

## Note

### Conformational analysis of a disaccharide fragment of the polysaccharide antigen of *Streptococcus pneumoniae* type 1 using n.m.r. spectroscopy and HSEA calculations

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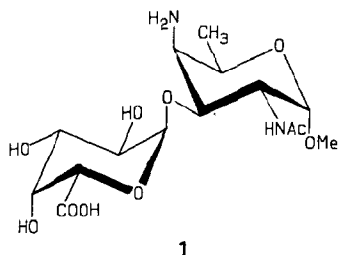
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The capsular polysaccharide of *Streptococcus pneumoniae* type 1 is composed of trisaccharide repeating-units  $\rightarrow 3$ )- $\alpha$ -D-GalpA-(1 $\rightarrow$ 3)- $\alpha$ -Sugp-(1 $\rightarrow$ 4)- $\alpha$ -D-GalpA-(1 $\rightarrow$ , in which Sug denotes 2-acetamido-4-amino-2,4,6-trideoxy-D-galactose<sup>1</sup>, and recently a disaccharide glycoside [ $\alpha$ -D-GalpA-(1 $\rightarrow$ 3)- $\alpha$ -Sugp-OMe (**1**)] related to this structure has been synthesized<sup>2</sup>. We now report on the conformational analysis of **1**, in order to investigate the conformational preferences of such a charged molecule using the simple approach by n.m.r. spectroscopy and HSEA calculations<sup>3,4</sup>.



A <sup>1</sup>H-n.m.r. spectrum for a solution of **1** in D<sub>2</sub>O is shown in Fig. 1A, and the parameters are given in Table I. The assignments, based on a first-order analysis from 1D and 2D spectra, were straightforward. The <sup>13</sup>C-n.m.r. data are given also in Table I, and the assignments were based on comparison with data for model compounds<sup>5</sup>.

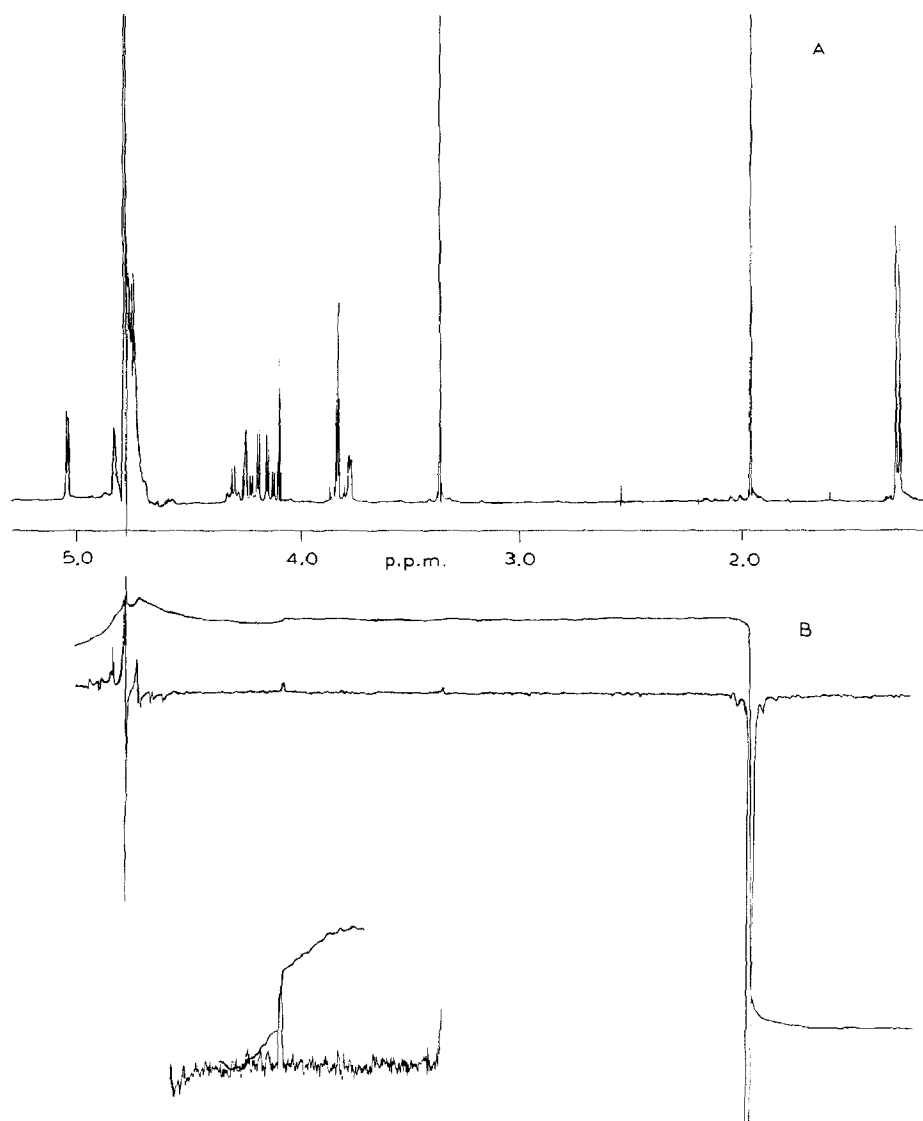


Fig. 1. A,  $^1\text{H}$ -N.m.r. (500 MHz) spectrum of a solution of **1** in  $\text{D}_2\text{O}$  at  $27^\circ$ ; B, difference n.o.e. experiment of **1** showing the result of saturation of the NAc group at 2.00 p.p.m. and the observed enhancement (2.3%) of H-5' at 4.12 p.p.m.

The conformational preference of **1** was assessed by determination of the n.o.e. on saturation of H-1', and enhancements of 5.5, 5.0, and 9.2%, respectively, were observed for the resonances of H-3, H-4, and H-2'. Furthermore, saturation of the NAc methyl group caused an enhancement of 2.3% of the resonance of H-5' (Fig. 1B).

Calculations of the interactions of the two units, using hard-sphere exo-

TABLE I

<sup>1</sup>H-N.M.R. DATA FOR **1**

<sup>1</sup> H- (δ in p.p.m., J in Hz)							
<i>H-1'</i>	<i>H-2'</i>	<i>H-3'</i>	<i>H-4'</i>	<i>H-5'</i>			
5.07	3.88	3.86	4.27	4.12			
3.3	10.2	2.9	1.6				
<i>H-1</i>	<i>H-2</i>	<i>H-3</i>	<i>H-4</i>	<i>H-5</i>	<i>H-6</i>	<i>NAc</i>	<i>OMe</i>
4.78	4.16	4.23	3.82	4.33	1.33	2.00	3.40
3.6	11.2	4.2	1.6	6.6			
<sup>13</sup> C (δ in p.p.m.)							
<i>C-1'</i>	<i>C-2'</i>	<i>C-3'</i>	<i>C-4'</i>	<i>C-5'</i>	<i>C-6'</i>		
98.2	68.5	70.6	71.7	73.6	176.4		
<i>C-1</i>	<i>C-2</i>	<i>C-3</i>	<i>C-4</i>	<i>C-5</i>	<i>C-6</i>	<i>NAc</i>	<i>OMe</i>
99.2	48.8	73.6	53.7	63.6	16.7	175.6	56.6
						23.0	
<i>N.O.e</i>							
<i>Proton saturated</i>			<i>Proton observed</i>			<i>Proton saturated</i>	<i>Observed</i>
<i>Observed n.O.e.</i>							
<i>H-1'</i>			<i>H-3</i>	<i>H-4</i>	<i>H-2'</i>	<i>NAc</i>	<i>H-5'</i>
			5.5%	5.0%	9.2%		2.3%
<i>Calculated n.O.e.</i>							
First-order global minimum			3.1%	4.6%	10.1%		3.1%
Full-matrix global minimum							
$\tau_c \times 10^{-9}$	$\tau_1 \times 10^{-10}$						
0.26	0.26		2.9%	4.5%	10.4%		3.0%
Full-matrix ensemble average							
$\tau_c \times 10^{-9}$	$\tau_1 \times 10^{-10}$	<i>Solvent</i>					
		<i>Relaxation</i>					
0.1	0.1		7.2	13.9	29.7		5.6
0.4	0.4		-1.4	-2.1	-4.4		0.1
0.29	0.29		2.0	3.3	7.0		1.9
0.26	0.26		2.9	4.9	10.4		2.4
0.23	0.23		3.8	6.5	13.9		3.0
0.26	0.26	5%	2.8	4.8	9.4		2.3
0.26	0.26	10%	2.7	4.6	8.5		2.2
0.26	0.26	25%	2.4	4.2	6.8		1.9

anomeric effect (HSEA) calculations<sup>3,4</sup>, gave the  $\phi/\psi$  isoenergy contour map shown in Fig. 2A, with a minimum energy conformation of  $\phi_H$  (*H-1'-C-1'-O-1'-C-3*)/ $\psi_H$  (*C-1'-O-1'-C-3-H-3*) ( $-42^\circ/-32^\circ$ ). The orientation of the NAc group was set as found in X-ray structures with the C-2-H-2 and the C=O bonds eclipsed. HSEA calculations do not include hydrogen atoms (such as OH, NH<sub>2</sub>, or C(OH)), which are in rapid exchange, but it proved to be important to include the coordinate

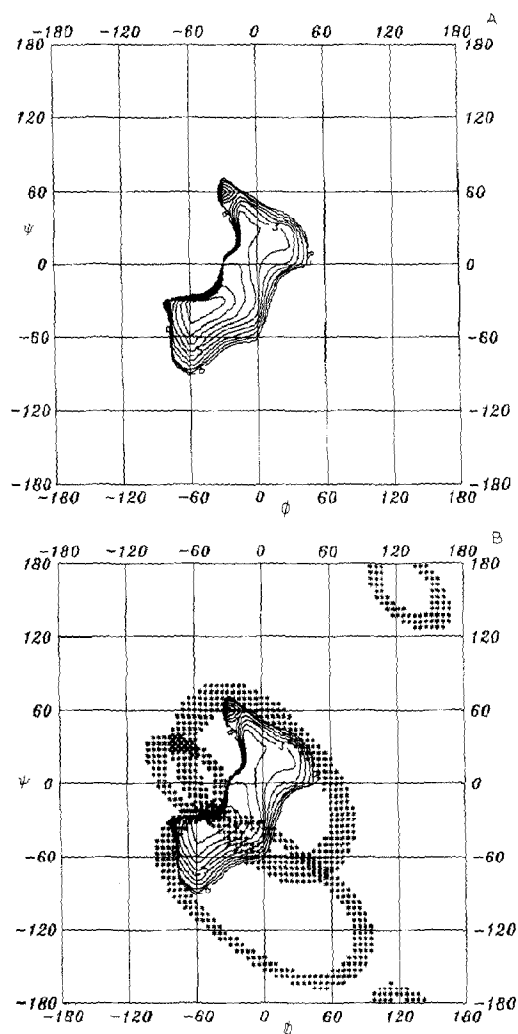


Fig. 2. A, Isoenergy contour diagram for rotation of  $\phi_H$  ( $-180^\circ$  to  $180^\circ$ ) and  $\psi_H$  ( $-180^\circ$  to  $180^\circ$ ) for compound 1; B, as in A but overlaid with the experimentally observed distance constraints from H-1' to H-3 ( $2.45\text{\AA} \pm 0.15$ ), H-1' to H-4 ( $2.45\text{\AA} \pm 0.15$ ), and H-5' to NAc ( $2.85\text{\AA} \pm 0.25$ ).

for the NH proton of the NHAc group in the calculations, in order to obtain a good agreement between the experimental data and the calculated conformational preference.

As discussed earlier<sup>4,6</sup>, the observation of one inter-residue n.O.e. and its assignment to a distance does not unequivocally determine  $\phi_H/\psi_H$ , but rather imposes restraints on the conformational map. This is demonstrated in Fig. 2B, where the experimentally observed n.O.e.s are presented as distance constraints from H-

1' to H-3 ( $2.45\text{\AA} \pm 0.15$ ), H-1' to H-4 ( $2.45\text{\AA} \pm 0.15$ ), and H-5' to NAc ( $2.85\text{\AA} \pm 0.25$ ). Only conformers with  $\phi_{\text{H}} -40^\circ$  to  $-60^\circ$  and  $\psi_{\text{H}} -20^\circ$  to  $-35^\circ$  will fulfill these experimental observations.

However, a more realistic approach to the evaluation of the experimental data is to use the conformational model to calculate the observed n.O.e.s. In Table I are shown the calculated n.O.e.s from the minimum energy conformation described above, using a simpler  $r^{-6}$  dependence<sup>4</sup> or using a full-matrix calculation<sup>7</sup> assuming dipole-dipole relaxation only and isotropic reorientation with correlation times of  $0.1\text{--}0.4 \times 10^{-9}\text{s}$  and  $0.1\text{--}0.4 \times 10^{-10}\text{s}$  for the internal motion of the Me-5 and NAc, respectively, in a three-fold jump model<sup>8</sup>. Furthermore, relaxation contributions from the solvent of 5, 10, and 25% are included in order to evaluate this contribution on the relaxation behaviour. The n.O.e.s are critically dependent on the isotropic correlation time. The agreement is fair, but a better evaluation of the experimental data is expected<sup>9</sup> if the average n.O.e. values are calculated using the whole energy surface (Fig. 2A). Therefore, an ensemble average relaxation matrix was calculated for all conformers in a  $10^\circ$  grid for  $\phi$  and  $\psi$ , starting from the minimum calculated above, and then averaging according to a Boltzmann distribution function at  $27^\circ$  for the respective relative energies. These results (Table I) show that the agreement with the experimental data is better than using a single conformer model, and that the best fit is obtained if a solvent relaxation of 5% is included in the calculations and assuming an isotropic reorientation of  $0.26 \times 10^{-9}\text{s}$ . Thus, it can be demonstrated that the conformational preference of **1** experimentally determined accords with that calculated, even though the charged atoms were treated as neutral spheres with van der Waals radii similar to the neutral atoms.

## EXPERIMENTAL

N.m.r. spectra were recorded with a Bruker AM 500 spectrometer operating at 500 MHz for  $^1\text{H}$  on a 0.1M solution of **1** in  $\text{D}_2\text{O}$  at neutral pH at  $27^\circ$  (internal acetone, 2.22 p.p.m.; DOH at 4.75 p.p.m.). A sweep width of 5000 Hz using 32k of computer memory, giving a digital resolution of 0.3 Hz/point, was used together with pulse angles of  $10\text{ }\mu\text{s}$  ( $60^\circ$ ). COSY experiments were made using Bruker standard software, and the n.O.e. experiments were performed in the difference mode. The  $^{13}\text{C}$ -n.m.r. spectra were recorded at 125.77 MHz at  $27^\circ$  (internal 1,4-dioxane, 67.4 p.p.m.). A sweep width of 25 000 Hz using a computer memory of 64k, giving a digital resolution of 0.8 Hz/point, was used together with a pulse angle of  $5\text{ }\mu\text{s}$  ( $90^\circ = 8.5\text{ }\mu\text{s}$ ).

The HSEA calculations were performed<sup>4</sup> on a IBM PS/2 system model 80 with a 387 math-coprocessor. The calculations of the ensemble average n.O.e.s were performed<sup>9</sup> on a TITAN (Ardent Computer Systems) computer. The coordinates for the  $\alpha$ -D-galacturonic acid residue were taken from the X-ray structure<sup>10</sup> and the protons attached as described<sup>3</sup>. The coordinates for the Sug unit were constructed by bond modification of the X-ray data of 2-acetamido-2-deoxy- $\alpha$ -D-galactose<sup>11</sup>, using the program Alchemy<sup>12</sup>.

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