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# Structure of δ-Cyclodextrin $13.75H_2O$

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Crystal and molecular structure of 13.75 hydrate of cycloamylose, δ-cyclodextrin, was studied by X-ray structure analysis. δ-cyclodextrin is not a doughnut-shaped molecule but rather elliptic, boat-shaped one.

Cyclodextrin(CyD) is a common name given for cyclic oligosaccharides composed of a number of α-1,4-linked D-glucoses, in which number 6, 7, and 8 are well known as α-, β-, and γ-CyD, respectively. Owing to an annular aperture of 5 - 8 Å, CyD is able to form inclusion complex with a variety of guest molecules.[1] As CyD hydrate is called as vacant CyD because of being no guest molecule without water in the host CyD, structure of CyD hydrate is the most important one to study the inclusion phenomena by CyD at atomic level. δ-CyD is also a cyclic oligosaccharide composed of nine α-1,4-linked D-glucoses. We succeeded to crystallize δ-CyD as its hydrate form for the first time and elucidated its structure by X-ray analysis. We report here briefly the crystal and molecular structure of δ-CyD $13.75H_2O$.

δ-CyD was prepared as follows; CyD powder(K-50, commercial product of Ensuiko Sugar Refining Co., Ltd.) was dissolved to make 20% aqueous solution, and reacted with β-amylose, pullulanase, and yeast at 30 °C, 24

h, then lees, yeast, α-, β-, and γ-CyD, and dextrin were removed. The resultant large ringed CyD was treated with pure glucoamylase to remove contaminated dextrin as glucose. Separation of δ-CyD from the mixture was done by a gel chromatography with TOYO PEAL HW-40S. Fractions were analyzed by HPLC and the fractions containing pure δ-CyD were collected and concentrated by vacuum evaporation. Crystallization of δ-CyD $13.75H_2O$ was performed by slow evaporation of the concentrated δ-CyD aqueous solution. The details of method will be published elsewhere in the near future.

A transparent colorless crystal of 0.01 x 0.18 x 0.40 mm size was used for the X-ray analysis. The crystal data are : $C_{54}H_{90}O_{45}$ $13.75H_2O$, F.W.= 1707.0, Monoclinic, $P2_1$, Z=2, a=20.881(3), b=11.538(1), c=16.222(2) Å, β= 104.33(1)° , V=3786.5(8) $Å^3$, $D_m$=1.474(1), $D_x$=1.497 Mg $m^{-3}$, μ=12.1 $cm^{-1}$. X-ray intensity data were measured on Rigaku automatic four circle diffractometer (AFC-5, Cu-Kα, λ=1.5418 Å, ω-2θ scan with a $2\theta<125°$). 5338 independent reflections with $|F_o| > 3\sigma(|F_o|)$ were used in the structure determination by SIR85[2] and in the following refinements by block-diagonal and full-matrix least-squares procedures. All the hydrogen atoms except for those of crystalline waters were assigned on a difference Fourier map. Occupancy factors for water oxygen atoms in disordered state were refined by full-matrix least-squares method. The final refinement was done by anisotropic temperature factors for oxygen and carbon atoms and isotropic ones for hydrogen atoms, and converged R to 0.053. All computations were carried out with IBM 3081-GX3 computer at the Information Processing Center, Shimane University.

The molecular structure of δ-CyD is shown in Figs. 1 and 2. The overall shape of δ-CyD is elliptic and its longer axis is parallel to a line from glucose unit G2 to G6 and shorter one from G1 to G4 or from G5 to G9. As a distance along the longer axis is about 10.3 ~ 11.2 Å (G6-C3-H... H-C3-G2 ~ G3-O4...O4-G7), and that along the shorter one is about 5.8 ~ 7.1 Å (G5-C5-H...H-C5-G9 ~ G1-O4...O5-G4), a naphthalene molecule (9.4 x 7.2 x 3.5 Å) is included loosely or rather freely, and an anthracene molecule

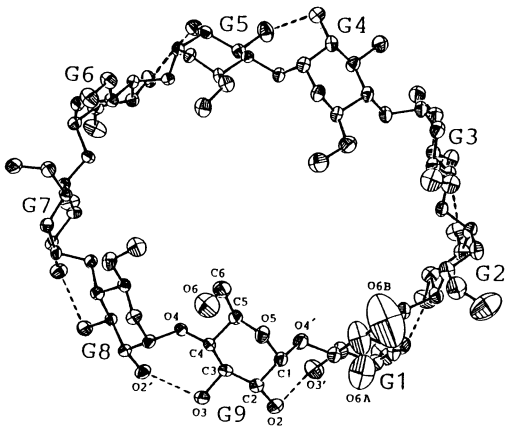


Fig. 1. Molecular structure and numbering of δ-cyclodextrin (ORTEP[3] drawing)

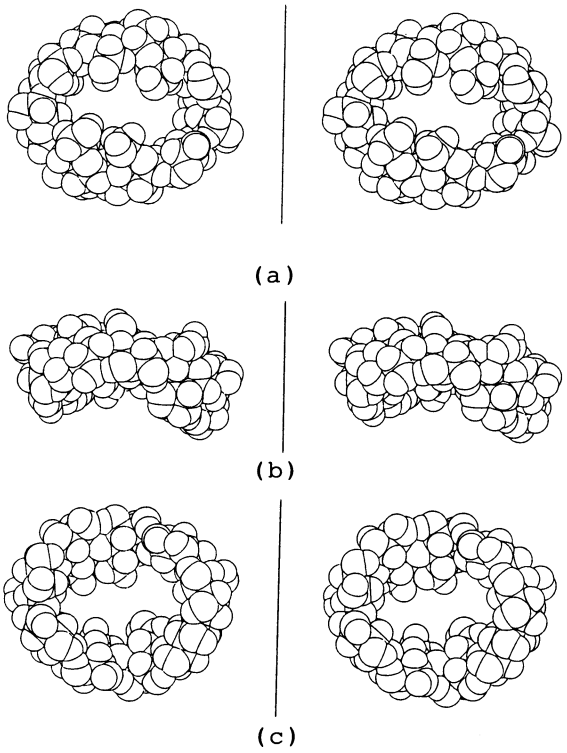


Fig. 2. Spacefilling drawing of δ-CyD (PLUTO,[4] stereo view a) view from O6 side, b) side view, c) from O2, O3 side)

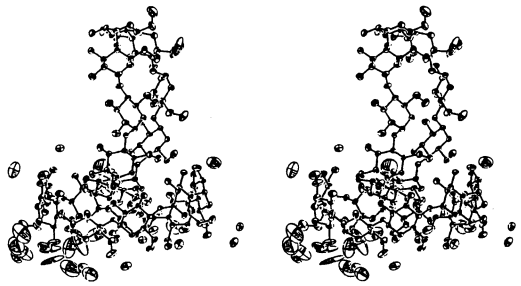

Fig. 3. A part of crystal structure δ-CyD $13.75H_2O$ (ORTEP, stereo view)

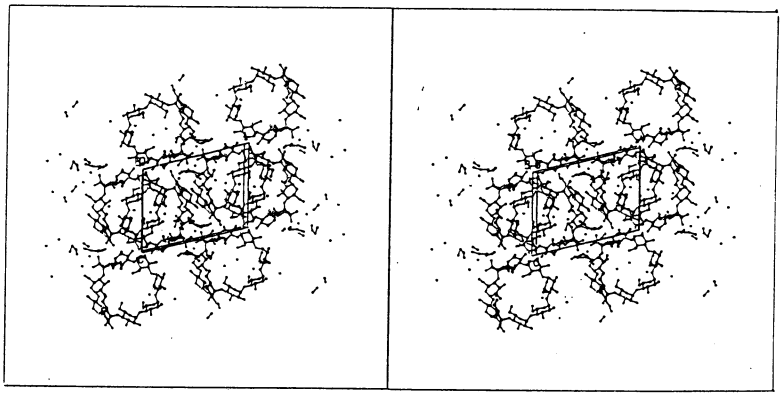

Fig. 4. Crystal structure of δ-CyD $13.75H_2O$ along b-axis

(11.6 x 7.2 x 3.5 Å) seems to fit well in δ-CyD cavity. Owing to the interglucose hydrogen bond between O2...O3', an annular aperture of δ-CyD is much wider at secondary hydroxyl group (O2, O3) side than that of primary (O6) side. Moreover, glucose units, G4, G5, G8, and G9 fall down inside of δ-CyD cavity. A δ-CyD molecule building by wire-model showed that the wider the maclocyclic ring became, the stronger stress at glucoxide bond angle of C1'-O4-C4 arose and it was impossible to construct a round, doughnut-shaped molecule. From side view of δ-CyD, the molecule takes a boat form or U character, that is, nine glucosidic oxygen atoms (O4) connecting neighboring glucose unit by α-1,4-linkage, are not in a plane. All glucose units take chair form. Bond lengths and angles of δ-CyD are normal. The conformations about the C5-C6 bond; C4-C5-C6-O6 and O5-C5-C6-O6 are trans and gauche for G3, G4, G5, G6, and G8, but those for G2, G7, and G9 are gauche and gauche respectively. Only O6 atom of G1 is in disordered state equally at gauche-gauche and trans-gauche conformations (O6A and O6B in Fig. 1). In an asymmetric unit, there are 23 positions for 13.75 water molecules in which each five water is in fully occupied state and lies around the wide space at O6 side of δ-CyD. The rest 8.75 waters are in disordered state with occupancy ranged from 0.16 to 0.87 at 18 positions and stay at the narrow space of O6 side, and form a water cluster by hydrogen bonds. Wide annular aperture of one δ-CyD is closed from O2, O3 side by wall of another δ-CyD molecule, and the opposite narrow aperture of the δ-CyD is packed with 13.75 waters as shown in Figs. 3 and 4.

References

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