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Structure of the α-Cyclodextrin (α-CD) Inclusion Complex with the Potassium Salt of γ-Aminobutyric Acid (GABA)

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Abstract. α-CD.GABA$^-$.K$^+$.10H$_2$O, $(C_6H_{10}O_5)_6$.$C_4H_8NO_2^-$.K$^+$.10H$_2$O, M_r = 1294·16, $P2_12_12$, a = 21·861 (2), b = 16·624 (3), c = 8·279 (1) Å, Z = 2, D_m = 1·457 (2), D_x = 1·429 Mg m^{-3}. The structure was determined from 1655 X-ray diffractometer data (Ni-filtered Cu $K\alpha$ radiation) and refined to R = 0·11. The host α-CD, with a channel-type structure, includes the guest GABA molecules in its cavities in a disordered arrangement; the molecular conformation of the GABA anions is *trans*-zigzag.

Introduction. The molecular conformation of GABA, a nervous inhibitory transmitter, takes two distinct forms, one folded (Tomita, Higashi & Fujiwara, 1973) and the other *trans*-zigzag (Tomita, 1965), obtained by crystallization from a neutral aqueous solution and from an aqueous hydrochloric acid solution, respectively. However, our efforts to obtain a GABA$^-$.K$^+$ crystal were not successful. Therefore, we attempted to determine the molecular conformation of GABA$^-$.K$^+$ when it is incorporated into a matrix of α-CD and is co-crystallized. Colorless prismatic crystals were obtained by slow cooling of equimolar amounts of α-CD, GABA and KOH in aqueous solution. A crystal, 0·45 × 0·44 × 0·41 mm, was sealed in a glass capillary with some of the mother liquor and X-ray diffraction intensities were measured in the 2θ–ω scan mode. A Fourier synthesis with the phases of α-CD as in the isomorphous potassium acetate complex (Hybl, Rundle & Williams, 1965) revealed the overall structure of the title compound. Two general positions with half occupancy are possible for the K$^+$ ion in an asymmetric unit because the monovalent GABA anion forms a 1:1 complex with α-CD. In a subsequent difference Fourier map the well resolved peaks around the twofold rotation axis could be interpreted as a *trans*-zigzag GABA molecule occupying 12 different positions; the residual electron density found at a position close to that of the cation was assigned to the water molecule (*W*K). Refinement of the structure was by a full-matrix least-squares method using 869 strong reflections, with constraints applied to the α-CD and GABA moieties. Final refinement by a block-diagonal

Table 1. *The final atomic coordinates with their estimated standard deviations in parentheses*

$$B_{eq} = \tfrac{4}{3} \textstyle\sum_i \sum_j B_{ij} \mathbf{a}_i . \mathbf{a}_j.$$

	Occupancy factor	x	y	z	B_{eq} (Å^2)
C(1,*G*1)	1·00	0·1522 (7)	0·2437 (14)	0·3475 (24)	4·44
C(2,*G*1)	1·00	0·1263 (8)	0·2887 (13)	0·4958 (26)	4·20
C(3,*G*1)	1·00	0·0574 (7)	0·2634 (13)	0·5162 (24)	3·74
C(4,*G*1)	1·00	0·0228 (7)	0·2814 (11)	0·3604 (22)	3·23
C(5,*G*1)	1·00	0·0528 (7)	0·2380 (13)	0·2171 (24)	3·97
C(6,*G*1)	1·00	0·0247 (9)	0·2683 (16)	0·0617 (23)	5·41
O(2,*G*1)	1·00	0·1611 (5)	0·2678 (9)	0·6350 (16)	4·80
O(3,*G*1)	1·00	0·0305 (5)	0·3077 (9)	0·6483 (16)	4·86
O(4,*G*1)	1·00	−0·0365 (5)	0·2450 (7)	0·3842 (15)	3·48
O(5,*G*1)	1·00	0·1173 (5)	0·2666 (8)	0·2112 (15)	4·11
O(6*A*,*G*1)	0·81	0·0511 (7)	0·2255 (14)	−0·0742 (18)	6·35
O(6*B*,*G*1)	0·19	0·037 (3)	0·339 (1)	0·013 (19)	19·08
C(1,*G*2)	1·00	0·2453 (8)	−0·0476 (13)	0·3499 (25)	4·04
C(2,*G*2)	1·00	0·2589 (8)	0·0044 (14)	0·4985 (26)	4·36
C(3,*G*2)	1·00	0·2121 (7)	0·0692 (13)	0·5148 (25)	3·90
C(4,*G*2)	1·00	0·2038 (7)	0·1145 (12)	0·3584 (25)	3·69
C(5,*G*2)	1·00	0·1948 (9)	0·0593 (13)	0·2133 (24)	4·17
C(6,*G*2)	1·00	0·2008 (12)	0·1083 (15)	0·0598 (25)	6·01
O(2,*G*2)	1·00	0·2639 (6)	−0·0460 (9)	0·6375 (17)	5·33
O(3,*G*2)	1·00	0·2273 (5)	0·1240 (8)	0·6408 (16)	4·33
O(4,*G*2)	1·00	0·1500 (5)	0·1623 (8)	0·3785 (16)	3·71
O(5,*G*2)	1·00	0·2424 (6)	−0·0019 (10)	0·2103 (15)	4·56
O(6*A*,*G*2)	0·80	0·1953 (9)	0·0577 (11)	−0·0725 (20)	5·86
O(6*B*,*G*2)	0·20	0·248 (5)	0·135 (6)	−0·007 (13)	10·10
C(1,*G*3)	1·00	0·0895 (7)	−0·2973 (12)	0·3530 (26)	3·96
C(2,*G*3)	1·00	0·1298 (8)	−0·2881 (12)	0·4993 (26)	4·17
C(3,*G*3)	1·00	0·1525 (7)	−0·2023 (13)	0·5185 (21)	3·69
C(4,*G*3)	1·00	0·1805 (7)	−0·1696 (12)	0·3636 (24)	3·55
C(5,*G*3)	1·00	0·1381 (8)	−0·1850 (13)	0·2146 (22)	3·76
C(6,*G*3)	1·00	0·1724 (10)	−0·1657 (16)	0·0593 (25)	6·05
O(2,*G*3)	1·00	0·0998 (6)	−0·3170 (9)	0·6396 (19)	5·49
O(3,*G*3)	1·00	0·1949 (5)	−0·1916 (9)	0·6458 (15)	4·62
O(4,*G*3)	1·00	0·1878 (5)	−0·0862 (8)	0·3814 (15)	3·75
O(5,*G*3)	1·00	0·1206 (5)	−0·2668 (8)	0·2133 (16)	4·06
O(6*A*,*G*3)	0·77	0·1323 (8)	−0·1787 (13)	−0·0711 (20)	5·83
O(6*B*,*G*3)	0·23	0·202 (4)	−0·222 (5)	0·005 (9)	8·80
K	0·50	0·3238 (6)	−0·0134 (9)	−0·0748 (14)	7·90
O(*W*K)	0·50	0·3248 (33)	−0·0127 (36)	−0·0728 (91)	20·56
O(*W*1)	1·00	0·3316 (7)	−0·1620 (11)	0·0649 (20)	7·71
O(*W*2)	1·00	0·3692 (11)	0·1270 (13)	0·0600 (24)	11·02
O(*W*3)	1·00	0·4339 (15)	−0·0027 (18)	−0·2903 (46)	19·59
O(*W*5)	1·00	0·4260 (16)	−0·0220 (18)	0·3585 (64)	25·63

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least-squares method with anisotropic temperature factors for the non-hydrogen atoms of α-CD, K^+ and five waters, and with isotropic ones for the remaining atoms including the H atoms in α-CD, reduced R to 0·11 for 1655 non-zero reflections. Atomic scattering factors were taken from *International Tables for X-ray Crystallography* (1974). The final positional parameters are given in Table 1.* All the numerical computations were carried out on an ACOS 700 computer of the Crystallographic Research Center, Institute for Protein Research, Osaka University, using the programs *UNICS* (1979) and *ORXFLS*4 (Busing, Martin & Levy, 1978).

Discussion. All the glucose units are in the usual $^4C_1$ conformation. The primary hydroxyl O(6) atoms occupy two positions [O(6*A*) and O(6*B*)] and their orientations around the C(6)—O(6) bond are *trans–gauche* and *gauche–gauche*. The average bond lengths [$\sigma_{\max}$ = 0·03 Å except for C(6)—O(6*B*) where σ = 0·18 Å] and angles [$\sigma_{\max}$ = 2° except for C(5)—C(6)—O(6*B*) where σ = 8°] in the α-CD molecule are shown in Fig. 1. They are normal compared with those found in other α-CD inclusion complexes (Saenger, 1980) with the exception of the disordered C(6)—O(6) bond with the smaller occupancy which is considerably shorter. The molecular structure of α-CD is well represented by the dihedral angles between the plane through the six glucosidic O(4) atoms, and those formed by the four atoms C(2), C(3), C(5) and O(5) of each glucose unit, which are all 98°. α-CD almost forms a distorted hexagonal prism but the side with the protruding secondary hydroxyl groups [O(2) and O(3)] is wider than that with the primary hydroxyl, O(6). The distances between the six O(4) atoms are shown in Table 2, of which three diagonal O(4)···O(4) distances are thought to be sensitive to the outer environment of the α-CD molecule. The glucose unit *G*2 participates in coordination bonds with K^+, whereas *G*1 and *G*3 are hydrogen bonded to the water molecules (Fig. 2).

As shown in Figs. 2 and 3, the guest GABA molecules, with reasonable molecular dimensions, are included in the α-CD cavities. They are distributed at 12 alternative positions in the cavity, namely those of

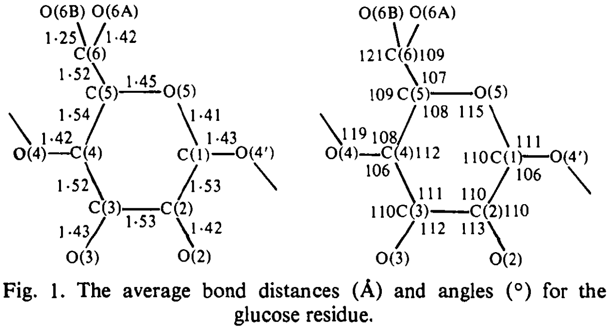

Fig. 1. The average bond distances (Å) and angles (°) for the glucose residue.

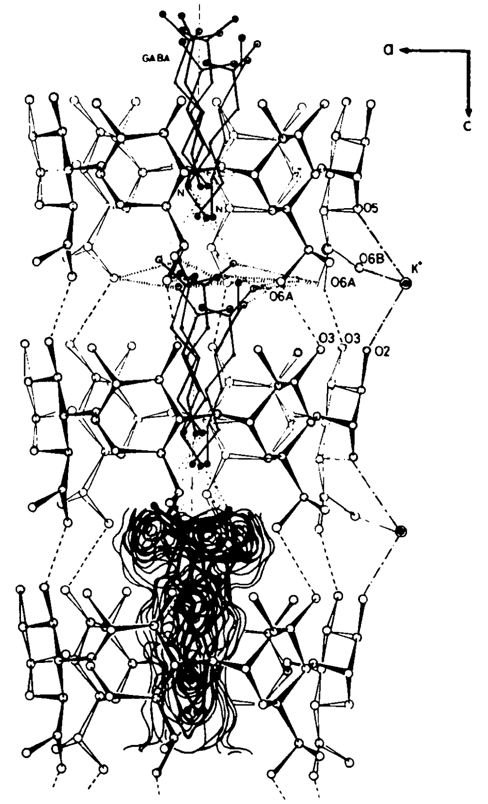

Fig. 2. Projection of the crystal structure of α-CD.-$GABA^-.K^+.10H_2O$ along the *b* axis with a superposition of the difference Fourier map, indicating the assignment of the guest GABA molecule. —·— indicates a coordinate bond, ----, ····, and ||||||||| indicate the host–host, guest–guest and host–guest hydrogen bonds, respectively.

Table 2. *The distances* (Å) *between the six glucosidic* O(4) *atoms of* α-CD

Asterisks indicate the atoms in the equivalent glucose unit related by a twofold rotation axis.

O(4,*G*1)–O(4,*G*2) = 4·30 (2)
O(4,*G*1)–O(4,*G*3) = 7·37 (2)
O(4,*G*1)–O(4,*G*1)* = 8·30 (2)
O(4,*G*2)–O(4,*G*3) = 4·21 (2)
O(4,*G*2)–O(4,*G*1)* = 7·21 (2)
O(4,*G*2)–O(4,*G*2)* = 8·49 (2)
O(4,*G*3)–O(4,*G*1)* = 4·23 (2)
O(4,*G*3)–O(4,*G*2)* = 7·49 (2)
O(4,*G*3)–O(4,*G*3)* = 8·70 (2)

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* Lists of structure factors, anisotropic thermal parameters, GABA and H atom coordinates, observed bond distances and angles of α-CD, dihedral angles in α-CD, and the geometry around K^+ have been deposited with the British Library Lending Division as Supplementary Publication No. SUP 35713 (16 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

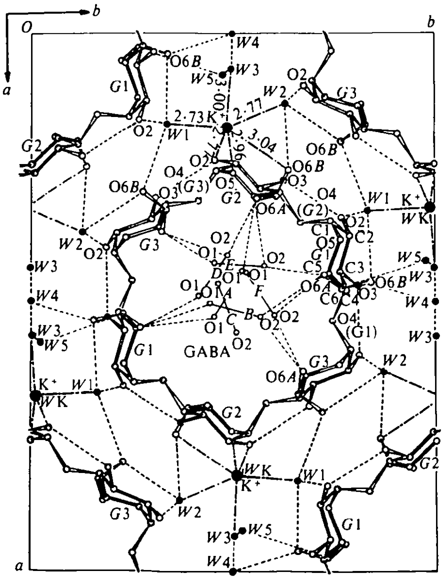

Fig. 3. Projection of the crystal structure of α-CD.-GABA$^-$.K$^+$.10H$_2$O along the *c* axis. Only the carboxyl O atoms of the guest GABA molecules (*A* to *F*) are shown in the α-CD cavity. ---- and —·— indicate hydrogen and coordinate bonds, respectively.

the first six disordered GABA molecules (*A*, *B*, *C* and their equivalents related by a twofold rotation axis) and those of the second six (*D*, *E*, *F* and their equivalents), separated from each other by about 1 Å along the *c* axis.

The GABA molecules are connected infinitely by intermolecular NH···O hydrogen bonds through the α-CD cavity. Such GABA molecules are fixed in the cavities in such a way that each carboxyl O atom of the disordered GABA molecules, except the GABA *C* molecule, is engaged in more than one hydrogen bond with the primary hydroxyl O(6*A*) of the host α-CD molecule, as evidenced by the O···O or O···N distances. Other parts of the guest molecule are in normal van der Waals contact with the host α-CD. The α-CD molecules are arranged into a channel-type structure, which is commonly found in α-CD complexes, *e.g.* that with sodium 1-propanesulfonate (Harata, 1977). The intermolecular OH···O hydrogen bond between the secondary hydroxyl O(3) and the primary hydroxyl O(6*A*), which has a *trans–gauche* conformation, connects each α-CD molecule to form a head-to-tail-type arrangement along the *c* axis as shown in Fig. 2. The K$^+$ cation is coordinated to six O atoms, constructing a disordered octahedron as shown in Fig. 3, where O(*W*1), O(*W*3), O(5) and O(6*B*) are roughly in a plane and the remaining two atoms, O(2) and O(*W*2), occupy the apices.

The coordination sphere around K$^+$ and the hydrogen-bond network formed by molecules of water of crystallization seem to be important in the stabilization of the host matrix structure. One α-CD channel is surrounded by four neighboring channels with opposite channel direction.

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Structure of Acetylacetonato[*N*-(methyl)thiobenzamidomethyl]palladium(II)

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Abstract. [Pd($C_5H_7O_2$)($C_9H_{10}NS$)], $C_{14}H_{17}NO_2PdS$, M_r = 369·8, orthorhombic, $P2_12_12_1$, a = 11·200 (2), b = 6·972(1), c = 19·034 (3) Å, V = 1486·4 (4) Å^3, Z = 4, D_x = 1·652 Mg m^{-3}, F(000) = 744, μ(Mo $K\alpha$) = 1·36 mm^{-1}. R = 0·024 for 1837 non-zero reflexions. The geometry around the Pd atom is square planar. The *N*-(methyl)thiobenzamidomethyl group is bound to the Pd atom through the Pd—C σ bond and the dona-

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