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4-Chloro-5-methylamino-2,3,6-pyridinetrione Monohydrate

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Monoclinic, $P2_1/c$, $a=5.276$ $b=19.31$ (3), $c=7.968$ (8) Å, $\beta=93.06$ (6)°, 25°C, $C_6H_5N_2O_3Cl \cdot H_2O$, $M=206.6$, $Z=4$, $D=1.695$ g cm⁻³. The exocyclic carbon–nitrogen bond has considerable double-bond character resulting in a planar structure.

Introduction

An X-ray diffraction study of 4-chloro-5-methylamino-2,3,6-pyridinetrione (I) was undertaken to identify the substituent positions in this compound and a series of related compounds (Johnston, 1971). The results also are of interest with regard to the valence structure assumed by I in the monohydrate crystal state.

Experimental

Efforts to recrystallize I from a variety of organic solvents gave twinned specimens exclusively. However, prismatic single crystals could be obtained as the monohydrate by recrystallization from aqueous solution. A crystal of approximate dimensions 0.20 × 0.05 × 0.50 mm was sealed within a 0.2 mm diameter Lindemann glass capillary. Preliminary Weissenberg and precession photographs showed diffraction sym-

metry $2/m$ and the systematic absences characteristic of space group $P2_1/c$. The crystal was aligned with a collinear with the φ axis of a Picker four-circle diffractometer, and the cell constants were determined by least-squares refinement of the setting angles of 23 reflections. Intensity data were taken by the θ - 2θ scan mode using Mo $K\alpha$ radiation monochromated by reflection from the 002 planes of highly oriented graphite. Within the sphere $\sin \theta < 0.461$ a total of 1943 unique reflections could be measured, of which the 1286 satisfying the condition $I > 3\sigma(I)$ were retained for solution and refinement. The 112 reflection was remeasured after each 50 reflections and showed r.m.s. stability of 1.6%. No absorption correction was made ($\mu=4.61$ cm⁻¹); transmission factors range from 0.92 to 0.98.

The crystal structure was solved by Patterson and Fourier methods and refined by full-matrix least-squares calculations minimizing $\sum w(|F_o| - |F_c|)^2$. All

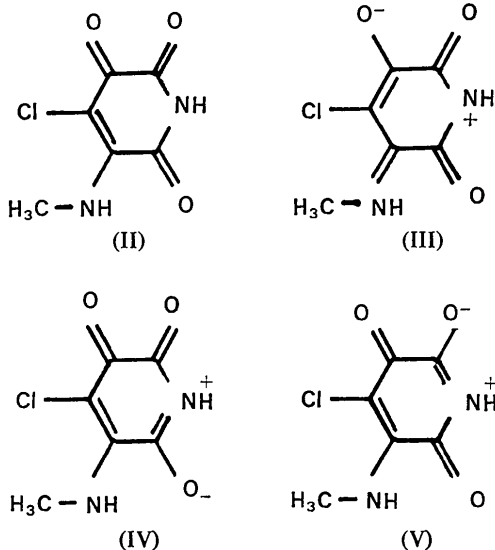
Table 1. Atomic parameters with standard errors

Errors in parentheses refer to last significant digit(s). Thermal parameters are of the form

$$\exp [-(h^2\beta_{11} + k^2\beta_{22} + l^2\beta_{33} + 2hk\beta_{12} + 2hl\beta_{13} + 2kl\beta_{23}) \times 10^4].$$

	x	y	z	$10^4\beta_{11}$	$10^4\beta_{22}$	$10^4\beta_{33}$	$10^4\beta_{12}$	$10^4\beta_{13}$	$10^4\beta_{23}$
N(1)	0.7074 (5)	0.2098 (1)	0.3693 (4)	204 (10)	20 (1)	144 (2)	-2 (5)	-69 (6)	-5 (2)
C(1)	0.5544 (6)	0.2587 (2)	0.2882 (4)	232 (12)	18 (1)	142 (6)	-0 (3)	-34 (7)	-3 (2)
C(2)	0.3283 (6)	0.2317 (2)	0.1769 (4)	206 (12)	21 (1)	108 (6)	2 (3)	-22 (7)	-2 (2)
C(3)	0.2938 (6)	0.1597 (2)	0.1641 (4)	182 (12)	20 (1)	110 (6)	0 (2)	-51 (6)	-2 (2)
C(4)	0.4536 (5)	0.1127 (2)	0.2484 (4)	187 (12)	18 (1)	113 (6)	-2 (3)	-12 (6)	-1 (2)
C(5)	0.6759 (6)	0.1396 (2)	0.3574 (4)	188 (11)	20 (1)	135 (6)	-2 (3)	-35 (6)	-2 (2)
O(1)	0.5917 (4)	0.3194 (1)	0.3036 (3)	353 (12)	19 (1)	250 (6)	-5 (2)	-135 (6)	-6 (2)
O(2)	0.1982 (4)	0.2756 (1)	0.1022 (3)	324 (10)	20 (1)	195 (5)	12 (2)	-108 (6)	3 (2)
Cl	0.0422 (2)	0.1360 (1)	0.0291 (1)	271 (3)	23 (1)	158 (2)	-5 (1)	-111 (2)	-3 (1)
N(2)	0.4479 (5)	0.0448 (1)	0.2479 (4)	268 (12)	19 (1)	167 (6)	-2 (3)	-86 (7)	1 (2)
C(6)	0.2597 (9)	-0.0023 (2)	0.1685 (8)	359 (20)	21 (1)	282 (12)	-18 (4)	-144 (12)	-0 (3)
O(3)	0.8199 (4)	0.0998 (1)	0.4295 (3)	300 (10)	23 (1)	213 (6)	4 (2)	-139 (6)	8 (2)
O(H ₂ O)	0.2698 (6)	0.4299 (2)	0.1340 (4)	375 (13)	23 (1)	256 (7)	-15 (3)	-139 (7)	8 (2)

and C(6), forms a dihedral angle of 4.6° with the ring plane given above.



The bond distances (Table 3) largely reflect the contributions of four principal valence structures (II–V), which are given in their apparent order of importance. All four forms require single bonds at C(1)–C(2) and C(4)–C(5), as verified by the respective bond lengths of

Table 3. Bond distances and angles with standard errors

Errors in parentheses refer to the last significant digit given, and were calculated from the variance-covariance matrix obtained in the final least-squares cycle.

Distances (Å)		Angles ($^\circ$)	
N(1)–C(1)	1.380 (4)	N(1)–C(1)–C(2)	117.0 (3)
C(1)–C(2)	1.539 (4)	C(1)–C(2)–C(3)	118.1 (3)
C(2)–C(3)	1.404 (4)	C(2)–C(3)–C(4)	122.6 (3)
C(3)–C(4)	1.388 (4)	C(3)–C(4)–C(5)	119.0 (3)
C(4)–C(5)	1.514 (4)	C(4)–C(5)–N(1)	117.8 (3)
C(5)–N(1)	1.368 (4)	C(5)–N(1)–C(1)	125.4 (3)
C(1)–O(1)	1.194 (4)	N(1)–C(1)–O(1)	122.3 (3)
C(2)–O(2)	1.225 (3)	O(1)–C(1)–C(2)	120.7 (3)
C(3)–Cl	1.725 (3)	C(1)–C(2)–O(2)	116.2 (3)
C(4)–N(2)	1.311 (4)	O(2)–C(2)–C(3)	125.6 (3)
N(2)–C(6)	1.466 (5)	C(2)–C(3)–Cl	113.6 (2)
C(5)–O(3)	1.205 (4)	Cl–C(3)–C(4)	123.7 (2)
N(1)–H(1)	0.84 (3)	C(3)–C(4)–N(2)	129.7 (3)
N(2)–H(2)	0.88 (3)	C(4)–N(2)–C(6)	129.6 (3)
C(6)–H(6A)	1.01 (4)	N(2)–C(4)–C(5)	111.2 (3)
C(6)–H(6B)	0.98 (5)	C(4)–C(5)–O(3)	120.2 (3)
C(6)–H(6C)	0.92 (4)	O(3)–C(5)–N(1)	122.0 (3)
Water O–H	0.87 (4)	C(5)–N(1)–H(1)	117 (2)
	0.77 (4)	C(1)–N(1)–H(1)	117 (2)
		C(4)–N(2)–H(2)	117 (2)
		C(6)–N(2)–H(2)	113 (2)
		N(2)–C(6)–H(6A)	105 (2)
		N(2)–C(6)–H(6B)	107 (3)
		N(2)–C(6)–H(6C)	107 (3)
		H(6A)–C(6)–H(6B)	114 (4)
		H(6A)–C(6)–H(6C)	115 (3)
		H(6B)–C(6)–H(6C)	108 (4)
		H–O–H (water)	107 (4)

1.539 and 1.514 Å. The most important ionic form is clearly (III), since C(4)–N(2) (1.311 Å) is the shortest C–N distance, and C(2)–O(2) (1.225 Å) is the longest carbonyl bond. The C–N bonds in the ring, C(1)–N(1) (1.380 ± 0.004 Å) and C(5)–N(1) (1.368 ± 0.004 Å) are, as expected, longer than the C–N bonds of 1.340 in pyridine itself (Bak, Hansen-Nygaard & Rastrup-Andersen, 1958). The differences between the distances C(1)–N(1) and C(5)–N(1) and between C(1)–O(1) and C(5)–O(3) are significant at the 3σ level and suggest that structure (IV) contributes slightly more than V. Not surprisingly, the shortest C–C bond is C(3)–C(4) (1.388 Å) followed by C(3)–C(2) (1.404 Å).

Resonance structure (III) is undoubtedly responsible for the methylamino ligand adopting a conformation coplanar with the ring. The bond angles C(6)–N(2)–C(4) (129.6°), N(2)–C(4)–C(3) (129.7°), and C(4)–C(3)–Cl (123.7°) are all significantly greater than the trigonal angle, indicating that this conformation is not achieved without some cost in strain energy. The locations of the methyl hydrogens are also consistent with a very close chlorine–methyl contact. The C(1)–N(1)–C(5) angle of 125.4° is typical for nitrogen atoms bearing an extra-annular hydrogen atom in 6-membered rings (Chatar Singh, 1965).

The crystal structure (Fig. 2) consists of two-dimensional sheets corresponding to the $\{10\bar{2}\}$ planes and held together by hydrogen bonds. One of the two water protons is approximately equidistant from oxygen atoms O(1) and O(2) of the basic molecule, as can be seen in Fig. 1, while the second water proton is directed toward O(3) of a molecule related by $x-1, \frac{1}{2}-y, z-\frac{1}{2}$.

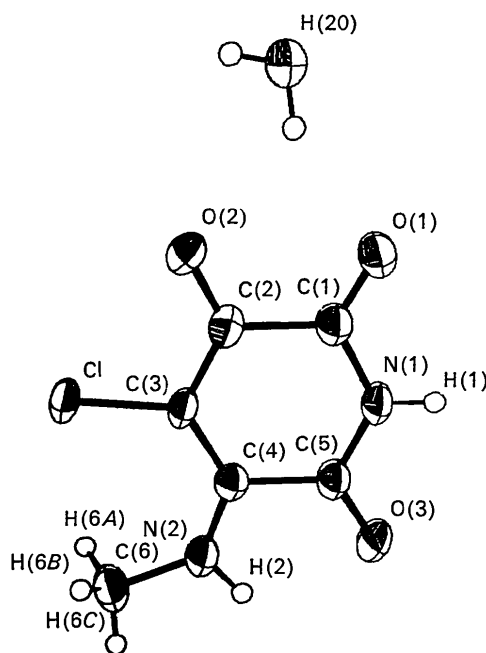


Fig. 1. Molecular structure with thermal ellipsoids drawn at 50% probability of occupancy.

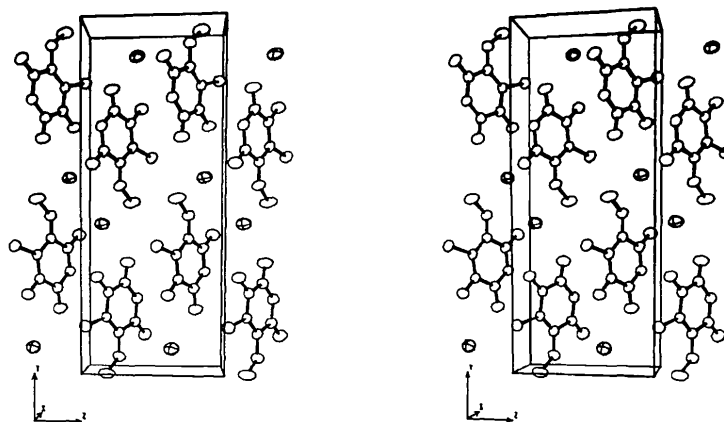


Fig. 2. Three-dimensional view of the crystal structure of 4-chloro-5-methylamino-2,3,6-pyridinetriene monohydrate.

The O-H...O distances are 3.001, 3.011, and 2.864 Å to O(1), O(2) and O(3) respectively. In addition, the amine [N(2)] hydrogen of a molecule related by $1-x, \frac{1}{2}+y, \frac{1}{2}-z$ forms an N-H...O bond of 2.808 Å to the H₂O oxygen. The basic molecule and that related by $x-1, \frac{1}{2}-y, z-\frac{1}{2}$ may also interact weakly through an N(1)-H...O(2) contact of 3.117 Å. We note that these hydrogen-bonded interactions are not only critical in determining the crystal structure of the monohydrate, but also may play an important role in stabilizing the valence structures inferred from the molecular bond lengths.

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The Crystal and Molecular Structure of the Tetraphenylarsonium Salt of the Monoanion of Adenine, [C₂₄H₂₀As]⁺[C₅N₅H₄]⁻·3H₂O*

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The tetraphenylarsonium salt of the monoanion of adenine crystallizes from aqueous solution as the trihydrate. The crystals are monoclinic, space group $P2_1/n$, with $a=9.878$ (4), $b=21.347$ (7), $c=13.407$ (4) Å, $\beta=103.19$ (3)° and $Z=4$. 2982 independent intensities (2418 above zero) were collected by counter methods. A structural solution was obtained by the heavy-atom method. The adenine anion is disordered in the crystal and accurate values for its bond lengths and angles have not been obtained. Full-matrix least-squares refinement based on the 2418 non-zero F 's led to an R value of 0.103 with all atoms treated isotropically.

Introduction

Our recent interest in the coordination chemistry of purines and pyrimidines (Kistenmacher, Marzilli &

Chang, 1973) has led to the synthesis and structural investigation of several cobalt(III) complexes containing the monoanion of adenine (I) as a coordinated ligand. In an effort to compare the bond lengths and angles in the free anion *versus* those in the complexed anion, we have undertaken a structural study of the tetraphenylarsonium salt of the monoanion of adenine. Our efforts to obtain accurate dimensions have been thwarted by a disordering of the adenine anions.

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