

## Note

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### Capsular polysaccharide of *Klebsiella* type 30: X-ray diffraction results and idealised chain conformation

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X-ray diffraction patterns have been obtained from oriented films of the sodium salt of *Klebsiella* capsular polysaccharide type 30 (K 30) by using methods similar to those reported previously<sup>1</sup> for *Klebsiella* type 57. The quality of the X-ray diffraction patterns (Fig. 1 shows a typical example) was poorer than that obtained for other

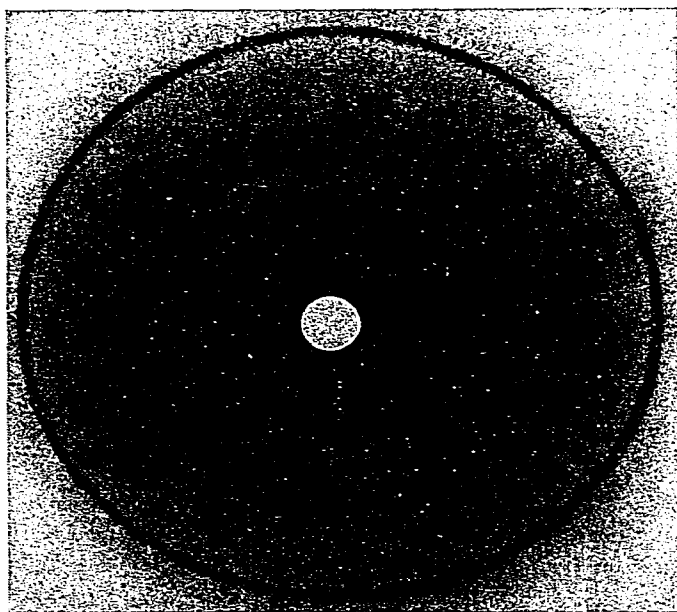


Fig. 1. X-ray diffraction pattern obtained from oriented films of the sodium salt of *Klebsiella* K 30. The chain direction is vertical. The series of meridional reflections (on the vertical bisector) index on a spacing of 1.52 nm, which correlates directly with the trisaccharide backbone-repeat.

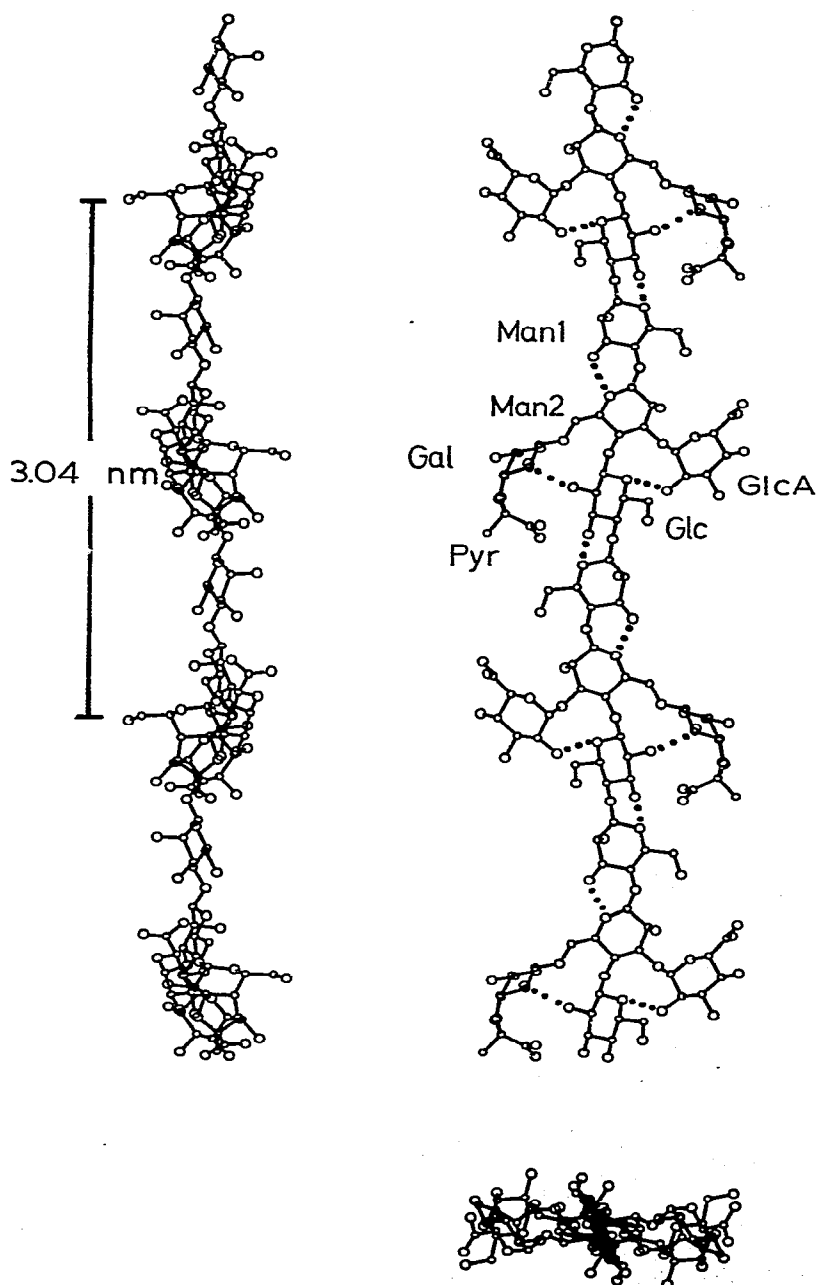


Fig. 2. Computer-drawn projections of the idealized, two-fold, helical model for *Klebsiella* K 30. Intrachain hydrogen-bonds are shown dotted. The incorporation of non-stoichiometric *O*-acetyl groups will upset the true repeat of  $2 \times 1.52 = 3.04$  nm.

*Klebsiella* serotypes<sup>2</sup>, but was sufficient to provide a series of clearly defined, meridional arcs. These arcs relate to repeats along the polysaccharide chain, and index on a one-dimensional lattice with spacing  $1.52 \pm 0.01$  nm.

The chemical structure of *Klebsiella* K 30 is given in the preceding paper by Lindberg *et al.*<sup>3</sup>. The three residues in the backbone, one  $\beta$ -D-glucosyl and two  $\beta$ -D-mannosyl, would be expected to exist in the condensed phase in the normal  ${}^4C_1$  conformation. Thus, all glycosidic linkages in the backbone would be 1,4-diequatorially arranged in common with the simpler homopolymers; namely, cellulose, mannan, and chitin. These polymonosaccharides exist as almost fully extended, helical chains in the condensed phase with an axial advance per saccharide ( $h_s$ ) in the range 0.515–0.505 nm<sup>4–6</sup>. The asymmetric backbone-repeat in K 30 is a trisaccharide, and therefore the value of the average advance per saccharide is  $1.52/3 = 0.507$  nm, which is nearly identical with the reported values of  $h_s$  for the extended two-fold helices, with ribbon-like appearance, of cellulose and mannan. Thus, we assert that the limited X-ray evidence supports a trisaccharide backbone-repeat with all glycosidic linkages disposed 1,4-diequatorial. Furthermore, the torsion angles about each glycosidic bond cannot be too far from that found in the cellulose, mannan, and chitin group of polymonosaccharides. If they were, a decrease in the value of  $h_s$  would be expected, similar to that observed in the three-fold helical structures of (1 $\rightarrow$ 4)-linked  $\beta$ -D-xylan<sup>7</sup> and *Watsonia primidata*<sup>8</sup>, and the five-fold helical structures of xanthan gum<sup>9</sup>. Thus, successive saccharide residues may be imagined to be rotated by 180° about the chain (helix) axis; because there are three different saccharide residues (one mannosyl residue has side-appendages that distinguish it structurally from the other mannosyl residue) in *Klebsiella* K 30, the final result is to produce a two-fold helix, with ribbon-like appearance, as illustrated by the idealized conformation shown in Fig. 2. This two-fold, ribbon-like, helical conformation is expected to occur for the fully extended chain in any 1,4-diequatorially linked polysaccharide containing an odd number of saccharide residues in the chemical repeating-unit for the backbone.

The poor crystallinity, lack of any well-defined layer lines, and very small, inter-chain, interference effects indicate that *Klebsiella* K 30 chains have been captured in an extended conformation, similar to the idealized model in Fig. 2, but with unco-ordinated variations about this "average" conformation. Our inability to crystallize this polysaccharide, using our annealing techniques<sup>10</sup>, indicates that the pentasaccharide repeating-unit<sup>3</sup> is idealized; in fact, Lindberg *et al.*<sup>3</sup> obtained poorly resolved n.m.r. spectra, and suggested that such a repeat only accounts for a proportion of the polymer. Only when the polysaccharide was *O*-deacetylated did the n.m.r. spectrum improve. A non-stoichiometric arrangement of *O*-acetyl groups would impair crystallinity, and would also be expected to perturb the model shown in Fig. 2 in a small, but random, fashion and destroy the precise two-fold nature of the helix. Thus Fig. 2, the atomic co-ordinates of which are given in Table I, should be thought of as the idealized model without *O*-acetyl groups attached.

TABLE I

CARTESIAN CO-ORDINATES OF THE MODEL SHOWN IN FIG. 2

Atom	x (nm)	y (nm)	z (nm)	Atom	x (nm)	y (nm)	z (nm)
<i><math>\beta</math>-D-Mannose (1)</i>				<i><math>\beta</math>-D-Mannose (2)</i>			
C-1	0.0492	-0.0173	-0.1246	C-1	0.0779	-0.0941	-0.6353
C-2	0.1261	0.0663	-0.2261	C-2	0.0710	-0.2059	-0.7385
C-3	0.0748	0.0399	-0.3668	C-3	0.1297	-0.1598	-0.8711
C-4	0.0761	-0.1095	-0.3964	C-4	0.0634	-0.0303	-0.9160
C-5	0.0030	-0.1856	-0.2863	C-5	0.0689	0.0732	-0.8042
C-6	0.0108	-0.3357	-0.3041	C-6	-0.0056	0.2005	-0.8386
O-1	0.1080	0.0000	0.0000	O-1	0.0115	-0.1361	-0.5207
O-2	0.2645	0.0339	-0.2192	O-2	-0.0646	-0.2447	-0.7576
O-3	0.1569	0.1086	-0.4615	O-3	0.1099	-0.2610	-0.9700
O-4	0.0115	-0.1361	-0.5207	O-4	0.1302	0.0227	-1.0303
O-5	0.0612	-0.1556	-0.1585	O-5	0.0085	0.0205	-0.6850
O-6	-0.0471	-0.3775	-0.4277	O-6	0.0481	0.2634	-0.9549
H-1	-0.0569	0.0118	-0.1260	H-1	0.1830	-0.0680	-0.6164
H-2	0.1166	0.1729	-0.2006	H-2	0.1248	-0.2941	-0.7008
H-3	-0.0279	0.0783	-0.3762	H-3	0.2379	-0.1436	-0.8596
H-4	0.1801	0.1447	-0.4026	H-4	-0.0415	-0.0501	-0.9427
H-5	-0.1031	-0.1568	-0.2860	H-5	0.1736	0.0996	-0.7837
<i><math>\beta</math>-D-Glucose</i>				<i><math>\alpha</math>-D-Glucuronic acid (side-group)</i>			
C-1	0.0513	0.0488	-1.1417	C-1	0.2259	-0.3275	-1.0164
C-2	0.1426	0.0886	-1.2569	C-2	0.1954	-0.3878	-1.1529
C-3	0.0625	0.1044	-1.3853	C-3	0.0889	-0.4957	-1.1409
C-4	-0.0195	-0.0211	-1.4122	C-4	0.1294	-0.5989	-1.5564
C-5	-0.1022	-0.0573	-1.2893	C-5	0.1647	-0.5300	-0.9053
C-6	-0.1773	-0.1877	-1.3057	C-6	0.2198	-0.6259	-0.8019
O-1	0.1302	0.0227	-1.0303	O-1	0.1099	-0.2610	-0.9700
O-2	0.2097	0.2097	-1.2241	O-2	0.1532	-0.2847	-1.2414
O-3	0.1514	0.1283	-1.4946	O-3	0.0710	-0.5596	-1.2674
O-4	-0.1080	0.0000	-1.5220	O-4	0.0224	-0.6900	-1.0125
O-5	-0.0167	-0.0724	-1.1749	O-5	0.2650	-0.4312	-0.9277
O-6	-0.2680	-0.1831	-1.4158	O-6a	0.3383	-0.6521	-0.7890
H-1	-0.0223	0.1285	-1.1238	O-6b	0.1275	-0.6800	-0.7250
H-2	0.2197	0.0115	-1.2710	H-1	0.3064	-0.2545	-1.0254
H-3	-0.0048	0.1910	-1.3762	H-2	0.2872	-0.4313	-1.1951
H-4	0.0479	-0.1044	-1.4369	H-3	-0.0068	-0.4498	-1.1120
H-5	-0.1758	0.0221	-1.2699	H-4	0.2104	-0.6556	-1.0726
				H-5	0.0748	-0.4821	-0.8636
<i>3,4-O-(1-Carboxyethylidene)-<math>\beta</math>-D-galactose (side-group)</i>							
C-1	0.0043	0.3925	-0.9813	H-1	0.0272	0.4627	-0.8997
C-2	0.0705	0.4405	-1.1098	H-2	0.0524	0.3674	-1.1900
C-3	0.0151	0.5760	-1.1510	H-3	0.0457	0.6521	-1.0777
C-4	-0.1370	0.5709	-1.1584	H-4	-0.1764	0.6723	-1.1744
C-5	-0.1940	0.5153	-1.0283	H-5	-0.1711	0.5842	-0.9457
C-6	-0.3442	0.4969	-1.0336	C-7	-0.0495	0.5672	-1.3798
O-1	0.0481	0.2634	-0.9549	C-8	-0.0841	0.4366	-1.4504
O-2	0.2113	0.4473	-1.0903	O-8a	0.0168	0.3835	-1.5164
O-3	0.0563	0.5920	-1.2869	O-8b	-0.1942	0.3842	-1.4474
O-4	-0.1584	0.5997	-1.2964	C-9	-0.0434	0.6629	-1.4926
O-5	-0.1372	0.3864	-1.0005	H-9a	-0.1368	0.6574	-1.5504
O-6	0.4118	0.6202	-1.0583	H-9b	-0.0305	0.7649	-1.4535
				H-9c	0.0415	0.6376	-1.5577

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