The Structure of the Cyclodextrin Complex. X. Crystal Structure of α-Cyclodextrin–Benzaldehyde (1 : 1) Complex Hexahyderate

Kazuaki HARATA,* Kaneto UEKAMA,† Masaki OTAGIRI,†
Fumitoshi HIRAYAMA,† and Hisashi OGINO††

Research Institute for Polymers and Textiles, 1-1-4, Yatabe-Higashi, Tsukuba, Ibaraki 305

† *Faculty of Pharmaceutical Sciences, Kumamoto University, 5-1, Oe-honmachi, Kumamoto 862*

†† *Kaken Chemical Co., Ltd., Honkomagome, Bunkyo-ku, Tokyo 113*

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The crystal structure of the α-cyclodextrin–benzaldehyde (1:1) complex hexahydrate, $C_{36}H_{60}O_{30}\cdot C_7H_6O\cdot 6H_2O$, was determined by the X-ray method. The crystal is monoclinic, the space group being $P2_1$ with $Z=2$. The cell dimensions are $a=7.932(1)$, $b=13.500(1)$, $c=24.704(2)$ Å, and $\beta=90.85(1)°$. The structure was solved by means of a Patterson map and a trial-and-error method combined with the rigid-body least-squares technique. Refinement was carried out by the block-diagonal least-squares method to the final R-value of 0.057 for 4565 reflections. α-Cyclodextrin molecules are stacked along the a axis in a head-to-tail fashion to form a channel-type structure. The α-cyclodextrin ring is tilted by an angle of 11.5° against the channel axis. Adjacent α-cyclodextrin molecules along the channel are linked by hydrogen bonds between the primary hydroxyl groups and the secondary hydroxyl groups, and O(2)···water···O(6) hydrogen-bond bridges. The guest benzaldehyde molecules are aligned inside the α-cyclodextrin column. The benzene ring is inserted into the α-cyclodextrin ring from the secondary hydroxyl side, while the carbonyl group is in the van der Waals contact with the primary hydroxyl side of the next α-cyclodextrin. The guest plane is nearly parallel to the channel axis, making an angle of 71.2° against the plane through six glycosidic oxygen atoms. Spaces between α-cyclodextrin columns are filled with water molecules. Many hydrogen bonds are observed among hydroxyl groups of α-cyclodextrin and water molecules, forming a hydrogen-bond network in the crystal.

Interaction of cyclodextrins with drugs has received considerable attention because the complexation may increase their solubility and chemical stability.[1] It was recently found that the photolysis and oxidation of benzaldehyde are significantly retarded by cyclodextrins,[2] several crystal structures of α-cyclodextrin complexes with benzene derivatives having been investigated by the X-ray method.[3–6] In this paper, the crystal structure of the benzaldehyde complex is discussed.

Experimental

α-Cyclodextrin and benzaldehyde in a 1:1 molar ratio were dissolved in degassed water at 80 °C. The solution was sealed under nitrogen and then cooled slowly to room temperature, colorless plate-like crystals being obtained. Experiments were carried out in the dark to avoid photolysis and oxidation of benzaldehyde. Measurements of lattice parameters and intensities were carried out on a Rigaku automatic four-circle diffractometer with graphite monochromated Cu $K\alpha$ radiation; 4565 independent reflections with $|F_o|>3\sigma(F)$ were collected up to 150° in 2θ by a θ-2θ scan technique. No corrections were made for absorption and extinction.

Crystal Data: $C_{36}H_{60}O_{30}\cdot C_7H_6O\cdot 6H_2O$, $F.W.=1187.1$, monoclinic, space group $P2_1$, $Z=2$, $a=7.932(1)$, $b=13.500(1)$, $c=24.704(2)$ Å, $\beta=90.85(1)°$, $V=2645.1$ Å^3, $D_x=1.490$, $D_m=1.495$ g·cm^{-3}.

Determination and Refinement of the Structure

The orientation of the α-cyclodextrin molecule in the crystal was easily deduced by inspection of a Patterson map. The position of the molecule was determined by the trial-and-error method. The positional and orientational parameters of each glucose residue were corrected by the rigid-body least-squares method. Benzaldehyde and water molecules were found on Fourier and difference-Fourier maps. A primary hydroxyl group (O(6,G1)) of α-cyclodextrin and a water molecule (W2) were statistically disordered. Their occupancy was estimated from an electron-density map, but the results were not refined. Seventy-three hydrogen atoms were found on a difference-Fourier map. The refinement of the structure was carried out by the block-diagonal least-squares method. The quantity minimized was $\Sigma w(|F_o|-|F_c|)^2$, with $w=1.0$ for all the reflections, the final R-value being 0.057. The atomic scattering factors were taken from "International Tables for X-Ray Crystallography."[7] The atomic coordinates are given in Table 1. Tables of anisotropic temperature factors of non-hydrogen atoms, atomic parameters of hydrogen atoms, observed and calculated structure factors, bond distances, angles, and conformation angles in α-cyclodextrin are kept at The Chemical Society of Japan (Document No. 8135).

Description of the Structure and Discussion

Outline of the Structure. The structure and numbering scheme of the complex are shown in Fig. 1, the atom numbering for α-cyclodextrin being the same as that used in the *m*-nitroaniline complex.[6] The α-cyclodextrin molecule is in the shape of a distorted hexagon, and is stacked along the a axis in the head-to-tail mode to form a typical channel-type structure (Fig. 2). The guest benzaldehyde molecule is linearly arranged in the channel, being fixed by the van der Waals force.

Table 1. Final atomic coordinates($\times 10^4$) and B_{eq}[a] (B/Å^2) of non-hydrogen atoms[b]

	x	y	z	B_{eq}/Å^2		x	y	z	B_{eq}/Å^2
C (1, G1)	−255 (8)	4863 (-)	1074 (2)	3.38	O (3, G4)	−755 (5)	11841 (4)	2788 (2)	3, 56
C (2, G1)	−1766 (7)	4418 (4)	1360 (2)	3.14	O (4, G4)	1591 (5)	10714 (3)	2212 (1)	2.78
C (3, G1)	−1781 (7)	4754 (5)	1943 (2)	2.88	O (5, G4)	3505 (4)	10793 (3)	3574 (2)	3.12
C (4, G1)	−99 (6)	4517 (4)	2227 (2)	2.64	O (6, G4)	5735 (5)	11444 (5)	2785 (2)	5.13
C (5, G1)	1313 (7)	5014 (5)	1908 (2)	3.26	C (1, G5)	1167 (7)	7134 (5)	4668 (2)	2.89
C (6, G1)	3057 (8)	4753 (7)	2131 (2)	4.74	C (2, G5)	−122 (7)	7898 (5)	4857 (2)	3.05
O (2, G1)	−3285 (5)	4696 (4)	1086 (2)	4.12	C (3, G5)	−202 (7)	8752 (4)	4458 (2)	2.67
O (3, G1)	−3088 (5)	4231 (4)	2220 (2)	3.82	C (4, G5)	1550 (6)	9178 (4)	4360 (2)	2.54
O (4, G1)	−195 (4)	4933 (3)	2753 (1)	2.66	C (5, G5)	2827 (7)	8356 (5)	4238 (2)	2.41
O (5, G1)	1248 (5)	4634 (4)	1360 (2)	3.70	C (6, G5)	4658 (8)	8698 (5)	4210 (1)	3.94
O (6A, G1)	3338 (12)	3665 (9)	2140 (6)	6.96	O (2, G5)	−1731 (5)	7402 (3)	4872 (2)	4.01
O (6B, G1)	4189 (11)	5503 (11)	1913 (5)	6.63	O (3, G5)	−1211 (5)	9556 (3)	4648 (2)	3.72
C (1, G2)	1222 (7)	8382 (5)	295 (2)	3.36	O (4, G5)	1363 (4)	9782 (3)	3885 (1)	2.61
C (2, G2)	−454 (7)	7997 (5)	61 (2)	3.23	O (5, G5)	2775 (5)	7601 (3)	4641 (2)	3.02
C (3, G2)	−1128 (7)	7177 (5)	417 (2)	3.32	O (6, G5)	5208 (5)	9167 (4)	4678 (2)	4.68
C (4, G2)	168 (7)	6399 (5)	558 (2)	3.13	C (1, G6)	192 (7)	4316 (4)	3198 (2)	2.72
C (5, G2)	1943 (7)	6829 (5)	696 (2)	3.07	C (2, G6)	−1178 (6)	4458 (4)	3623 (2)	2.73
C (6, G2)	3336 (8)	6072 (6)	636 (3)	4.40	C (3, G6)	−1101 (6)	5500 (5)	3845 (2)	2.86
O (2, G2)	−1594 (6)	8806 (4)	17 (2)	4.24	C (4, G6)	679 (6)	5762 (4)	4040 (2)	2.47
O (3, G2)	−2519 (6)	6741 (4)	126 (2)	5.00	C (5, G6)	1920 (6)	5573 (4)	3588 (2)	2.61
O (4, G2)	−496 (5)	5898 (3)	1025 (2)	3.12	C (6, G6)	3764 (6)	5759 (5)	3738 (2)	3.31
O (5, G2)	2375 (5)	7606 (3)	329 (2)	3.39	O (2, G6)	−2787 (5)	4272 (3)	3374 (2)	3.35
O (6, G2)	4852 (5)	6426 (4)	884 (2)	5.15	O (3, G6)	−2243 (4)	5560 (3)	4295 (2)	3.36
C (1, G3)	2173 (7)	11225 (5)	1754 (2)	3.24	O (4, G6)	631 (4)	6798 (3)	4157 (1)	2.36
C (2, G3)	696 (8)	11355 (5)	1355 (2)	4, 03	O (5, G6)	1807 (4)	4554 (3)	3423 (2)	2.81
C (3, G3)	72 (7)	10348 (5)	1161 (2)	3.58	O (6, G6)	4214 (5)	5188 (4)	4194 (2)	4.19
C (4, G3)	1526 (7)	9768 (4)	921 (2)	2.84	C (1, BA)	−3464 (10)	7678 (6)	2464 (2)	5.38
C (5, G3)	2996 (7)	9705 (5)	1326 (2)	3.22	C (2, BA)	−2535 (13)	7891 (9)	2950 (3)	8.36
C (6, G3)	4584 (8)	9247 (6)	1081 (3)	4.60	C (3, BA)	−812 (13)	8043 (7)	2923 (4)	9.79
O (2, G3)	−586 (6)	11928 (4)	1601 (2)	5.37	C (4, BA)	−96 (11)	8007 (9)	2436 (4)	7.51
O (3, G3)	−1186 (6)	10519 (4)	749 (2)	4.97	C (5, BA)	−961 (12)	7822 (8)	1974 (7)	6.97
O (4, G3)	890 (5)	8802 (3)	806 (1)	3.14	C (6, BA)	−2637 (10)	7628 (7)	1989 (3)	5.68
O (5, G3)	3478 (5)	10675 (3)	1502 (2)	3.37	C (7, BA)	−5337 (15)	7511 (12)	2433 (6)	11.53
O (6, G3)	4976 (7)	9725 (5)	588 (2)	6.43	O (1, BA)	−6114 (10)	7653 (10)	2872 (4)	14.26
C (1, G4)	2037 (7)	10752 (5)	3883 (2)	3.09	O (W1)	5591 (10)	2476 (7)	1885 (3)	10.14
C (2, G4)	676 (8)	11422 (5)	3636 (2)	3.34	O (W2A)	5162 (9)	8564 (6)	−364 (3)	4.33
C (3, G4)	344 (7)	11131 (4)	3046 (2)	2.87	O (W2B)	6029 (16)	8378 (10)	−873 (5)	5.16
C (4, G4)	1997 (6)	11116 (4)	2731 (2)	2.56	O (W3)	6020 (8)	11803 (5)	823 (3)	7.51
C (5, G4)	3287 (7)	10456 (5)	3019 (2)	3.04	O (W4)	6256 (6)	12450 (4)	3756 (2)	4.84
C (6, G4)	5028 (7)	10476 (6)	2774 (3)	4.46	O (W5)	5192 (14)	11258 (9)	4717 (4)	14.70
O (2, G4)	−826 (6)	11347 (4)	3946 (2)	4.29	O (W6)	6388 (8)	8179 (4)	5649 (2)	6.62

a) $B_{eq}=8\pi^2(U_1+U_2+U_3)/3$ where U_1, U_2, and U_3 are the principal components of U matrix. b) The occupancy factors for O(6A, G1), O(6B, G1), O(W2A), and O(W2B) are 0.5, 0.5, 0.6, and 0.4, respectively.

Conformation of α-Cyclodextrin. Average bond distances and angles in six glucose residues are shown in Fig. 3. The C–C bond distances are in the range 1.518—1.533 Å. The C(1)–C(2) and C(4)–C(5) bonds are somewhat longer than the C(2)–C(3) and C(3)–C(4) bonds. The anomeric C–O bonds (1.411 and 1.414 Å) are shorter than the other C–O bonds (1.421—1.437 Å). The C(3)–C(4)–O(4) and C(6)–C(5)–O(5) angles are relatively small, the C(4)–C(5)–C(6) angle (113.7°) being large. The same tendency has been observed in the uncomplexed α-cyclodextrin and in the α-cyclodextrin complexes with some other guests.[3,8] The larger C(4)–C(5)–C(6) angle may be ascribed to the repulsive interaction between the C(6) methylene group and the adjacent glucose residue. The C(4)–O(4)–C(1′) glycosidic oxygen angles are in the range 117.7—119.7° in good agreement with those of other α-cyclodextrin complexes.[3-6,8] Except for the G1 and G2 residues, the primary hydroxyl group is in the *gauche-gauche* conformation. The G2 residue has the hydroxyl group with the *gauche-trans* conformation, the primary hydroxyl group of the G1 residue being statistically disordered showing the *gauche-gauche* and *gauche-trans* conformations for O(6A,G1) and O(6B,G1), respectively (Fig. 1).

The hexagonal α-cyclodextrin ring is elliptically distorted owing to the inclusion of the planar molecule, as seen from the diagonal distances measured between

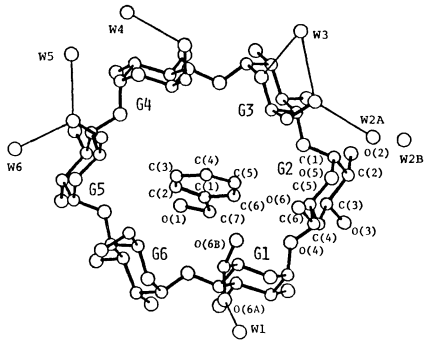

Fig. 1. Structure and numbering scheme of the α-cyclodextrin–benzaldehyde complex hexahydrate. The water molecules are shown by W1, W2A, W2B, W3, W4, W5, and W6, in which W2A and W2B denote the disordered W2 water. The disordered primary hydroxyl group of the G1 residue is denoted by O6A and O6B. Intermolecular contacts less than 3.1 Å are shown by thin lines.

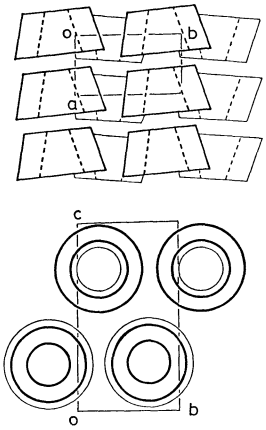

Fig. 2. Schematic drawings of the packing feature of α-cyclodextrin in the crystal.

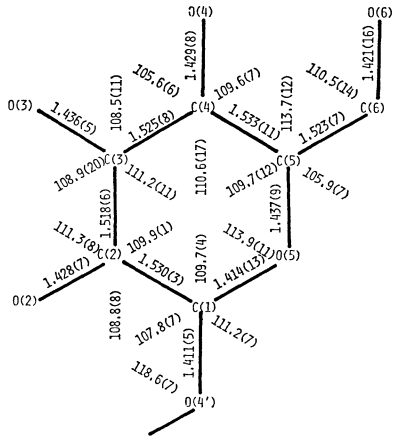

Fig. 3. Average bond distances (l/Å) and angles (ϕ/°) over six glucose residues. Standard deviations in parentheses were estimated according to the equation: $\sigma=[\sum_{i=1}^{6}(x_i-\bar{x})^2/5]^{1/2}$, where x_i referes to the bond distance or angle in the i-th glucose residue, and $\bar{x}$ is the average value.

TABLE 2. GEOMETRICAL DATA FOR α-CYCLODEXTRIN RING

I. O(4)···O(4) distances

Distance (l/Å)		Distance (l/Å)	
O(4, G1)···O(4, G2)	4.466	O(4, G5)···O(4, G6)	4.126
O(4, G1)···O(4, G6)	4.328	O(4, G1)···O(4, G4)	8.047
O(4, G2)···O(4, G3)	4.110	O(4, G2)···O(4, G5)	8.905
O(4, G3)···O(4, G4)	4.357	O(4, G3)···O(4, G6)	8.714
O(4, G4)···O(4, G5)	4.327		

II. Torsion-angle index (I), tilt-angle (II), glycosidic oxygen angle (III), and the angle made by the planes through O(4'), C(1), C(4), and O(4) (IV)

Residue	I(ϕ/°)	II(ϕ/°)	III(ϕ/°)	IV(ϕ/°)
G1	117	19.5	118.8	27.6(G1-G2)
G2	143	19.9	117.8	13.3(G2-G3)
G3	122	15.7	118.4	13.0(G3-G4)
G4	123	10.9	117.7	12.2(G4-G5)
G5	140	11.8	119.7	15.4(G5-G6)
G6	122	18.3	119.3	14.0(G6-G1)

TABLE 3. LEAST-SQUARES PLANES AND DEVIATIONS OF ATOMS FROM THE PLANE

The plane equation is of the $AX+BY+CZ=D$ from, where X, Y, and Z are the coordinates in Å unit along the a, b, and c* axis, respectively.

I. The plane through six O(4) atoms

$0.980X-0.196Y-0.049Z=-1.878$

G1	0.089	G4	0.013
G2	−0.192	G5	−0.120
G3	0.144	G6	0.066

II. Benzaldehyde

$-0.140X+0.979Y-0.144Z=9.697$

C1	−0.039	C5	0.047
C2	−0.034	C6	−0.028
C3	−0.015	C7	−0.040
C4	0.031	O1	0.078

the glycosidic oxygen atoms in Table 2. The conformation of each glucose residue is affected by such distortion. The distance between the adjacent glycosidic oxygen atoms is in the range 4.110—4.466 Å. The O(4)···O(4) distance is closely related to the conformation of pyranose ring characterized by the torsion-angle index.[3] The shorter O(4)···O(4) distance gives the large torsion-angle index. This is ascribed to the smaller conformation angles of C(2)–C(3)–C(4)–C(5) and C(3)–C(4)–C(5)–O(5) and the larger angles of O(5)–C(1)–C(2)–C(3) and C(5)–O(5)–C(1)–C(2).

A tilt-angle between the plane through six glycosidic oxygen atoms and the plane through O(4'), C(1), C(4), and O(4) atoms of each glucose residue was proposed as a convenient measure to describe the orientation of each glucose residue relative to the macro-cyclic ring.[9] In the benzaldehyde complex, the tilt-angles are in the range 10.9—19.9, the average value being 16.0°. These values are similar to those found in the m-nitroaniline complex,[6] but considerably larger than those of complexes with other aromatic

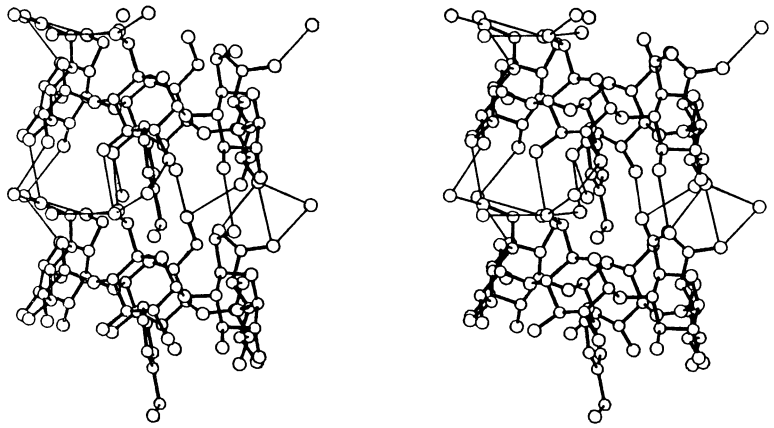

Fig. 4. A stereo-drawing of the packing feature of the complex with associated water molecules. Thin lines denote intermolecular contacts less than 3.1 Å.

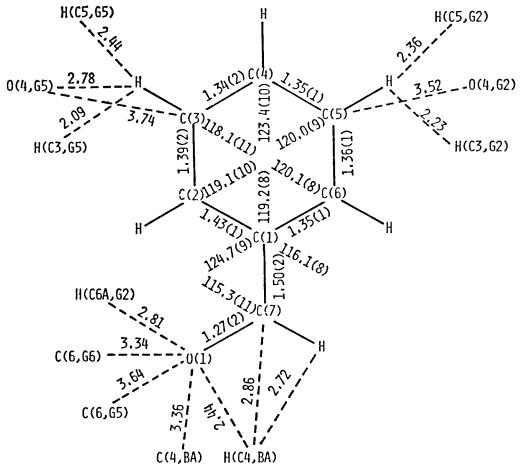

Fig. 5. Bond distances (l/Å) and angles (ϕ/°) in benzaldehyde and selected intermolecular distances (l/Å) between α-cyclodextrin and benzaldehyde. Estimated standard deviations in benzaldehyde are given in parentheses.

guests (average values of 10—12°).[9] Since the packing of α-cyclodextrin in the crystal is nearly the same in the complexes with *m*-nitroaniline and benzaldehyde, we propose another example to support the suggestion that the tilt-angle is largely determined by the packing of α-cyclodextrin in the crystal.

The O(2)···O(3) contact between the adjacent glucose residues is also important to interpret the α-cyclodextrin conformation. The greatest O(2)···O(3) distance is 3.695 Å observed between the G1 and G2 residues, while the other O(2)···O(3) distances are in the range 2.857—2.994 Å. We see from Table 2 that the C(4)–O(4)–C(1′) angle scarecely affects the O(2)···O(3) distance; the greatest O(2)···O(3) distance is observed between the most tilted residues, but the O(2,G2)···O(3,G3) distance is the smallest in spite of the large tilt of the G2 and G3 residues. The O(2)···O(3) distance is more sensitive to the angle made by two planes through O(4′), C(1), C(4), and O(4) of the corresponding glucose residues. The largest angle of 27.6° is found between the G1 and G2 residues, while the other values are in a relatively small region (12.2—15.4°) in accordance with the distribution of the O(2)···O(3) distances.

α-Cyclodextrin-Guest Interaction. Figure 5 shows bond distances and angles in benzaldehyde and intermolecular distances between α-cyclodextrin and benzaldehyde. There is no unusual value in bond distances and angles in benzaldehyde, the planarity of the molecule being fairly good (Table 3). The α-cyclodextrin ring includes about two-third of the benzene ring, while the carbonyl group protrudes from the secondary hydroxyl side and is inserted into the next α-cyclodextrin ring from the primary hydroxyl side (Fig. 4). The benzaldehyde molecule is tilted towards the G1 residue, making an angle of 71.2° against the O(4) plane. The value differs significantly from those found in the α-cyclodextrin complexes with benzene derivatives, in which the aromatic plane is nearly perpendicular to the O(4) plane.[3,5] In those complexes, the benzene ring is deeply inserted into the α-cyclodextrin ring. The benzaldehyde plane is nearly parallel to the C(3,G2)···C(3,G5) diagonal. The relatively short hydrogen···hydrogen contacts are observed between the benzene ring and the C(3) methine groups; H(C3,G5)···H(C3,BA) of 2.09 Å and H(C3,G2)···H(C5,BA) of 2.23 Å. Such a short intermolecular distance is also found between the benzaldehyde molecules; H(C4,BA)···O(1,BA) of 2.44 Å. It is noteworthy that the carbonyl group does not form a hydrogen bond with α-cyclodextrin, and the benzaldehyde molecule is fixed in the α-cyclodextrin ring by the van der Waals contact. In the α-cyclodextrin complexes with other aromatic guests, the guest molecule is hydrogen-bonded to the next α-cyclodextrin or adjacent water molecules. Although the inclusion geometry of the sodium benzenesulfonate complex is similar to the benzaldehyde complex, the sulfonato group of the guest is hydrogen-bonded to primary hydroxyl groups which are in the *gauche-trans* conformation.[4] In the benzaldehyde complex, the nearest primary hydroxyl group is in the *gauche-gauche* conformation, being oriented in the opposite direction. The carbonyl group is so deeply inserted into the α-cyclodextrin ring that it can not form a hydrogen bond with the primary hydroxyl group even when it is in the *gauche-trans* conformation.

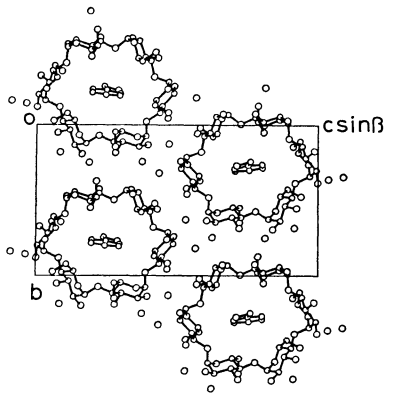

Fig. 6. Crystal structure viewed down the a axis.

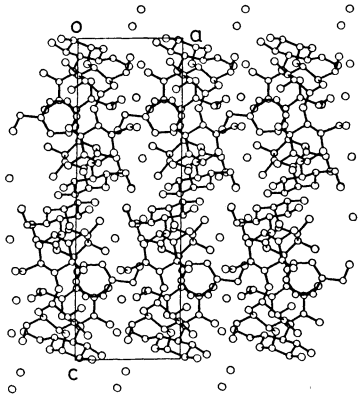

Fig. 7. Crystal structure viewed down the b axis.

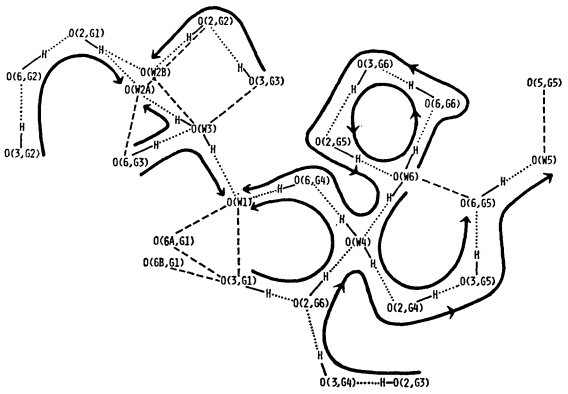

Fig. 8. A schematic drawing of the hydrogen-bond network in the crystal. Arrows indicate the direction of the O–H bond. Intermolecular O···O contacts less than 3.0 Å are shown by broken lines.

Molecular Packing and Hydrogen Bonds. Crystals of the α-cyclodextrin–benzaldehyde complex are built up of the stack of α-cyclodextrin molecules along the a axis to form endless columns. The projections of the crystal structure are shown in Figs. 6 and 7. The α-cyclodextrin molecule is nearly parallel to the a axis, being tilted by 11.5°. The guest benzaldehyde molecules are aligned inside the column with their planes parallel to the ac plane; the angle between these planes is 11.7°. The repetition unit along the column axis (7.932 Å) is almost the same as that of the *m*-nitroaniline complex (8.054 Å), but shorter by 0.3 Å than that of the sodium benzenesulfonate complex. Since the channel axis is perpendicular to the two-fold screw axis, the α-cyclodextrin molecule of the symmetry-related column is arranged up-side-down. These α-cyclodextrin columns are closely packed in the crystal, spaces between columns being filled with water molecules.

So far, no details of hydrogen-bond scheme have been described in the α-cyclodextrin complexes with the channel-type structure.[4,5] A number of hydrogen-bonding contacts were defined in the benzaldehyde complex since most of the hydrogen atoms were found. Five intramolecular hydrogen bonds are formed between the adjacent glucose residues: O(3,G1)–H···O(2,G6), O(3,G3)–H···O(2,G2), O(2,G3)–H···O(3,G4), O(2,G4)–H···O(3,G5), and O(3,G6)–H···O(2,G5). No hydrogen-bonding contact is observed between the G1 and G2 residues, but they are linked by the O(3,G2)–H···O(6,G2)–H···O(2,G1) hydrogen bonds. The adjacent α-cyclodextrin molecules along the channel are connected by the direct hydrogen bonds and hydrogen-bonding linkages involving water molecules. The G2, G4, G5, and G6

Table 4. Hydrogen-bond distances (*l*/Å) and angles (φ/°) and intermolecular distances (*l*/Å) less than 3.0 Å

Estimated standard deviations are in the ranges 0.006—0.008 Å for the distance, 0.06—0.10 Å for the distance involving the hydrogen atoms, and 1.0—4.0° for the O-H···O angle.

O	H	O		DISTANCES O-H	H···O	O···O	ANGLES O-H···O
O(2,G1)	-H(O2,G1)	O(W2A)	(e)	1.09	1.89	2.767	135
O(2,G1)	-H(O2,G1)	O(W2B)	(e)	1.09	1.85	2.855	152
O(3,G1)	-H(O3,G1)	O(2,G6)		0.99	1.88	2.857	168
O(2,G2)	-H(O2,G2)	O(W2A)	(b)	0.96	1.83	2.746	158
O(2,G2)	-H(O2,G2)	O(W2B)	(b)	0.96	2.03	2.933	157
O(3,G2)	-H(O3,G2)	O(6,G2)	(b)	0.78	2.08	2.855	174
O(6,G2)	-H(O6,G2)	O(2,G1)	(b)	1.08	1.86	2.804	144
O(2,G3)	-H(O2,G3)	O(3,G4)		0.96	2.01	2.939	169
O(3,G3)	-H(O3,G3)	O(2,G2)		0.86	2.23	2.950	141
O(6,G3)	-H(O6,G3)	O(W3)		0.91	2.29	2.825	111
O(2,G4)	-H(O2,G4)	O(3,G5)		1.05	1.94	2.994	176
O(3,G4)	-H(O3,G4)	O(6,G4)	(b)	1.08	1.91	2.836	142
O(6,G4)	-H(O6,G4)	O(W1)	(a)	1.05	1.63	2.623	157
O(2,G5)	-H(O2,G5)	O(W6)	(b)	1.10	1.64	2.663	154
O(3,G5)	-H(O3,G5)	O(6,G5)	(b)	0.81	2.11	2.891	162
O(6,G5)	-H(O6,G5)	O(W5)		1.04	2.29	2.825	111
O(2,G6)	-H(O2,G6)	O(W4)	(d)	1.02	1.74	2.747	169
O(3,G6)	-H(O3,G6)	O(2,G5)		1.10	1.82	2.891	165
O(6,G6)	-H(O6,G6)	O(3,G6)	(b)	0.92	1.96	2.862	169
O(W3)	-H(1,W3)	O(W1)	(c)	1.32	1.51	2.802	163
O(W3)	-H(2,W3)	O(W2A)	(g)	1.00	2.20	2.791	116
O(W4)	-H(1,W4)	O(2,G4)	(b)	0.94	1.87	2.789	165
O(W4)	-H(2,W4)	O(6,G4)		1.19	1.62	2.782	166
O(W6)	-H(1,W6)	O(6,G6)	(h)	0.78	2.20	2.783	132
O(W6)	-H(2,W6)	O(W4)	(f)	1.11	1.69	2.761	162
O(3,G1)		O(6A,G1)	(b)			2.940	
O(3,G1)		O(6B,G1)	(b)			2.854	
O(3,G1)		O(W1)	(b)			2.715	
O(6,G1)		O(W1)				2.490	
O(3,G3)		O(W3)	(b)			2.822	
O(6,G3)		O(W2A)				2.832	
O(5,G5)		O(W5)	(h)			2.885	
O(6,G5)		O(W6)				2.919	
O(W2B)		O(W3)	(g)			2.680	

Code	Symmetry operator		
None	x,	y,	z
a	x	1+y,	z
b	-1+x,	y,	z
c	x,	-1+y,	z
d	-1+x,	-1+y,	z
e	-x,	-1/2+y,	-z
f	1-x,	1/2+y,	1-z
g	1-x,	-1/2+y,	-z
h	1-x.	-1/2+y,	1-z

residues are linked by the O(3)···O(6) hydrogen bond. In the G2, G4, and G5 residues, the O(3) hydroxyl group donates the hydrogen atom, while the O(6) hydroxyl group acts as a donor in the G6 residue. Although no hydrogen atom of the O(6A,G1) and O(6B,G1) hydroxyl group was found, the intermolecular distance (Table 4) indicates that they are hydrogen-bonded to the O(3,G1) hydroxyl group of the adjacent α-cyclodextrin. The O(2) hydroxyl groups are also involved in the hydrogen bonds connecting the adjacent α-cyclodextrins. The O(6,G2) hydroxyl group donates the hydrogen atom to O(2,G1). O(2, G4) and O(6,G4) are linked through the O(2,G4)··· H–O(W4)–H···O(6,G4) hydrogen-bond bridge.

Water molecules are located in two intermolecular spaces. W1, W2A, W2B, and W3 fill the space encircled by the G1, G2, and G3 residues. W2 is statistically disordered, occupying two positions. The water molecules are linked by the O(W1)···H–O(W3)–H··· O(W2A) hydrogen-bond bridge. Although no hydrogen atoms of the W2B water molecule were found, the O(W3)···O(W2B) distance of 2.680 Å suggests a hydrogen-bond formation. W4, W5, and W6 occupy the space encircled by the G4, G5, and G6 residues. W4 and W6 are connected by the O(W6)–H···O(W4) hydrogen bond, W5 being isolated and only hydrogen-bonded to O(6,G5).

In the crystal, a hydrogen-bond network is constructed by circles and chains of hydrogen bonds (Fig. 8). The four-membered hydrogen-bond circle is formed by O(2,G5), O(3,G6), O(6,G6), and W6. O(2,G4), O(3,G5), O(6,G5), O(W6), and O(W4) form a five-membered ring, but the circle is not closed since the O(W6) and O(6,G5) forms no hydrogen bond in spite of a suitable distance of 2.919 Å. In the five-membered ring composed of O(3,G1), O(2,G6), O(W4), O(6,G4) and O(W1), the O(W1)–H bond should be oriented to O(3,G1) to close the circle.

The α-cyclodextrin packing in the present crystal resembles that in the *m*-nitroaniline complex, but their crystal property is quite different; the crystal of the *m*-nitroaniline complex easily breaks up in the air. This may be mainly due to the conformation of G1, G2, and G3 residues and water molecules hydrogen-bonded to them. The primary hydroxyl group of the G1 residue in the benzaldehyde complex is disordered and that of the G2 residue is in the *gauche-trans* conformation. On the other hand, in the *m*-nitroaniline complex, the primary hydroxyl groups of the G2 and G3 residues are disordered, and the *gauche-gauche* conformation is found in the G1 residue. Four water molecules in the *m*-nitroaniline complex are located in the same positions as those of W3, W4, W5, and W6 in the benzaldehyde complex, but the other two water molecules occupy different sites.

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