N-Acetylated Domains in Heparan Sulfates Revealed by a Monoclonal Antibody against the Escherichia coli K5 Capsular Polysaccharide

DISTRIBUTION OF THE COGNATE EPITOPE IN NORMAL HUMAN KIDNEY AND TRANSPLANT KIDNEY WITH CHRONIC VASCULAR REJECTION*

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The Escherichia coli K5 capsular polysaccharide has the same (GlcUA\(\rightarrow\)GlcNac)\(_n\) structure as the nonsulfated heparan sulfate/heparin precursor polysaccharide. A monoclonal antibody (mAb 865) against the K5 polysaccharide has been described (Peters, H., Jürs, M., Jann, B., Jann, K., Timmis, K. N., and Bitter-Sauermann, D. (1985) Infect. Immun. 50, 459–466). In this report, we demonstrate the binding of anti-K5 mAb 865 to N-acetylated sequences in heparan sulfates and heparan sulfate proteoglycans but not to heparin. This is shown by direct binding and fluid phase inhibition of mAb 865 in an enzyme-linked immunosorbent assay. In this system we found that the binding of the mAb decreased with increasing sulfate content of the polysaccharide. By testing chemically modified K5 and heparin polysaccharides, we found that each of the modifications that occur during heparan sulfate (HS) synthesis (N-sulfation, C-6 epimerization, and O-sulfation) prevents recognition by mAb 865. Samples of heparan sulfate from human aorta (HS-II) were selectively degraded so as to allow the separate isolation of N-sulfated and N-acetylated block structures. N-Sulfated oligosaccharides (obtained after N-deacetylation by hydrazinolysis followed by nitrous acid deamination at pH 3.9) were not recognized by mAb 865, in contrast to N-acetylated oligosaccharides (obtained after nitrous acid deamination at pH 1.5), although the reactivity was lower than for intact HS-II. Analysis of the latter's pH 1.5 deamination products by gel filtration indicated that a minimal size of 18 saccharide units was necessary for antibody binding. These results lead us to propose bivalent antibody-heparan sulfate interaction, in which both F(ab) domains of the mAb interact with their epitopes, both of which are present in a single large (>18 saccharide units) N-acetylated domain and additionally with single epitopes present in two N-acetylated sequences (each <18 saccharide units) bridged by a short N-sulfated domain. Immunohistochemistry with mAb 865 on cryostat sections of normal human kidney tissue, revealed its binding to most but not all renal basement membranes. However, all renal basement membranes contain heparan sulfate, as shown by a mAb against heparitinase-digested heparan sulfate stubs (mAb 3G10). This finding indicates that not all heparan sulfate chains present in basement membranes express the mAb 865 epitopes. Besides the normal distribution, mAb 865 staining was found in fibrotic and sclerotic lesions in vessels, interstitium, and mesangium in transplant kidneys with chronic vascular rejection. Occasionally, a decrease of staining was observed within tubulo-interstitium and glomeruli. These findings show that N-acetylated sequences in heparan sulfates can be demonstrated by anti-K5 mAb 865 in normal and diseased kidneys.

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The biosynthesis of heparan sulfate (HS)\(^1\) involves the formation of a nonsulfated (GlcUA\(\beta1,4\)\(\rightarrow\)GlcNAc\(\alpha1,4\))\(_n\) precursor polysaccharide N-acetylheparosan, which subsequently undergoes a series of polymer modification reactions. These reactions start with N-deacetylation/N-sulfation of GlcNAc residues, which is followed by C-5 epimerization of GlcUA to IdceA units, and finally by O-sulfation at various positions (1). The GlcUA C-5 epimerization and O-sulfation reactions occur in the close vicinity of N-sulfate groups, pointing to a key role for the glucosaminyl N-deacetylase/N-sulfotransferase enzyme in determining the overall extent of modification of the HS chain. Structural analysis of HS from various sources has revealed that these modifications tend to colocalize in block sequences, separated by relatively unmodified domains (2–6). The extent of biosynthetic modification, affecting the number, length, and substitution patterns of the modified domains as well as their position along the HS chain, may differ among cell types (7), alter during proliferation (8), and change as a result of cell transformation (9, 10).

Many biological activities of heparan sulfate proteoglycans (HSPGs) are due to interactions between the HS polysaccharide side chains and a variety of proteins such as extracellular matrix molecules, enzymes, enzyme inhibitors, growth factors, and other cytokines (1, 11–13). These interactions can be either specific, dependent on defined sulfation patterns within given sequences of sugar residues, as described for antithrombin (14),

\(^{1}\) The abbreviations used are: HS, heparan sulfate(s); ELISA, enzyme-linked immunosorbent assay; HSPG, heparan sulfate proteoglycan(s); mAb, monoclonal antibody; PBS, phosphate-buffered saline.
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ELISA—Binding properties of mAb 865 to polysaccharides were tested in ELISA. Polysaccharides (50 μg/ml) were coated overnight at room temperature in PBS to the wells of polystyrene flat-bottom microtiter plates (NUNC Maxisorp, Life Technologies, Inc., Breda, The Netherlands), 100 μl/well. Alternatively, HSPG (1 μg/ml) was coated under the same conditions. Wells were washed 8 times with PBS containing 0.05% Tween 20 (PBS-T) and incubated for 2 h at room temperature with PBS containing 1% gelatin, 120 μl/well, to avoid nonspecific antibody binding. After washing with PBS-T, the dilution range of mAb 865 in PBS-T, 100 μl/well, was incubated for 1 h at room temperature in the ELISA plates. Detection of the mAb and substrate reaction was identical to the inhibition ELISA and has been described before (34). The mAb 865 inhibition ELISA is based on the inhibition of mAb 865 binding to coated K5 or HS-II by liquid phase polysaccharides, HS-II-derived oligosaccharides, or intact HSPGs. Percentage of inhibition was calculated as \((1 - (A450 \text{ with inhibitor}/A450 \text{ without inhibitor})) \times 100\%\). 

**MATERIALS AND METHODS**

**Glycosaminoglycans and Heparan Sulfate Proteoglycans—** HS (preparation HS-II) was isolated from human aorta, essentially according to Iversen (26). HS from pig intestine, the E. coli K5 capsular polysaccharide, with the same GlcUA–GlcNAc, structure as the nonsulfated HS/heparin precursor polysaccharide (24) and chemically O-sulfated K5 polysaccharide were kindly provided by Dr. G. van Dedem (Organon Corp., Oss, The Netherlands). N-Sulfated K5 was given by Dr. B. Casu (Instituto di Chimica e Biochimica G. Ronzoni, Milan, Italy). Intact heparin (stage 14) from pig intestinal mucosa was obtained from Inoleus Iverius (25). HS from pig intestine, the buffered saline (PBS).

**Expression of the Anti-K5 mAb 865 Epitope in Heparan Sulfates and Heparan Sulfate Proteoglycans—** The binding of the anti-K5 mAb 865 to HS was tested in ELISA with a low sulfated HS preparation (0.6 sulfate groups/disaccharide; isolated from human aorta, designated as HS-II), a high sulfated HS preparation (1.5 sulfate groups/disaccharide; isolated from porcine intestine), and heparin (2.5 sulfate groups/disaccharide) and compared with the binding to the nonsulfated K5 polysaccharide. From Fig. 1A it becomes clear that HSes are recognized by the mAb, especially the low sulfated HS-II, although to a lesser extent than the K5 polysaccharide. The mAb did not bind to heparin. Since the coating efficiency of these polysaccharides might be unequal due to differences in negative charge, we tested the same preparations in a fluid phase inhibition ELISA. HS-II was used to coat the ELISA plates. Results are shown in Fig. 1B and are essentially the same as found in the direct ELISA (Fig. 1A). The inhibitory activity of HS-II was ±3000-fold lower than that of K5. Since high sulfated HS demonstrated only weak inhibition and heparin did not inhibit at all, it is suggested that the extent of chain modification is inversely correlated with antibody binding. In control experiments mAb 865 was tested for its binding to other glycosaminoglycans such as chondroitin sulfate A and C, dermatan sulfate, and hyaluronic acid and to dextran sulfate and DNA, which all were completely negative. These control experiments exclude the possibility that the binding of mAb 865 to HS is due to nonspecific, charge-based interactions.

Next to glycosaminoglycans, the mAb was also tested for binding to isolated HSPG from mouse Engelbreth-Holm-Swarm sarcoma (perlecan) and from rat glomerular basement
membranes. Both HSPGs were recognized by mAb 865 in the direct ELISA and as fluid phase inhibitor (Fig. 1, C and D), Engelbreth-Holm-Swarm HSPG expressing more mAb 865 epitopes/mg core protein than glomerular basement membrane HSPG.

Heparitinase digestion of the HSPGs abolished all binding of mAb 865, whereas the binding of antibodies against the core proteins of both HSPGs were not affected by this treatment (not shown), thereby confirming HS specificity of mAb 865.

**Recognition of Chemically Modified K5 and Heparin Polysaccharides by mAb 865—HS differs in three major regards from K5: (i) $N$-sulfation of GlcN units, (ii) C-5 epimerization of hexuronic acid residues, and (iii) O-sulfation at different positions. To investigate whether the epitope requirements in HS and K5 are identical, the effect of chemical modification of the K5 polysaccharide on antibody binding was studied in the inhibition ELISA with K5 as coated antigen (Table I). Complete $N$-sulfation of K5 abolished all binding to the mAb. To evaluate the effect of C-5 epimerization we tested completely ($N$- and O-) desulfated, $N$-reacetylated heparin. This preparation differs from K5 in one major regard, i.e. the occurrence of IdceA units ($\pm 80\%$ of the total hexuronic acid contents). From Table I it is inferred that such units completely prevent antibody binding. We also tested an O-sulfated K5 polysaccharide preparation containing an average of $-1.2$ O-sulfate (but no N-sulfate) groups/disaccharide unit. The locations of the O-sulfate groups were not defined but would presumably primarily involve C-6 of the GlcN units, along with C-2 and/or C-3 of the GlcUA units. The results in Table I clearly show that O-sulfation of K5 polysaccharide completely prevents mAb 865 binding. From these experiments we concluded that each of the modifications known to occur during HS synthesis ($N$-sulfation, C-5 epimerization, and O-sulfation) prevents recognition by anti-K5 mAb 865.

Requirements of the mAb 865 Epitopes in the HS Chain—In order to define the requirements of the mAb 865 epitopes in the HS chain more precisely, samples of HS-II were selectively degraded to isolate separately $N$-sulfated and $N$-acetylated block structures of the molecule (see “Materials and Methods”). These oligosaccharides were then tested in the mAb 865 inhibition ELISA using HS-II as coated antigen. The results in Fig. 2 demonstrate complete loss of reactivity for the $N$-sulfated oligosaccharides. In contrast to this, the $N$-acetylated oligosaccharides are still recognized by mAb 865, although to a considerably lower extent. Nitrous acid degradation at pH 3.9 alone, i.e. not preceded by $N$-acetylation, had no influence on antibody binding, which indicates that $N$-unsubstituted GlcN units are not located within the epitopes. In this respect, anti-K5 mAb 865 clearly differs from another anti-HS mAb (JM-403) that we described recently, whose epitope is dependent on the presence of $N$-unsubstituted glucosamine units in HS (37). The fact that the heavily modified, heparin-like $N$-sulfated block sequences of the HS chains (obtained after nitrous acid deamination at pH 3.9 of $N$-deacetylated HS-II) lacked all mAb 865 binding suggests to us that the epitope is located in the $N$-acylated regions of HS. If this is true, why is there a considerable loss of...
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Table 1

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<th>Treatment</th>
<th>Characteristic</th>
<th>IC&lt;sub&gt;50&lt;/sub&gt; μg/ml</th>
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<tr>
<td>Native K5</td>
<td>100% (1,4GlcA→1,4GlcNac)&lt;sub&gt;α&lt;/sub&gt;, no sulfation, no IdceA units</td>
<td>0.4</td>
</tr>
<tr>
<td>N-Sulfated K5</td>
<td>All GlcN units are sulfated, no O-sulfates</td>
<td>&gt;100</td>
</tr>
<tr>
<td>N,O-Desulfated, N-reacetylated heparin</td>
<td>No sulfation, ≥80% IdceA units</td>
<td>&gt;100</td>
</tr>
<tr>
<td>O-Sulfated K5</td>
<td>1.2 O-sulfate groups/disaccharide, no N-sulfates</td>
<td>&gt;100</td>
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Fig. 2. Fluid phase inhibition of mAb 865 binding to HS-II from human aorta by HS-II-derived oligosaccharides. Inhibition was performed with native HS-II (○——○), N-sulfated oligosaccharides of HS-II (isolated after N-deacetylation by hydrazinolysis followed by deamination at pH 3.9; •——•), N-acetylated oligosaccharides of HS-II (isolated after deamination at pH 1.5; O——O); HS-II treated with nitrous acid at pH 3.9 alone, i.e. not preceded by N-deacetylation (+——+).

Inhibitory capacity of the N-acetylated domains, which are obtained after nitrous acid pH 1.5 cleavage of HS? From the work of others we know that a size of five sugar residues is sufficient for monovalent antibody binding (38). Therefore, we analyzed the minimal binding size of N-acetylated oligosaccharides derived from HS-II, which still demonstrate binding to the mAb. To this end, a 3-mg sample of HS-II was deaminated by nitrous acid, pH 1.5. The resulting oligosaccharides were subsequently separated by gel filtration on a Bio-Gel P-10 column. From Fig. 3 it becomes clear that only large, N-acetylated oligosaccharides ≥18 residues bound to mAb 865. This finding suggests that bivalent epitope recognition is required for adequate binding of the mAb.

Immunohistology with mAb 865 on Normal Human Renal Tissue—The epitopes detected by mAb 865 in cryostat sections of human renal tissue were expressed in most but not all basement membranes in a linear fashion. Glomerular basement membranes were moderately positive, while Bowman's capsule and mesangial matrix were more prominent (Fig. 4A). Basement membranes of endothelial cells of peritubular capillaries and other blood vessels, including the basal laminae surrounding vascular smooth muscle cells were strongly positive (Fig. 4C). Tubular basement membrane staining varied from strongly positive to completely negative (Fig. 4, A and C). In two kidney specimens of older patients moderate interstitial fibrosis and mesangial matrix accumulation were found, which were stained with mAb 865 (not shown). HS specificity of the staining was demonstrated by pretreatment of the sections with heparitinase, which completely prevented all staining (not shown). On the other hand, all renal basement membranes were stained by mAb 3G10, which reacts with the residual HS stubs remaining after enzymatic cleavage by heparitinase (Fig. 4, B and D). The resultant 3G10 epitope contains an essential, terminal, 4,5-unsaturated uronate residue and thus can serve as a general HS marker, of which staining intensity is independent of HS modifications (36). These results demonstrate the presence of HS in all renal basement membranes, some of them being negative for the mAb 865 epitope. The most likely explanation points toward differences in modification/sulfation of HS in the various basement membranes, highly modified HS being negative and low sulfated HS being positive for mAb 865.

Distribution of mAb 865 Epitopes in Transplant Kidneys with Chronic Vascular Rejection—Since we observed in some normal kidney biopsies that interstitial and periglomerular fibrosis and mesangial sclerosis were associated with a higher binding of mAb 865, we analyzed renal transplant biopsies with chronic vascular rejection. Chronic vascular rejection in kidney transplants is morphologically characterized by severe narrowing of arteries due to intima fibrosis and interstitial fibrosis with tubular atrophy. Sometimes a glomerulopathy,

Fig. 3. mAb 865 recognition of pH 1.5 deamination products of HS-II. A 3-mg sample of HS-II was subjected to nitrous acid degradation at pH 1.5 followed by gel filtration of the fragments on a Bio-Gel P-10 fine column as described under "Materials and Methods." Effluent fractions were analyzed for hexuronic acid by the carbazole reaction (panel A, A 530, •——•) and for mAb 865 reactivity in the inhibition ELISA (panel B, percentage of inhibition, O——O). The number of monosaccharides of the separated oligosaccharides is indicated at the top of each peak in panel A. The column was calibrated by dextran blue (V<sub>b</sub>) and "H-labeled heparin disaccharides.
The present study deals with the expression of HS in mammary glands.

**DISCUSSION**

The expression of HS in mammary glands was quantified by immunohistochemical staining of formalin-fixed paraffin-embedded sections using antibodies specific for HS. The results showed a significant increase in HS expression in the mammary glands of the experimental group compared to the control group. These findings suggest that HS may play a role in the development and progression of mammary gland diseases.

**Table**

<table>
<thead>
<tr>
<th>Gene</th>
<th>mRNA</th>
<th>Protein</th>
<th>Activity</th>
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<tr>
<td>HS</td>
<td>High</td>
<td>High</td>
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<td></td>
<td>Low</td>
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**Figure**


**Conclusion**

The results of this study suggest that HS plays a critical role in the development and progression of mammary gland diseases. Further studies are needed to fully understand the mechanisms by which HS contributes to these processes.
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value agrees with the calculated distance between both Fab arms of an immunoglobulin molecule (39). Simultaneous bonding of both F(ab) antibody domains will strongly promote the interaction. It is noteworthy that a comparable type of bivalent bonding has been described recently for the interaction of interferon-γ dimer with HS (18). In this elegant study it was shown that the high affinity binding domain for interferon-γ in HS is composed of two terminal N-sulfated domains, linked together by an intervening N-acetylated domain. The interferon-γ dimer bound to both N-sulfated terminal regions, while a monovalent interferon-γ-HS interaction was insufficient for stable binding. Our finding that deamination at pH 1.5 results in partial loss of antibody recognition suggests that in native HS, not only the large N-acetylated domains (= 18 saccharide units) but also smaller N-acetylated sequences bridged by a short N-sulfated domain, are recognized by mAb 865. Cleavage of the HS polysaccharide at N-sulfated glucosamine residues (deamination at pH 1.5) thus abolishes bivalent antibody recognition of such small N-acetylated sequences. Alternatively, the extended minimal polymer size of 18 saccharide units needed for antibody recognition might be explained by assuming a conformational epitope. For example, in a helical polymer structure, a much longer primary sequence will be required for maintenance of a conformational epitope.

Immunofluorescence studies on human kidney sections with mAb 865 revealed that the carbohydrate epitope is not evenly distributed among the HS subspecies of this tissue. All basement membranes, as expected, were found to contain HS, as evidenced by the anti-HS stub mAb 3G10. However, the polysaccharide present in some tubular basement membranes stained poorly with mAb 865, suggesting the existence of HS isoforms lacking the corresponding epitope. The most likely explanation for this is the existence of a high sulfated HS isoform in these particular tubular basement membranes. This is supported by the finding that another anti-HS mAb (JM-403), which recognizes epitopes with N-unsubstituted glucosamine units in low sulfated HS isoforms (37), shows the same staining pattern. Alternatively, the N-acetylated domains may be inappropriately spaced for antibody binding. Staining with mAb 865 was also observed in mild fibrosis and sclerosis, which is found in normal renal tissue, secondary to aging. This led us to the analysis of renal tissue with more extensive fibrosis. To be inappropriately spaced for antibody binding. Staining with mAb 865 revealed that the carbohydrate epitope is not evenly distributed among the HS polysaccharide at N-sulfated glucosamine residues (deamination at pH 1.5) thus abolishes bivalent antibody recognition of such small N-acetylated sequences. Alternatively, the extended minimal polymer size of 18 saccharide units needed for antibody recognition might be explained by assuming a conformational epitope. For example, in a helical polymer structure, a much longer primary sequence will be required for maintenance of a conformational epitope.

Thus, N-acetylated oligosaccharides isolated after nitrous acid deamination of HS from bovine lung were found to be more effective inhibitors of mesangial cell proliferation than either the intact polymer or highly sulfated oligosaccharides from the same source (41). Moreover, it has been shown that HS fragments obtained after digestion with heparinase (yielding low sulfated GlcUA- and GlcNAc-rich oligosaccharides) inhibited endothelial cell proliferation induced by acidic fibroblast growth factor, in contrast to HS fragments obtained after digestion with heparinase (yielding high sulfated IDEa-rich oligosaccharides) (42). Moreover, it has been reported that small K5 fragments and N-acetylated oligosaccharides derived from HS inhibited normal angiogenesis (43). These data indicate that mAb 865-positive HS present in the extracellular matrix may represent a pool of immobilized precursors of antiproliferative and antiangiogenic oligosaccharides. It has been demonstrated that biologically active oligosaccharides may be released from the matrix by the action of various endoglycosidases (44-48). While the substrate specificities of these enzymes have not yet been elucidated in detail, it has been suggested that certain enzyme species may preferentially cleave nonsulfated regions in the HS chain (49), whereas others require sulfate groups for substrate recognition (50-52). We thus may envisage an elaborate system of distinct bioactive oligosaccharides, generated by the action of endoglycosidases on HS substrates composed of sulfated and nonsulfated regions.

**REFERENCES**

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