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Imidazole–Trimethyl Phosphate System: Characterization of the Hydrogen Bonding by Fast-Atom-Bombardment Mass Spectrometry and X-ray Crystallography

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The hydrogen-bonding properties of imidazole and its derivatives are of considerable importance in biochemistry. Of special interest is the ability of imidazole to form strong, easily polarizable hydrogen bonds as this may play an important role in a number of biochemical functions including proton conductivity in membranes[1] and protein oxygen binding.[2] An apparently simple example of a strong, easily polarizable hydrogen bond to imidazole has recently been reported to occur in the imidazole–trimethyl phosphate system.[3,4] Infrared and multinuclear NMR spectroscopy revealed the presence of the hydrogen bond and several other features of interest in the system but gave little information on the structure of the complex formed. We now wish to report the first use of fast-atom-bombardment mass spectrometry (FAB MS) as a means of characterizing a complex containing a strong hydrogen bond. The structure of the complex has been independently confirmed by conventional X-ray crystallography.

Table I. Positive Ion FAB MS of the Complex in Glycerol[a]

m/z	rel intensity	assignment[b]	*m/z*	rel intensity	assignment[b]
69	100	$(I + H)^+$	195	17.60	$(IP + H)^+$
109	1.01	$(P - OH)^+$	263	2.40	$(IP + I + H)^+$
127	6.24	$(P + H)^+$	321	2.43	$(IP + P + H)$
137	3.21	$(I_2 + H)^+$	390	0.55	$(IP + H_2)^+$

[a] The sample was inserted on a stainless steel probe tip into the mass spectrometer (a kratos MS-30 with a DS-55 data system) and sputtered into the gas phase as ions by bombardment with 6 keV neutral xenon atoms. [b] I = imidazole; P = $(MeO)_2PO_2H$; IP = complex.

Ordinary electron-impact mass spectrometry (EI MS) of the crystals isolated from an equimolar mixture of imidazole and trimethyl phosphate gave the highest mass peak at *m/z* 126 followed by peaks characteristic of the fragmentation of imidazole and the phosphate. Such an experiment requires thermal volatilization of the complex and subjects it to bombardment with electrons, the combination of which effectively precludes the use of EI MS for the analysis of hydrogen bonding. In an attempt to overcome this problem we have used FAB MS, which as a soft ionization technique that does not require sample heating may allow the direct observation of hydrogen-bonded species.

The FAB MS of the crystalline complex dissolved in glycerol shows the three most intense peaks occurring at *m/z* 69, 127, and 195. Significant higher mass peaks at *m/z* 263, 321, and 390 were also observed in a remarkably clear spectrum. It is interesting to note that the complex is obviously strong enough to survive the hydrogen-bonding competition provided by the hydroxylic solvent and that it does not significantly dissociate in solution as this would be expected to produce intense fragments containing glycerol. We believe that the observed spectrum is only consistent with a polymeric complex of imidazole with $(MeO)_2PO_2H$ (Table I).

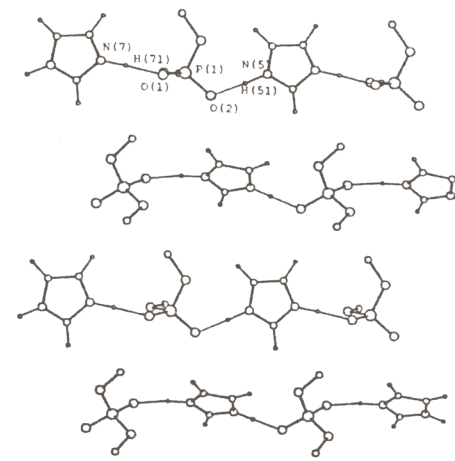

Figure 1. Diagram of the packing and chain-type structure of the imidazole–$(MeO)_2PO_2H$ complex. The positions of the hydrogen atoms have been geometrically calculated.

In order to disprove the possibility that the observed imidazole–phosphate species were produced by reactions between fragment species in the desorption–ionization process, systems containing imidazole and weaker hydrogen-bond electron donors were investigated. The FAB MS of imidazole–Ph_2O, imidazole–Ph_2CO, and imidazole–dioxane systems in glycerol gave spectra very similar to that of imidazole itself with no evidence of any peaks due to the hydrogen-bonded complexes. The more powerful hydrogen-bond electron donor Ph_2SO does, however, appear to form strong hydrogen bonds to imidazole. The FAB MS of this system in glycerol shows a peak at *m/z* 271, which can be assigned to a protonated imidazole–Ph_2SO hydrogen-bonded complex ion. The relative intensity of this peak is approximately one-half of the intensity of the corresponding (imidazole–phosphate + H^+) ion peak.

The observed crystal structure of the imidazole–phosphate complex is in excellent agreement with the structure deduced from the FAB MS data and is shown in Figure 1. The complex contains infinite chains of imidazole–$(MeO)_2PO_2H$ units. The two N–O distances are 2.68 (1) and 2.67 (1) Å, i.e., equal within experimental error, and the bond angles are 171.0 (4)° and 176.5 (4)°, which are consistent with the presence of strong NHO hydrogen bonds.

The successful application of FAB MS to the analysis of a hydrogen-bonded complex suggests that this technique may well become a routine analytical method for the study of strong hydrogen bonding.[4] The information obtained is complementary to that obtained from other "fast" analytical technqiues such as infrared and NMR spectroscopy. While FAB MS cannot provide the same detailed information as X-ray crystallography, it is a much simpler technique and it can be used to study liquids or solutions thus removing the need for a crystalline sample.

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Registry No. Ph_2O, 101-84-8; Ph_2CO, 119-61-9; Ph_2SO, 945-51-7; imidazole, 288-32-4; trimethyl phosphate, 512-56-1; dioxane, 123-91-1.

Supplementary Material Available: Tables of atomic coordinates, anisotropic thermal parameters, bond lengths, bond angles, and observed and calculated structure factors (9 pages). Ordering information is given on any current masthead page.

(1) Zundel, G. In "The Hydrogen Bond, Recent Developments in Theory and Experiments"; Schuster, P., Zundel, G., Sandorfy, C., Eds.; North-Holland: Amsterdam, 1976; Chapter 15.

(2) For recent examples see: Shaanan, B. *Nature (London)* **1982**, *296*, 683. Phillips, S.E.V.; Schoenhorn, B. P. *Ibid.* **1981**, *292*, 81. Quinn, R.; Nappa, M.; Valentine, J. S. *J. Am. Chem. Soc.* **1982**, *104*, 2588. La Mar, G. N.; De Ropp, J. S.; Chacko, V. P.; Satterlee, J. D.; Erman, J. E. *Biochim. Biophys. Acta* **1982**, *708*, 317 and references therein.

(3) Clark, J. H.; Green, M.; Madden, R. G. *J. Chem. Soc., Chem. Commun.* **1983**, 136.

(4) For general discussions on strong hydrogen bonding, see: Emsley, J. *Chem. Soc. Rev.* **1980**, 91. And Chapter 12 in ref 1.

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