**Comamonas testosteronan synthase, a bifunctional glycosyltransferase that produces a unique heparosan polysaccharide analog**

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Glycosaminoglycans (GAGs) are linear hexosamine-containing polysaccharides. These polysaccharides are synthesized by some pathogenic bacteria to form an extracellular coating or capsule. This strategy forms the basis of molecular camouflage since vertebrates possess naturally occurring GAGs that are essential for life. A recent sequence database search identified a putative protein from the opportunistic pathogen *Comamonas testosteroni* that exhibits similarity with the *Pasteurella multocida* GAG synthase PmHS1, which is responsible for the synthesis of a heparosan polysaccharide capsule. Initial supportive evidence included glucuronic acid (GlcUA)-containing polysaccharides extracted from *C. testosteroni* KF-1. We describe here the cloning and analysis of a novel *Comamonas* GAG synthase, CtTS. The GAG produced by CtTS in vitro consists of the sugars α-D-GlcUA and N-acetyl-α-d-glucosamine, but is insensitive to digestion by GAG digesting enzymes, thus has distinct glycosidic linkages from vertebrate GAGs. The backbone structure of the polysaccharide product [α-(1→4)-D-GlcUA-(1→3)-α-N-acetyl-D-glucosamine]$_n$ was confirmed by nuclear magnetic resonance. Therefore, this novel GAG, testosteronan, consists of the same sugars as the biomedically relevant GAGs heparosan (N-acetyl-heparosan) and hyaluronan but may have distinct properties useful for future medical applications.

**Keywords:** *Comamonas* / glycosaminoglycan / glycosyltransferase / heparosan / polysaccharide

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**Introduction**

Certain pathogenic microbes employ extracellular capsules of host-like glycans to evade host defenses and to increase virulence (DeAngelis 2002). Previous work in our laboratory and others has identified very distinct types of microbial glycosaminoglycan (GAG) synthases, the bifunctional enzymes that assemble GAG polysaccharides. These synthases include peripheral membrane-associated two domain enzymes such as the *Pasteurella multocida* GAG synthases PmHS1 (hyaluronan, HA; DeAngelis and White 2002; DeAngelis and Padgett-McCue 2000; DeAngelis and White 2004; Figure 1A) and KfoC (chondroitin) from *Escherichia coli* K4 (Ninomiya et al. 2002), as well as integral membrane proteins with unknown domain structures such as the *Streptococcus pyogenes* HA synthase (DeAngelis et al. 1993) and the *Chlorella* virus paramecium bursaria chlorella virus (PBCV)-1 HA synthase (DeAngelis et al. 1997). All the known GAG synthases employ uridine diphosphate (UDP)-sugar precursors to form the repeating disaccharide units (DeAngelis 2002). The *Streptococcus* HA synthase has some similarity with vertebrate HA synthases at the amino acid sequence level (Weigel and DeAngelis 2007), but the bacterial chondroitin and heparosan synthases (HSs) are quite different from their vertebrate counterparts (DeAngelis and Padgett-McCue 2000; DeAngelis and White 2002).

Recently, we reported the distinct catalytic phenotypes exhibited by the two *P. multocida* HSs (Sismey-Ragatz et al. 2007). As a part of our efforts to better understand the mechanism of these GAG synthases, including the structure/function relationship that manifests donor and acceptor specificity, a search of the NCBI sequence databases identified a potential bifunctional glycosyltransferase (GT) (YP_03542636; 32% identity, Supplementary data, Figure S1) in the genome of the *Comamonas testosteroni* KF-1 isolate with a region of sequence similarity with the carbohydrate-active enzymes (CAZy) (http://www.cazy.org) GT45 family of GTs (Cantarel et al. 2009; Drummond et al. 2010). The CAZy GT45 family of proteins contains only eight members; as of January 2011, the CAZy GT database contained 92 families with ~65,000 GT modules. The bifunctional *P. multocida* HSs contain this relatively rare GT45 domain that in combination with a GT2 domain synthesizes the GAG heparosan that comprises the capsule of type D *P. multocida*. 

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The ability for *C. testosteroni* (Gul et al. 2007) and endophthalmitis (Reddy et al. 2009), meningitis (Arda et al. 2003; Jin et al. 2008), bacteremia that has been found in various hospital infections including meningitis (Arda et al. 2003; Jin et al. 2008), bacteremia, and K

The polysaccharide backbone produced by CtTS is a precursor polysaccharide to heparan sulfate and testosteronan synthase. By further clariﬁcation, we performed activity assays with conﬁrmed lysates from recombinant bacteria expressing CtTS using two different UDP-sugars simultaneously in polymerization reactions in vitro. Speciﬁcally, we employed radiolabeled UDP-[3H]GlcUA (glucuronic acid) as a traceable precursor and either unlabeled UDP-GlcNAc, UDP-GalNAc or UDP-Glc as the second precursor. Signiﬁcant activity was seen in the presence of UDP-GlcNAc, but not with UDP-GalNAc or UDP-Glc (Figure 2, top); without any UDP-hexosamine, the signal due to incorporation of [3H]GlcUA was the same as vector-alone control lysates. This result was conﬁrmed with the converse polymerization experiment which was performed with radiolabeled UDP-[3H]GlcNAc and unlabeled UDP-GlcUA. To assess if this uronic acid was the preferred donor, we also performed radiochemical incorporation assays with UDP-[3H]GlcNAc in the presence of either UDP-GlcUA, UDP-galacturonic acid, UDP-iduronic acid (Weïwer et al. 2008) or UDP-Glc as the second precursor; only the reaction mixtures containing UDP-GlcUA showed signiﬁcant incorporation (Figure 2, bottom). Therefore, simultaneous incubation of lysates containing the recombinant CtTS gene product with both UDP-GlcUA and UDP-GlcNAc was required for the polymeric signal. In summary, we hypothesize that CtTS is a bifunctional enzyme capable of forming polysaccharide composed of GlcNAc and GlcUA in vitro. These are the same two sugars found in both HA and heparosan. By further
studying acceptor specificity and using GAG-degrading enzymes that are specific for these GAGs, we set forth to characterize the nature of the polysaccharide formed by CtTS in vitro.

**Acceptor specificity of CtTS**

To identify the acceptor preference of CtTS, we performed radiolabeled sugar polymerization assays in the presence of various GAG acceptors. In many, but not all, GAG synthases, exogenous cognate polysaccharide will increase the signal in sugar incorporation assays by bypassing the slower de novo initiation phase (DeAngelis 1999; Jing and DeAngelis 2004); the elongation phase is much more rapid thus higher activity is observed. Typically, non-cognate GAG polymers with different glycosidic linkage patterns are very poor or non-functional acceptors for the known GAG synthases in vitro. HA, unsulfated chondroitin and heparosan as well as polysaccharide extract from *C. testosteroni* were tested. HA and heparosan tetrasaccharides were also tested for their abilities to act as acceptors. CtTS showed a clear preference for the *Comamonas* polysaccharide, but was also able to use heparosan (Figure 3). To confirm that CtTS is able to directly extend a heparosan acceptor so as to rule out an artifactual stabilizing or conformational effect in the radioassays, we also tested an $^{125}$I-labeled tetrasaccharide heparosan acceptor in vitro in the presence of only UDP-GlcNAc for single sugar addition, or UDP-GlcNAc and UDP-GlcUA for polymerization. The *C. testosteroni* synthase was able to extend $^{125}$I-labeled heparosan tetrasaccharide (Supplementary data, Figure S2).

In summary, lysates containing the recombinant CtTS gene product are capable of utilizing heparosan and *Comamonas* polysaccharide as acceptors, but not HA or chondroitin. The failure to extend HA, which consists of the same sugars as heparosan (which is extended), indicates that the glycosidic linkages are not compatible with a structure required for polysaccharide extension. This could be due to either lack of acceptor binding or binding in a mode that does not orient the acceptor in an appropriate configuration with respect to the donor sugar for extension. The chondroitin acceptor contains a GalNAc sugar in place of GlcNAc and may also be unable to bind, or binds in a way that it cannot be extended. The finding that heparosan is extended by CtTS in vitro, but not as well as the *Comamonas* extract, suggests that the two polysaccharides share some structural features, but are not identical.

**Metal dependence of CtTS**

Many GTs require a divalent cation (e.g. Mg$^{2+}$, Mn$^{2+}$, Ca$^{2+}$ etc.) in order to coordinate the UDP-sugar donor molecule for nucleophilic attack by the acceptor molecule. The *Streptococcus* HA synthase prefers Mg$^{2+}$, whereas the *Pasteurella* HA and HSSs prefer Mn$^{2+}$ (DeAngelis 1996). The difference in metal preference in vitro may be an indication of differences in coordination geometry at the active site structures and/or in the reaction mechanisms.

Using radiolabeled sugar incorporation assays performed in the presence of one or both of these divalent cations, we observed that lysates containing the recombinant CtTS gene product prefer Mg$^{2+}$. The presence of 5 mM Mn$^{2+}$ supported GT activity, but activity achieved in the presence of 5 mM
Mg$^{2+}$ was roughly five times as for Mn$^{2+}$ (Supplementary data, Figure S3). Metal is required as the chelator ethylenediaminetetraacetic acid (EDTA) eradicated the polymerization signal. Control assays in which lysates were pretreated with 2 mM EDTA then excess (7 mM) Mg$^{2+}$ or Mn$^{2+}$ were added back confirm that a divalent cation is required for CtTS activity.

**Analysis of *C. testosteroni* polysaccharide**

The native target polysaccharide yield from 1 L culture of *C. testosteroni* in chemically defined medium (CDM) after 24 h was ~2 mg. Using complete acid hydrolysis of the purified polysaccharide extract into monosaccharides, followed by anion exchange chromatography, we observed GlcUA and GlcNac (data not shown); the presence of GlcUA was consistent with the presence of a UDP-glucose 6-dehydrogenase gene adjacent to the *CtTS* gene in the *C. testosteroni* KF-1 genome. Gel analysis of the cetylpyridinium chloride (CPC) precipitated the native polysaccharide and the synthetic polysaccharide made with recombinant CtTS in vitro revealed products with apparent molecular weights of ~60 kDa based on the HA standards.

The preference for heparosan acceptor over HA and chondroitin in the radiochemical incorporation assays (Figure 3) as well as the sequence similarity with PmHS1 and PmHS2 initially suggested that CtTS was akin to HS. However, both the native polysaccharide and the synthetic polysaccharide were insensitive to degradation by heparin lyase III or ovine testicular hyaluronidase (Figure 4) as well as *Streptomyces hyalurolyticus* HA lyase or *Proteus vulgaris* chondroitinase ABC. The synthetic polysaccharide has no possibility of any putative polymerization modifications made by *Comamonas* in vivo that could block the action of the GAG digesting enzymes. Because of this finding, we believe that while CtTS is able to utilize heparosan as an acceptor molecule due to a hypothetical shared structural feature, this GAG is not the native substrate.

Due to our inability to digest the *C. testosteroni* polysaccharide with known GAG-degrading enzymes, partial acid hydrolysis was employed to produce oligosaccharides that would be suitable for further analysis. Thin-layer chromatography (TLC) was used to optimize the conditions (not shown) and confirmed the presence of sugar oligomers after hydrolysis. MALDI-ToF (matrix-assisted laser desorption/ionization-time of flight) mass spectrometry analysis yielded a ladder pattern of mass peaks that is indicative of a backbone with a repeating disaccharide pattern (i.e. 1:1 ratio of N-acetyl-hexosamine to uronic acid; Figure 5). Indeed, the fragment mass values were virtually identical to those seen with both heparosan and HA. The in vitro synthesized polymer mass spectral data were virtually identical to the native polysaccharide; however, it should be noted that such acidic conditions would also potentially remove labile modifications of the backbone. Under our conditions, many N-acetyl groups are removed (as in heparosan or HA). Therefore, in theory, the native polysaccharide could contain derivatives of the more well-known monosaccharide units, but such putative modifications may escape detection after hydrolysis.

These mass spectral data, in combination with the in vitro synthesis of this GAG and the inability to digest both the in vitro and native polysaccharide with various known GAGases led us to conclude that this polysaccharide backbone was in fact a new GAG with distinct glycosidic linkages from those of both HA and heparosan. In keeping with the tradition of naming GAGs based on their initial origin, we have called this new polysaccharide backbone “testosteronan”.

**Nuclear magnetic resonance determination of a novel GAG**

One-dimensional $^1$H and $^{13}$C spectroscopy were initially used to evaluate the structure of both the native and the synthetic polysaccharides. These polysaccharides had similar but not identical spectral properties with 14 carbon signals, consistent...
with a repeating disaccharide unit of GlcUA and GlcNAc. The anomeric signals of each type of monosaccharide residues were assigned based on their characteristic downfield positions (Supplementary data, Figure S4). Next, two-dimensional COSY (COrrelation SpectroscopY; $^{1}$H-$^{1}$H) and HMQC (Heteronuclear Multiple-Quantum Coherence experiment; $^{13}$C-$^{1}$H) (Supplementary data, Figures S5, S6, S10 and S11) experiments were used to assign all signals to each proton and carbon within the two polysaccharides (Table 1). Two-dimensional ge-HMQC-TOCSY (TOTAal Correlation SpectroscopY; Figure 6) confirmed all of these assignments. Figure 6 shows the HMQC (green) spectrum of native Comamonas polysaccharide overlaid onto ge-HMQC-TOCSY (red) spectrum. Two-dimensional TOCSY ($^{1}$H-$^{1}$H) (Supplementary data, Figures S7 and S12) was used to obtain all possible correlations within each spin system. Finally, two-dimensional NOESY (Nuclear Overhauser Effect SpectroscopY; Figures 7 and 8) was used to assign nuclear overhauser effect (NOE) signals between the anomeric protons and H-4 protons of the adjacent saccharide residue across the glycosidic linkage to provide linkage positions.

Based on these spectral data, the structure of the native polysaccharide backbone could be definitively assigned as [-4-D-GlcUA-$\alpha1,4$-D-GlcNAc-$\alpha1$-$\beta$], but the proton at the 3-position of the GlcNAc residue was shifted downfield by 1.354 ppm, compared with the synthetic polysaccharide to 5.222 ppm, suggesting it carried a deshielding modification. One hypothesis is that during biosynthesis of testosteronan, the polysaccharide is polymerized by the CtTS synthase and then during a post-polymerization step or reaction, the C3 hydroxyl is modified. An alternative model is that a novel hexosamine unit is used by this organism in vivo but that the enzyme tolerates GlcNAc as observed in our in vitro tests. To date, we have been unable to determine the nature of the modification that causes this unusual shift in the C3 atom position. We have ruled out the possibility of sulfation [by X-ray photoelectron spectroscopy (XPS)] and phosphorylation [by $^{31}$P NMR (nuclear magnetic resonance) and XPS]. We analyzed the sample at pH 9, but the unusual NMR signal remained thus ruling out the possibility of a potential base-labile O-acetyl unit or an inter-residue lactone.

The synthetic polysaccharide was produced in vitro with pure precursors, UDP-GlcUA and UDP-GlcNAc. The $^{1}$H and $^{13}$C signals of the GlcUA residue in synthetic polysaccharide resonated at nearly identical chemical shift values as those observed for the native polysaccharides. The chemical shift values for the $^{1}$H and $^{13}$C signals for the GlcNAc residue were different for the two polysaccharides, particularly those at the 3-position. Moreover, overlap (even at 800 MHz field strength) between the proton at the 4-positions of both the GlcNAc and GlcUA residues in the synthetic polysaccharide initially made it impossible to definitively assign linkage positions. When the probe temperature was elevated up to 338 K, the GlcUA and GlcNAc anomeric signals could be partially separated (Supplementary data, Figure S8) but their linkage positions could still not be assigned by NOESY due to peak broadening. This problem was overcome by reducing the pH (the pH equivalent in deuterated water) of the synthetic polysaccharide sample from 6.9 to 3.6 (Supplementary data, Figure S9) allowing its structure to be definitely assigned as [-4-D-GlcUA-$\alpha1,4$-D-GlcNAc-$\alpha1$-$\beta$].

Table 1. Chemical shift values (pD 7.0, 25°C) and assignments of $^{1}$H and $^{13}$C NMR shifts for C. testosteronan polysaccharides

<table>
<thead>
<tr>
<th>Residue/position</th>
<th>Native polysaccharide</th>
<th>Synthetic polysaccharide</th>
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<tr>
<td></td>
<td>$^{13}$C</td>
<td>$^{1}$H</td>
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<tr>
<td>GlcUA1</td>
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<td>GlcUA2</td>
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<tr>
<td>GlcNAc (CH$_3$)</td>
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Discussion

GAGs are hydrophilic polysaccharides that can play signaling, structural, and protective roles in the human body. These properties make GAGs desirable molecules for therapeutics and tissue engineering. In the current work, we have identified a bifunctional GAG synthase, CtTS, which is responsible, in part, for forming an extracellular polysaccharide in the bacterium C. testosteronan KP-1. The GAG backbone formed by the action of CtTS, testosteronan, consists of the same chemical composition as both heparan and HA, but has distinct glycosidic linkages. Heparan is [-4-D-GlcUA-$\beta1,4$-D-GlcNAC-$\alpha1$-$\beta$], while HA is [-4-D-GlcUA-$\beta1,3$-D-GlcnAc-$\beta1$-$\beta$]. Our NMR studies have been able to confirm that this new GAG backbone has the structure [-4-D-GlcUA-$\alpha1,4$-D-GlcNAc-$\alpha1$-$\beta$]. Therefore, the testosteronan backbone has identically configured GlcNAc units as heparan; this observation probably explains why heparan served as an acceptor for CtTS in vitro, but not as efficiently as the native polymer found in Comamonas extracts.

Some bacterial pathogens utilize polysaccharide capsules with molecular structures similar or identical to their host organism to avoid host defenses, such as antibodies, phagocytes or complement. Although the differences in the testosteronan structure may appear to be detrimental for the Comamonas microbe’s strategy of molecular mimicry, some capsular glycans are not identical to host GAGs, but are still employed as virulence factors. Specific examples include: (i) heparan of P. multocida type D and E. coli K5, which is employed without sulfation or epimerization, and (ii) a fructosylated version of chondroitin is used by E. coli K4 (DeAngelis 2002).

The glycosidic linkages of testosteronan are responsible for the polysaccharide’s insensitivity to digestion by all GAG-degrading enzymes tested thus far, but it should be susceptible to vertebrate lysosomal exoglycosidases. This property of testosteronan may prove useful for generating longer-lasting polysaccharides or biomaterials provided the
molecule does not promote an immunological response in the human body. Additionally, it is intriguing to consider the potential for this molecule to possess anticoagulant or anti-proliferative activity after chemical or enzymatic sulfation (Kuberan et al. 2003; Chen et al. 2005; Liu R et al. 2010). This is due to the similar structure to that of heparosan, which is the precursor molecule to heparin, the highly sulfated, epimerized form of the same molecule. The only difference between heparosan and testosteronan is the change from β- to α-linkage configuration between the GlcUA and the GlcNAc residues. Therefore, any binding protein or factor that relies on this structure (or the conformation it assumes) may not interact with the testosteronan backbone as well as with that of heparosan, but conversely, other proteins that do not rely on this structure may be minimally affected. If such a scenario exists, then the basis for more selective therapeutics exists. Future studies will assess this and other possible applications for testosteronan.

CtTS serves as the source of a new GT domain (GT93) for protein engineering, as well as expanding the pool of characterized GT45-containing enzymes. By mining genomes for related or similar sequences to CtTS and other GAG synthases, we may both elucidate GT mechanisms as well as generate new catalytic tools capable of producing novel polysaccharides.

**Materials and methods**

**Materials**

Wild-type *C. testosteroni* KF-1 (DSM# 14576) was obtained from the German Collection of Microorganisms and Cell Cultures (DSMZ, Braunschweig, Germany). The strain was grown in CDMs which is free of other polysaccharides and animal extracts (van De Rijn and Kessler 1980; JRH Biosciences, Lenexa, KS). All reagents were from Sigma (St Louis, MO) unless otherwise noted. Oligonucleotide primers were synthesized by Integrated DNA Technologies, Inc. (Coralville, IA).

**Isolation and analysis of capsular polysaccharide**

Wild-type *C. testosteroni* KF-1 was grown in CDM for 24 h at 30°C with shaking at 250 rpm. Cells were then removed from the culture by centrifugation. Spent media was treated with 0.1 μg/μL DNase/RNase for 2 h at room temperature to degrade nucleic acids. The anionic polysaccharide fraction was precipitated by addition of 1% CPC for 1 h at room temperature. The pellet was collected by centrifugation (2000 × g, 60 min), washed with water and resuspended in 1 M NaCl. The solution was clarified by centrifugation and the supernatant was ethanol precipitated (70% v/v final). The ethanol precipitation/1 M NaCl dissolution procedure was repeated twice and then the pellet was washed with 70% ethanol.
Finally, the pellet was resuspended in water, treated with 0.1 μg/μL DNase/RNase for 1 h (20 mM Tris, pH 7.2, 1 mM MgCl₂) and extracted with CHCl₃ to remove proteins from the sample. This polysaccharide extract was further fractionated by anion exchange chromatography (HiTrap Q HP 1 mL column, GE LifeSciences, Uppsala, Sweden) using a 0.05–2 M ammonium formate gradient (1 mL/min for 93 min). The resulting fractions were analyzed by polyacrylamide gel electrophoresis [PAGE; 1× tris-borate-EDTA (TBE), 6% acrylamide] with staining by Alcian Blue. Fractions containing the target polysaccharide (~0.6–0.75 M ammonium formate) were pooled and lyophilized three times from water to remove the volatile ammonium formate. The polysaccharide pool was then treated with protease K (1 μg/μL enzyme, 50 mM NaOAc, pH 7.4, overnight at 30°C) to destroy any contaminating proteins. In certain preparations, as noted, other HA-like polysaccharides were digested with ovine testicular hyaluronidase prior to protease K digestion. Digest reactions were CHCl₃ extracted to remove enzymes and exchanged via ultrafiltration into water (Microcon 30 kDa, 3× with 500 μL rinses). The retentate containing polysaccharide was purified on a PD-10 column (GE LifeSciences) to remove remaining low-molecular-weight contaminants. Briefly, the column was equilibrated, loaded and eluted as per manufacturer’s instructions using 0.2 M ammonium formate buffer. The void volume fractions containing polysaccharide were pooled and lyophilized 3×. Uronic acid content was measured by the carbazole assay (Bitter and Muir 1962) with GlcUA standard. Resulting polysaccharide was used for NMR and monosaccharide analysis.

For monosaccharide analysis, polysaccharides were subjected to acid hydrolysis; 30–100 μg of polysaccharide was incubated in 300 μL of 2-N-trifluoroacetic acid (TFA) for 6 h at 100°C. Finally, reactions were cooled to room temperature and dried in a rotary evaporator. Samples were dissolved in 50 μL of water and 20 μL was subjected to anion exchange chromatography with pulsed amperometric detection on a Dionex DX600 instrument as described previously (DeAngelis et al. 2002; Dionex, Inc., Sunnyvale, CA).

**Cloning and expression of C. testosteroni synthase**

Genomic DNA was extracted from the wild-type C. testosteroni microbe grown in CDMs employing the UltraClean Microbial DNA Sample Kit (MO BIO, Carlsbad, CA) and used as a template for polymerase chain reaction (PCR) using primers designed to amplify the predicted 1923 bp coding sequence (sense: ATGAGCGCGCATGTATAGATTG GCCAATG; antisense: TCATTTCACCATCATCTTTTAA TCTCAG). The resulting PCR product was cloned into the pTrcHis-TOPO vector (Invitrogen, Carlsbad, CA) according to the manufacturer’s instructions and transformed into E. coli TOP-10F° cells with selection on LB/ampicillin plates at 30°C. The plasmids of transformants were screened by

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**Fig. 7.** ¹H–¹H NOESY spectrum of the native *Comamonas* polysaccharide at pH 6.9; T 328 K. The GlcUA residues are labeled G and the GlcNAc residues are labeled N. The spectrum was recorded at 800 MHz on a Bruker Avance II spectrometer with probe temperature of 328 K. Mixing time 400 ms; delay time 1.5 s; acquisition time 0.852 s.
restriction digest and DNA plasmids positive for the correctly oriented insert were confirmed by sequencing both strands (Oklahoma Medical Research Foundation sequencing facility). Plasmid was then transformed into phage lysin-expressing freeze/thaw lysis E. coli XJa cells according to the manufacturer’s instructions (Zymo Research, Orange, CA). For protein production, cultures of E. coli XJa in Superior Broth (AthenaES, Baltimore, MD) with ampicillin (50 μg/mL), carbenicillin (50 μg/mL) and l-arabinose (3.25 mM final; to induce the lysin enzyme) were grown at 30°C. Expression of target protein was induced by addition of iso-propyl β-d-1-thiogalactopyranoside (0.2 mM final) at OD600 0.35. At 1 h post-induction, growth was supplemented with fructose (12.8 mM final) and growth proceeded for ~16 h before cells were harvested by centrifugation (3000 × g, 30 min at 4°C). The cell pellet was resuspended in 50 mM Tris, pH 7.2, with protease inhibitors pepstatin, benzamidine, N-[N-(l-3-trans-carboxyoxirane-2-carbonyl)-l-leucyl]-agmatine, leupeptin on ice and subjected to two freeze/thaw cycles to allow the phage lysin to degrade the cell walls. The lysates were then clarified by centrifugation (20,000 × g, 30 min at 4°C). Protein content was measured by the Bradford assay with a BSA standard (Thermo Fisher Scientific, Waltham, MA).

GT activity assays
Radiolabeled sugar incorporation assays (25 μL, 30 min at 22°C) were performed using clarified lysates (60 μg total protein) in the presence of 0.05 mM UDP-GlcUA or UDP-GlcNAc as carrier with UDP-[3H]GlcUA or UDP-[3H] GlcNAc (0.1 μCi/assay; NEN Perkin Elmer, Waltham, MA) with various unlabeled UDP-sugars (1 mM) or no second sugar as a negative control. The reaction buffer was 50 mM Tris, pH 7.2, 5 mM MgCl2; these conditions were obtained after limited optimization trials. Certain reactions used acceptors (1 μg) to bypass de novo initiation including HA, heparosan or C. testosteroni polysaccharide (sonicated 10 min on ice to increase the number of termini).

Reactions were incubated at the indicated temperatures for the times noted, and then stopped with 2% final sodium dodecyl sulfate and separated by descending paper chromatography (65:35 ethanol/1 M ammonium acetate buffer, Whatman 3MM paper). This method enables the separation of GAG polysaccharides with greater than ~14 sugar units, which remain at the origin, from smaller oligomers and unincorporated nucleotide sugars that migrate down the strip. The origin of the strip was cut out and subjected to liquid scintillation counting (Biosafe, RPI Corp., Mt Prospect, IL).

Production of synthetic polysaccharide
To produce larger amounts of the polysaccharide synthesized by the recombinant enzyme in vitro, 200 μL reaction mixtures were employed containing 10 mM each of unlabeled UDP-GlcNAc and UDP-GlcUA, 5 mM MgCl2 and 50 mM Tris, pH 7.2, with 40 ng/μL heparosan tetrasaccharide as

Fig. 8. 1H–1H NOESY spectrum of the synthetic Comamonas polysaccharide at pH 3.6; T 328 K. The GlcUA residues are labeled G and the GlcNAc residues are labeled N. The spectrum was recorded at 600 MHz on a Bruker Avance II spectrometer with probe temperature of 328 K. Mixing time 400 ms; delay time 1.5 s; acquisition time 0.852 s.
acceptor at 30°C overnight using clarified lysates (3 mg/mL total protein). Synthetic polysaccharide was purified using the same methods as the native polysaccharide extract following (and including) the final CHCl₃ extraction, ultrafiltration and PD-10 column; the yield was 0.6 mg.

Digestion of native and synthetic polysaccharide with GAG-degrading enzymes

Purified synthetic or native polysaccharide was treated with heparin lyase III from *Pedobacter heparinus* (previously *Flavobacterium heparinum*; kindly supplied by Jian Liu, University of North Carolina; 0.2 mg/mL, 50 mM Tris, pH 7.2, at 30°C) or ovine testicular hyaluronidase (0.4 mg/mL, 30 mM ammonium acetate, pH 5.5, at 30°C) to help characterize the polysaccharide being produced by CtTS. Polysaccharides were analyzed post-treatment with either 6% PAGE (1× TBE) stained with Ailcan Blue (Min and Cowman 1986) or 2% agarose gels [1× tris-acetate-EDTA (TAE)] with Stains-all detection (Lee and Cowman 1994). Nearly mono-disperse HA standards (Hyalose, LLC, Oklahoma City, OK) were used to estimate size (Jing and DeAngelis 2004). As a positive control for complete and specific digestion, we employed internal standards of authentic HA or heparosan as appropriate; the use of GAGs with molecular weights differing from the *C. testosteroni* polysaccharides allowed analysis of the test and standard samples in the same reaction and gel lane.

Acid hydrolysis of Ct native polysaccharide extract

Purified native *Comamonas* polysaccharide was partially fragmented with 1 M HCl at 95°C for 15 min. The resulting hydrolyzed oligosaccharides were then analyzed by either TLC (silica plates with *n*-butanol, acetic acid, H₂O, 2:1:1 and staining by naphthoresorcinol) or MALDI-ToF mass spectrometry. MALDI-ToF mass spectrometry was performed in a reflector negative mode using an Ultraflex II instrument (Bruker Daltonics, Billerica, MA), with the matrix 6-aza-2-thiothymine at a concentration of 5 mg/mL in 50% acetonitrile, 0.1% TFA. HA oligosaccharides were employed as mass calibrants. Spectra were analyzed using mMass 3 (Strohalm et al. 2010).

NMR studies

The native *Comamonas* and synthetic polysaccharides were analyzed by one-dimensional ¹H and two-dimensional COSY, HMQC, TOCSY, NOESY and ge-HMQC-TOCSY experiments to elucidate their structure. All NMR experiments were acquired on Bruker Avance II Ultrasheild 600 MHz (14.1 T) and 800 MHz (18.8 T) NMR instruments equipped with an ultrasensitive HCN cryoprobe with a z-axis gradient. The spectra were mostly acquired at a probe temperature of 298 and 328 K. Polysaccharides (~0.5–1.5 mg) were dissolved in 0.4 mL of 99.996% deuterium oxide (²H₂O; Sigma) and freeze-dried to remove exchangeable protons. The residual water peak served as a reference (HOD, 4.76 ppm); typical silane standards were not employed due to water insolubility or lack of volatility that would interfere with subsequent analyses. The chemical shift of the water peak yields reliable chemical shift values for polysaccharides (Liu Z et al. 2010). For one-dimensional ¹H-NMR spectra, sweep width of 20.5 ppm and acquisition time of 2.65 s were employed. For the ¹H–¹H COSY, ¹H–¹H TOCSY and NOESY spectra, 512 experiments resulting in 4096 data points for a spectral width of 10 ppm were measured. Proton-detected HMQC experiments used 10 and 78 ppm spectral widths in the ¹H dimension and ¹³C dimension, respectively. A mixing time of 400 ms with 1.5 s relaxation delay and a mixing time of 50 ms with 1 s relaxation delay were used in NOESY and ge-HMQC-TOCSY experiments, respectively. The two-dimensional NMR data sets were processed by Topspin version 2.1.4 and cross-peak assignments were carried out using an NMR assignment software Sparky (Goddard and Kneller 2001).

XPS studies

XPS measurements (1 mg sample/test) were carried out in a PHI 5400 instrument (Physical Electronics, Chanhassen, MN) with a 200 W AI Kalphy mono probe beam. The spectrometer was configured to operate at high resolution with pass energy of 117.40 eV.

Supplementary data

Supplementary data for this article is available online at http://glycob.oxfordjournals.org/.

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Conflict of interest statement

None declared.

Abbreviations

CAZy, Carbohydrate-Active enZymes; CDM, chemically defined medium; COSY, COrrelation SpectroscopY; CPC, cetylpyridinium chloride; EDTA, ethylenediaminetetraacetic acid; GAG, glycosaminoglycan; ge, gradient-enhanced; GlcNAc, N-acetyl-glucosamine; GlcUA, glucuronic acid; HA, hyaluronan; HAS, hyaluronan synthase; HMQC, Heteronuclear Multiple-Quantum Coherence experiment; HOD, chemical structure; HS, heparosan synthase; KF, strain...
name; MALDI-ToF, matrix-assisted laser desorption/ionization-time of flight; NMR, nuclear magnetic resonance; NOE, nuclear overhauser effect; NOESY, Nuclear Overhauser Effect Spectroscopy; PAGE, polyacrylamide gel electrophoresis; PBCV, paramaecium bursaria chlorella virus; PCR, polymerase chain reaction; TAE, tri-acetate-EDTA; TBE, tri-borate-EDTA; TFA, trifluoroacetic acid; TLC, thin-layer chromatography; TOCSY, T0tal Correlation Spectroscopy; UDP, uridine diphosphate; XPS, X-ray photoelectron spectroscopy.

References


