Binding affinities of vascular endothelial growth factor (VEGF) for heparin-derived oligosaccharides

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Synopsis
Heparin and HS (heparan sulfate) exert their wide range of biological activities by interacting with extracellular protein ligands. Among these important protein ligands are various angiogenic growth factors and cytokines. HS binding to VEGF (vascular endothelial growth factor) regulates multiple aspects of vascular development and function through its specific interaction with HS. Many studies have focused on HS-derived or HS-mimicking structures for the characterization of VEGF₁₆₅ interaction with HS. Using a heparinase 1-prepared small library of heparin-derived oligosaccharides ranging from hexasaccharide to octadecasaccharide, we systematically investigated the heparin-specific structural features required for VEGF binding. We report the apparent affinities for the association between the heparin-derived oligosaccharides with both VEGF₁₆₅ and VEGF₉₅, a peptide construct encompassing exclusively the heparin-binding domain of VEGF₁₆₅. An octasaccharide was the minimum size of oligosaccharide within the library to efficiently bind to both forms of VEGF and a tetradecasaccharide displayed an effective binding affinity to VEGF₁₆₅ comparable to unfractionated heparin. The range of relative apparent binding affinities among VEGF and the panel of heparin-derived oligosaccharides demonstrate that the VEGF binding affinity likely depends on the specific structural features of these oligosaccharides, including their degree of sulfation, sugar-ring stereochemistry and conformation. Notably, the unique 3-O-sulfo group found within the specific antithrombin binding site of heparin is not required for VEGF₁₆₅ binding. These findings afford new insight into the inherent kinetics and affinities for VEGF association with heparin and heparin-derived oligosaccharides with key residue-specific modifications and may potentially benefit the future design of oligosaccharide-based anti-angiogenesis drugs.

Key words: heparin, heparin-binding domain (HBD), heparin-derived oligosaccharide, solution affinity, surface plasmon resonance (SPR), vascular endothelial growth factor (VEGF)

INTRODUCTION

Heparin and HS (heparan sulfate) are structurally related members of the GAG (glycosaminoglycan) family consisting of repeating disaccharide subunits of 1→4 linked hexuronic acid, β-D-GlcA (glucuronic acid) or α-L-IdoA (iduronic acid) and glucosamine, α-D-GlcNAc (N-acetylgalactosamine) or α-D-GlcNS (N-sulfoglucosamine) [1,2]. The hexuronic acid residues in these GAGs are frequently found to be modified with a 2-O-sulfo group. The glucosamine residue is commonly modified with a 6-O-sulfo group [GlcNS6S (6-O-sulfo-N-acetylglucosamine)] and in rare cases with a 3-O-sulfo group [GlcNS3S (3-O-sulfo-N-sulfoglucosamine) and GlcNS3S6S (3,6-O-sulfo-N-sulfoglucosamine)]. Heparin is more highly sulfated than its undersulfated counterpart HS, with an average of 2–3 sulfo groups per disaccharide compared with 0–2 sulfo groups per disaccharide for HS [1,2]. Despite their differences, heparin and HS contain identical disaccharide sequences, but in different ratios. Unique sequences, such as the pentasaccharide comprising the ATIII (antithrombin III) binding site, are found in both heparin and HS [1,2].

Heparin and HS are biosynthesized as PGs (proteoglycans) as one or more GAG chains that are covalently attached to a core
protein [3]. While heparin-PGs are stored in mast-cell granules, HS-PGs are ubiquitously expressed on the cell surface of most cell types and in the ECM (extracellular matrix), where they exert a wide range of biological functions through interaction with a variety of protein ligands involved in diverse cellular processes [4–7]. These interactions are principally based on ionic or H-bonding forces between the sulfo and carboxy groups in the saccharide backbone and basic amino-acid residues in the heparin (or HS)-binding protein [8,9]. HS-induced cellular functions are believed to be highly dependent on the structure of the engaged polysaccharide [8–10].

VEGF (vascular endothelial growth factor) is a heparin-binding angiogenic growth factor that regulates multiple aspects of vascular development and function, including stimulation of vasculogenesis and angiogenesis by promoting endothelial cell proliferation and migration [11,12]. For more than two decades, research has shown that the VEGF family of growth factors and its receptors play pivotal roles in tumour angiogenesis by regulating tumour growth, invasion and metastasis [13,14]. As a result of alternative mRNA splicing, VEGF exists in a number of isoforms with each having different biological properties. The polypeptide backbone of the predominant VEGF165 isoform contains two structurally independent domains. Plasmin cleavage of VEGF165 generates a homodimer consisting of two disulfide bond-linked N-terminal polypeptides (residues 1–110, VEGF110) and two identical 55-residue C-terminal fragments (residues 111–165, VEGF55) [15]. The 110-residue N-terminal ‘receptor binding’ domain contains the dimerization sites, the binding sites for the tyrosine kinase receptors FLT-1 (FMS-like tyrosine kinase 1) and KDR (kinase insert domain-containing receptor) [also referred to as VEGFR1 (VEGF receptor 1) and VEGFR2 respectively]. The C-terminal HBD (heparin-binding domain) contains the binding sites for heparin and the KDR co-receptor neuropilin [16]. VEGF isoforms have diverse HBD structures, whereas the receptor-binding domain is invariant [15].

Emerging studies on the inhibition of tumour angiogenesis via the targeting of relevant angiogenic growth factors have shown promising primary results both in vitro and in vivo for therapies using heparin and HS-based oligosaccharides [17–19]. These compounds competitively bind to heparin-binding growth factors, preventing their interaction with cell surface HS-PGs and cytokine receptors and hence inhibit angiogenesis [17]. LMWH (low-molecular-mass heparin), for example, has been demonstrated to be a potent inhibitor of FGF2 (fibroblast growth factor 2) and VEGF mediates human microvascular endothelial cell proliferation [20,21]. Recent evidence has implicated the significance of HS oligosaccharides on suppression of endothelial cell migration, tube formation and signalling induced by VEGF165 and FGF2 [22]. Nevertheless, how the complex structure of heparin and HS saccharide affect angiogenesis with regard to the distinct binding affinities towards their protein ligands and abilities to activate the respective signalling pathways still remains largely unexplored. Previous attempts have been made on elucidating the structural features within HS that contribute to its binding with VEGF165 [22,23]. In the present study we report the VEGF binding affinities of a small library of heparinase I-prepared heparin-derived oligosaccharides with sizes ranging from hexasaccharide to octadecasaccharide. Influences including oligosaccharide size and sulfation towards heparin-specific VEGF165 and VEGF55 binding are investigated using SPR (surface plasmon resonance).

MATERIALS AND METHODS

Materials

Recombinant human VEGF165 was purchased from R&D System (Minneapolis, MN, U.S.A.). VEGF55, corresponding to residues 111–165 of VEGF165, was produced by plasmin (Haematologic Technologies, Essex Junction, VT, U.S.A.) cleavage of VEGF165 as previously described [24,25]. Cloning, expression and purification of the recombinant heparinase 1 (EC 4.2.2.7) from Flavobacterium heparinum in Escherichia coli were performed essentially as described previously [26]. Heparin sodium salt was obtained from porcine intestinal mucosa (Celsius Laboratories, Cincinnati, OH, U.S.A.). SA (streptavidin) sensor chip and HBS-EP buffer [10 mM Hepes, pH 7.4, 150 mM NaCl, 3.0 mM EDTA and 0.005 % (v/v) surfactant P20] were purchased from Biacore (GE Healthcare, Uppsala, Sweden). Buffers were filtered (0.22 µm) and degassed before use. SPR measurements were performed on a Biacore 3000 (Biacore).

Preparation of the oligosaccharide library from heparin

A series of homogeneous oligosaccharides with sizes ranging from disaccharide to hexadecasaccharide have been isolated and sequenced from fractionated heparin in our laboratory [27]. Briefly, heparin was digested by heparinase 1 (1.5 unit/g) at 30°C until 30% completion. The reaction mixture was then fractionated by gel permeation chromatography on a Bio-Gel P-10 column (BioRad, Hercules, CA, U.S.A.) to obtain uniform-sized oligosaccharides. Fractions were subsequently desalted on a Bio-Gel P-2 column and freeze-dried. For oligosaccharides with defined structures, the freeze-dried uniform-sized oligosaccharides with the dp (degree of polymerization) from dp6 to dp16 were further purified and separated on a semi-preparative SAX-HPLC column (Shimadzu, Kyoto, Japan) equipped with a 5 µm Spherisorb column of dimension 2.0 cm × 25 cm (Waters, Milford, MA, U.S.A.). Chromatographically purified peaks were analysed by LC (liquid chromatography)-MS (Agilent 1100 LC/MSD, Agilent Technologies, Wilmington, DE, U.S.A.) under conditions previously described [27,28]. The structure of each purified oligosaccharide was determined by 1D (one-dimensional) and 2D (two-dimensional) NMR measured at 298 K on a Bruker Avance 600 II MHz (14.1 T) NMR spectrometer equipped with a cryo-probe with z-axis gradients [27,29].

Immobilization of biotinylated heparin on to the SA sensor chip

Biotinylated heparin was prepared by homogeneously reacting sulfo-N-hydroxysuccinimide long-chain biotin (Pierce,
Rockford, IL, U.S.A.) with free amino groups of unsubstituted glucosamine residues in the polysaccharide chain (2.8 wt% of D-GlcN) according to published procedures [30,31]. The biotinylated heparin was immobilized to SA chip according to the manufacturer’s protocol. Briefly, 20 μl of the solution of the heparin–biotin conjugate (0.1 mg/ml) in HBS-EP running buffer was injected over flow cell 2 of the SA chip at a flow rate of 10 μl/min. The successful immobilization of heparin was confirmed by the observation of a ~ 100 RU (resonance unit) increase in the sensor chip. The control flow cell 1 was prepared by 1 min injection with saturated biotin.

**SPR-based kinetics measurement of the interaction between VEGF and heparin**

A series of VEGF protein samples were prepared by dilution in HBS-EP buffer to final concentrations ranging from 0.63 to 10 nM and from 10 to 150 nM for VEGF165 and VEGF55 respectively. Protein samples were injected at a flow rate of 30 μl/min. At the end of sample injection (180 s), HBS-EP buffer was passed over the sensor surface for 180 s during which VEGF dissociation was monitored. After dissociation, the sensor surface was regenerated by injecting 2 M NaCl to remove all the binding proteins. The response was monitored as a function of time (sensorgram) at 25°C. Apparent rate constants for chip association were obtained in global fits to the SPR data at multiple protein concentrations with residuals for the resulting fits being used to assess the goodness of the fit. BIAevaluation version 4.0.1 software was used for all SPR data analysis.

**Inhibition of VEGF binding to the heparin-coated chip by heparin-derived oligosaccharides in solution**

A VEGF165 (5 nM) or VEGF55 (100 nM) sample was premixed with 1 μM of each uniform-sized heparin oligosaccharide mixture (dp6–dp18) or each structurally defined oligosaccharide (dp8–dp16) in HBS-EP buffer. The mixed solution was injected over the heparin chip at a flow rate of 30 μl/min for 180 s after which the dissociation and the regeneration steps were performed as described above. For each set of experiments, a control run with protein only was performed to confirm that the chip surface was undergoing complete regeneration and validate that the results obtained among the experiments are comparable.

Apparent binding constants for the defined structures with sizes from dp8 to dp16 were evaluated based on an SPR solution affinity assay as previously described [32]. For each K_d measurement, samples containing 5 nM VEGF165 or 100 nM VEGF55 with various concentrations of oligosaccharide (diluted from 1 to 10 nM stock solutions) were prepared in HBS-EP buffer. Binding was monitored using equivalent conditions for sample injection, dissociation and regeneration conditions as described above. The process of protein (P) pre-equilibrated with ligand (L) can be expressed as:

\[ P + L \rightleftharpoons P \cdot L \] (1)

The equilibrium equation is:

\[ [L][P] = K_d[L \cdot P] \] (2)

The free concentrations at equilibrium for protein and ligand are

\[ [P] = ([P]_{total} - [L \cdot P]) \text{ and } [L] = ([L]_{total} - [L \cdot P]) \] (3)

Substitution of these expressions into the equilibrium equation and rearranging and solving for [L·P] give:

\[ [L \cdot P] = \frac{([L]_{total} + [P]_{total} + K_d)}{2} - \sqrt{\left(\frac{([L]_{total} + [P]_{total} + K_d)^2}{4} - [L]_{total}[P]_{total}\right)} \] (4)

Therefore the free protein concentration can be expressed as:

\[ [P] = \frac{([L]_{total} + [P]_{total} + K_d)}{2} + \sqrt{\left(\frac{([L]_{total} + [P]_{total} + K_d)^2}{4} - [L]_{total}[P]_{total}\right)} \] (5)

If binding is not mass-transport limited, in which case the initial binding rate (r) is proportional to the concentration of free protein and the maximum binding rate (r_m) measured in the absence of ligand is proportional to the total protein concentration, free protein concentration can be calculated by:

\[ [P] = \frac{r}{r_m}[P]_{total} \] (6)

The initial binding response for each sensorgram was measured 10 s before the end of injection and was subsequently employed to estimate the free protein concentration using eqn (6). The calculated free protein concentration [P] was plotted against total oligosaccharide concentration [L]_{total} and fit to eqn (5) to determine the apparent K_d values [32]. Analysis of duplicate or triplicate experiments was conducted at each oligosaccharide concentration in order to better estimate errors in the acquired data and fitted values.

**RESULTS**

**Preparation of heparin-derived oligosaccharide library**

As part of an ongoing effort in our laboratory to understand the highly complex structure of heparin and its structure–function relationships, a small structurally characterized heparin oligosaccharide library was assembled through the controlled, partial de-polymerization of porcine intestinal mucosa heparin using heparinase 1 and purification of the resulting cleavage products. This small library contains oligosaccharides of sizes between hexa-saccharide (dp6) and hexadecasaccharide (dp16), with a number of these oligosaccharides being isolated and studied for the first time, affording new reagents for these heparin-binding protein activity studies.
Oligosaccharides with sizes ranging from dp6 to dp18 were examined in our present study. The purified oligosaccharides from dp8 to dp16 in our library shared a common motif that made them particularly valuable for this structure-dependent binding study. These oligosaccharide motifs could be divided into three groups (a, b and c), differing in the five sugar residues located at their reducing end (Figure 1). The components in each size group are structural analogues differing in the number of central trisulfated GlcNS6S–IdoA2S disaccharide units. The a motif consisted of only octasaccharide 8a and decasaccharide 10a, since the distribution of this specific motif is susceptible to heparinase 1. The unique feature of the a motif is the presence of a GlcA residue immediately adjacent to the reducing end. The b motif is characterized by clusters of trisulfated disaccharide repeating units of IdoA and glucosamine residues and is representative of the canonical heparin structure. The c motif contains a four-residue stretch at its reducing end with a unique combination of sugar residue modifications that corresponds to a key portion of the high-affinity ATIII binding site in heparin (Figure 1).

**Binding kinetics of VEGF to immobilized heparin**

SPR response curves were recorded for VEGF samples at a range of concentrations being injected and flowed over a heparin sensor chip. The binding kinetics and relative apparent affinities were calculated from these results as described in the Materials and methods section and are summarized in Figure 2 and Table 1. The sensograms of VEGF165–heparin and VEGF55–heparin binding displayed uniquely different shapes. Both sets of sensograms of the VEGF55–heparin and VEGF165–heparin interactions fit well with the 1:1 Langmuir binding model, which is consistent with a monophasic-binding process. The apparent microscopic on-rate and off-rate constants for VEGF55–heparin binding were both greater than those for VEGF165–heparin binding. Standard curves were constructed by plotting relative response values as a function of protein concentration (Figures 2C and 2D). For both VEGF165 and VEGF55, the relative response from binding was detected to have a linear dependence on protein concentration with extrapolated fits that pass through the origin within experimental error, indicating that the binding experiments were not limited by mass transport.
Table 1  Kinetics and relative apparent affinities of VEGF binding to immobilized heparin

<table>
<thead>
<tr>
<th>Interaction</th>
<th>$k_{on}^{app}$ (1/ms)</th>
<th>$k_{off}^{app}$ (1/s)</th>
<th>$K_D^{app}$ (nM)</th>
<th>$K_D$ (nM)*</th>
</tr>
</thead>
<tbody>
<tr>
<td>VEGF165-heparin</td>
<td>$8.6 \times 10^3$</td>
<td>$6.9 \times 10^{-4}$</td>
<td>80</td>
<td>40–157</td>
</tr>
<tr>
<td>VEGF55-heparin</td>
<td>$3.1 \times 10^5$</td>
<td>$6.1 \times 10^{-2}$</td>
<td>197</td>
<td>N.R.</td>
</tr>
</tbody>
</table>

*Literature values.

Figure 2  Kinetics of VEGF165– or VEGF55–heparin interactions

SPR sensorgrams showing change in binding response to various concentrations of injected proteins of (A) VEGF165 from 0.63 to 10 nM (from bottom to top) and (B) VEGF55 from 10 to 150 nM (from bottom to top). The black curves in (A, B) are the fitting curves using models from BIAevaluate version 4.0.1. Protein standard curves for (C) VEGF165 and (D) VEGF55 were prepared by plotting the binding response (RU) as a function of the injected protein concentration.

Inhibition of VEGF association to heparin-coated chips by heparin-derived oligosaccharides

In the solution competition experiments, heparin oligosaccharides were pre-equilibrated with VEGF and the mixtures were passed over an immobilized heparin surface. Protein in complex with oligosaccharide in solution is distinguished from unbound protein in that the oligosaccharide bound state is not able to associate with the heparin immobilized chip surface. The partitioning of VEGF in bound and unbound states results in a decrease in the binding response as compared with the control experiment obtained in the absence of oligosaccharide. Thus productive binding of the oligosaccharides corresponds to a decrease in response that is directly related to the binding affinity for the formation of the VEGF–oligosaccharide complex. Uniform-sized oligosaccharide mixtures purified from fractionated heparin were first screened for their binding to VEGF165 and VEGF55. In Figure 3(B), the relative VEGF–heparin binding responses in the presence of oligosaccharide are plotted as a percentage of the response detected in the control experiment and compared among oligosaccharides increasing in length from dp6 to dp18. As shown in Figure 3, competition for binding to the chip surface was detected in both VEGF165 and VEGF55 exclusively in the presence of oligosaccharides containing eight or more sugar residues. Competition from oligosaccharides of dp10 resulted in a stronger inhibition of $\sim 35\%$ for both proteins. The level of inhibition increased correspondingly with the increase in oligosaccharide chain length. The dp18 mixture, the largest fragment employed in the present study, elicited
greater than 80% decrease in VEGF₁₆₅ binding to the chip surface. No detectable binding inhibition was seen by oligosaccharides with a chain length shorter than dp8 (Figure 3, dp2 and dp4; results not shown), even at relatively high oligosaccharide concentrations (i.e. no effect on heparin–VEGF binding was detected in the presence of dp6 in excess of 50 μM; results not shown). These results indicate that the binding for VEGF₁₆₅ requires a heparin sequence longer than the hexasaccharide.

Oligosaccharides with defined structures were investigated next to better understand the VEGF binding specificity. Oligosaccharides composed entirely of trisulfated disaccharide units (structures in group b) exhibited the highest level of competitive binding to both VEGF₁₆₅ and VEGF₅₅ (Figure 4). Octasaccharide 8a and decasaccharide 10a, with a GlcA residue adjacent to the reducing end, showed approx. 15% and 5% lower inhibition compared with their counterparts in group b for VEGF₁₆₅ and VEGF₅₅ respectively. Oligosaccharides in group c showed the lowest binding capacity among the three structure motifs. This motif contains part of the high-affinity ATIII recognition site including a 3-O-sulfo group on the reducing-end glucosamine and lacks 2-O-sulfo groups at the two hexuronic acid residues and one N-sulfo group at the glucosamine residue closest to the reducing end (see Figure 1). An increase in oligosaccharide chain length was able to partially offset the unfavourable sulfation pattern of group c structures, reflected by more similar levels of inhibition observed for motif b and c oligosaccharides at dp12, dp14 and dp16. The results suggest that, for a given sized oligosaccharide, binding for VEGF is highly dependent on their specific structures with respect to the degree of sulfation and backbone flexibility associated with the presence of IdoA residues. It is noteworthy that the unique 3-O-sulfation within heparin did not remarkably promote binding such that the effect of under sulfation of neighbouring residues could be counterbalanced.

Kₐ measurement by solution affinity assay
Quantification of apparent binding affinity of the heparin-derived oligosaccharides for VEGF binding was performed by analysis of SPR-based solution affinity experiments. In these competition binding studies, inhibition of VEGF association with the
Binding affinities of VEGF for heparin structures

Figure 5 Representative apparent $K_d$ measurement for heparin decasaccharides binding to VEGF

SPR sensograms showing change in (A) 5 nM VEGF165 binding to heparin on treatment with various concentrations of decasaccharide 10b from 0 to 4 μM or (B) 100 nM VEGF55 binding to heparin on treatment with various concentrations of decasaccharide 10c from 0 to 8 μM. The free protein concentration was calculated and plotted as a function of total oligosaccharide concentration for (C) VEGF165 and (D) VEGF55. The $K_d$ values were determined by fitting the data points in eqn (1). See the Materials and methods section for details.

heparin immobilized on the chip surface was measured at various concentrations of oligosaccharides. Apparent $K_d$ values were calculated through fitting the SPR data that demonstrate the dependence of the relative binding responses on oligosaccharide concentration. A simplified binding model was employed to obtain the apparent $K_d$ values for both forms of VEGF in that no better fits were observed with more advanced models for VEGF165 which contain two identical HS-binding sites [33]. Representative SPR sensograms for VEGF165–decasaccharide 10b and VEGF55–decasaccharide 10c interactions are shown in Figures 5(A) and 5(B) respectively. For oligosaccharides with eight residues and more, binding responses decreased with increasing oligosaccharide concentrations. Figures 5(C) and 5(D) show plots of unbound VEGF as a function of total oligosaccharide from which the $K_d$ value was calculated. The apparent $K_d$ values for each heparin-derived oligosaccharide are summarized in Table 2. Similar dissociation constants were obtained for VEGF165 and VEGF55 toward specific dp8 or dp10 oligosaccharides. As oligosaccharide length increased from dp10 to dp16, the apparent binding affinity increased from the low micromolar to the low nanomolar range. The apparent $K_d$ values for the tetradecasaccharide and hexadecasaccharide were as low as ~100 nM, which was nearly equivalent to the $K_d$ measured here for VEGF165 binding (80 nM) with unfractionated heparin, suggesting comparable protein-binding affinity between heparin and heparin oligosaccharide with a size of dp14 and above. In all cases, the relative affinities among the three oligosaccharide motifs tested here demonstrate a VEGF binding preference towards motif b that contains the canonical sulfation pattern and sugar geometry of heparin in contrast to the alternative structures in motifs a and c which are also commonly found in heparin and heparin sulfate materials (Table 2).

**DISCUSSION**

Emerging evidence now supports the view that VEGF is as a key anti-angiogenic target for various types of human cancers [13,14]. The VEGF family of growth factors regulates tumour angiogenesis by interacting with its receptors (VEGFRs) through several different mechanisms [34]. Heparin and HS regulate VEGF signal activation through driving a cooperative binding mechanism between VEGF and the co-receptor of VEGFR2, neuropilin [35]. Structural features within HS that promote VEGF–HS binding have been previously investigated by using HS-derived or HS-like oligosaccharides with various lengths and sulfation patterns [22,23]. However, there is a dearth of information on the
wards undersulfated octasaccharides the trisulfated IdoA–GlcN disaccharide and at a lesser degree to
towards octasaccharide structure of an oligosaccharide. VEGF bound with strongest affinity
demonstrates that binding is dependent on the specific struc
tures and GlcA compositions (Figures 3 and 4). This result
VEGF binding to unfractionated heparin to a greater extent than
this library provided for the systematic heparin binding charac
sulfation patterns and sugar-ring geometries. Binding studies with
structurally defined oligosaccharide library varying in length,
binding for both VEGF165 and its HBD VEGF55 requires an
within heparin relative to HS.
that are associated with greater sulfation and structural plasticity
productive binding and preferred heparin-like structural aspects
determined here for both VEGF165 and VEGF55 towards a small
heparin–VEGF recognition, the relative binding affinities were
complex relative to HS-derived candidates.
ors that block formation and activation of the VEGF signalling
ent in the ECM and on most cell surfaces, the greater affinity
and signal activation. Although HS represents a major compon
physiological saline buffer [23]. In the present study, we show
that, under the same physiological conditions, a heparin-derived
octasaccharide consisting of mostly trisulfated disaccharide re
repeating units is the smallest oligosaccharide that can bind both
VEGF55 and VEGF165. The one disaccharide unit difference in
length between the minimum binding size of VEGF165 for hep
arin hexasaccharide in our present study might be explained
physiological conditions. In fact, for HS oligosaccharides, dp10
was found to be the shortest size capable of binding VEGF165 in
physiological saline buffer [23]. In the present study, we show
that, under the same physiological conditions, a heparin-derived
octasaccharide consisting of mostly trisulfated disaccharide re
repeating units is the smallest oligosaccharide that can bind both
VEGF55 and VEGF165. The one disaccharide unit difference in
length between the minimum binding size of VEGF165 for hep
arin and HS may come from a higher sulfation level of the heparin
sequence. An in vivo study has shown that heparin octasacchar
ides appear to inhibit VEGF-induced angiogenesis in H460 hu
man lung carcinoma [36]. Nevertheless, longer oligosaccharides
may be required for stronger inhibition against VEGF55 and the
VEGF165-induced endothelial cell responses [22,37,38].
Our results also demonstrate that the minimum size of hep
arin oligosaccharide that conveys the equivalent apparent binding
affinity with unfractionated heparin for VEGF165, binding is a hepa
arin tetradecasaccharides (dp14). Moreover, no significant differ
ence was found for the binding constants of dp14 (90–100 nM)
and dp16 (100–110 nM) with that of heparin measured in our
experiment (80 nM) (Table 2), suggesting comparable VEGF165
binding capability between these oligosaccharides and heparin.
This finding provides an important guideline for the optimal size
requirement in oligosaccharide-based anti-tumour drug design.
Previous studies found that the heparin fragment of 16 or 18 sugar
units inhibited the binding of VEGF165 to its receptors, while
larger fragments potentiated the binding [39,40]. A number of
LMWHs have been developed as potential anti-angiogenesis
agents. Not surprisingly, the oligosaccharides comprising these
polydisperse LMWH formulations contain species sufficiently
long for supporting angiogenic cytokine activity including VEGF
[41]. The occurrence of one of the common heparin-associated
toxicity for oligosaccharide-based drugs, HIT (heparin-induced
thrombocytopenia), also depends on longer heparin oligosac
charides required for the formation of the antigenic complex
with PF4 (platelet factor 4) [42]. Therefore our results indicate
that heparin oligosaccharides of the optimal length might be
sufficient for VEGF165 binding and inhibition and that longer
compounds might simply induce coagulation and autoimmune
related side effects without providing improved anti-angiogenic
activity.
The oligosaccharide library we prepared represents the three
prominent structure motifs within the heparin polysaccharide

Table 2  Summary of apparent $K_{d}$ values for heparin-derived
oligosaccharides binding with VEGF
Results shown are means ± S.D. ($n > 3$).

<table>
<thead>
<tr>
<th>Ligand</th>
<th>$K_{d}$ VEGF165</th>
<th>$K_{d}$ VEGF55</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hp dp8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>8a</td>
<td>7.2 ± 0.4 μM</td>
<td>6.5 ± 0.8 μM</td>
</tr>
<tr>
<td>8b</td>
<td>5.5 ± 0.7 μM</td>
<td>4.8 ± 0.4 μM</td>
</tr>
<tr>
<td>8c</td>
<td>14.1 ± 3.3 μM</td>
<td>7.3 ± 1.0 μM</td>
</tr>
<tr>
<td>Hp dp10</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10a</td>
<td>1.8 ± 0.4 μM</td>
<td>1.5 ± 0.1 μM</td>
</tr>
<tr>
<td>10b</td>
<td>1.3 ± 0.3 μM</td>
<td>1.4 ± 0.2 μM</td>
</tr>
<tr>
<td>10c</td>
<td>2.4 ± 0.3 μM</td>
<td>2.3 ± 0.1 μM</td>
</tr>
<tr>
<td>Hp dp12</td>
<td></td>
<td></td>
</tr>
<tr>
<td>12b</td>
<td>471 ± 96 nM</td>
<td>950 ± 200 nM</td>
</tr>
<tr>
<td>12c</td>
<td>570 ± 38 nM</td>
<td>1.9 ± 0.2 μM</td>
</tr>
<tr>
<td>Hp dp14</td>
<td></td>
<td></td>
</tr>
<tr>
<td>14b</td>
<td>90 ± 5 nM</td>
<td>358 ± 49 nM</td>
</tr>
<tr>
<td>14c</td>
<td>103 ± 11 nM</td>
<td>799 ± 191 nM</td>
</tr>
<tr>
<td>Hp dp16</td>
<td></td>
<td></td>
</tr>
<tr>
<td>16b</td>
<td>113 ± 26 nM</td>
<td>478 ± 54 nM</td>
</tr>
<tr>
<td>16c</td>
<td>105 ± 14 nM</td>
<td>584 ± 105 nM</td>
</tr>
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</table>
(Figure 1). In the present study, we also investigated the VEGF binding affinity in response to each of these heparin structures. Experiments using defined oligosaccharide structures showed that the canonical trisulfated oligosaccharide (b) exhibited highest binding affinity for VEGF in each size class. This observation is consistent with previous findings that 2-O, 6-O and N-sulfo groups in HS all contribute to the strength of protein binding [23]. The different binding capacity between oligosaccharide motifs a and b indicates an important role of the IdoA residue for VEGF binding as previously reported, since the presence of 2-O-sulfo groups affect binding to a much lesser extent than N-sulfo and 6-O sulfo groups [43,44]. An undersulfated domain corresponding to a fragment of the ATIII binding site (c) appears to further reduce interaction with VEGF, suggesting the important contribution of N-sulfo group and that the addition of a 3-O-sulfo group cannot compensate for the loss of the N-sulfo group.

We also characterized and compared the heparin-binding properties between the full-length VEGF165 and the single heparin binding fragment VEGF55 to determine whether oligosaccharide binding is significantly influenced by structural regions beyond the HBD within VEGF165. The SPR sensorgram for VEGF55–heparin binding shows a different shape with that for VEGF165–heparin binding, suggesting differences in the binding kinetics. The ability of heparin oligosaccharides to inhibit VEGF binding to unfractionated heparin showed similar trends for VEGF165 and VEGF55. Although nearly equivalent results were obtained for VEGF55 and VEGF165 with a particular octasaccharide, increasingly greater inhibition was observed for VEGF165 by large oligosaccharides (dp > 10). This observation was confirmed by the lower apparent Kd values for VEGF165 binding with these larger oligosaccharides relative to VEGF55. This apparent increase in affinity is likely due to the avidity effect of the VEGF165 dimer in a cooperative binding mechanism provided by the linear array of polyvalent binding sites presented by extended heparin oligosaccharides [45]. It has also been previously reported that larger heparin fragments are able to simultaneously bind the two HBDs of VEGF165 and that such a bridging effect may stabilize and enhance binding [23,39]. However, modelling results suggest that oligosaccharides greater than 25 residues in length would likely be required for binding both HBDs [23]. Interestingly, while the non-canonical heparin-like structure of motif c was tolerated within the binding site as demonstrated by appreciable binding affinity of the 8c, the similar binding affinities between 12c and 10b and that between 14c and 12b suggest that little added benefit in binding affinity is provided when this motif is presented in addition to alternative binding units that contain canonical heparin structure. Our results from the binding studies with VEGF165 clearly indicate that there is no significant difference between the intrinsic binding characteristics of the isolated HBD and the VEGF165 dimer towards short oligosaccharides. These results offer novel insight into the binding properties of VEGF–heparin recognition that are free of the many inherent complications in interrogating the VEGF165 dimer.

In conclusion, a heparin-derived oligosaccharide library with sizes ranging from dp6 to dp18 allowed us to better characterize the heparin-specific binding of VEGF165. The minimum size among these heparin oligosaccharides for VEGF165 binding under physiological conditions was an octasaccharide but a tetradecasaccharide bound VEGF165 with comparable affinity to that of heparin. The trisulfated heparin oligosaccharides bound VEGF165 with the greatest affinity. The relatively rapid rate constants and modest inherent affinity for VEGF55–heparin association are consistent with a binding model in which the HBD is able to rapidly sample alternative binding modes along heparin chains in search for preferred heparin-like oligosaccharide sequences and heparin-dependent binding partners. Similar oligosaccharide libraries have been demonstrated to be useful in a number of previous studies for identification of critical structural features required for specific interactions with various HS binding proteins [46–53]. The SPR-based solution inhibition provides a fast and sensitive way for qualitative and quantitative screening of these libraries for candidates with maximum inhibitory effect towards protein–HS binding. Increasingly recognized for their therapeutic advantages due to a lower toxicity and a general effect towards multiple HS/heparin-dependent growth factors and metastasis related enzyme such as heparanases [54], heparin- and HS-derived oligosaccharides represent an exciting new approach for future anti-tumour drug development upon the elucidation of their structure–function relationship with the targeted angiogenic molecules.

**AUTHOR CONTRIBUTION**

Wenjing Zhao, Scott McCallum, Fuming Zhang and Robert Linhardt

designed the study. Wenjing Zhao carried out the experiments and drafted the manuscript. Fuming Zhang carried out the SPR data analysis. Zhongping Xiao produced the heparin-derived oligosaccharide library. Robert Linhardt directed the project and revised the manuscript before submission.

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**REFERENCES**


20 Norrby, K. (2000) 2.5 kDa and 5.0 kDa heparin fragments specifically inhibit microvessel sprouting and network formation in VEGF165-mediated mammalian angiogenesis. Int. J. Exp. Pathol. 81, 191–198
and modulate its biological activity. Glycobiology 9, 705–711
45 McGhee, J. D. and Hippel, P. H. V. (1974) Theoretical aspects of
DNA–protein interactions: cooperative and non-cooperative binding
of large ligands to a one-dimensional homogeneous lattice. J. Mol.
Biol. 86, 469–489
46 Jemth, P., Kreuger, J., Kusche-Gullberg, M., Sturiale, L.,
oligosaccharide libraries for identification of protein-binding
heparan sulfate motifs: exploring the structural diversity by
screening for fibroblast growth factor (FGF) 1 and FGF2 binding.
J. Biol. Chem. 277, 30567–30573
47 Barth, H., Schafer, C., Adah, M. I., Zhang, F. M., Linhardt, R. J.,
Toyoda, H., Kinoshita-Toyoda, A., Toida, T., van Kuppevelt, T. H.,
Depla, E. et al. (2003) Cellular binding of hepatitis C virus
envelope glycoprotein E2 requires cell surface heparan sulfate.
J. Biol. Chem. 278, 41003–41012
48 Peterson, F. C., Elgin, E. S., Nelson, T. J., Zhang, F. M., Hoeger,
T. J., Linhardt, R. J. and Volkman, B. F. (2004) Identification and
characterization of a glycosaminoglycan recognition element of the
C chemokine lymphotactin. J. Biol. Chem. 279, 12598–12604
Structural determinants of heparan sulfate interactions with slit
50 Suk, J. Y., Zhang, F. M., Balch, W. E., Linhardt, R. J. and Kelly, J. W.
Biochemistry 45, 2234–2242
51 Zhang, F. M., McLellan, J. S., Ayala, A. M., Leahy, D. J. and
Linhardt, R. J. (2007) Kinetic and structural studies on
interactions between heparin or heparan sulfate and proteins of
the hedgehog signaling pathway. Biochemistry 46, 3933–3941
52 Zhang, F. M., Zhang, Z. Q., Lin, X. F., Beenken, A., Eliseenkova,
analysis of heparin/heparan sulfate interacting with fibroblast
growth factor. Fibroblast growth factor receptor complexes.
Biochemistry 48, 8379–8386
53 Ra, H. J., Harju-Baker, S., Zhang, F. M., Linhardt, R. J., Wilson,
C. L. and Parks, W. C. (2009) Control of promatrilysin (MMP7)
activation and substrate-specific activity by sulfated
glycosaminoglycans. J. Biol. Chem. 284, 27924–27932
clinical significance of heparanase in cancer metastasis and

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