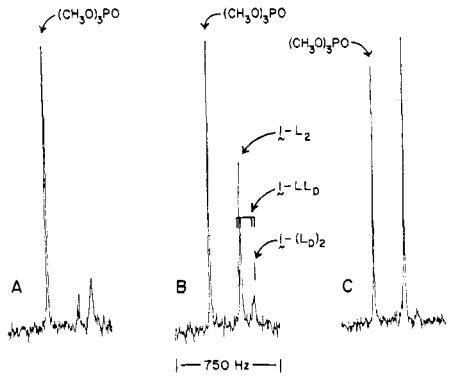


**Figure 7.** Representative $\{^1H\}$-$^{31}P$ NMR spectra used to follow the conversion of **1**-$[P(C_2D_5)_3]_2$ to **1**-$[P(C_2H_5)_3]_2$ by exchange with added triethylphosphine.

observed. Typical spectra are shown in Figure 7. When the appearance of $(C_2H_5)_3P$-Pt was observed, the first-order rate constants obtained for 200, 100, and 20 μL of added $(C_2H_5)_3P$ were 6.3, 8.3, and $1.2 \times 10^{-4}$ $s^{-1}$, respectively. For the exchange reaction with 10 μL of added $(C_2H_5)_3P$, the exchange was followed by observing the decrease of free $(C_2H_5)_3P$ and yields a first-order rate constant of $1.0 \times 10^{-4}$ $s^{-1}$. With the assumption that the exchange was first-order in $(C_2H_5)_3P$, the calculated second-order rate constants would be 0.4, 0.9, 5.6, and $9.1 \times 10^{-4}$ $M^{-1}$ $s^{-1}$.

**Photolyses of dineopentylmercury and 1** were carried out at ambient temperature by using cyclohexane as solvent. The progress of the photolysis of **1** was monitored by $^{31}P$ NMR spectroscopy. During the reaction, the resonance of **1** and free triethylphosphine disappeared and were replaced by a 1:4:1 triplet at $\delta$ +41 ($(Et_3P_3)Pt^0$, $J_{Pt-P}$ = 4226 Hz).

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**Supplementary Material Available:** Table IA of mass spectral data used in analyzing isotopic compositions (3 pages). Ordering information is given on any current masthead page.

# Complexation of Metal Ions by Monensin. Crystal and Molecular Structure of Hydrated and Anhydrous Crystal Forms of Sodium Monensin

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**Abstract:** The conformations of the sodium–monensin complex observed in anhydrous and dihydrate crystal forms are nearly identical with one another, with the previously reported $Ag^+$ complex, and with a complex with sodium bromide. The dihydrate crystallizes in the orthorhombic space group $P2_12_12_1$ ($a$ = 16.387 (4) Å, $b$ = 18.684 (4) Å, $c$ = 12.792 (3) Å, $Z$ = 4) and the anhydrous complex crystallizes in the monoclinic space group $P2_1$ ($a$ = 9.218 (5) Å, $b$ = 12.702 (1) Å, $c$ = 16.274 (7) Å, $\beta$ = 101.02 (1)°, $Z$ = 2). The conformations of all of the metal complexes differ from that of the free acid in the carboxylic acid conformation, the heat-to-tail hydrogen bonding, and the conformation of one of the five-membered rings. Although individual torsion angle differences between uncomplexed and complexed monensin seldom exceed 15°, the positions of three of the coordinating oxygens are shifted by 1.0, 1.9, and 2.1 Å relative to the oxygens in the invariant part of the molecule. A comparison of the complexed and uncomplexed structures suggests that complexation could easily be initiated by association of a metal ion with an ether oxygen, O(7), which is near the surface of the free acid. Two other oxygen atoms, O(6) and O(4), in the invariant part of the molecule are then positioned to displace additional water of hydration from the ion. No change in the monesin conformation is necessary during this step, but a minor rearrangement of the intramolecular hydrogen bonds must take place. This rearrangement initiates a change in head-to-tail hydrogen bonding and the repositioning of the O(8), O(9), and O(11) atoms so that the remaining solvent is displaced from the metal ion completing the coordination. If the ability of monensin to complex metal ions is in part attributable to the flexibility of the five-membered C ring it may be possible to modify monensin by methyl substitutions on this ring, stabilizing a particular conformation.

Ionophores are natural or synthetic compounds that facilitate transport of ions across membranes. Comparison of the crystal structures of complexed and uncomplexed ionophores provides information concerning the flexibility of these molecules and the coordination of the complex ions. These data may provide an explanation for the ion specificity of a particular compound and the mechanism of ion capture and release.[1]

Monensin (Figure 1) is a monocarboxylic acid that has specificity for $Na^+$ ions.[2] The crystal structures of the silver monensin complex[3] revealed that the molecule adopts a cyclic conformation with the carboxylic oxygens [O(1) and O(2)] on one end hydrogen bonded to the hydroxyls at the other end [O(10) and O(11)]. The molecule surrounds the silver ion and provides it with irregular sixfold coordination. The crystal structure of the hydrated free acid of monensin also possesses head-to-tail hydrogen bonding, but two different hydrogen bonds link the ends of the molecule together [O(2) → O(11) and O(10) → O(4)].[4] Steinrauf has noted that the substituents on carbon atoms C(3) and C(4) are

(1) G. D. Smith and W. L. Duax, *J. Am. Chem. Soc.*, **98**, 1578 (1976).
(2) B. C. Pressman and D. H. Haynes, "The Molecular Basis of Membrane Function", Prentice-Hall, Englewood Cliffs, N.J., 1969, p 221.
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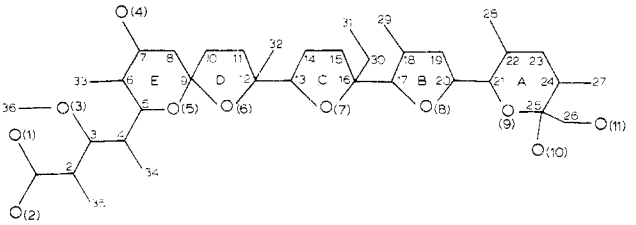

**Figure 1.** Chemical structure, numbering scheme, and ring identification for monensin.

significantly rotated (26°) from the more probable staggered conformation when the molecule exists as a complex, and furthermore, if this bond is rotated to bring these substituents into the staggered position, the associated hydrogen bond shifts would be consistent with a transition to the uncomplexed form.[5] The crystal structure of the sodium bromide complex of monensin[6] showed that its conformation is quite similar to that of the conformation of the $Na^+$ and $Ag^+$ salts despite the fact that the former compound is anhydrous while the latter is a dihydrate. The crystal structures of the anhydrous and of the dihydrated sodium salts reported here provide additional data on the flexibility of the monensin molecule and illustrate the differences between the geometries of the charged and uncharged $Na^+$ complex and also the differences between the solvated and unsolvated forms.

## Experimental Section

Single crystals of the dihydrate of the sodium complex of monensin $C_{36}H_{61}O_{11}Na\cdot 2H_2O$ were grown from an ethanol–water solution and are nearly isomorphous with the $P2_12_12_1$ silver ion complex ($a$ = 16.387 (4) Å, $b$ = 18.684 (4) Å, and $c$ = 12.792 (3) Å, $Z$ = 4, $\rho_c$ = 1.23 g/cm$^{-3}$). A single crystal (0.08 × 0.28 × 0.40 mm) was mounted and a total of 3697 independent data (sin $\theta_{max}/\lambda$ = 0.587) were collected on an Enraf-Nonius CAD-4 diffractometer, using nickel-filtered copper radiation. Intensities were corrected for Lorentz and polarization factors but not for extinction or absorption ($\mu$(Cu K$\alpha$) = 8.648 cm$^{-1}$). On the basis of the $2\sigma(I)$ test, 2067 data were considered observed. The variance of each $F$ was calculated according to the method of Stout and Jensen[7] [$\sigma^2(F) = k/4(Lp)$ [$\sigma^2(I) = (0.06I)^2$]; $w(F) = 1/\sigma^2(F)$]. Unobserved data were given zero weight.

The starting coordinates were those reported for the silver ion complex of monensin.[3] The structure was refined by full-matrix least-squares, treating all atoms anisotropically. Hydrogen atom contributions were included for the final two cycles of least-squares by calculating their positional parameters at the end of each cycle; the refinement converged to a residual of 0.067 for the observed data and 0.142 for all data. A final difference map based on heavy-atom contributions alone failed to reveal the positions of the hydrogen atoms bound to oxygen although many of the remaining hydrogen atoms could be located. The ethyl group attached to C(16) was found to be disordered as was observed in the silver ion complex.

Single crystals of an anhydrous sodium complex of monensin $C_{36}H_{61}O_{11}Na$ were grown from diethyl ether; no attempt was made to exclude water vapor from the crystallizing media. The crystals are monoclinic, space group $P2_1$ ($a$ = 9.218 (5) Å, $b$ = 12.702 (1) Å, $c$ = 16.274 (7) Å, $\beta$ = 101.02 (1)°, $Z$ = 2, $\rho_c$ = 1.230 g/cm$^3$). With use of a needle-shaped crystal (0.1 × 0.1 × 0.8 mm), a total of 4016 indepennet data (3672 with $I > 2\sigma_I$) were collected as described above. The intensities were reduced to structure factor amplitudes, and phase angles sufficient for location of the nonhydrogen atoms were derived by using the direct methods program QTAN.[8] Electron density peaks corresponding to 54 of the 61 hydrogen atoms were found from difference electron density maps. The other hydrogens were placed in geometrically expected positions. The hydrogen atoms were included in structure factor calculations with isotropic thermal parameters of 5.0 but were not refined. The refinement converged to a residual of 0.044 for the observed data and 0.048 for all data. Although the ethyl group attached to C(16) appeared to be ordered in the structure, it is noteworthy that it has relatively high thermal motion and the terminal C–C bond is anomalously short.

(5) L. K. Steinrauf and M. N. Sabesan, "Metal-Ligand Interactions in Organic Chemistry and Biochemistry", Pullman and Goldblum, Eds., D. Reidel Publishing Co., Boston, Mass. 1977, p 43.

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(8) D. A. Langs and G. T. DeTitta, *Acta Crystallogr., Sect. A*. **A31**, S16 (1975).

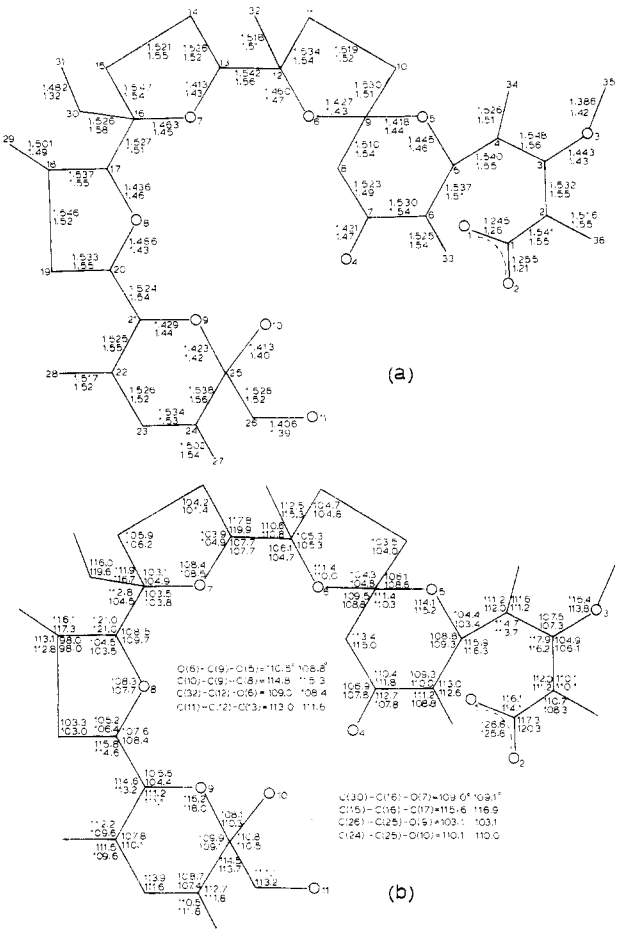

**Figure 2.** (a) Bond lengths and (b) valence angles for anhydrous (above) and dihydrate crystal forms of the sodium complex of monensin.

**Table I.** Carbon-Carbon Distances (Å) in Monensin Molecules in Five Crystal Forms[a]

| | C(sp$^3$)–C(sp$^3$) | |
|---|---|---|
| cryst form | range | av |
| anhydrous $Na^+$ complex | 1.504→1.549 | 1.529 (11) |
| dihydrate $Na^+$ complex | 1.486→1.561 | 1.522 (18) |
| NaBr complex | 1.490→1.584 | 1.532 (21) |
| hydrated free acid | 1.493→1.558 | 1.524 (14) |
| dihydrate $Ag^+$ complex | 1.477→1.619 | 1.537 (34) |

[a] Numbers in parentheses are standard deviations.

## Results

The bond lengths and valence angles for the two monensin molecules are compared in Figure 2. The ranges and average values of the 30 sp$^3$–sp$^3$ carbon bonds in all five monensin structures are compared in Table I. The C(30)–C(31) distance was omitted from this average due to disorder present in most structures. These averages are shorter than the expected value of 1.54 Å in all structures except the silver complex. Although some of the bonds may be foreshortened due to thermal motion, the consistently short averages suggest electronic balance in the molecule favoring such short bonds. Although differences are small and not significant, both sodium complexes have shorter averages, 1.529 and 1.522, than the sodium bromide salt, 1.532.

The torsion angles of the monensin molecules in the anhydrous and dihydrate sodium complexes and the free-acid crystal form are given in Table II. The deviation of the individual backbone torsion angles of the metal complexes of monensin from those of the free acid (Table II) is illustrated in Figure 3a; the deviation of the ring torsion angles from those of the free acid is illustrated

**Table II**

| | atoms | anhydrous | dihydrate | free acid |
|---|---|---|---|---|
| (a) Backbone Torsion Angles $\tau$ (Deg) for the Anhydrous and the Hydrated Forms of the Sodium-Monensin Complex and for the Free-Acid Form[a] | | | | |
| 1 | O(1)-C(1)-C(2)-C(3) | −107.0 (3) | −122.1 (8) | −110.7 |
| 2 | O(2)-C(1)-C(2)-C(3) | 72.6 (3) | 59.7 (10) | 69.2 |
| 3 | C(1)-C(2)-C(3)-C(4) | 54.1 (3) | 62.5 (9) | 57.5 |
| 4 | C(2)-C(3)-C(4)-C(5) | −77.2 (2) | −82.0 (8) | −75.8 |
| 5 | C(3)-C(4)-C(5)-O(5) | −171.8 (2) | −176.9 (6) | −176.2 |
| 6 | C(4)-C(5)-O(5)-C(9) | −173.0 (2) | −173.6 (6) | −170.5 |
| 7 | C(5)-O(5)-C(9)-O(6) | 64.7 (2) | 64.9 (7) | 59.0 |
| 8 | O(5)-C(9)-O(6)-C(12) | 89.3 (2) | 88.3 (7) | 92.1 |
| 9 | C(9)-O(6)-C(12)-C(13) | 125.8 (2) | 128.1 (7) | 122.3 |
| 10 | O(6)-C(12)-C(13)-O(7) | 60.3 (2) | 63.1 (8) | 56.8 |
| 11 | C(12)-C(13)-O(7)-C(16) | −165.5 (2) | −167.0 (7) | −161.7 |
| 12 | C(13)-O(7)-C(16)-C(17) | 153.7 (2) | 147.4 (7) | 138.3 |
| 13 | O(7)-C(16)-C(17)-O(8) | −69.0 (2) | −69.2 (8) | −68.7 |
| 14 | C(16)-C(17)-O(8)-C(20) | −162.1 (2) | −163.9 (7) | −156.2 |
| 15 | C(17)-O(8)-C(20)-C(21) | −119.0 (2) | 116.4 (7) | −124.1 |
| 16 | O(8)-C(20)-C(21)-O(9) | 50.9 (2) | 50.8 (8) | 64.0 |
| 17 | C(20)-C(21)-O(9)-C(25) | −175.1 (2) | 175.3 (6) | 176.5 |
| 18 | C(21)-O(9)-C(25)-C(26) | 178.6 (2) | 180.0 (6) | 176.0 |
| 19 | O(9)-C(25)-C(26)-O(11) | −58.3 (3) | −54.2 (8) | −65.4 |
| (b) Intraring Torsion Angles $\tau$ (Deg) for the Anhydrous and the Hydrated Forms of the Sodium-Monensin Complex and for the Free-Acid Form[b] | | | | |
| 1 | O(5)-C(5)-C(6)-C(7) | −59.3 (2) | −57.8 (8) | −57.8 |
| 2 | C(5)-C(6)-C(7)-C(8) | 53.1 (3) | 51.5 (9) | 51.1 |
| 3 | C(6)-C(7)-C(8)-C(9) | −48.6 (3) | −46.0 (10) | −49.0 |
| 4 | C(7)-C(8)-C(9)-O(5) | 49.4 (3) | 46.0 (10) | 50.8 |
| 5 | C(8)-C(9)-O(5)-C(5) | −57.2 (2) | −54.3 (8) | −59.6 |
| 6 | C(9)-O(5)-C(5)-C(6) | 62.7 (2) | 62.0 (8) | 64.0 |
| 7 | O(6)-C(9)-C(10)-C(11) | 32.8 (3) | 33.7 (9) | 32.4 |
| 8 | C(9)-C(10)-C(11)-C(12) | −29.2 (3) | −27.2 (9) | −29.8 |
| 9 | C(10)-C(11)-C(12)-O(6) | 15.3 (3) | 11.1 (9) | 16.7 |
| 10 | C(11)-C(12)-O(6)-C(9) | 5.8 (2) | 10.3 (8) | 3.9 |
| 11 | C(12)-O(6)-C(9)-C(10) | −24.3 (2) | −27.7 (8) | −22.8 |
| 12 | O(7)-C(13)-C(14)-C(15) | 29.5 (3) | 34.9 (9) | 39.6 |
| 13 | C(13)-C(14)-C(15)-C(16) | −9.7 (3) | −20.1 (9) | −29.2 |
| 14 | C(14)-C(15)-C(16)-O(7) | −12.6 (3) | −1.1 (9) | 8.8 |
| 15 | C(15)-C(16)-O(7)-C(13) | 33.0 (3) | 24.2 (9) | 17.0 |
| 16 | C(16)-O(7)-C(13)-C(14) | −39.8 (3) | −38.2 (9) | −35.6 |
| 17 | O(8)-C(17)-C(18)-C(19) | 44.2 (2) | 45.1 (8) | 40.8 |
| 18 | C(17)-C(19)-C(19)-C(20) | −40.2 (2) | −39.7 (8) | −39.0 |
| 19 | C(18)-C(19)-C(20)-O(8) | 23.3 (2) | 21.9 (9) | 24.8 |
| 20 | C(19)-C(20)-O(8)-C(17) | 5.0 (2) | 7.3 (8) | 1.5 |
| 21 | C(20)-O(8)-C(17)-C(18) | −31.8 (2) | −33.4 (8) | −26.9 |
| 22 | O(9)-C(21)-C(22)-C(23) | −53.4 (3) | −48.4 (9) | −47.2 |
| 23 | C(21)-C(22)-C(23)-C(24) | 53.3 (4) | 54.7 (9) | 50.6 |
| 24 | C(22)-C(23)-C(24)-C(25) | −53.5 (4) | −59.1 (9) | −56.8 |
| 25 | C(23)-C(24)-C(25)-O(9) | 52.8 (3) | 58.0 (8) | 60.9 |
| 26 | C(24)-C(25)-O(9)-C(21) | −59.0 (3) | −58.1 (8) | −63.2 |
| 27 | C(25)-O(9)-C(21)-C(22) | 59.9 (3) | 53.0 (8) | 55.5 |

[a] Numbers in the left-hand column correspond to torsion angle designations in Figure 3a. [b] Numbers in the left-hand column corresponds to torsion angle designations in figure 3b.

in Figure 3b. With the exception of the positioning of the carboxylic acid group in the anhydrous sodium complex, the conformations of all of the complexed molecules differ from the free acid in a nearly identical fashion. The most dramatic differences between the complexed and free-acid conformations are in the A rings, the C rings, the carboxylic acid conformations, and the conformation about the C(16)–O(7), C(20)–C(21), and C(25–C(26) bonds.

The A rings in all five molecules have distorted chair conformations but differ in the nature and the degree of the distortion. The sodium bromide complex differs from the other three ion complexes in the conformation of the A ring. This is probably due to a difference in hydrogen bonding to the O(10) hydroxyl (see below). The five-membered C rings have a greater variation of conformation due to the potential for pseudorotation. The C ring has a C(13)-O(7) half-chair conformation in the anhydrous

**Table III.** Sodium Ion Coordination in (a) the Hydrated and (b) Anhydrous Crystal Forms

| | dist, Å | | angle, deg a | angle, deg b |
|---|---|---|---|---|
| O(4)-Na | (a) 2.336 (7) | -O(6) | 76.5 (3) | 73.9 |
| | (b) 2.346 (2) | -O(7) | 139.1 (3) | 134.1 |
| | | -O(8) | 106.8 (3) | 106.4 |
| | | -O(9) | 98.3 (3) | 101.2 |
| | | -O(11) | 114.0 (3) | 114.8 |
| O(6)-Na | (a) 2.358 (6) | -O(7) | 69.0 (3) | 67.6 |
| | (b) 2.411 (2) | -O(8) | 112.9 (3) | 113.7 |
| | | -O(9) | 173.8 (3) | 174.4 |
| | | -O(11) | 118.6 (3) | 117.4 |
| O(7)-Na | (a) 2.543 (7) | -O(8) | 69.2 (3) | 69.3 |
| | (b) 2.529 (2) | -O(9) | 114.4 (3) | 115.6 |
| | | -O(11) | 101.6 (3) | 104.7 |
| O(8)-Na | (a) 2.443 (7) | -O(9) | 65.1 (3) | 64.8 |
| | (b) 2.408 (2) | -O(11) | 119.5 (3) | 120.7 |
| O(9)-Na | (a) 2.447 (6) | -O(11) | 66.5 (3) | 66.9 |
| | (b) 2.513 (2) | | | |
| O(11)-Na | (a) 2.449 (7) | | | |
| | (b) 2.381 (2) | | | |

**Table IV.** Oxygen-Oxygen Contacts (Å) of Less Than 3.0 Å

| | | | |
|---|---|---|---|
| (a) Hydrated Sodium Complex | | | |
| O(1)-O(11) | 2.51 | O(3)-O(1w) | 2.95 |
| O(2)-O(10) | 2.64 | O(4)-O(2w) | 2.86 |
| O(4)-O(10) | 2.96 | O(11)-O(1w) | 2.85 |
| O(4)-O(6) | 2.92 | O(10)-O(2w) | 2.87 |
| O(10)-O(11) | 2.90 | O(1w)-O(2w) | 2.83 |
| (b) Anhydrous Sodium Complex | | | |
| O(1)-O(11) | 2.58 | O(4)-O(6) | 2.86 |
| O(2)-O(10) | 2.62 | O(10)-O(11) | 2.83 |
| O(4)-O(10) | 2.74 | | |

sodium complex, a C(13) envelope conformation in the sodium hydrate complex, and a conformation midway between a C(13) envelope and a C(13)–C(14) half-chair in the free acid. The O(8)–C(20)–C(21)–O(9) torsion angle is near the expected value in the free-acid form (64.0°) but is as small as 45.8° in one of the complexes. It is conceivable that coordination reduces the repulsive interaction between O(8) and O(9), thus permitting this reduction.

The sodium ion has severely distorted octahedral coordination (Figure 4). The coordination is nearly identical in the solvated and anhydrous forms of the sodium complexes (Table III). Although solvent interaction from O(4), O(10), and O(11) is correlated with minor adjustments in the coordination, the average Na–O distances remain the same, 2.43 (7) Å. The oxygen–oxygen contacts shorter than 3.0 Å are compared in Table IV. Although some hydrogen positions could not be located, the hydrogen bonding in the anhydrous form appears to be unambigous. The carbonyl oxygens accept hydrogen bonds from hydroxy oxygen O(10) and O(11), and hydroxy O(4) donates a hydrogen bond to O(10). The intramolecular hydrogen bonds between both oxygens of the carboxyl group and the two hydroxy groups at the other end of the molecule that produce a pseudocyclic conformation are also present in the hydrated sodium and silver complexes. The large conformational changes in the free-acid hydrate are accompanied by changes in hydrogen bonding. The O(4) hydroxyl appears to act as an intramolecular hydrogen bond acceptor from O(10) and donor to O(6). In the sodium bromide complex there is a change in hydrogen bonding with only a small change in conformation. Since O(2) is a hydroxyl in the acid, it is the donor in the hydrogen bond to O(10). The O(10) donates a hydrogen bond to the bromide ion which occupies a position analogous to that filled by one of the water molecules in the hydrated sodium complex. All intermolecular hydrogen bonds involving water are considerably longer than the intramolecular bonds. In addition to a hydrogen bond between the two independent molecules, each water molecule is involved in two hydrogen bonds to the ionophore.

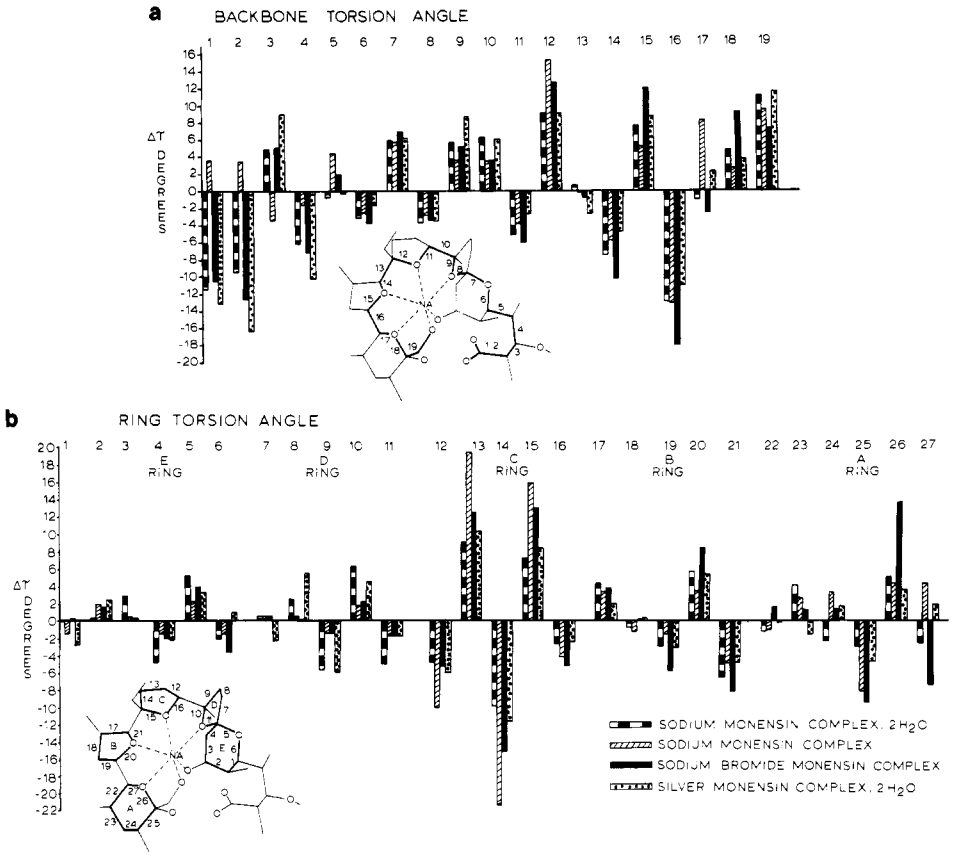


**Figure 3.** (a) The differences in the backbone torsion angles of metal ion complexes of monensin from those of the free acid. (b) The differences in intraring torsion angles of metal complexes of monensin from those of the free acid. $\Delta\tau = \tau$(complexed) $- \tau$(free acid).

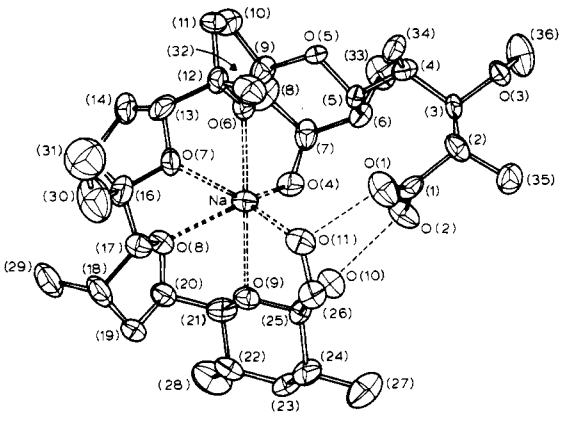


**Figure 4.** ORTEP drawing of the monensin sodium complex in the hydrated crystals illustrating head to tail hydrogen bonding and sixfold coordination of the sodium ion.

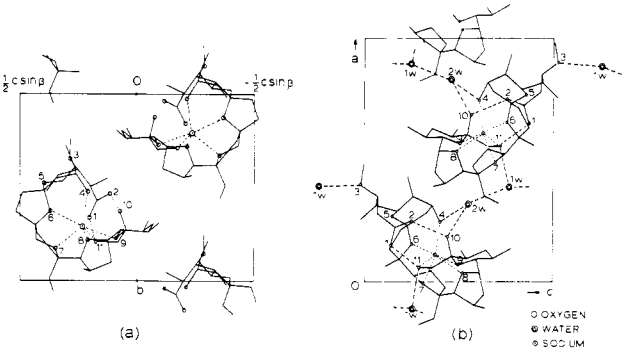


**Figure 5.** (a) Packing of sodium–monensin complexes in anhydrous crystals viewed along the 9.2-Å $a$ axis. (b) Packing and hydrogen bonding in a single monensin water layer viewed along the 18.7-Å $b$ axis. A second layer related by the screw axis parallel to $b$ accounts for the doubling of the cell side.

The crystal packing of the anhydrous and hydrated sodium complexes are compared in Figure 5. In the dihydrate a water–ionophore layer is perpendicular to the $y$ axis. Adjacent layers are related by the screw axis parallel to $y$, and there are no hydrogen bonds between layers. In the anhydrous form the arrangement of monensin molecules in the layers is only slightly altered, the $b$ cell side is halved and adjacent "layers" are related by translation.

## Discussion

Although hydrogen-bonded solvent and crystal-packing forces in the free-acid form may distort the conformation from the minimum energy position for the isolated molecule, the distortion is certainly less than that imposed by ion coordination. This is particularly well illustrated by the sodium bromide–monensin complex in which the ionophore exists as a free acid but adopts the conformation observed for the anionic forms of monensin. Consequently most of the differences between the complexed and free-acid conformations are probably related to a rearrangement required to accomodate the ion and successfully coordinate it. The B, D, and E rings are seen to be the least flexible portions of the molecules and the least affected by complex formation. The spiro junction between the D and E rings is a major factor restricting their flexibility, and the methyl substituent at C(18) stabilizes the C(18) envelope conformation of the B ring. The conformations of monensin in the free-acid form and the anhydrous sodium complex are compared in Figure 6 by performing a least-squares fit of the conformationally similar portion of the molecules, atoms C(4) → C(13), O(4), O(5), and O(6) that make up the spiro-fused ring and adjacent atoms. It is interesting to note that while the magnitudes of the differences in the individual torsion angles are comparable on either side of this reference fragment (i.e., the acid end and the A-ring end), the net effects upon the ends are quite dissimilar. The magnitudes of the shifts of atoms O(1), O(2), O(8), O(9), and O(11) in going from the uncomplexed to the complexed form are 0.4, 0.3, 1.0, 1.9, and 2.1 Å, respectively. The

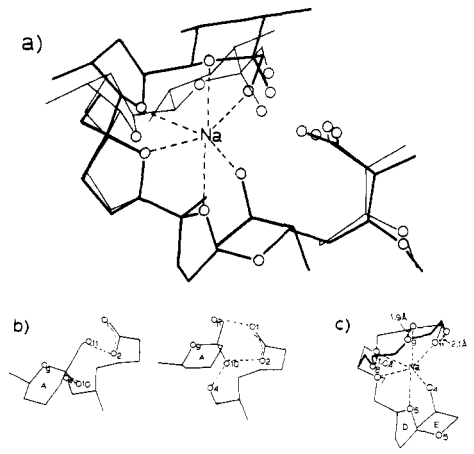


**Figure 6.** (a) A comparison of the conformations of the monensin molecules as the free acid (light line) and the anhydrous sodium complex (this comparison was made by making a least-squares fit of the least flexible portion of the molecule [atoms C(4) to C(13) and O(4) to O(6)]). (b) Differences in head-to-tail hydrogen bonding. (c) Differences in positions of oxygens of coordination.

changes in the O(1) to C(4) region internally compensate to leave the acid group little changed in relation to the reference fragment. The change in the C(13) to C(22) region on the other hand produces a concerted movement of oxygens O(8), O(9), and O(11) to bring them in position to coordinate incoming ions.

Complexation is almost certainly a process of sequential exchange of water of hydration for coordination to the oxygens of monensin. In the free acid the O(7) atom of the C ring is solvated, demonstrating it to be one of the most accessible of the coordinating oxygens. Complexation could easily be initiated by association of a metal ion with O(7). Two other oxygens, O(6) and O(4), in the invariant position of the molecule, are positioned to displace additional water of hydration and induce a rearrangement in the hydrogen bonding, namely, the disruption of the hydrogen bond between O(6) and O(4) followed by the reversal of the donor–acceptor relationship in the O(4)–O(10) intramolecular hydrogen bond. This displacement of three solvent molecules by three coordinating oxygens requires no appreciable change in the conformation of monensin. In the transformation of the free acid to the complexed form, O(2) loses its acidic proton and accepts a hydrogen bond from O(10) while O(11) becomes a hydrogen bond donor to O(1). The disruption of the O(4)–O(6) hydrogen-bonding scheme appears to be the driving force for this rearrangement in head-to-tail hydrogen bonding. At the same time, small torsion angle changes permit O(8), O(9), and O(11) to move the 1–2 Å which is necessary to displace the remaining solvent from the metal ion and to complete the coordination.

The conformational change in the C ring and in the C(13)–O(7)–C(16)–C(17) torsion angle is the hinge upon which the molecular rearrangement turns. The flexibility of the C ring could be restricted by methyl substitution at C(14) or C(15). If the ability of monensin to complex metal ions is in part attributable to the flexibility of this ring, it may be possible to modify monensin's activity by such substitutions.

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**Supplementary Material Available:** Tables of bond distances, bond angles, structure factors, atomic coordinates, and thermal parameters (38 pages). Ordering information is given on any current masthead page.

# Imidazolate Complexes of Iron and Manganese Tetraphenylporphyrins

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**Abstract:** The possible importance of partially or completely deprotonated imidazole ligation in the hemoproteins has led us to investigate imidazolate, $Im^-$, complexes of iron(II,III) and manganese(II,III) *meso*-tetraphenylporphyrin (TPP). Tetrabutylammonium imidazolate is a convenient reagent for the synthesis of isolable complexes. By steric and stoichiometric control the stereochemistry can be manipulated to give complexes with most possible coordination numbers and spin states. $[Mn(Im)_2(TPP)]^-$ is the first example of a low-spin Mn(III) porphyrin complex and demonstrates the greater ligand field strength of imidazolate over imidazole. The X-ray crystal structure of the polymer $[Mn(Im)(TPP)]_n$ is reported. It shows layers of parallel chains with alternate layers having their quasi-linear chains approximately orthogonal to each other. There is a short–short/long–long alternation of Mn–N(Im) bond lengths (2.186 (5) and 2.280 (4) Å) interpreted as reflecting alternating predominantly low- and high-spin Mn(III) atoms along the polymeric chain. The average Mn–N(porph) bond distance is 2.019 (4) Å. Crystal data: $a$ = 20.073 (3) Å, $b$ = 16.885 (3) Å, $c$ = 22.590 (5) Å, $\beta$ = 104.36 (2)°, space group $C2/c$, $Z$ = 8 (Mn(Im)(TPP) units).

## Introduction

The ubiquity of "neutral" imidazole ligation to iron by histidine residues in the hemoproteins has led to speculation that partially or completely deprotonated imidazole ligation may also be important.[3-10] Imidazolate ($Im^-$)[11] arises from complete deprotonation whereas hydrogen bonding of the N–H proton to bases

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