We show the identification and characterization of small 6-mer peptides that target the extracellular ligand-binding domain of all three VEGF receptors. These peptides specifically prevent the binding of VEGF family members to all three receptors and downstream signaling but do not affect other angiogenic RTKs and their ligands. One of the selected peptides was also very effective at preventing pathological angiogenesis in a mouse model of retinopathy, normalizing the vasculature to levels similar to those of a normal developing retina. Collectively, our results suggest that these peptides are pan-VEGF inhibitors directed at a common binding pocket shared by all three VEGFRs. These peptides and the druggable binding site they target might be important for the development of novel and selective small-molecule, extracellular ligand-binding inhibitors of RTKs (eTKIs) for angiogenic-dependent diseases.

INTRODUCTION

Angiogenesis is the formation of new blood vessels from preexisting ones, an important process in physiological and pathological conditions (1). For example, tumors cannot grow beyond a few cubic millimeters without proper supply of nutrients and oxygen, and abnormal growth of blood vessels in the retina may result in legal blindness in children and adults (2, 3). Cancer and retinopathy are examples of diseases in which patients already benefit from currently available angiogenesis inhibitors (4, 5), and a growing number of diseases, from tumor formation to other nonneoplastic dysfunctions, share pathological angiogenesis as an underlying cause or as an important component for disease progression (3). Hence, the search for novel therapeutic options, such as antiangiogenic agents, is a valuable approach to improving treatment for these diseases.

Several molecules are important for angiogenesis, but it is well accepted that the vascular endothelial growth factor (VEGF, also known as VEGF-A) and family members [VEGF-B, VEGF-C, VEGF-D, and placental growth factor (PIGF)], along with their corresponding receptors (VEGFR-1, VEGFR-2, and VEGFR-3), are key factors in this process (6–8). Currently available antiangiogenic therapies for cancer and retinopathy are focused on neutralizing VEGF, their receptors, or pathways activated by these growth factors (5, 7, 9).

The three VEGF receptors have been implicated in angiogenesis, and they all belong to the receptor tyrosine kinase (RTK) family. There are more than 50 different RTKs encoded in the human genome, which are organized in 20 different families (10), and because they participate in key cellular processes, RTKs have been of great interest for drug development, including angiogenesis (10–12). Currently, two kinds of RTK inhibitors (TKIs) are in use in the clinic: small molecules directed to the adenosine triphosphatase (ATPase) intracellular kinase domain and antibodies that target the extracellular ligand-binding domain (13, 14). Although small-molecule TKIs offer significant advantages in terms of bioavailability (that is, oral administration), they often lack specificity because of the similarity of the ATPase tyrosine kinase domain shared by all family members (10, 15, 16). Although the broad-spectrum effect of TKI might be desirable in specific settings (for example, oncologic therapy, given the heterogeneous nature of cancer cells), it is also more likely to induce unwanted effects or develop drug resistance due to mutations. Thus, researchers have used different approaches to identifying new druggable sites in the kinase domain to improve selectivity and to overcome drug resistance (16). Although there have been important advances in the field, specificity is still an important challenge for the development of new TKI molecules.

Conversely, the extracellular ligand-binding portion of these receptors is the most diverse region of RTKs in terms of protein structure and, therefore, more attractive for the development of selective drugs (10, 17). In effect, several monoclonal antibodies that target the extracellular domain of an individual RTK have been approved for clinical use, including angiogenesis (5, 7). The trouble with monoclonal antibodies, albeit very specific down to a single-family member, is that they are expensive to produce, lack cell permeability, and have to be administered to patients in hospitals. Orally available molecules would be preferred, so there is a need to find novel alternatives for the development of small selective TKI molecules; targeting the ligand-binding domain of RTKs with small molecules may be an important option (17–19). These extracellular ligand-binding TKIs could offer significant advantages over current drugs by combining the bioavailability and cell permeability of small molecules with the specificity of targeting the ligand-binding domain with monoclonal antibodies (17, 18).

As an example of this strategy, we showed in previous studies that a small tripeptide targeting the extracellular ligand-binding domain of VEGFR-1 and neuropilin-1 (NRP-1) (20, 21) inhibited retinal neovascularization (17). This tripeptide, which can be applied topically to the eye, combines the selectivity of a monoclonal antibody with the advantages of a small-molecule compound, possibly...
as an unrecognized candidate class of TKI (17). These results have been further validated in a preclinical study that uses a nonhuman primate model of retinal disease, emphasizing the potential for targeting the extracellular domain of transmembrane receptors involved in angiogenesis (19).

Here, we expanded on these previous studies to target another receptor from the VEGF family, the VEGFR-3. We chose this receptor because it is highly expressed by the endothelial tip cells. These are specialized endothelial cells found at the tip of sprouting vessels whose function is believed to be the coordination of vessel formation and migration toward the VEGF gradient (22, 23). Blockage of endothelial tip cells with anti-VEGFR-3 monoclonal antibody prevents retinal angiogenesis (24). Although we were successful in identifying a peptide that targeted the extracellular domain of VEGFR-3 from a phage display library, we noticed that, once the peptides were synthesized and used outside the phage context, they lost their selectivity toward VEGFR-3. The synthetic peptides also interact with VEGFR-1 and VEGFR-2, neutralize binding of VEGF family members to all three receptors, and inhibit neovascularization in vivo in the retina. Hence, it is the first pan-VEGF inhibitor directed at the extracellular domain...
of an RTK that we have knowledge of. In summary, our study suggests that members of the VEGF receptor family share a common original binding site, which might be important for drug development.

RESULTS
Identification of peptides that target the extracellular domain of VEGFR-3
We used phage display in vitro to isolate peptides that target the extracellular domain of VEGFR-3. Recombinant mouse VEGFR-3 extracellular portion (Tyr to Asp) was immobilized on microtiter plates and incubated with an X6 (X = any amino acids) peptide phage display library. This particular library was chosen because it encodes peptides with relatively small molecular weights (average molecular weight of 6-mer peptides is 660 g/mol) while maintaining diversity greater than 10^7 possible peptides. The X6 phage display library that we built has an estimated ~10^9 individual peptides, and it is likely to encode several copies of all conceivable combinations possible for 6-mer peptides (6.4 x 10^7 unique peptide combinations), excluding...

Fig. 2. Peptides PCAIWF and WVCSGG interact with the ligand-binding domain of VEGFR-3. (A) Binding of phage PCAIWF to immobilized VEGFR-3 in the presence or absence of VEGF-A or VEGF-C (10 ng/ml). (B) Binding of phage PCAIWF to immobilized VEGFR-3 in the presence of increasing concentrations of VEGF-C. Percentage relative to phage binding in the absence of VEGF-C. (C) Cartoon showing the three-dimensional structure of the complex VEGF-C (red) bound to VEGFR-2 IgD2-3 (shown in orange and green, respectively) (Protein Data Bank #2X1W). (D) Analysis by SDS–polyacrylamide gel electrophoresis of purified recombinant IgD2 and IgD2-3 proteins containing the ligand-binding domain of VEGFR-3. (E) Binding of phage PCAIWF to VEGFR-3 and its recombinant Ig domains immobilized on microtiter wells in the presence or absence of the synthetic peptide PCAIWF or its scramble version, IFCAPW. Phage binding was quantified by ELISA using an anti-bacteriophage sera. (F) Binding of VEGF-C to microtiter wells coated with immobilized recombinant ligand binding domains IgD2 and IgD2-3 of VEGFR-3 in the presence or absence of synthetic peptides PCAIWF and WVCSGG or the scramble control peptide (IFCAPW). For phage experiments (A and B), bars represent mean ± SEM from triplicate plating; for ELISA assays (E to G), bars represent means ± SEM from duplicate wells. Statistics, Student’s t test [not significant (N.S.), P > 0.05; *P ≤ 0.05 and ***P ≤ 0.001].
peptides toxic to the bacteria or the bacteriophage. After three rounds of selection, we observed an approximately sixfold enrichment in the number of recovered phage compared to the previous round of selection (Fig. 1A), indicating that we had successfully enriched for peptides targeting our ligand. Randomly selected phage clones were analyzed by sequencing to identify their DNA inserts and coding peptides; only two peptide sequences were found encoded in all phage genomes analyzed: PCAIWF (58%) and WVCSGG (42%) (Fig. 1B).

PCAIWF and WVCSGG peptides are selective and bind to the same site in VEGFR-3

To validate the interaction of phage PCAIWF and WVCSGG and determine its specificity for VEGFR-3, we used a phage binding assay. All three VEGF receptors were individually immobilized on a plate and incubated with phage PCAIWF or WVCSGG or with a control insertless phage (Fd). We observed that phages PCAIWF and WVCSGG bind to VEGFR-3 but not to the other receptors, VEGFR-1 and VEGFR-2 (Fig. 1C and D), including the two other non-RTKs, NRP-1 and NRP-2, which have been described as co-receptors for VEGF. Moreover, binding was independent of the receptor’s species of origin because both phages bound to mouse and human VEGFR-3. No binding was observed when control phage Fd was used in the assays. Because all three receptors used in our assays are produced as recombinant proteins fused to the Fc domain of human immunoglobulin G1 (IgG1), these results also rule out the possibility that PCAIWF and WVCSGG phages bind to the Fc fusion portion present in these receptors. Finally, to exclude the possibility that random mutations in phage are responsible for receptor interaction, we found that binding of phage PCAIWF to VEGFR-3 is mediated specifically by the peptide because phage binding was inhibited by the cognate synthetic PCAIWF peptide (Fig. 1E). A control peptide had no effect on phage binding to this receptor.

Peptides PCAIWF and WVCSGG have no obvious motif in common or sequence similarity, but they both share two residues, a tryptophan and a cysteine. To assess whether they actually bind to the same site in VEGFR-3, we performed a competition assay. When synthetic peptide PCAIWF in solution was added to our binding assay, it prevented the binding of phage WVCSGG to VEGFR-3 (Fig. 1F). These results indicate that both peptides target the same site in VEGFR-3. Inhibition by peptide PCAIWF was dose-dependent with a median inhibitory concentration (IC50) below 30 μg/ml (Fig. 1G, black circles). Because both peptides have an unpaired cysteine residue with a free sulfhydryl group, we pondered whether a disulfide bridge formed between the peptide and VEGFR-3 was actually responsible for the interaction between these two molecules. To test this, we synthesized a new version of the peptide by replacing serine with cysteine. Although the peptide PSAIWF can no longer form a disulfide bridge, it was also effective at preventing the binding of phage PCAIWF to VEGFR-3, albeit with a lower efficiency (IC50 of ~200 μg/ml).
VEGF-C and VEGF-D, with IgD3 also contributing to the binding domain of VEGFR-3 as a recombinant protein to test for PCAIWF binding. The extracellular portion of VEGFR-3 was produced and purified, and the ligand-binding domain of VEGFR-3 was used to further validate these results. We observed that, when synthetic peptides PCAIWF and WVCSGG were added to the assay, both prevented binding of VEGF-C to IgD2 and IgD2-3 (Fig. 2F and G). Together, these results indicate that peptide PCAIWF interacts with the ligand-binding domain of VEGFR-3 and prevents VEGF-C interaction with the receptor.

**Synthetic PCAIWF is a pan-VEGF inhibitor**

Having shown that phage PCAIWF binds to the ligand-binding domain of VEGFR-3 but not to other VEGF receptors and modulates the binding of VEGF-C to this receptor, we asked whether peptides PCAIWF and WVCSGG were selective for the binding of VEGF-C to VEGFR-3. To answer this question, we set up a fluorophore-linked immunosorbent assay (FLISA) to evaluate the effect of PCAIWF on the binding of the three main angiogenic ligands (VEGF-A, PlGF, and VEGF-C) to all three RTK VEGF receptors (Fig. 3A). Because peptides PCAIWF and WVCSGG target the same site in the receptor, we decided to concentrate our studies on the PCAIWF peptide. The VEGF receptors were individually immobilized on plates and incubated with their respective ligands in the presence or absence of the synthetic peptide PCAIWF or PSAIWF. As control, we used a synthetic peptide containing the same amino acid residues of PCAIWF but in a distinct sequence (scramble). To our surprise, we observed that the synthetic peptide PCAIWF inhibits the binding of all VEGF members that we tested to their respective receptors (Fig. 3, B to F). Briefly, peptide PCAIWF inhibited the binding of VEGF-C to VEGFR-3 (Fig. 3B) and VEGFR-2 (Fig. 3C), prevented the binding of PlGF to VEGFR-1 (Fig. 3D), and also blocked the binding of VEGF-A to VEGFR-2 (Fig. 3E) and VEGFR-1 (Fig. 3F). These inhibitions were specific and were not affected by the control scramble peptide. Moreover, the synthetic peptide PSAIWF containing a serine residue instead of cysteine also inhibited the binding to all VEGF factors tested (albeit with lower affinity), again indicating that the sulfhydryl residue is important, but not essential, for binding (Fig. 3, B to F). Notably, we observed the binding of synthetic peptides PCAIWF and WVCSGG to VEGFR-3 and to VEGFR-1 (Fig. 3D) and rat NRP-2 (D) in the presence or absence of synthetic peptides PCAIWF and WVCSGG or the scramble control peptide (IFCAPW). Growth factor and neuropilin bound to the wells were quantified by FLISA using immunospecific antibodies and fluorescent detection. Bars represent means ± SEM from duplicate wells. Statistics, ANOVA (Tukey’s multiple comparison test) (N.S., P > 0.05).

Fig. 4. PCAIWF does not affect other angiogenic RTK or neuropilin binding. (A to D) Recombinant proteins for the human FGFR-1 (A), PDGFR-β (B), and VEGFR-1 (C and D) extracellular domains were immobilized on microtiter wells and incubated with the human ligands FGF-1 (A), PDGF-BB (B), human NRP-1 (C), and rat NRP-2 (D) in the presence or absence of synthetic peptides PCAIWF and WVCSGG or the scramble control peptide (IFCAPW). Growth factor and neuropilin bound to the wells were quantified by FLISA using immunospecific antibodies and fluorescent detection. Bars represent means ± SEM from duplicate wells. Statistics, ANOVA (Tukey’s multiple comparison test) (N.S., P > 0.05).

**PCAIIWF interacts with the ligand-binding domain of VEGFR-3**

To map the binding site of peptide PCAIWF within VEGFR-3, we performed a competition assay. Phage PCAIWF was incubated with VEGFR-3 in the presence or absence of its natural ligand, VEGF-C. As control, we used VEGF-A, which does not bind to this receptor. Only VEGF-C prevents the binding of phage PCAIWF to the receptor (Fig. 2A) in a dose-dependent manner (Fig. 2B). To corroborate these findings, we observed that binding of phage WVCSGG to VEGFR-3 is also inhibited by VEGF-C but not by VEGF-A. These data suggest that phage PCAIWF binds to the ligand-binding domain of VEGFR-3. To further validate these results, we produced the ligand-binding domain of VEGFR-3 as a recombinant protein to test for PCAIWF binding. The extracellular portion of VEGFR-3 is composed of seven immunoglobulin-like (Ig) domains, and the Ig domain 2 (IgD2) has been identified as the main binding site for VEGF-C and VEGF-D, with IgD3 also contributing to the interaction (Fig. 2C) (25). To confirm that peptide PCAIWF interacts with this domain, we produced IgD2 and IgD2-3 domains from human VEGFR-3 (Fig. 2D) and used the recombinant proteins in our phage assay. Phage PCAIWF binds to VEGFR-3 IgD2 and IgD2-3 domains with similar levels compared to the full-length extracellular VEGFR-3 protein, whereas the control phage Fd did not bind to any of the protein tested. Binding to the recombinant Ig domains could be prevented by the synthetic peptide PCAIWF but not by the control peptide (Fig. 2E). To confirm that our recombinant IgD2 and IgD2-3 domains were functional, we tested for the capacity to bind VEGF-C. VEGF-C binds to both recombinant ligand-binding domains IgD2 (Fig. 2F) and IgD2-3 (Fig. 2G). We observed that, when synthetic peptides PCAIWF and WVCSGG were added to the assay, both prevented binding of VEGF-C to IgD2 and IgD2-3 (Fig. 2, F and G). Together, these results indicate that peptide PCAIWF interacts with the ligand-binding domain of VEGFR-3 and prevents VEGF-C interaction with the receptor.
angiogenesis and have similar structural architecture compared to the VEGFR: ligand-binding moieties constituted of immunoglobulin folds. Neuropilins have also been described as ligands for the VEGF receptors (27, 28). It has been described that NRP-1 binds with high affinity to VEGFR-1 (Kd ~ 1.8 nM) (27). In agreement with these studies, we observed a strong interaction between NRP-1 and NRP-2 with VEGFR-1 using the FLISA binding assay. These interactions were not affected by peptide PCAIWF or WVCSGG (Fig. 4, C and D).

Binding of growth factors to RTKs triggers the activation of signaling events that are important for cell growth and survival. To assess whether peptide PCAIWF could prevent VEGFR-mediated activation of downstream signaling, lymphatic endothelial cells (LECs) were stimulated with VEGF-A, VEGF-C, or FGF-1. LECs were selected because they express high levels of VEGFR-3, VEGFR-2, and FGFR-1 and respond to these three growth factors by activating the extracellular signal–regulated protein kinases 1 and 2 (ERK1/2) pathway (29, 30). We observed that phosphorylation of ERK1/2 increases upon stimulation of LECs with VEGF-A, VEGF-C, or FGF-1; as expected, peptide PCAIWF inhibited the phosphorylation of ERK1/2 induced by VEGF-A and VEGF-C but had no effect on the phosphorylation of ERK1/2 induced by FGF-1 (Fig. 5, A and B). In all cases, the scramble synthetic control peptides had no effect on this downstream signaling event. Together, these results indicate that the effect of peptide PCAIWF is specific and selective for RTKs of the VEGF family.

**Pan-VEGF inhibitor PCAIWF prevents retinal neovascularization in a mouse model**

VEGF inhibitors have shown promising results for the treatment of ocular diseases with an angiogenic component. To assess whether synthetic peptide PCAIWF could inhibit neovascularization, we performed two angiogenesis assays: endothelial tube formation in Matrigel and the oxygen-induced retinopathy (OIR) model (in vivo). For the endothelial cell tubulogenesis assay, peptides PCAIWF and scramble were embedded in the Matrigel layer, and human umbilical vein endothelial cells (HUVECs) were stimulated with VEGF-A or VEGF-C (31). In both cases, we observed inhibition of tube formation by peptide PCAIWF but not by the control scramble peptide or vehicle alone (Fig. 6A). Tube formation was reduced by ~50% in both cases (VEGF-A and VEGF-C), suggesting that other growth factors present in the Matrigel, which are not affected by peptide PCAIWF, might be stimulating the endothelial cells (Fig. 6B) and preventing the full inhibition of tubulogenesis. Next, we assessed the effect of PCAIWF in an in vivo mouse model.
formed as early as P12 because young mice have their eyelids shut and they are not fully open until P14 to P15 (36). Two days after treatment, the retinas were analyzed, and neovascularization was quantified (37). We observed that the retinas of animals treated with peptide PCAIWF showed a significant reduction in the amount of blood vessels (total vascular area) (Fig. 7, A and B) and vascular sprouting and ramifications (Fig. 7, C and D). No alteration in the number of vessels and their ramifications was observed when the animals were treated with the scramble control peptide or vehicle only.

One of the hallmarks of the OIR model is the formation of tufts due to the outgrowth of blood vessels protruding into the vitreous cavity. We noticed that treatment with peptide PCAIWF significantly reduced tuft formation in number and size (Fig. 8A). To further evaluate the effect of the treatment with the peptide on tuft formation, we performed confocal laser scanning microscopy to gain information on the vascular layer deep in the retina (Fig. 8B). Confocal images were obtained at 2.4-μm intervals and assembled with the aid of computer software (Fig. 8C), which allowed us to determine the thickness of the vascular layer and to visualize blood vessels migrating toward the vitreous chamber (tufts). As expected, normal C57BL/6 mice that were not subjected to the OIR model have a homogeneous vascular layer of approximately 39 ± 1.3 μm (Fig. 8D) that is positioned between the ganglion and the outer plexiform layers of the normal retina (19). When mice are treated by OIR, the vascular layer changes shape and becomes thicker (75 ± 2.7 μm) because of a series of tufts of vessels extending toward the vitreous humor (Fig. 8, D and E). These projections are almost absent in OIR mice treated with peptide PCAIWF in which the thickness of the vascular layer reduces to 44 ± 3.9 μm, similar to normally developing retinas in C57BL/6 mice (Fig. 8, D and E). Animals treated with vehicle only showed no significant reduction (67 ± 3.7 μm) in vascular layer thickness (Fig. 8D). In summary, the small-molecule pan-VEGF inhibitory peptide PCAIWF prevents pathological angiogenesis in vivo in one of the most widely used animal models for retinopathy of prematurity, suggesting that this peptide might have important uses in the development of novel antiangiogenic inhibitors for retinopathy and other human diseases.

DISCUSSION

Antiangiogenic therapy has been firmly established by numerous clinical trials using drugs aimed at the central factors involved in this process: VEGF and its receptors. Unfortunately, despite the significant benefits of these drugs, there are important questions in antiangiogenic therapy that have not been solved. For example, not all patients respond to anti-VEGF therapy, and others eventually develop resistance (38). Why do some tumors respond to antiangiogenic therapy (colorectal) and others do not (pancreatic)? The ingenious hypothesis [proposed by Folkman (39)] that tumors would starve to death if not properly nourished by blood vessels is an impeccable and compelling concept, but researchers are still puzzled as to why antiangiogenic compounds have not achieved the expected efficacy (5, 7). Although this conundrum is likely to be multifaceted, targeting molecules other than VEGF-A and VEGFR-2 might help improve efficacy. In effect, in ophthalmology, clinical studies with aflibercept have shown better efficacy compared to bevacizumab and ranibizumab (40). The latter two drugs exclusively target VEGF-A, whereas aflibercept is the only one that, in addition to VEGF-A, neutralizes two other members of the family, VEGF-B and PIGF. Drugs with a broader effect may do better in angiogenesis therapy.

The OIR model is a well-accepted animal model for the study of human diseases, such as retinopathy of prematurity and, to a certain extent, diabetic retinopathy (32, 33). The retinal vasculature in mice develops and matures after birth, a process that is controlled by oxygen tension and, therefore, VEGF levels (34). By exposing mice at postnatal day 7 (P7) to 75% oxygen, VEGF expression is down-regulated, and its concentration in the eye is substantially reduced. This inhibits neovascularization that would otherwise be active in physiological retinas, with the formation of a central zone of vaso-obliteration. Once the mice at P12 are returned to room air (normal oxygen levels, 21%), vascularization has stopped and the retina experiences severe hypoxia; VEGF expression rises above normal, resuming vascularization, but it is now in a pathological state that exacerbates the angiogenic process, resulting in a retinopathic condition, which peaks at P17 (32–34). In mice, it eventually resolves within a few days, but in premature babies exposed to high oxygen concentrations in neonatal care units, if severe enough, the ongoing retinopathy may result in retinal detachment and blindness (retinopathy of prematurity) (35).

To assess whether our pan-VEGF peptide inhibitor PCAIWF could prevent pathological angiogenesis in the OIR model, mice at P15 (3 days after exposure to 75% oxygen) were treated with a single intravitreal injection of peptide PCAIWF. Peptide treatment could not be per-
All VEGF family members and the three receptors are expressed in the retina and play distinct and important roles in angiogenesis. For example, studies with animal models indicate that VEGF-B is dispensable for neovascularization but is essential for retinal endothelial cell survival, and antibodies targeting VEGF-B inhibit choroid and retina neovascularization (41). PI GF has also been implicated in pathological angiogenesis (42, 43) and is said to have contributed to the development of diabetic retinopathy (44). VEGF-C and VEGF-D are expressed in the ischemic retina (45) and the subretinal vascular membrane of an age-related macular degeneration patient (46), and blockage of VEGFR-3 with monoclonal antibodies prevents neovascularization in the retina (24), suggesting that they also contribute to neovascularization in the retina. Furthermore, these growth factors have different effects in the type of newly formed blood vessels and in their stability and permeability (47).

However, targeting all members of the VEGF family is challenging. Monoclonal antibodies are selective to a single receptor. Similarly, molecules like VEGF-trap ( aflibercept), which is composed of the ligand-binding domain of VEGFR-1 fused to an Ig constant region, will target multiple members of the VEGF family (VEGF-A, VEGF-B, and PI GF) but will miss others (VEGF-C and VEGF-D) (48). An alternative is to use small TKIs, such as sunitinib, which is a pan-VEGF inhibitor. Unfortunately, these molecules also affect other angiogenic RTKs, resulting in important side effects, such as cardiotoxicity, such as in the case of sunitinib and PDGFR-β (49). Therefore, drugs with similar activity to peptides PCAIWF and WVCSSG (neutralization of all VEGFRs through the extracellular domain) could have important applications in the clinic for the development of true pan-VEGF inhibitors.

In a previous study (19), we have successfully developed a small tripeptide (now denominated Vasotide) into a prodrug candidate. Nevertheless, it is not very often that peptides are suitable for drug development. They are prone to proteolysis and suffer the same limitations in terms of biodistribution as monoclonal antibodies. For instance, peptides PCAIWF and WVCSSG are not found in the vitreous humor if applied topically to the retina, which seems to preclude their use in eye drop formulations. Because they are small molecules, they probably will have short half-lives in the eye and will not be good drug candidates for repeated intravitreal injections (granting that we...
Fig. 8. PCAIWF prevents neovascularization in the vitreal cavity. (A) Assembly of confocal microscopy images of P17 retinas of normal neonatal C57BL/6 mice or with OIR treated with PCAIWF (n = 4 retinas) or not (n = 10 retinas) by a single intravitreal injection (1 µl) of vehicle only (DMSO) or peptide PCAIWF (30 µg). Yellow arrowheads indicate vascular complexity (tufts). (B) Schematic representation of a mouse retina showing the location of the retinal vascular layer and the images obtained by confocal laser scanning microscopy to gain information on vascular depth. (C) Computer-assisted assembly of the laser scanning confocal images of P17 retinas (obtained at 2.4-µm intervals) of neonatal CS7BL/6 mice with OIR treated or not treated with vehicle or peptide PCAIWF. (D) Quantification of the retinal vascular thickness. (E) Drawing outlining the retinal, its layers, and blood vessels protruding or not into the humor vitreous. Statistics, ANOVA (Tukey’s multiple comparison test) (***P < 0.005). Error bars represent means ± SEM.
have not performed pharmacokinetic studies yet). The hydrophobicity and relative small molecular weight of peptides PCAIWF and WVCSGG (736 and 608 Da, respectively) are not far from the rule of five (Lipinski’s rule), which suggests that their binding site is likely a druggable region in these receptors. With better knowledge of the structural requirements for VEGFR binding, these peptides might be important leads for drug development. Small molecules, such as peptides PCAIWF and WVCSGG, might comprise a new class of drugs, the extracellular ligand-binding inhibitors of receptor tyrosine kinas (eTKIs). Despite all the difficulties associated with peptide drug development, given the strong antiangiogenic effect of PCAIWF in vivo following a single dose and without any optimization, it is possible that, if properly formulated (that is, slow-release formulations), peptide PCAIWF might be a drug candidate for the treatment of human retinopathy. Notably, peptides PCAIWF and WVCSGG are fairly soluble in Matrigel compared to aqueous media. Matrigel has a composition similar to that of the vitreous humor, rich in collagen, collagen-like proteins (vitrosin), and glycosaminoglycans, which may help solubilize the peptides in the eye. Collectively, drugs based on PCAIWF and WVCSGG might be interesting alternatives for antiangiogenic therapy because the neutralization of all VEGFRs could be achieved with a single compound.

The change of specificity of peptides PCAIWF and WVCSGG depending on the context in which they are presented to the receptors is noteworthy. These peptides are fairly specific for VEGFR-3 if fused to the bacteriophage coat protein but become more permissive in solution as synthetic-free peptide molecules. These data suggest that peptides that are identified by combinatorial approaches (such as phage display) should be carefully validated, and one should not assume the peptide’s specificity without considering the contexts in which the peptide is presented (bacteriophage or in solution). It also highlights another important aspect: Distinct families of RTK might retain an original binding site shared by family members. Peptides PCAIWF and WVCSGG prevent ligand binding and inhibit angiogenesis in vivo (PCAIWF). These results suggest that, if these binding sites are present in other RTKs, original sites might be important druggable domains. Studies using the FGF receptor family corroborate this idea. A small experimental TKI molecule (SSR128129E) binds to and prevents the activation of all four FGF receptors (17). Different from peptides PCAIWF and WVCSGG, this FGF receptor inhibitor does not interact with the ligand-binding domain of the receptors and is likely to exert its effect through a putative allosteric domain. The exact binding site and mechanism by which PCAIWF and WVCSGG exert their effect and prevent ligand interaction are still unknown; whether they bind directly to the ligand domains of VEGFRs or to an allosteric adjacent binding site remains to be determined. An important difference is that peptides identified by phage display often mimic natural ligands for their target (20, 50–53). Peptide PCAIWF does not share significant primary sequence similarity to any of the VEGF family members. Thus, if peptide PCAIWF were to bind to an allosteric binding site in the VEGF receptor family, it would be interesting to identify the natural ligand for this putative domain. Further studies will be necessary to answer these questions.

In summary, and in a larger context, our work suggests that RTKs might have family-specific common binding sites that modulate ligand interaction with the receptors. Notwithstanding the great advances in drug design for better RTK inhibitors, selectivity is still an important challenge to the field (16). Identification of these original binding sites shared by members of RTK-distinct families may contribute well to this milestone and to the design of novel and better molecules with the exquisite selectivity necessary to target this important superfamily of receptors that are highly relevant in many human diseases.

**MATERIALS AND METHODS**

**Materials**

All recombinant growth factors and their respective receptors were obtained commercially from R&D Systems. Antibodies and other reagents were obtained commercially: anti-human VEGF (AF-293-NA), anti-human VEGF-C (AF752), anti-human PIGF (AF-264-PB), anti-human PDGF-BB (AF-220-NA), anti-human FGF-basic (AF-233-NA), anti-mouse/rat NRP-1 (AF566), and anti-mouse/rat NRP-2 (AF567) were from R&D Systems; anti-fd Bacteriophage-Biotin Conjugate (B2661) was from Sigma-Aldrich; secondary antibodies IRDye 680LT Donkey anti-goat IgG and IRDye 680LT Streptavidin were from LI-COR. The gas admixture (75% oxygen and 25% nitrogen) used for the OIR mouse model was obtained from Air Products.

**Phage library construction**

The linear heptapeptide phage display (X6) library was built as previously described (54) but with modifications. Briefly, the fUSE55 vector (provided by G. Smith, University of Missouri, Columbia, MO) was prepared in large scale using the Maxiprep kit (Qiagen) followed by two consecutive CsCl equilibrium gradient purifications. Equimolar amounts of oligonucleotides 5′-CAGCAAGGACGACTGCTNNKNNKKNNKKNGGGCGGGCGTGGGGCGGAA-3′ and 5′-TTGGGCCACCGGCG-3′ (where N = any nucleotide and K = T or G) were converted to double-stranded DNA with Klenow enzyme (as recommended by the manufacturer) (New England Biolabs) and purified using a P500 Maxiprep column (Qiagen). The vector (500 µg) and oligonucleotide insert (20 µg) digested with the restriction enzyme Bg II were ligated using T4 DNA ligase (New England Biolabs). The ligation product was purified using a P500 Maxiprep column and transformed into electrocompetent Escherichia coli MC1061 cells, resulting in 1.4 × 10^9 transformants, of which 1.2 × 10^8 contained inserts coding for peptides. Bacteria were cultured for ~20 hours, and phages were purified from culture supernatants by the polyethylene glycol/Nacl method (20).

**Synthetic peptides**

Peptides were synthesized and purified by high-performance liquid chromatography to a purity greater than 95% by Bachem or Chinese Peptide Company. Two control peptides were used in this study: peptide CARAC (referred to as control) (20) and the scramble version of the peptide PCAIWF, sequence IPACPWI (referred to as scramble).

**Biopanning on VEGFR-3 and phage binding assays**

Phage assays were performed as previously described (20, 50). To isolate peptides targeting VEGFR-3, microtiter wells were coated with recombinant mouse VEGFR-3/Fc [1 µg in 50 µl of phosphate-buffered saline (PBS)] [10 mM Na2HPO4, 1.8 mM KH2PO4, 137 mM NaCl, and 2.7 mM KCl (pH 7.4)], blocked with PBS supplemented with 3% bovine serum albumin (BSA), and incubated with the X6 phage peptide library (10^10 TU) in 50 µl of PBS supplemented with 1% BSA (PBS/BSA) for 2 hours at room temperature. The wells were then washed, and bound phages were recovered by bacterial infection and amplified for the next cycle of selection. After the third round of selection, random bacterial colonies were selected for DNA sequencing to identify the phage coding peptides. Briefly, each bacterial colony was dispersed in 50 µl of PBS, and 2 µl was used to subject the pII gene
encoding the random DNA insert [5′-GCAAGCTGATTTAAGCGATA-CAATT-3′ (forward) and 5′-CCCTCAGTTAGCGTAAGCGATCT-3′ (reverse)] to polymerase chain reaction (PCR) using Taq DNA polymerase (Thermo Fisher Scientific) in a thermal cycler (Bio-Rad) (94°C for 2 min, followed by 35 cycles at 94°C for 15 s, 60°C for 20 s, and 72°C for 45 s). DNA sequencing was performed by the Sanger method in the DNA sequencing facility at the Chemistry Institute, University of São Paulo. For the phage binding assays, the procedure was similar. Wells of microtiter plate were coated with the specified ligand (overnight at 4°C), incubated with the specified phage (10⁸ TU in 50 µl of PBS) for 2 hours at room temperature, and washed, and bound phage was quantified by either colony count or phage-FLISA. The latter was performed using an anti-Fd bacteriophage conjugated to biotin, followed by IRDye 680LT Streptavidin, and plates were scanned in the Odyssey Infrared Imaging Scanner. For the competition assays, phage incubation was performed in the presence or absence of different concentrations of the specified synthetic peptide or growth factor. In all experiments, the insertless phage Fd was used as control.

**Recombinant VEGFR-3 ligand-binding domain**

The complementary DNA encoding the full-length human VEGFR-3 (pDON233-FL1T4) was obtained from Addgene and used to PCR ampiclons encoding the ligand-binding domains of human VEGFR-3 [IgD2: 5′-GTGAGACATATGGAGCAGCCAATCTAC-3′ (forward) and 5′-GATCTCGAGGAGCTCGTTGCCTGTGAT-3′ (reverse); IgD2-3: same forward primer used for IgD2 and 5′-GACCTCGAGGAAGGATTTCATGTGAC-3′ (reverse)]. The ampiclons were cloned into pET21a and used to produce the corresponding recombinant proteins (IgD2, residues 136 to 229; IgD2-3, residues 136 to 332) using Rosetta(DE3)pLysS cells (EMD Millipore). The recombinant proteins were purified from inclusion bodies. Briefly, cells were lysed by sonication and centrifuged (10,000 g for 10 min at 4°C), the insoluble pellets were washed twice with wash buffer [50 mM tris, 1 mM MEQTA, 1 mM EDTA, 2.5 mM magnesium phosphate, 1 mM NaF, 1 mM glycophosphate, 1 mM Na₂VO₄, and the protease and phosphatase inhibitor cocktail (Sigma)]. The detection of phosphorylated and total forms of ERK1/2 was performed by Western blotting using specific antibodies (mouse IgG anti-p44/p42 MAPK ERK1/2, 3A7, #9107; rabbit IgG anti-phospho-p44/p42 MAPK ERK1/2 Thr202/Yyr204, 197G2, #4377; Cell Signaling) according to the manufacturer’s recommendations. Total ERK was detected using goat anti-mouse IgG conjugated to IRDye 680LT (LI-COR), and phospho-ERK1/2 was detected using donkey anti-rabbit IgG conjugated to IRDye 800CW (LI-COR). The immunoblots were quantified using the Odyssey Infrared Imaging system (LI-COR).

**Endothelial cell tube formation assay**

HUVECs (HUVEC-C, American Type Culture Collection CRL-1730) were seeded onto 96-well plates coated with 80 µl of Matrigel (BD Biosciences, 354234) containing 1% DMSO and supplemented or not supplemented with peptide PCAIWF or scramble (500 µg/ml). Cells (1.5 × 10⁴ cells per well) were incubated in RPMI 1640 (Thermo Fisher Scientific) containing VEGF-A (30 ng/ml) or VEGF-C (100 ng/ml). Quantification of endothelial network formation was performed by counting the number of tubes formed per field (objective, 4×) using an inverted (bright-field) microscope (Nikon) (31).

**Animals**

The Institutional Animal Care and Use Committees at the Chemistry Institute of the University of São Paulo approved all animal experimentation (protocol number 10/2010). This study followed the Association for Research in Vision and Ophthalmology statement for the use of animals in ophthalmic and vision research. C57BL/6 mice (Taconic) maintained at the animal facility of the Chemistry Institute and Pharmacy School of the University of São Paulo were used for all experiments.

**OIR neovascularization and peptide treatment**

The OIR mouse model was performed as described previously (17, 32, 37). Briefly, the animals were exposed to 75% oxygen from P7 to P12, along with their nursing mothers. Four experiments were performed with similar results. The initial three experiments were performed with a homemade oxygen chamber, and the last experiment was performed on a Biospherix Hyperoxia Chamber equipped with a ProOx 110 oxygen controller (Biospherix). At P12, the animals were returned to room air (20.8% oxygen) and organized in groups, and 3 days later...
(P15), they were treated with vehicle (DMSO) only or with 30 μg of each individual peptide by intravitreal injection (peptides were solu-
ibilized in DMSO solution at 30 mg/ml; injection of 1 μl per eyeball). Animals weighing less than 6 g were not used for the study.

Whole-mount retina preparation and neovascularization quantification
At P17 (2 days after treatment), the animals were enucleated, their eyeballs were fixed in PBS containing 4% paraformaldehyde, and the retina was dissected under a stereomicroscope. The blood ves-
sels in the retinas were then stained with isocyanate B4 conjugated with Alexa Fluor 594 (Life Technologies), mounted with VECTA-
SHIELD (Vector Laboratories), and examined in an epifluorescent microscope (Nikon). The neovascularization was quantified as previously described (32). Briefly, images from whole-mount retinas were obtained at ×100 magnification using the same exposition time for all samples. Images for the same retina were merged into a single picture using Adobe Photoshop CS3. Quantification of total neovascularization (NV) was performed by selecting the flu-
orescent areas containing the neovessels and counting the total number of pixels. A similar procedure was used to determine the total number of pixels in the whole retina (RA). The percentage of retinal vascularization was then calculated with the formula (NV/RA) ×
10. Representative confocal images of retinas were performed on a Zeiss LSM510 META microscope and used to determine vessel sprouts and bifurcations by counting the number of branch points per identical 167-μm × 167-μm fields (two fields per quadrant and a total of eight fields per retina) for each animal retina. For the laser scanning micro-
copy, confocal images spanning the whole retina were obtained at 2.4-μm intervals using the 10× objective (final magnification, ×70). The three-dimensional retina was reconstructed with the Zeiss Zen software.

Statistical analysis
Statistics were performed using GraphPad Prism software. Error bars are presented as means ± SD. Statistical significance was determined by Student’s t test or the two-way ANOVA test set at P < 0.05.

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