

Effects of Calcium Interactions on the Conformations of Sugars: Crystal Structure of Myo-Inositol–Calcium Bromide Pentahydrate

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X-ray diffraction data were used to determine the crystal structure of a hydrated calcium bromide complex of myo-inositol. Crystals of $C_6H_{12}O_6 \cdot CaBr_2 \cdot 5H_2O$ are triclinic, space group $P\bar{1}$, with $a = 7.513$ (3), $b = 8.280$ (3), $c = 15.035$ (3) Å, $\alpha = 70.43$ (3), $\beta = 82.06$ (3), $\gamma = 68.08$ (4)°, $Z = 2$, $\rho(\text{obs}) = 1.90$ and $\rho(\text{calc}) = 1.910$ g cm⁻³. Intensity data for 2724 independent reflections were collected with an automated diffractometer by use of nickel-filtered copper radiation. A trial structure, obtained by direct and Fourier methods, was refined by least-squares to $R = 0.039$. The calcium ion binds four water molecules and two symmetry-related myo-inositol molecules. One myo-inositol molecule is coordinated to the calcium ion through its O(2) and O(3) hydroxyl groups, and the second is coordinated through its O(5) and O(6) hydroxyl groups. The four hydroxyl groups and four water molecules that interact with the calcium ion form a distorted square-antiprism coordination polyhedron. A comparison of this and other crystal structures of myo-inositol indicates that the calcium interactions produce small distortions in the conformation of the sugar. At both chelation sites, there are changes ranging up to 15° in torsion angles and up to 5° in bond angles, with resultant decreases of about 0.2 Å in the intramolecular spacing between the hydroxyl groups that are chelated to calcium. These conformational changes are consistent with those observed in other crystal structures of calcium–sugar complexes.

Introduction

Many simple carbohydrates bind to calcium ions in solution, and a number of crystalline calcium halide complexes of sugars have been isolated from water (Rendleman, 1966). We are currently investigating the crystal structures of a series of these complexes (Bugg & Cook, 1972; Bugg, 1973; Cook & Bugg, 1973*a, b, c*) in order to elucidate the factors involved in calcium–carbohydrate interactions. Thus far, we have found that most uncharged sugars chelate calcium ions through pairs of adjacent hydroxyl groups, and our results have suggested that the calcium–hydroxyl interactions generally produce small conformational changes in the sugars at the calcium-binding sites. We have determined the crystal structure of a hydrated calcium bromide complex of myo-inositol (Fig. 1) to further investigate the effects that calcium interactions exert on the conformations of sugars. Myo-inositol is a particularly suitable choice for this purpose, since conformational data for the uncomplexed sugar are available from the crystallographic studies of myo-inositol (Rabinowitz & Kraut, 1964) and of myo-inositol dihydrate (Lomer, Miller & Beevers, 1963).

Experimental

Clear, platelike crystals of the complex were grown by evaporating an aqueous solution that contained a 1:2 molar mixture of myo-inositol and calcium bromide. Weissenberg and oscillation photographs showed the crystals to be triclinic, thus indicating that the space

group was either $P1$ or $P\bar{1}$. A crystal fragment with approximate dimensions of $0.25 \times 0.12 \times 0.14$ mm was mounted on a Picker FACS-1 diffractometer with the a axis of the crystal slightly inclined to the ϕ axis of the diffractometer. Approximate cell parameters for use in collecting intensity data were calculated by a least-squares analysis of the angular settings of twelve high-angle reflections ($Cu K\alpha_1$, $\lambda = 1.54051$ Å).

Intensity data were collected with the diffractometer by use of nickel-filtered copper radiation, a scintillation counter, and a θ – 2θ scanning technique. Measurements were made for the 2724 independent reflections with $2\theta \leq 128^\circ$. Three strong, medium-angle reflections that were monitored periodically did not vary significantly during data collection. Immediately after data collection, accurate values for the cell parameters were determined by a least-squares analysis of 2θ values for 14

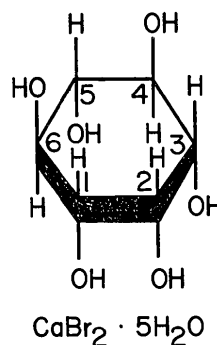


Fig. 1. Structural formula of the hydrated inositol-calcium bromide complex.

high-angle reflections (Cu $K\alpha_1$); these cell parameters were not significantly different from those obtained prior to the measurement of intensity data. The cell parameters, along with other crystal data, are listed in Table 1. The reduced cell can be obtained by the transformation matrix

$$S = \begin{pmatrix} -1 & 0 & 0 \\ 0 & -1 & 0 \\ 0 & -1 & 1 \end{pmatrix}.$$

Table 1. *Crystal data*

Stoichiometry	$C_6H_{12}O_6 \cdot CaBr_2 \cdot 5H_2O$
Z	2
Space group	$P\bar{1}$
ρ (calculated)	1.910 g cm^{-3}
ρ (observed)	1.90 g cm^{-3}
μ	100.6 cm^{-1}
Cell dimensions	
a	$7.513 (3) \text{ \AA}$
b	$8.280 (3)$
c	$15.035 (3)$
α	$70.43 (3)^\circ$
β	$82.06 (3)$
γ	$68.08 (4)$

(Density was measured by flotation in a mixture of benzene, carbon tetrachloride, and dibromoethane.)

Reflections that had scan counts below background levels were assigned intensity values of 0.0 and were included in all subsequent calculations. All intensities were assigned variances, $\sigma^2(I)$, according to the statistics of the scan and background counts plus a correctional term $(0.03S)^2$, S being the scan counts. The intensities and their variances were corrected for Lorentz

and polarization factors, and absorption corrections were applied by using the computer program *ORABS* (Wehe, Busing & Levy, 1962). The data were then scaled by means of a Wilson (1942) plot.

A Howells, Phillips & Rogers (1950) plot indicated that the crystal structure was centrosymmetric, and the observed density (Table 1) indicated that there were two formula units per unit cell. Consequently, we presumed that the space group was $P\bar{1}$; this assumption was corroborated by the final structural results. Trial coordinates for the calcium and bromide ions were obtained by direct methods, with the use of Long's (1965) computer program for sign determination by reiterative application of Sayre's (1952) relationship. The other nonhydrogen atoms were located in a Fourier map that was calculated by using phase angles derived from the three ions. The trial structure was refined by using a modified version of the full-matrix least-squares program *ORFLS* (Busing, Martin & Levy, 1962; Busing, 1971). The quantity minimized was $\sum w(F_o^2 - F_c^2/k^2)^2$, where k is a scale factor and weight w is equal to $1/\sigma^2(F_o^2)$. Scattering factors for the calcium cation (Ca^{2+}), the bromide anions (Br^-), and carbon and oxygen atoms, as well as anomalous dispersion correction factors for all nonhydrogen atoms except carbon, were from *International Tables for X-ray Crystallography* (1962). Hydrogen atom scattering factors were from Stewart, Davidson & Simpson (1965). Hydrogen atoms were located in a difference Fourier map that was calculated during the latter stages of refinement. All positional parameters, anisotropic temperature factors for the heavy atoms, isotropic temperature factors for the hydrogen atoms, and Zachariasen's (1963) isotropic extinction parameter g (as formulated by Coppens & Hamilton, 1970) were included in the refinement. The final R index, $(\sum ||F_o| - |F_c|| / \sum |F_o|)$, in-

Table 2. *Final heavy-atom parameters and their standard deviations*

Values have been multiplied by 10^4 . Temperature factors are in the form $T = \exp(-\beta_{11}h^2 - \beta_{22}k^2 - \beta_{33}l^2 - 2\beta_{12}hk - 2\beta_{13}hl - 2\beta_{23}kl)$. $W1-W5$ are oxygen atoms of the water molecules. Final value of the isotropic extinction parameter is $g = 0.005 (2)$.

	x	y	z	β_{11}	β_{22}	β_{33}	β_{12}	β_{13}	β_{23}
Br(1)	2191 (1)	7300 (1)	888 (1)	178 (1)	188 (1)	27 (1)	-101 (1)	5 (1)	-18 (1)
Br(2)	2084 (1)	5310 (1)	4063 (1)	135 (1)	134 (1)	32 (1)	-29 (1)	-2 (1)	-18 (1)
Ca	8853 (1)	2306 (1)	2633 (1)	92 (1)	112 (1)	25 (1)	-42 (1)	2 (1)	-18 (1)
C(1)	5045 (5)	-1540 (4)	3801 (2)	91 (7)	99 (6)	21 (2)	-37 (5)	-2 (2)	-10 (2)
O(1)	4713 (4)	-1639 (3)	4769 (2)	116 (5)	135 (5)	18 (1)	-24 (4)	-3 (2)	-7 (2)
C(2)	6885 (5)	-1117 (4)	3437 (2)	82 (6)	102 (6)	25 (2)	-35 (5)	-4 (2)	-14 (2)
O(2)	6820 (4)	519 (3)	3596 (2)	141 (6)	158 (5)	23 (1)	-91 (4)	15 (2)	-33 (2)
C(3)	7170 (4)	-813 (4)	2380 (2)	76 (6)	108 (6)	29 (2)	-45 (5)	9 (3)	-28 (3)
O(3)	8718 (3)	-118 (3)	2075 (2)	73 (5)	149 (5)	32 (1)	-56 (4)	21 (2)	-38 (2)
C(4)	5388 (5)	567 (4)	1814 (2)	92 (7)	113 (6)	18 (2)	-47 (5)	7 (2)	-18 (2)
O(4)	5638 (4)	526 (4)	862 (2)	137 (6)	188 (6)	19 (1)	-83 (5)	10 (2)	-21 (2)
C(5)	3614 (4)	83 (4)	2205 (2)	79 (6)	100 (6)	22 (2)	-29 (5)	0 (2)	-18 (2)
O(5)	1922 (3)	1455 (3)	1748 (1)	81 (5)	163 (5)	16 (1)	-20 (4)	-6 (2)	-10 (2)
C(6)	3322 (4)	-61 (4)	3245 (2)	78 (6)	103 (6)	20 (2)	-44 (5)	6 (2)	-12 (2)
O(6)	1549 (3)	-356 (3)	3581 (2)	74 (5)	119 (5)	29 (1)	-43 (4)	6 (2)	-13 (2)
W1	8010 (5)	-2436 (4)	211 (2)	156 (7)	166 (6)	33 (1)	-34 (6)	-8 (2)	-24 (2)
W2	8069 (5)	4009 (5)	998 (2)	207 (8)	164 (7)	28 (2)	-45 (6)	-9 (3)	-23 (3)
W3	105 (5)	4626 (4)	2478 (3)	234 (8)	191 (7)	38 (2)	-149 (6)	20 (3)	-34 (3)
W4	5718 (5)	4636 (5)	2538 (3)	136 (7)	234 (8)	40 (2)	30 (6)	13 (3)	-15 (3)
W5	8606 (7)	2688 (6)	4190 (2)	354 (11)	298 (9)	34 (2)	-225 (9)	43 (3)	-59 (3)

cluding all reflections, is 0.039. The goodness-of-fit, $[\sum w(F_o^2 - F_c^2k^2)^2 / (m - s)]^{1/2}$, where m is the number of reflections used and s is the number of parameters refined, is 2.18. During the last cycle of refinement, no parameter shifted more than one-fifth of its estimated standard deviation. A final three-dimensional difference Fourier map showed several peaks and troughs with magnitudes ranging from 0.6 to $1.5 \text{ e } \text{Å}^{-3}$ in the immediate vicinities of the bromide ions; there were no other peaks or troughs in excess of 0.4 Å^{-3} .

Table 2 lists the final heavy-atom parameters and their estimated standard deviations. Table 3 gives the hydrogen-atom parameters and their estimated standard deviations. The estimated errors in positional coordinates are about 0.001 Å for bromide and calcium ions, $0.002\text{--}0.005 \text{ Å}$ for carbon and oxygen atoms, and $0.04\text{--}0.10 \text{ Å}$ for hydrogen atoms. Observed and calculated structure factors are listed in Table 4.

Results and discussion

Crystal packing and calcium coordination

The crystal-packing and hydrogen-bonding schemes are depicted in Fig. 2. Hydrogen-bond lengths and angles are given in Table 5. The sugar molecules, water molecules, and bromide ions form a cohesive hydrogen-bonded network that uses all hydrogen atoms covalently bonded to oxygen atoms. The bromide ions are hydrogen bonded to water molecules and to hydroxyl groups. There are no direct calcium–bromide contacts (the shortest Br–Ca distance is 4.5 Å), but several of the water molecules and hydroxyl groups form bridges between the calcium and bromide ions.

Surrounding the calcium ion is a shell composed of eight oxygen atoms from hydroxyl groups and water molecules. Fig. 3 depicts the environment of the cal-

Table 3. *Hydrogen-atom parameters and their standard deviations*

Positional parameters have been multiplied by 10^3 .

	<i>x</i>	<i>y</i>	<i>z</i>	<i>B</i> (Å ²)
H(C1)	522 (5)	−269 (5)	370 (2)	2.2 (0.7)
H(O1)	558 (7)	−261 (6)	505 (3)	4.3 (1.0)
H(C2)	791 (6)	−212 (5)	375 (3)	2.9 (0.8)
H(O2)	649 (6)	54 (5)	407 (3)	2.7 (0.8)
H(C3)	747 (5)	−192 (5)	224 (2)	2.5 (0.8)
H(O3)	931 (6)	−51 (5)	176 (3)	3.0 (0.8)
H(C4)	520 (6)	187 (6)	190 (3)	3.5 (0.9)
H(O4)	606 (7)	121 (7)	57 (3)	5.5 (1.2)
H(C5)	384 (5)	−114 (5)	215 (2)	1.8 (0.7)
H(O5)	200 (5)	159 (5)	129 (2)	1.9 (0.7)
H(C6)	313 (5)	115 (5)	332 (2)	1.9 (0.7)
H(O6)	168 (5)	−129 (5)	363 (2)	1.8 (0.7)
H(W1)	723 (9)	−157 (8)	36 (4)	6.2 (1.6)
H'(W1)	889 (9)	−227 (8)	28 (4)	5.6 (1.7)
H(W2)	809 (9)	515 (10)	75 (4)	7.1 (1.8)
H'(W2)	791 (6)	371 (6)	69 (3)	2.2 (1.0)
H(W3)	65 (8)	488 (7)	209 (4)	4.2 (1.4)
H'(W3)	42 (8)	480 (7)	286 (4)	4.4 (1.4)
H(W4)	502 (8)	466 (8)	296 (4)	5.4 (1.4)
H'(W4)	511 (9)	518 (8)	206 (4)	5.8 (1.5)
H(W5)	794 (11)	246 (11)	447 (5)	9.1 (2.5)
H'(W5)	906 (12)	326 (12)	430 (5)	12.1 (2.9)

cium ion, which binds two symmetry-related myo-inositol molecules and four water molecules. One myo-inositol molecule chelates the calcium ion through its O(2) and O(3) hydroxyl groups (an axial-equatorial pair), and the second myo-inositol molecule chelates the calcium ion through its O(5) and O(6) hydroxyl groups (an equatorial-equatorial pair). The stereochemistry of the calcium–ion coordination shell is shown in more detail in Fig. 4. The eight oxygen atoms form a distorted square–antiprism with calcium–oxygen distances ranging from 2.37 to 2.52 Å . The average distance for the calcium–hydroxyl contacts is 2.49 Å ,

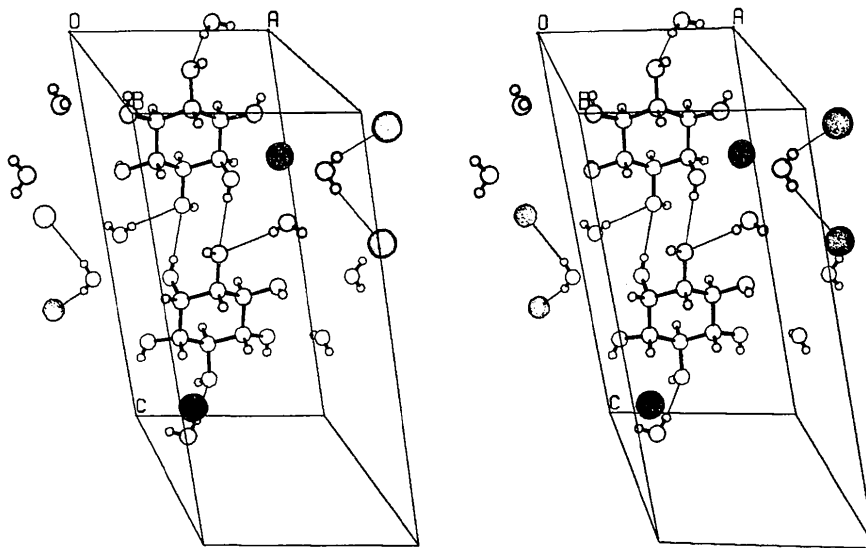


Fig. 2. Stereo drawing in which the crystal packing is viewed approximately down the *b* axis. Spotted circles represent bromide ions, solid black circles—calcium ions, heavy lines—the covalent bonds, and light lines—the hydrogen bonds. [This drawing and those in Figs. 3–5, were prepared by using the program ORTEP (Johnson, 1965)].

Table 4. Observed and calculated structure factors

From left to right, the columns contain values of l , $10F_o$, and $10F_c$.

Table with multiple columns containing numerical data for structure factors. The columns are labeled with l, 10Fo, and 10Fc. The data is organized in a grid-like format with rows and columns of numbers.

and for the four calcium–water contacts the average distance is 2.41 Å. Within the calcium shell there are several short oxygen–oxygen contacts, however, no hydrogen bonds exist between the oxygen atoms of the shell. The calcium–oxygen distances and the geometry of the coordination shell are in agreement with those found for other sugar–calcium halide complexes (Bugg & Cook, 1972; Bugg, 1973; Cook & Bugg, 1973*b*) and for several calcium salts of sugar acids (Cook & Bugg, 1973*a*; Norrestam, Werner & von Glehn, 1968; Furberg & Hellend, 1962; Balchin & Carlisle, 1965).

Calcium interactions with various epimers of inositol in aqueous solution have been studied by Angyal & Davies (1971), who found that myo-inositol binds calcium only weakly, whereas several other epimers of

inositol interact strongly with calcium. These investigators concluded that an axial–equatorial–axial arrangement of three hydroxyl groups is necessary for strong binding of calcium ions to six-membered sugar rings, apparently because this arrangement allows the three hydroxyl groups to interact simultaneously with a single calcium ion. Recent studies have provided additional evidence that, in aqueous solution, calcium ions bind strongly only to those sugars that possess at least three hydroxyl groups that are oriented suitably for calcium chelation (Angyal, 1972). In contrast, the myo-inositol molecule in the calcium bromide complex uses only two adjacent hydroxyl groups at each site that binds calcium ions. Similarly, in the crystal structures of calcium halide complexes of lactose (Bugg,

Table 5. *Hydrogen bond distances and angles*

The estimated standard deviations are about 0.003 Å for donor–acceptor distances, 0.06 Å for hydrogen–acceptor distances, and 3° for donor–hydrogen–acceptor angles.

Donor atom	Hydrogen atom	Acceptor atom	Distances (Å)		Donor–hydrogen–acceptor angle (°)
			Donor–acceptor	Hydrogen–acceptor	
O(1)	H(O1)	Br(2) <i>b</i>	3.201	2.36	177
O(2)	H(O2)	O(1) <i>b</i>	2.859	2.17	160
O(3)	H(O3)	Br(1) <i>c</i>	3.416	2.76	166
O(4)	H(O4)	Br(1) <i>d</i>	3.265	2.58	155
O(5)	H(O5)	W1 <i>f</i>	2.780	2.13	171
O(6)	H(O6)	Br(2) <i>g</i>	3.291	2.57	172
W1	H(W1)	O(4) <i>a</i>	2.830	2.02	171
W1	H'(W1)	Br(1) <i>c</i>	3.342	2.62	162
W2	H(W2)	W1 <i>h</i>	2.766	1.87	177
W2	H'(W2)	Br(1) <i>d</i>	3.410	2.78	168
W3	H(W3)	Br(1) <i>e</i>	3.329	2.71	152
W3	H'(W3)	Br(2) <i>e</i>	3.274	2.55	170
W4	H(W4)	Br(2) <i>a</i>	3.319	2.57	166
W4	H'(W4)	Br(1) <i>a</i>	3.440	2.67	161
W5	H(W5)	O(1) <i>b</i>	3.009	2.37	168
W5	H'(W5)	Br(2) <i>i</i>	3.437	2.97	124

Summetry codes

<i>a</i>	<i>x</i>	<i>y</i>	<i>z</i>	<i>b</i>	$-x+1$	$-y$	$-z+1$	<i>c</i>	$x+1$	$y-1$	<i>z</i>
<i>d</i>	$-x+1$	$-y+1$	$-z$	<i>e</i>	$x+1$	<i>y</i>	<i>z</i>	<i>f</i>	$-x+1$	$-y$	$-z$
<i>g</i>	<i>x</i>	$y-1$	<i>z</i>	<i>h</i>	<i>x</i>	$y+1$	<i>z</i>	<i>i</i>	$-x+1$	$-y+1$	$-z+1$

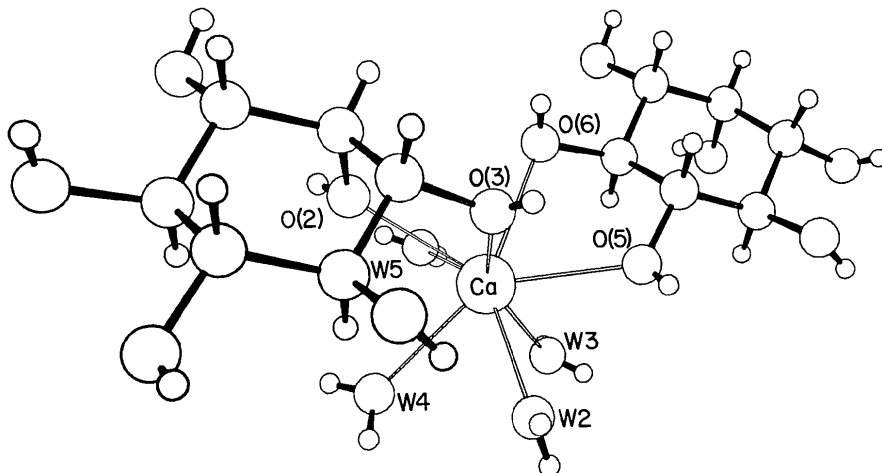


Fig. 3. Environment of the calcium ion.

1973; Cook & Bugg, 1973c), galactose (Bugg & Cook, 1972), trehalose (Cook & Bugg, 1973b), and fucose (Cook & Bugg, 1973b) the sugar moieties are chelated

to calcium ions through pairs of hydroxyl groups. Thus in the crystalline calcium complexes of sugars, it appears that pairs of adjacent hydroxyl groups can serve as effective calcium-chelation sites.

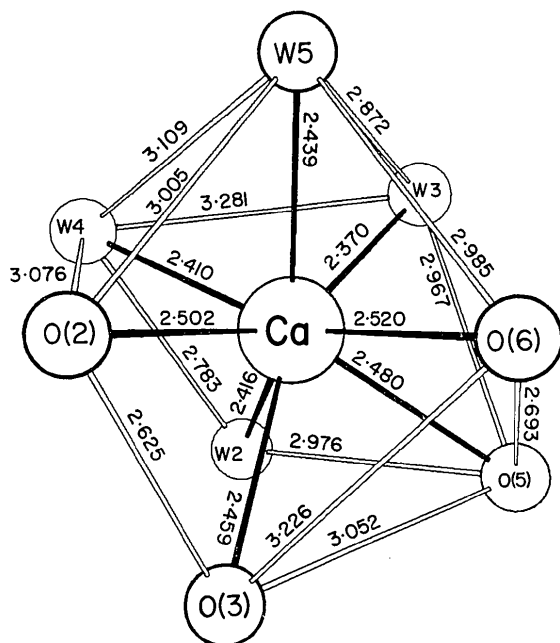


Fig. 4. Stereochemistry of the calcium-ion coordination shell. All oxygen-oxygen contacts shorter than 3.25 Å are shown, along with the calcium-oxygen distances. *W2*, *W3*, *W4*, and *W5* are oxygen atoms of water molecules. The estimated standard deviations are about 0.003 Å for Ca-O distances and about 0.004 Å for O-O contacts.

Conformation of the sugar

Fig. 5 shows the conformation, thermal ellipsoids, and bond lengths for myo-inositol. The sugar ring is in the expected chair conformation. Conformational and bond angles are listed in Tables 6 and 7 respectively.

The conformation of the myo-inositol molecule in the calcium complex can be compared with that in the crystal structures of myo-inositol dihydrate and myo-inositol (which contains two crystallographically independent myo-inositol molecules). Torsion angles and bond angles for these two other crystal structures are listed in Tables 6 and 7 respectively. The major differences between the myo-inositol molecule in the calcium complex and in the other crystal structures occur at the sites where calcium ions interact with the sugar. For most torsion angles involving the hydroxyl groups coordinated to calcium [atoms O(2), O(3), O(5) and O(6)] significant differences are evident between uncomplexed molecules and those in the calcium complex (Table 6). For example, the O(2)-C(2)-C(3)-O(3) and O(5)-C(5)-C(6)-O(6) torsion angles differ by about 9 and 15°, respectively, from the corresponding values of the uncomplexed molecules. Similarly, several of the bond angles (Table 7) at the calcium-binding sites are different from those in the crystal structures of myo-inositol and myo-inositol dihydrate. Concomitant with the changes in torsion and bond angles, the hydroxyl groups

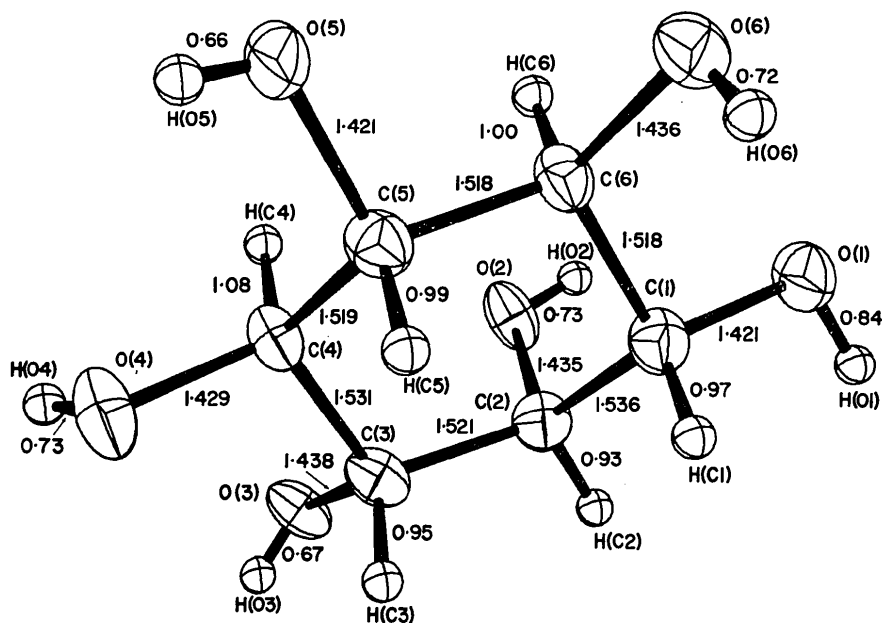


Fig. 5. Conformation and bond lengths of the myo-inositol molecule. Estimated standard deviations in bond lengths are about 0.004 Å for those bonds involving only nonhydrogen atoms and about 0.06 Å for those bonds involving hydrogen atoms. Non-hydrogen atoms are represented by thermal ellipsoids which are defined by the principal axes of thermal vibration and are scaled to include 50% probability. The hydrogen atoms are represented by spheres of 0.1 Å radius.

at both chelation sites are pulled closer together, resulting in O(2)-O(3) and O(5)-O(6) spacings that are about 0.2 Å shorter than in the crystal structures of myo-inositol and myo-inositol dihydrate.

The effects that calcium interactions exert on the conformation of myo-inositol are similar to those observed in other crystal structures of sugar-calcium complexes (Bugg & Cook, 1972). For example, if the

Table 6. *Conformational torsion angles involving nonhydrogen atoms of myo-inositol in the calcium complex and in the crystal structures of myo-inositol (which contains two crystallographically independent molecules designated as I and II), and of myo-inositol dihydrate*

Weighted-average values for myo-inositol I and II and myo-inositol dihydrate are listed in the fifth column. Those angles in the calcium complex that differ by more than 8° from the corresponding weighted-average values are denoted by an asterisk. Estimated standard deviations are about 0.3° in the calcium complex and in myo-inositol, 1-2° in myo-inositol dihydrate and 0.2° for the weighted-average values. Torsion angles are defined according to Klyne & Prelog (1960).

	Myo-inositol- CaBr ₂ ·5H ₂ O	Myo-inositol (I)	Myo-inositol (II)	Myo-inositol dihydrate	Weighted average
C(6)-C(1)-C(2)-C(3)	- 54.2°	- 59.8°	- 58.6°	- 57°	- 59.2°
C(6)-C(1)-C(2)-O(2)	64.9	61.6	60.8	62	61.2
O(1)-C(1)-C(2)-C(3)	-174.3*	176.4	175.9	-176	176.3
O(1)-C(1)-C(2)-O(2)	- 55.2*	- 62.2	- 64.7	- 58	- 63.3
C(1)-C(2)-C(3)-C(4)	50.6	58.3	56.4	59	57.4
C(1)-C(2)-C(3)-O(3)	170.1*	-175.2	-177.3	-179	-176.3
O(2)-C(2)-C(3)-C(4)	- 71.2	- 63.2	- 64.0	- 60	- 63.5
O(2)-C(2)-C(3)-O(3)	48.4*	63.4	62.4	62	62.9
C(2)-C(3)-C(4)-C(5)	- 51.6	- 56.2	- 53.9	- 60	- 55.1
C(2)-C(3)-C(4)-O(4)	-169.4	-176.9	-174.7	-176	-175.8
O(3)-C(3)-C(4)-C(5)	-170.7*	178.6	-179.5	179	179.5
O(3)-C(3)-C(4)-O(4)	71.5*	57.9	59.8	63	58.9
C(3)-C(4)-C(5)-C(6)	55.9	56.1	53.7	57	54.9
C(3)-C(4)-C(5)-O(5)	173.9	177.2	176.4	177	176.8
O(4)-C(4)-C(5)-C(6)	175.4	175.9	173.3	175	174.6
O(4)-C(4)-C(5)-O(5)	- 66.6	- 62.9	- 64.0	- 65	- 63.5
C(4)-C(5)-C(6)-C(1)	- 60.2	- 56.8	- 55.4	- 56	- 56.1
C(4)-C(5)-C(6)-O(6)	174.8*	-177.0	-175.1	-176	-176.0
O(5)-C(5)-C(6)-C(1)	178.5	-177.2	-177.5	-174	-177.3
O(5)-C(5)-C(6)-O(6)	53.5*	62.5	62.8	66	62.7
C(5)-C(6)-C(1)-C(2)	59.0	58.5	57.5	58	58.0
C(5)-C(6)-C(1)-O(1)	-179.7	-178.6	-177.0	179	-177.9
O(6)-C(6)-C(1)-C(2)	-177.8	179.8	178.1	176	178.9
O(6)-C(6)-C(1)-O(1)	- 56.5	- 57.3	- 56.4	- 63	- 57.0

Table 7. *Bond angles involving nonhydrogen atoms in the calcium complex and in the crystal structures of myo-inositol and myo-inositol dihydrate*

Weighted-average values for myo-inositol I and II and myo-inositol dihydrate are listed in the fifth column. Those angles in the calcium complex that differ by more than 3° from the corresponding weighted-average values are denoted by an asterisk. Estimated standard deviations are about 0.2° for the calcium complex and for myo-inositol (molecules I and II), 1-2° for inositol dihydrate, and 0.2° for the weighted-average values.

	Myo-inositol- CaBr ₂ ·5H ₂ O	Myo-inositol (I)	Myo-inositol (II)	Myo-inositol dihydrate	Weighted average
C(1)-C(2)-C(3)	111.6°	110.0°	109.4°	106°	109.6°
C(2)-C(3)-C(4)	112.9	110.1	111.9	115	111.1
C(3)-C(4)-C(5)	111.3	111.2	110.9	107	111.0
C(4)-C(5)-C(6)	110.6	111.6	113.4	110	112.5
C(5)-C(6)-C(1)	110.1	109.5	109.3	109	109.4
C(6)-C(1)-C(2)	110.7	109.9	111.3	115	110.7
O(1)-C(1)-C(2)	110.4	110.3	111.6	109	110.9
O(1)-C(1)-C(6)	108.4*	111.9	111.6	107	111.7
O(2)-C(2)-C(1)	111.2	110.1	110.2	111	110.2
O(2)-C(2)-C(3)	106.8	110.0	108.6	110	109.3
O(3)-C(3)-C(2)	107.7*	111.1	110.9	107	110.9
O(3)-C(3)-C(4)	108.4*	113.5	112.4	109	112.9
O(4)-C(4)-C(3)	109.5	108.3	108.1	110	108.2
O(4)-C(4)-C(5)	106.8*	109.8	110.1	107	109.9
O(5)-C(5)-C(4)	111.7	108.6	108.9	107	108.7
O(5)-C(5)-C(6)	106.1*	109.8	109.9	110	109.9
O(6)-C(6)-C(5)	109.8	110.7	110.3	107	110.4
O(6)-C(6)-C(1)	113.0*	109.0	108.9	110	109.0

lactose conformation in lactose-CaBr₂·7H₂O (Bugg, 1973) and lactose-CaCl₂·7H₂O (Cook & Bugg, 1973*b*, *c*) is compared with that in the crystal structure of lactose monohydrate (Fries, Rao & Sundaralingam, 1971), it is apparent that both the glucose and galactose moieties of lactose are distorted by calcium interactions; as in the crystal structure of the myo-inositol complex, calcium binding to adjacent hydroxyl groups results in a decrease of about 0.2 Å in the intramolecular spacing between the hydroxyl oxygen atoms. Similarly, conformations of the glucose moieties of the disaccharide, α,α-trehalose are noticeably different in the crystal structures of trehalose-CaBr₂·3H₂O complex (Cook & Bugg, 1973*b*) and trehalose dihydrate (Brown *et al.*, 1972), with the major differences occurring at calcium-binding sites. As in the crystal structure of the myo-inositol complex, calcium interactions induce subtle conformational distortions in lactose and trehalose with torsion-angle changes of 5–10° and bond-angle changes of 3–5°. It is not presently clear whether these distortions in individual sugars are sufficient to produce significant alterations in the overall conformations of oligo- and polysaccharides. In the calcium halide complexes of lactose and trehalose, the torsion angles about the bridge bonds between the sugar moieties deviate only slightly from those found for the uncomplexed disaccharides, and it is likely that the small differences are due simply to crystal-packing forces. However, more significant changes may be induced in oligosaccharides that are large enough to assume folded conformations in which calcium ions can form intramolecular cross-links between sugar residues. We are currently investigating this possibility.

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