X-Ray Crystal Structure of the Permethylated β-Cyclodextrin Complex with *m*-Iodophenol. A Stabilized Skew-Boat Pyranose Conformation in the Distorted Macrocyclic Ring

Kazuaki Harata

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

In the crystalline inclusion complex of permethylated β-cyclodextrin with *m*-iodophenol, the host molecule has a glucose unit with an unusual $^{0}S_{2}$ skew-boat conformation and shows markedly distorted macrocyclic conformation.

It has been shown that the round macrocyclic ring of cyclodextrins and partially methylated cyclodextrins is stabilized by the formation of intramolecular O(2)---O(3′) hydrogen bonds between adjacent glucose units.[1—3] By permethylation, all the intramolecular hydrogen bonds are blocked, and the steric hindrance involving methyl groups at the O(2),O(3) side of the molecule causes the collapsed bucket-shape of the macrocyclic ring.[4] However, in the structures of permethylated cyclodextrins reported to date, the pyranose ring of each glucose unit is always in the normal $^{4}C_{1}$ chair conformation. Here we report the first glucose unit with the $^{0}S_{2}$ skew-boat conformation in the crystalline inclusion complex of permethylated β-cyclodextrin (2,2′,-2″,2‴,2⁗,2⁗′, 2⁗″, 3,3′,3″,3‴,3⁗,3⁗′,3⁗″,6,6′,6″,6‴,6⁗,6⁗′, 6⁗″-henicosa-*O*-methyl-β-cyclodextrin) with *m*-iodophenol.†

Figure 1 shows the structure of a complete molecule of the complex. Unlike the G5 unit, the six 2,3,6-tri-*O*-methylglucose units are in the $^{4}C_{1}$ chair conformation. The G5 unit is in the $^{0}S_{2}$ skew-boat conformation, as shown in Figure 2. The C(1), C(2), C(4) and C(5) atoms are not coplanar. The C(1) and O(5) atoms are not coplanar. The C(1) and O(5) atoms are above the plane containing C(3), C(4), and C(5), while the C(2) atom is below the plane. Some torsion angles describing the conformation of the glucose units are given in Table 1. The C(2)–O(2), C(3)–O(3), and C(4)–O(4) bonds, which are equatorial in the units with the $^{4}C_{1}$ conformation, are axial and the C(2)–O(2) and C(4)–O(4) bonds are *trans* to the C(3)–O(3) bond. The O(4)–O(4′) distance in the G5 unit is 4.80 Å,

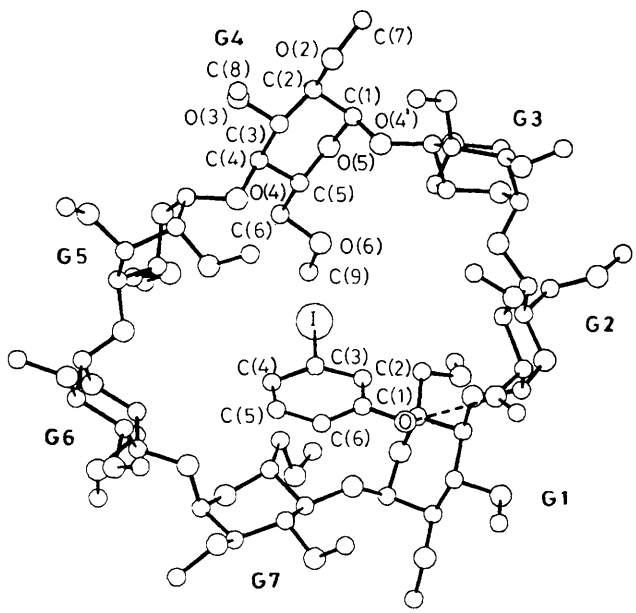

Figure 1. The structure of the permethylated β-cyclodextrin complex with *m*-iodophenol. The dashed line denotes the host–guest hydrogen bond.

† *Crystal data:* $C_{63}H_{112}O_{35}.C_{6}H_{5}OI$, M = 1649.6, orthorhombic, space group $P2_12_12_1$, a = 15.669(3), b = 20.798(4), c = 25.486(4) Å, U = 8305(2) Å^3, Z = 4, D_c = 1.319 g cm^{-3}. 4927 Independent reflections with $|F_o| \geq 3\sigma(F)$ were collected on a Nicolet P3/F diffractometer with graphite-monochromated Cu-K_α radiation. (θ—2θ scan mode) The structure was solved by the heavy atom method combined with phase refinement by the tangent formula and refined to R = 0.072 by the block-diagonal least-squares method. Atomic co-ordinates, bond lengths and angles, and thermal parameters have been deposited at the Cambridge Crystallographic Data Centre. See Notice to Authors, Issue No. 1.

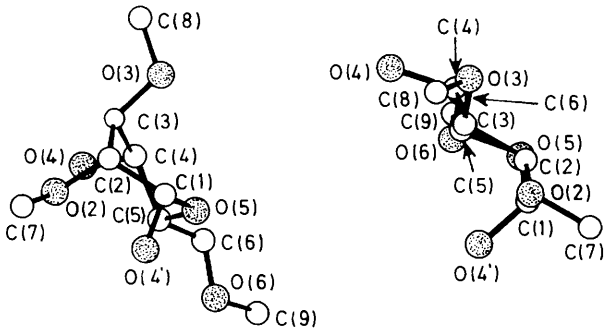

Figure 2. The $^{0}S_{2}$ skew-boat conformation of the G5 unit (left) and the $^{4}C_{1}$ chair conformation of the G4 unit (right). Oxygen atoms are shaded.

significantly longer than the corresponding distances in the other units (4.15—4.68 Å). The macrocyclic ring is in the shape of the ellipitically distorted bucket. The distances measured from the centre of gravity of seven O(4) atoms to each O(4) atom are in the range 4.17—5.48 Å. The guest *m*-iodophenol molecule is included within the host cavity. The hydroxyl group of *m*-iodophenol is hydrogen-bonded to O(2,G2) of the host. The guest shows no significant contacts with the G5 unit.

In our earlier paper,[4] we indicated that permethylation affects not only the macrocyclic conformation but also the conformation of the pyranose ring of constituent glucose units. The structure presented herein demonstrates that permethylation even causes the change in the conformation of pyranose ring. The $^{0}S_{2}$ conformation of the G5 unit may relieve the repulsive interaction of methyl groups at the O(2),O(3) side, since the O(2)Me and O(3)Me methoxy groups of the G5 unit are oriented so as to be as far as possible from the methoxy groups of the adjacent units.

Table 1. Comparison of torsion angles (ϕ/°) describing the $^{0}S_{2}$ pyranose conformation of the G5 unit and the corresponding average values for the other six units having the $^{4}C_{1}$ chair conformation.

	$^{0}S_{2}$	$^{4}C_{1}$
C(1)–C(2)–C(3)–C(4)	51	−53
C(2)–C(3)–C(4)–C(5)	−14	52
C(3)–C(4)–C(5)–O(5)	−43	−56
C(4)–C(5)–O(5)–C(1)	72	64
C(5)–O(5)–C(1)–C(2)	−35	−63
O(5)–C(1)–C(2)–C(3)	−29	57
O(2)–C(2)–C(1)–O(4')	−31	56
O(2)–C(2)–C(3)–O(3)	170	68
O(3)–C(3)–C(4)–O(4)	−138	−73
O(4)–C(4)–C(5)–C(6)	87	71

Received, 17th March 1988; Com. 8/01085D

References

1 W. Saenger in 'Inclusion Compounds,' ed. J. L. Atwood, J. E. D. Davies, and D. D. MacNicol, Academic Press, London, 1984, vol. 2, p. 231.
2 M. Czugler, E. Eckle, and J. J. Stezowski, *J. Chem. Soc., Chem. Commun.*, 1981, 1291.
3 K. Harata, *Chem. Lett.*, 1986, 2057.
4 K. Harata, K. Uekama, M. Otagiri, and F. Hirayama, *J. Inclusion Phenom.*, 1984, **1**, 279.