The Conformations of Oligosaccharides. III. The Crystal and Molecular Structure of Melibiose Monohydrate*

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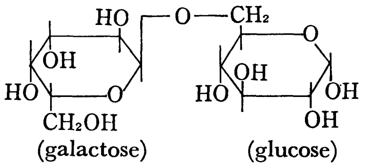
The crystal structure of α-melibiose monohydrate ($C_{12}H_{22}O_{11}\cdot H_2O$) was determined by direct methods using two-dimensional cosine invariants. The space group is $P2_12_12_1$, with $Z=4$ and unit cell dimensions of $a=15.814$ (5), $b=10.924$ (5), $c=8.903$ (4) Å. The structure was refined to $R=0.044$ for 1439 reflections measured with Mo$K\alpha$ radiation. Difference synthesis indicated the partial (15%) random substitution of α-melibiose molecules by the β-anomer. The molecular conformation of α-melibiose is almost the same as that previously found in the melibiose moiety of raffinose, although some of the bond lengths and angles are significantly different. The molecules are linked by complex hydrogen-bond systems which consist of six-link finite chains and five-membered closed loops.

The crystal structure of α-melibiose monohydrate has been determined as a part of a series of reports on the X-ray diffraction of carbohydrates.[1,2] α-Melibiose (*O*-α-D-galactopyranosyl-(1→6)-α-D-glucopyranoside) is the principal disaccharide of the melibiose group. It contains a galactose and a glucose moiety as shown in (I). The first purpose of this investigation was to compare the conformation of the melibiose unit in different intermolecular environments, *i.e.*, in this molecule and in the melibiose moiety of raffinose (Berman 1970).[3] The second purpose was to compare the bond lengths and bond angles common to melibiose and raffinose. The hydrogen bond scheme in the crystal is also of interest.



(I)

Experimental

Crystal Data. $C_{12}H_{22}O_{11}\cdot H_2O$, mol wt=360.3, orthorhombic, $a=15.814$ (5), $b=10.924$ (5), $c=8.903$ (4) Å, $U=1538.0$ Å^3. $D_m=1.54$ g·cm^{-3} (by flotation), $Z=4$, $D_c=1.556$ g·cm^{-3}. Mo$K\alpha$ radiation, $\lambda=0.7107$ Å, μ (Mo$K\alpha$) $=1.32$ cm^{-1}. Space group $P2_12_12_1$ (D_2^4, No. 19).

The crystal was grown by slow evaporation from a saturated aqueous solution of commercially available α-melibiose monohydrate. Unit cell parameters were determined using a standard Philips PW1100 X-ray diffractometer computer program, which investigates rows in the reciprocal lattice through the origin and scans the four highest weighted reflections and their anti-reflections (weighted by intensity and sin θ). The centers of gravity of these eight profiles are then used in a least-squares refinement of the spacing for that row.

Intensity Measurement. A crystal with the dimensions 0.22×0.30×0.18 mm was used to measure the cell parameters and intensities with a Philips PW 1100 four-circle automatic diffractometer. The $\omega/2\theta$ scan method was employed (scan speed 0.03° s^{-1}, scan width $1°+0.3°\times\tan\theta$). The background was measured for 15 s on either side of the peak. Data were collected to a maximum θ of 27.5° with graphite-monochromated Mo$K\alpha$ radiation ($\lambda=0.7107$ Å). Of the 2062 independently measured reflections, 1439 were considered to be observed with $I>2.5\,\sigma(I)$, where $\sigma(I)=[(0.04I)^2+S+TAU^2\times B]^{1/2}$ S=scan count, B=total background count, and TAU=ratio of scan time to total background time. The intensities were corrected for Lorentz and polarization factors but not for absorption.

Structure Determination and Refinement. The structure was determined by a phasing procedure, based on the two-dimensional structure invariants cos ($\phi_1+\phi_2+\phi_3$) whose values were calculated with the following modified triple product formula[4] at an E threshold level of 1.85:

$$\cos(\phi_1+\phi_2+\phi_3)\simeq\frac{K\Psi}{|E_1E_2E_3|}+\frac{R_3}{|E_1E_2E_3|}\qquad(1)$$

where

$$\Psi=\langle(|E_{\vec{k}}|^{1/2}-\overline{|E|^{1/2}})(|E_{\vec{h}_1+\vec{k}}|^{1/2}-\overline{|E|^{1/2}})\times$$
$$(|E_{-\vec{h}_1+\vec{k}}|^{1/2}-\overline{|E|^{1/2}})\,\Big|\,|E_{\vec{k}}|>t\rangle_{\vec{k}},$$
$$\overline{|E|^{1/2}}=\langle|E_{\vec{k}}|^{1/2}\rangle_{\vec{k}},$$
$$\phi_i=\phi_{\vec{h}_i},\ |E_i|=|E_{\vec{h}_i}|,\quad i=1,2,3$$
$$R_3=\frac{\sigma_3}{4\sigma_2^{3/2}}\left[\frac{3}{2}(|E_1E_2|^2+|E_2E_3|^2+|E_3E_1|^2)\right.$$
$$\left.+|E_1|^2+|E_2|^2+|E_3|^2-\frac{7}{2}\right],$$

$h_1+h_2+h_3=0$, and the parameter K is the sliding scale factor. The phasing process was similar to that described by Duax, Weeks and Hauptman (1972).[5] The positions of 24 non-hydrogen atoms were easily located from the E-map and further confirmed by a least-squares refinement. Six cycles of isotropic block-diagonal least-squares refinement followed by two cycles of anisotropic refinement resulted in an R ($=\sum||F_o|-|F_c||/\sum|F_o|$) value of 0.082. A difference map revealed hydrogen atoms attached to all carbon atoms and some of the hydroxyl hydrogen atoms. The electron density (1.22 e·Å^{-3}) of the peak at the position for the hydrogen atom attached to C(1) was about three times that of the other peaks (0.31—0.52 e·Å^{-3}). The second difference map after three cycles of anisotropic refinements, in which hydrogen atoms were included with an isotropic temperature factor, revealed the remaining hydrogen atoms. This map additionally showed a residual electron density of 0.95 e·Å^{-3} near the position assigned to H(Cl), which probably indicates the presence of a small amount of the β-anomer. The β-oxygen atom was located at about 1.38 Å from C(1). A similar example was found in the structure of α-lactose monohydrate (Fries, Rao and Sundaralingam, 1971).[6] Refinement of the carbon, oxygen and hydrogen parameters and of the occupancy factors for αO(1) and βO(1) was completed

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* The papers in *Chem. Lett.*, **1973**, 83 and *Bull. Chem. Soc. Jpn.*, **47**, 1872 (1974) are designated as parts I and II, respectively, of this series.

TABLE 1. FRACTIONAL ATOMIC COORDINATES AND THERMAL PARAMETERS IN MELIBIOSE MONOHYDRATE
The anisotropic temperature factor is of the form of $\exp[-(\beta_{11}h^2+\beta_{22}k^2+\beta_{33}l^2+\beta_{12}hk+\beta_{13}hl+\beta_{23}kl)]$.
Numbers in parentheses refer to standard deviations of the last place.

	$x\times10^4$	$y\times10^4$	$z\times10^4$	$\beta_{11}\times10^4$	$\beta_{22}\times10^4$	$\beta_{33}\times10^4$	$\beta_{12}\times10^4$	$\beta_{13}\times10^4$	$\beta_{23}\times10^4$
C(1)	2398(2)	384(4)	6648(4)	23(1)	83(4)	89(5)	1(4)	4(5)	13(8)
C(2)	2672(2)	−935(4)	6784(4)	24(1)	80(4)	56(4)	−18(4)	15(4)	−2(7)
C(3)	3567(2)	−1082(3)	7376(4)	32(2)	57(3)	55(4)	13(4)	6(4)	−9(7)
C(4)	4186(2)	−230(3)	6600(4)	24(1)	68(3)	58(4)	9(4)	7(4)	−36(7)
C(5)	3829(2)	1068(3)	6589(4)	22(1)	66(3)	59(4)	5(4)	6(4)	−24(7)
C(6)	4380(2)	2009(3)	5860(4)	28(1)	56(3)	88(5)	−9(4)	−11(5)	8(7)
C(1′)	5135(2)	2547(3)	3694(4)	27(1)	35(3)	105(5)	4(4)	7(5)	−2(7)
C(2′)	5058(2)	2492(3)	1983(4)	24(1)	74(3)	94(5)	−20(4)	6(5)	46(7)
C(3′)	5351(2)	1247(3)	1417(4)	37(2)	72(4)	90(5)	−41(4)	2(5)	4(8)
C(4′)	6245(2)	980(3)	2011(4)	38(2)	47(3)	109(5)	9(4)	29(5)	−15(8)
C(5′)	6255(2)	1103(3)	3716(4)	29(1)	44(3)	117(5)	−1(4)	16(5)	31(7)
C(6′)	7130(2)	954(4)	4390(5)	33(2)	78(4)	143(7)	11(5)	2(6)	50(9)
O(1)	2243(2)	828(3)	8069(3)	39(1)	72(3)	80(4)	30(4)	32(4)	−3(6)
O(2)	2089(2)	−1624(2)	7667(3)	33(1)	85(3)	87(3)	−34(3)	26(3)	−15(5)
O(3)	3845(2)	−2307(2)	7222(3)	38(1)	58(2)	113(4)	13(3)	14(4)	6(5)
O(4)	5000(2)	−253(2)	7308(3)	24(1)	83(3)	131(4)	12(3)	−27(4)	−47(6)
O(5)	3022(1)	1065(2)	5848(3)	22(1)	65(2)	77(3)	2(3)	−1(3)	20(5)
O(6)	4550(1)	1730(2)	4324(3)	24(1)	57(2)	71(3)	−21(3)	6(3)	0(5)
O(2′)	4235(2)	2812(3)	1525(3)	27(1)	128(4)	128(4)	0(3)	−15(4)	109(7)
O(3′)	5319(2)	1176(3)	−171(3)	52(1)	131(4)	79(4)	−65(4)	3(4)	−33(6)
O(4′)	6806(2)	1837(3)	1326(3)	30(1)	90(3)	115(4)	−4(3)	23(4)	6(6)
O(5′)	5972(1)	2311(2)	4153(3)	23(1)	59(2)	92(3)	−7(3)	1(3)	4(5)
O(6′)	7096(2)	939(3)	5998(3)	49(1)	123(4)	134(5)	36(4)	−37(5)	18(7)
W	6408(2)	−1477(3)	6203(3)	42(1)	97(3)	111(4)	−4(3)	−20(4)	0(6)
βO(1)	1618(11)	463(16)	6136(19)	3.51(4)[a]					

	$x\times10^3$	$y\times10^3$	$z\times10^3$	B		$x\times10^3$	$y\times10^3$	$z\times10^3$	B
H(C1)	186	53	604	2.4	H(C6′)	749	172	414	3.9
H(C2)	266	−129	583	1.6	H′(C6′)	738	9	401	2.4
H(C3)	358	−87	838	1.4	H(O1)	209	144	799	5.1
H(C4)	426	−49	559	1.4	H(O2)	208	−139	842	2.7
H(C5)	376	123	758	1.6	H(O3)	359	−268	770	4.4
H(C6)	487	206	646	3.8	H(O4)	498	7	−188	5.2
H′(C6)	411	277	590	2.2	H(O2′)	387	239	180	4.9
H(C1′)	501	340	402	1.8	H(O3′)	566	160	−53	5.2
H(C2′)	548	309	158	2.0	H(O4′)	728	157	133	5.6
H(C3′)	494	65	180	3.2	H(O6′)	685	6	610	8.2
H(C4′)	642	14	175	2.5	H(W)	617	−165	539	6.6
H(C5′)	590	48	414	1.8	H′(W)	593	−103	663	6.8

a) Isotropic temperature parameter. The occupancy parameters of O(1) and βO(1) are 0.848 and 0.152, respectively.

by the full matrix least-squares program. The total of the occupancy parameters was constrained to unity through the refinement. The function minimized was $\sum w(|F_o|-k\times|F_c|)^2$, where $w=1/\sigma(F)^2$. The final cycle gave an R value of 0.044 for all reflections. The occupancy parameter of αO(1) was 0.848 and that of βO(1) was 0.152. The atomic scattering factors used were those of the International Tables for X-ray Crystallography[7] and for the hydrogen atoms, those of Stewart, Davidson, and Simpson (1965).[8] The final positional and thermal parameters are given in Table 1; corresponding structure factors are listed in Table 2.**

Discussion

The molecular conformation of melibiose monohydrate is shown in Fig. 1, where the atomic numbering of the galactose moiety is primed.

Bond Lengths and Angles. The bond lengths and angles involving carbon and oxygen atoms are shown in Fig. 2, excluding those involving the βO (1) atom. The standard deviations are 0.004—0.005 Å for C–C and C–O bonds and 0.3° for the valence bond angles. E.s.d's for the C–H and O–H distances are 0.03—0.04 Å. The C(1)–βO(1) length is 1.32 Å. The C(2)–C(1)–βO(1) and O(5)–C(1)–βO(1) angles are 110.0° and 116.2°, respectively. The C(5)–C(6) bond length of the (1→6) linkage is 1.496 Å, which is rather short for a

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** Table 2 has been submitted to, and is kept by the office of the Chemical Society of Japan, 5, 1-Chome, Kanda-Surugadai, Chiyoda-ku, Tokyo 101. (Document No. 7614).

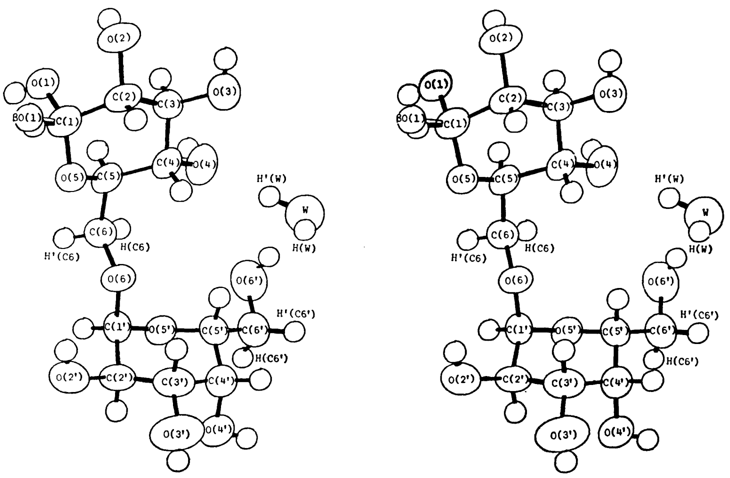

Fig. 1. Molecular conformation and atomic numbering in melibiose monohydrate. The 74% probability thermal ellipsoids are shown for the carbon and oxygen atoms.

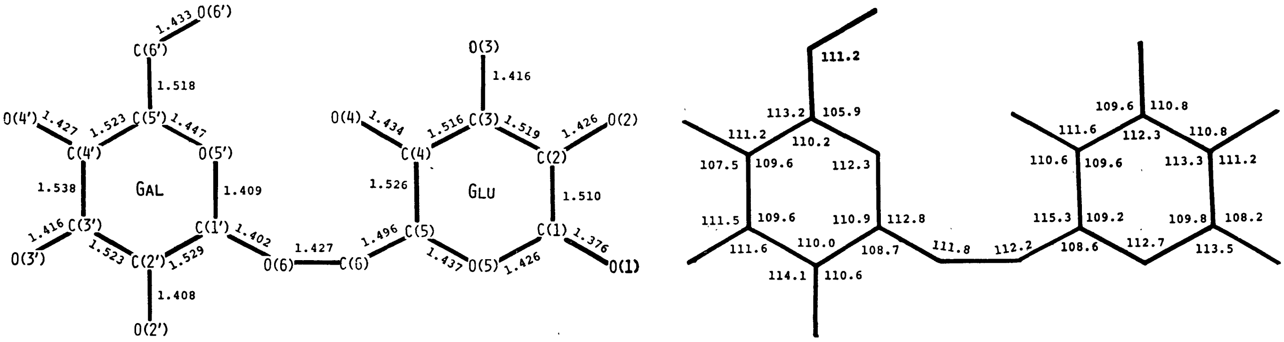

Fig. 2. Bond lengths (l/Å) and bond angles (ϕ/°).

Table 3. Comparison of C–O bond lengths for hemi-acetal groups in di- and trisaccharides

Compound	Pyranose ring	Configuration of C(1)-O(1) bond	C(5) — O(5) — C(1)—O(1)—R				References
α-Melibiose	Glu[a]	axial	1.437Å	1.426Å	1.376Å	H	this work
	Gal[b]	axial	1.447	1.402	1.402	$C_6H_{11}O_5$	
β-Lactose	Gal	equatorial	1.440	1.413	1.402	$C_6H_{11}O_5$	2
	Glu	equatorial	1.436	1.431	1.388	H	
α-Lactose	Gal	equatorial	1.448	1.427	1.389	$C_6H_{11}O_5$	6
	Glu	axial	1.425	1.443	1.387	H	
β-Cellobiose	Glu	equatorial	1.436	1.425	1.397	$C_6H_{11}O_5$	10
	Glu	equatorial	1.437	1.435	1.381	H	
Methyl β-cellobioside	Glu	equatorial	1.430	1.432	1.390	$C_6H_{11}O_5$	11
	Glu	equatorial	1.432	1.434	1.379	CH_3	
Trehalose	Glu	axial	1.433	1.421	1.415	$C_6H_{11}O_5$	14
	Glu	axial	1.431	1.404	1.422	$C_6H_{11}O_5$	
Methyl β-mal Topyranoside	Glu	axial	1.440	1.408	1.416	$C_7H_{13}O_5$	15
	Glu	equatorial	1.430	1.427	1.375	$C_6H_{11}O_5$	
Sucrose (X-ray)	Glu	axial	1.443	1.413	1.428	$C_6H_{11}O_5$	16, 17
(Neutron)			1.439	1.411	1.422		
Isomaltulose	Glu	axial	1.430	1.427	1.397	$C_6H_{11}O_5$	18
Melezitose	Glu	axial	1.435	1.405	1.424	$C_{12}H_{21}O_{10}$	1
	Glu	axial	1.436	1.419	1.415	$C_{12}H_{21}O_{10}$	
Planteose	Glu	axial	1.430	1.416	1.415	$C_{12}H_{21}O_{10}$	9
	Gal	axial	1.444	1.418	1.414	$C_{12}H_{21}O_{10}$	
Raffinose	Glu	axial	1.433	1.419	1.402	$C_6H_{11}O_5$	3
	Gal	axial	1.436	1.422	1.428	$C_{12}H_{21}O_{10}$	
1-Kestose	Glu	axial	1.441	1.410	1.417	$C_{12}H_{21}O_{10}$	19

a) Glu=glucopyranose ring. b) Gal=galactopyranose ring.

Table 4. Important torsion angles in the glucose and galactose moieties

	Glucose moiety		Galactose moiety	
Intracyclic torsion angles	C(1)–C(2)	50.4°	C(1′)–C(2′)	57.3°
	C(2)–C(3)	−46.3	C(2′)–C(3′)	−53.8
	C(3)–C(4)	49.1	C(3′)–C(4′)	54.3
	C(4)–C(5)	−57.7	C(4′)–C(5′)	−57.1
	C(5)–O(5)	65.6	C(5′)–O(5′)	61.6
	O(5)–C(1)	−61.0	O(5′)–C(1′)	−61.3
Extracyclic torsion angles	O(1)–C(1)–C(2)–O(2)	51.6°	O(6)–C(1′)–C(2′)–O(2′)	59.7°
	O(2)–C(2)–C(3)–O(3)	64.9	O(2′)–C(2′)–C(3′)–O(3′)	57.3
	O(3)–C(3)–C(4)–O(4)	−64.5	O(3′)–C(3′)–C(4′)–O(4′)	57.4
	O(4)–C(4)–C(5)–C(6)	56.3	O(4′)–C(4′)–C(5′)–C(6′)	−56.8
			O(5′)–C(5′)–C(6′)–O(6′)	65.6
			C(4′)–C(5′)–C(6′)–O(6′)	−173.5

C–C single bond. In planteose[9] also, the C(5)–C(6) bond of the (1→6) linkage is 1.494 Å. However, the corresponding bond in raffinose[3] is not markedly short (1.520 Å). A slight shortening of the exocyclic C(5)–C(6) bond has been observed in many carbohydrate structures.[2,6,10–12]

The C(1)–O(1) and C(1′)–O(6) bond lengths of melibiose are rather short. This shortening effect in the anomeric positions has been generally observed in oligosaccharides[13] and investigated theoretically.[14,15] The C–O bonds in both pyranoside rings show the same type of systematic disproportion. The C(1′)–O(5′) and C(5′)–O(5′) bond lengths in the galactose moiety are 1.409 and 1.447 Å, respectively, the latter bond being longer than the former by about 9σ. The same trend is observed in glucose moiety. The ring C–O and anomeric C–O bond lengths for the hemi-acetal group in di- and trisaccharides which contain glucose or galactose moiety are listed in Table 3. When R (the substituent at O(1)) is H or CH$_3$, the C(1)–O(1) lengths are markedly short. Systematic disproportion is not observed in ring C–O distances. When R is a pyranosyl group and O(1) is in an equatorial position, the mean distance of the C(1)–O(1) bonds is 1.391 Å. When O(1) is in an axial position, the corresponding mean distance is 1.416 Å, which is slightly longer than that of the axial C(1)–O(1) bond. The systematic disproportion, C(5)–O(5)>O(5)–C(1), is distinctly observed in both α- and β-pyranosides, excluding methyl β-cellobioside and isomultulose. The mean distances of C(5)–O(5) and O(5)–C(1) are 1.438 and 1.415 Å, respectively. There is a correlation between C(1)–O(1) and the ring C–O lengths of di- and trisaccharides given in Table 3. The difference between the C(5)–O(5) and O(5)–C(1) bond lengths becomes small with a shortening of the C(1)–O(1) bond. The difference becomes large with a lengthening of the C(1)–O(1) bond to the normal C–O single bond length.

The valence angles shown in Fig. 2 are not remarkable. The C(5)–C(6)–O(6) angle is 112.2°, which is larger by 4.2° than the corresponding angle in raffinose. The C(1′)–O(6)–C(6) angle is 111.8°

Molecular Conformation. The conformational angles in the pyranose rings are listed in Table 4. The torsion angles of the galactose moiety range from 53.8° to 61.6° with an average value of 57.6°. Those of the glucose moiety range more widely from 46.3° to 65.6° with an average value of 55.0°. The corresponding angles in the melibiose moiety of raffinose range from 52.7° to 59.5° and from 53.8° to 62.2° for the glucose and galactose moieties, respectively. The torsion angles around the ring C–O bonds are the largest, while those around C(2)–C(3), C(3)–C(4), C(2′)–C(3′), and C(3′)–C(4′), which are at the positions opposite to the ring C–O bonds, are the smallest. In the glucose moiety of melibiose, this trend is distinct. The difference between the torsion angles C(1)–C(2)–C(3)–C(4) and C(2)–C(3)–C(4)–C(5) is −95.4°, while the difference between the torsion angles C(4)–C(5)–O(5)–C(1) and C(5)–O(5)–C(1)–C(2) is 126.6°. This indicates smaller puckering in the region of C(3) and larger puckering in the region of O(5). Also, in the exocyclic torsion angles, those of the glucose moiety range more widely than those of the galactose moiety.

The conformation of the C(5′)–C(6′) bond of the galactose moiety is *plus synclinal,* while that of the corresponding bond of raffinose is *antiperiplanar.* From intramolecular interactions, these two conformations seem to be equally preferable, while *minus synclinal* conformation should be unfavorable because this conformation would have short O(6′)···O(4′) intramolecular contact.

Table 5. A comparison of the torsion angles of the (1→6) linkage in melibiose and raffinose

	Melibiose	Raffinose
O(5)–C(5)–C(6)–O(6)	−63.3°	−64.8°
C(4)–C(5)–C(6)–O(6)	59.6	58.4
C(5)–C(6)–O(6)–C(1′)	−173.9	−169.5
C(6)–O(6)–C(1′)–C(2′)	−160.5	−167.6
C(6)–O(6)–C(1′)–O(5′)	76.1	71.9

The conformation around the (1→6) linkage is of interest in that it determines the overall molecular form, and gives basic data which can be used to construct a model of macromolecular polysaccharides with a (1→6) linkage. The torsion angles around the (1→6) linkage in melibiose and raffinose are listed in Table 5. The conformations around the bridge bond of these two compounds are almost the same. The C(1′)–O(6) conformation is *plus synclinal,* the C(6)–O(6) conforma-

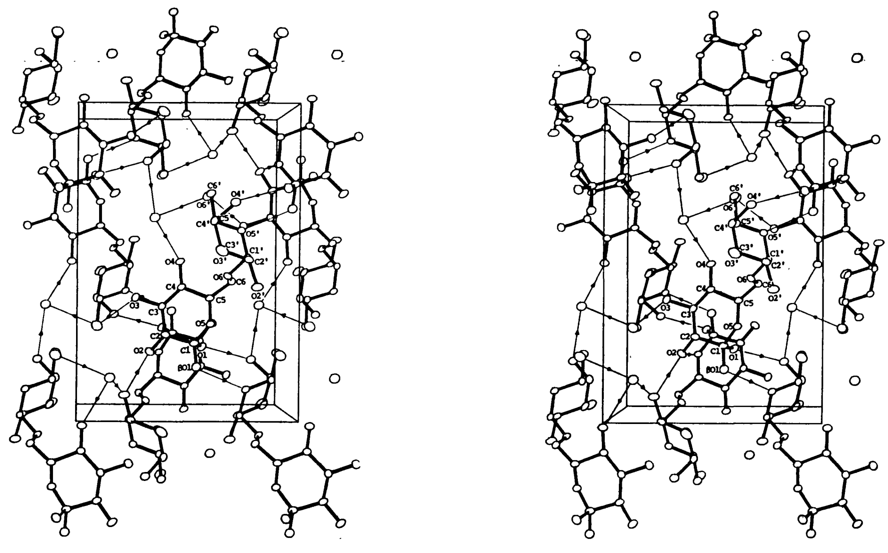

Fig. 3. Stereogram of melibiose monohydrate viewed down the c axis showing the packing and the hydrogen bonding scheme including that of the disordered oxygen atom βO(1).

Table 6. Hydrogen bonding

i	j	k	l	j-l	j-k	i-j-l	j-k-l	Symmetry code of l
C(1)	O(1)	H(O1)	O(4′)	2.697 Å	0.71 Å	124.2°	156°	(h)
C(2)	O(2)	H(O2)	O(5)	2.902	0.72	117.8	167	(d)
C(3)	O(3)	H(O3)	O(6′)	2.898	0.72	114.4	172	(l)
C(4)	O(4)	H(O4)	O(3′)	2.780	0.82	120.5	161	(b)
C(2′)	O(2′)	H(O2′)	O(2)	2.666	0.78	119.6	169	(f)
C(3′)	O(3′)	H(O3′)	O(3)	2.797	0.79	127.1	154	(i)
C(4′)	O(4′)	H(O4′)	W	2.854	0.81	122.7	162	(e)
C(6′)	O(6′)	H(O6′)	W	2.861	1.04	95.1	178	(a)
	W	H(W)	O(2′)	2.745	0.84		172	(k)
	W	H′(W)	O(4)	2.777	0.97		176	(a)
C(1)	βO(1)		O(5′)	2.683		118.4		(h)

Symmetry code

The letters refer to the symmetry operations to be applied to the coordinates listed in Table 1.

(a)	x,	y,	z	(g)	$-1/2+x$,	$1/2-y$,	$-z$
(b)	x,	y,	$1+z$	(h)	$-1/2+x$,	$1/2-y$,	$1-z$
(c)	x,	y,	$-1+z$	(i)	$1-x$,	$1/2+y$,	$1/2-z$
(d)	$1/2-x$,	$-y$,	$1/2+z$	(j)	$1-x$,	$1/2+y$,	$3/2-z$
(e)	$3/2-x$,	$-y$,	$-1/2+z$	(k)	$1-x$,	$-1/2+y$,	$1/2-z$
(f)	$1/2-x$,	$-y$,	$-1/2+z$	(l)	$1-x$,	$-1/2+y$,	$3/2-z$

tion is *antiperiplanar*, and the C(5)–C(6) conformation is *minus synclinal*. C(5), C(6), O(6), and C(1′) in melibiose are coplanar to within 0.04 Å. The same conformation of the (1→6) linkage is maintained in these two compounds in different intermolecular environments.

Hydrogen Bonding. The arrangement of the molecules in the structure is shown in Fig. 3. The molecules are linked by the complex system of hydrogen bonds given in Table 6. There are two major hydrogen bond sequences. One comprises a six-link finite chain:

$$\begin{array}{cccccc} O(1) \longrightarrow & O(4') \longrightarrow & W \longrightarrow & O(2') \longrightarrow & O(2) \longrightarrow & O(5) \\ (c) & (g) & (i) & (a) & (f) & (a) \end{array}$$

where → indicates the donor direction and the small letters refer to the symmetry codes given in Table 6. The other system consists of a five-membered closed loop:

$$\begin{tikzcd} \underset{(a)}{O(4)} \arrow[r] & \underset{(b)}{O(3')} \arrow[r] & \underset{(j)}{O(3)} \arrow[d] \\ \underset{(a)}{W} \arrow[u] & & \underset{(a)}{O(6')} \arrow[ll] \end{tikzcd}$$

As shown in Table 6, the separation between βO(1) and O(5′) (2.683 Å) corresponds to the hydrogen bond distances. When the α-anomer in the crystalline melibiose is replaced by a β-anomer, the hydrogen bond, O(1)···O(4′), is missing, but there appears to be one compensating hydrogen bond between βO(1) and O(5′). Thus, the β-anomer can easily be accomodated in the crystal.

Each hydroxyl group except O(1)–H participates in two hydrogen bonds, in one as a donor and in the other as an acceptor. O(1)–H serves only as a donor. A water molecule serves as a donor for two hydrogen bonds and an acceptor for two others. The ring oxygen O(5) takes part in hydrogen bonds as an acceptor. About 15% of the O(5′) atoms should be hydrogen bond acceptors. The glycosidic linkage oxygen atom is not involved in hydrogen bonds, just as in all crystal structures of di- and trisaccharides. There are no intramolecular hydrogen bonds.

Computer Programs

All calculations were performed on a FACOM 270/30 computer at the Computer Center of Osaka City University using the following programs: RSSFR-3,[20) HBLS-IV,[20) RSFLS-4,[20) MTPF (calculation of cosine invariants),[21) PHASE III (tangent refinement),[22) BOND (molecular dimensions),[23) and TECS (stereoscopic drawing of crystal and molecular structures).[24)

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