Models for the Methylmercury–Protein Interaction: a Comparison of the Molecular Structures of Methyl-L-cysteinatomercury(II) and Methyl-DL-methioninemercury(II)

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Summary X-ray crystal structure determinations have shown that the essential amino-acid L-cysteine is bound to methylmercury(II) via a deprotonated sulphydryl group, whereas methionine is co-ordinated via an amino group in their respective 1:1 complexes.

COMPLEXES with amino-acids and peptides have been extensively utilised as models for the interaction of metal ions with protein and enzyme molecules. In this context the binding of heavy-metal ion pollutants such as Cd^{2+} , Hg^{2+} , and RHg^+ , which pose environmental hazards has assumed significance. We describe a comparison of the molecular structures of methylmercury(II) complexes of the essential amino-acids L-cysteine and DL-methionine as determined by X-ray diffraction. The cysteine complex has been directly implicated in poisoning by methylmercury-(II) and in metabolic processes leading to the synthesis of methylmercurythiomethyl in shellfish.¹ Although the essential features of methionine metabolism are established,² the rôle of methionine residues in complexing organomercury(II) poisons is currently unclear.

The L-cysteine complex $MeHgSCH_2CH(N+H_3)CO_2^{-}, H_2O$ (I) was obtained from the reaction of MeHgOH with L-cysteine in aqueous ethanol.

Crystal data: $HgC_4H_9NO_2S,H_2O$, orthorhombic crystals, space group $P2_12_12_1$, a = 6.386(6), b = 26.026(13), c = 5.282(4) Å, Z = 4, $D_c = 2.676$, $D_m = 2.65$ g cm⁻³. Crystals of the methionine complex MeHgMeS(CH₂)₂CH(NH₂)CO₂-(II) from aqueous ethanol are monoclinic, space group $P2_1/c$, a = 7.048(9), b = 5.826(4), c = 25.320(5) Å, $\beta = 93.15$ (21)°, Z = 4, $D_c = 2.34$, $D_m = 2.38$ g cm⁻³. The structures were solved by the heavy-atom method using 980 and 1027 observed reflections for (I) and (II) respectively measured on a GEXRD6 automatic diffractometer. Refinement by least-squares methods proceeded to R values of 0.065 for (I) and 0.099 for (II). ORTEP plots of the structures are shown in the Figure.

The principal structural features of (I) are the co-ordination of the amino-acid in the zwitterionic form $-SCH_2CH_2(N^+H_3)CO_2^-$ to MeHg⁺ via a deprotonated sulphydryl group such that an almost linear C-Hg-S unit is formed. Both Hg–C(4) [2·09(4) Å] and Hg–S [2·352(12) Å] distances are normal for 2-co-ordinate Hg^{II}. However, a scan of intra- and inter-molecular contacts (≤ 3.5 Å) revealed a weak intramolecular Hg–O(2) bond to a carboxylate oxygen





atom. The Hg-O(2) distance $[2\cdot84(2) \text{ Å}]$ is comparable to a value of $2\cdot88 \text{ Å}$ in *cis*- β -benzoylvinylmercuric chloride³ and is shorter than the sums of van der Waals radii for mercury and oxygen (*ca.* $3\cdot0 \text{ Å}$).⁴ By contrast, in (II) the amino-acid is bound to MeHg⁺ via the amino group with an Hg–N bond length of $2 \cdot 06(4)$ Å similar to the Hg–N distance of $2 \cdot 10$ Å in H₂NHgCl.⁵ That the mercury–nitrogen interaction in (II) is strong is evident from a comparison with the Hg–N bond lengths (av. $2 \cdot 61$ Å) in Cl₃CHgCl,C₁₂H₈N₂.⁶ Apparently, free amino groups can interact strongly with the charged CH₃Hg⁺ ion despite predictions to the contrary.¹ It is also noteworthy that the thioether group is not involved in complexation. Recent n.m.r. studies for Hg^{II}–methionine complexes in acidic aqueous solution have been interpreted in terms of mercury(II) thio ether binding.⁷ Although the C(1)-Hg-N angle is 173(2)°, the presence of two additional weak Hg-O (carboxylate) bonds is shown by the intramolecular Hg-O(1) distance of 2.67(3) Å and an intermolecular Hg-O(2) contact of 2.72(3) Å. These contacts presumably reflect ionic interactions resulting from the zwitterionic nature $[CH_3-Hg^+-NH_2CH(CO_2^-)CH_2CH_2SCH_3]$ of the complex.

We are grateful to the Department of the Environment, Inland Waters Directorate, for financial support of this work.

(Received, 6th June 1974; Com. 653.)

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