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**Bis(dicyclohexylammonium) 2,6-Pyridinedicarboxylate Dihydrate**

SEIK WENG NG

Institute of Advanced Studies, University of Malaya, 50603  
Kuala Lumpur, Malaysia. E-mail: h1nswen@cc.um.edu.my

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**Abstract**

In the title compound,  $2C_{12}H_{24}N^+ \cdot C_7H_3NO_4^{2-} \cdot 2H_2O$ , one of the ammonium cations is linked to the dianion  $[N \cdots O = 2.717(3), 2.846(3) \text{ \AA}]$  to form an eight-membered ring; this monoanionic entity is linked to an adjacent entity through the second ammonium cation and a disordered water molecule  $[N \cdots O = 2.871(3), 2.908(3); O \cdots O 2.602(6), 2.778(6) \text{ \AA}]$  to form a linear chain. The second water molecule links two chains through the disordered water molecule  $[O \cdots O = 2.674(7), 2.825(9) \text{ \AA}]$  into a ribbon running parallel to the *a* axis.

**Comment**

Whereas dicyclohexylamine reacts with monocarboxylic acids to yield ammonium carboxylates, as displayed by dicyclohexylammonium *O*-(*N,N*-dimethylthiocarbamoyl)acetate (Ng, 1993), this secondary amine affords an ammonium hydrogen dicarboxylate when reacted with dicarboxylic acids. The acidic proton in the dicyclohexylammonium hydrogen trithiocarbodiglycolate (Ng, 1995) and in dicyclohexylammonium hydrogen oxalate (Ng, 1994) is held by one of the two carboxylate ends of the anion. The amine reacts with 2,6-pyridinedicarboxylic acid to give a bis(dicyclohexylammonium) derivative containing two water molecules, (I). Bond dimensions involving the planar anion are similar to those of the parent acid, which crystallizes as a monohydrate that adopts a hydrogen-bonded sheet structure (Takusagawa, Hirotsu & Shimada, 1973). The dicyclohexylammonium–water interactions  $[2.871(3), 2.908(3) \text{ \AA}]$  are longer than those  $[2.738(6), 2.741(6) \text{ \AA}]$  found in dicyclohexylammonium *N,N*-dimethyldithiocarbamoylacetate hydrate (Ng, 1992), which adopts a three-dimensional network structure.

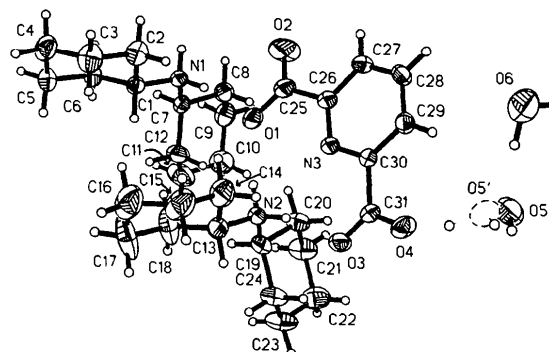
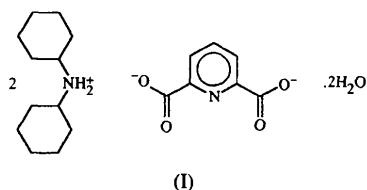


Fig. 1. ZORTEP (Zsolnai & Pritzkow, 1996) plot of bis(dicyclohexylammonium) 2,6-pyridinedicarboxylate dihydrate at the 30% probability level. H atoms are drawn as spheres of arbitrary radii.

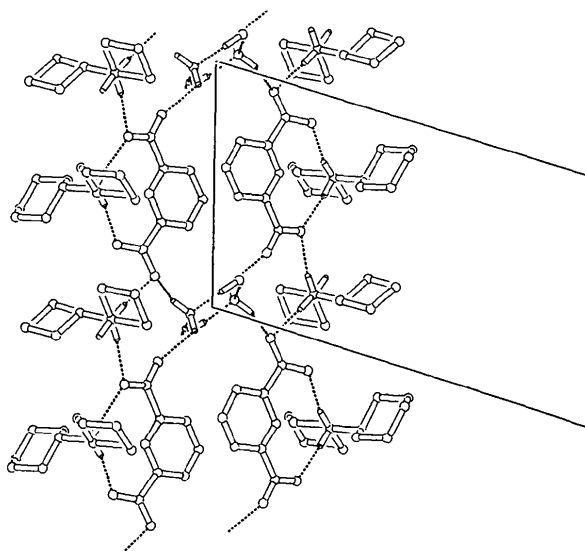
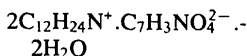


Fig. 2. Plot showing the hydrogen-bonding interactions when viewed along *b*.

**Experimental**

The compound was obtained as crystals on slow evaporation of an ethanol solution containing dicyclohexylamine and 2,6-pyridinedicarboxylic acid in a 2:1 molar ratio.

**Crystal data** $M_r = 565.78$ 

Monoclinic

 $P2_1/n$  $a = 10.579(1) \text{ \AA}$  $b = 18.1356(9) \text{ \AA}$  $c = 17.507(2) \text{ \AA}$  $\beta = 106.044(6)^\circ$  $V = 3228.1(6) \text{ \AA}^3$  $Z = 4$  $D_x = 1.164 \text{ Mg m}^{-3}$  $D_m$  not measuredMo  $K\alpha$  radiation $\lambda = 0.71073 \text{ \AA}$ 

Cell parameters from 25

reflections

 $\theta = 10\text{--}11^\circ$  $\mu = 0.080 \text{ mm}^{-1}$  $T = 298(2) \text{ K}$ 

Irregular block

 $0.53 \times 0.53 \times 0.53 \text{ mm}$ 

Colorless

**Data collection**

Enraf–Nonius CAD-4 diffractometer  
 $\omega$  scans  
 Absorption correction:  $\psi$  scan (North, Phillips & Mathews, 1968)  
 $T_{\min} = 0.922$ ,  $T_{\max} = 0.958$   
 5858 measured reflections  
 5664 independent reflections

3326 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.0181$   
 $\theta_{\text{max}} = 24.97^\circ$   
 $h = -12 \rightarrow 12$   
 $k = 0 \rightarrow 21$   
 $l = 0 \rightarrow 20$   
 3 standard reflections  
 frequency: 60 min  
 intensity decay: none

**Refinement**

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.067$   
 $wR(F^2) = 0.195$   
 $S = 1.107$   
 5664 reflections  
 370 parameters  
 H atoms: riding model with  $U(\text{H}) = 1.5U_{\text{eq}}(\text{C}, \text{N})$ ; water H atoms were calculated,  $U = 0.10 \text{ \AA}^2$

$w = 1/[\sigma^2(F_o^2) + (0.1P)^2]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\text{max}} < 0.001$   
 $\Delta\rho_{\text{max}} = 0.370 \text{ e \AA}^{-3}$   
 $\Delta\rho_{\text{min}} = -0.267 \text{ e \AA}^{-3}$   
 Extinction correction: none  
 Scattering factors from *International Tables for Crystallography* (Vol. C)

Table 1. Selected geometric parameters ( $\text{\AA}$ ,  $^\circ$ )

O1—C25	1.246 (4)	N1...O1	2.871 (3)
O2—C25	1.217 (4)	N1...O4 <sup>i</sup>	2.908 (3)
O3—C31	1.235 (3)	N2...O1	2.846 (3)
O4—C31	1.245 (3)	N2...O3	2.717 (3)
N1—C1	1.499 (3)	O5...O2 <sup>ii</sup>	2.602 (6)
N1—C7	1.496 (3)	O5...O4	2.778 (6)
N2—C13	1.493 (3)	O5...O6	2.674 (7)
N2—C19	1.499 (3)	O5'...O2 <sup>ii</sup>	2.656 (6)
N3—C26	1.337 (3)	O5'...O4	2.710 (5)
N3—C30	1.339 (3)	O6...O5 <sup>iii</sup>	2.825 (9)
C1—N1—C7	116.8 (2)	O1—C25—O2	124.0 (3)
C13—N2—C19	119.6 (2)	O1—C25—C26	118.6 (3)
C26—N3—C30	118.7 (2)	O2—C25—C26	117.5 (3)
N1—C1—C2	108.2 (2)	N3—C26—C25	117.2 (2)
N1—C1—C6	112.2 (2)	N3—C26—C27	122.0 (2)
N1—C7—C8	109.1 (2)	N3—C30—C29	122.2 (2)
N1—C7—C12	112.3 (2)	N3—C30—C31	115.5 (2)
N2—C13—C14	108.5 (2)	O3—C31—O4	124.6 (2)
N2—C13—C18	112.7 (3)	O3—C31—C30	117.8 (2)
N2—C19—C20	108.1 (2)	O4—C31—C30	117.7 (2)
N2—C19—C24	110.8 (2)		

Symmetry codes: (i)  $1 + x, y, z$ ; (ii)  $x - 1, y, z$ ; (iii)  $-x, -y, -z$ .

Data collection: *CAD-4-VAX/PC* (Enraf–Nonius, 1988). Cell refinement: *CAD-4-VAX/PC*. Data reduction: *NRCVAX* (Gabe, Le Page, Charland, Lee & White, 1989). Program(s) used to solve structure: *SHELXS86* (Sheldrick, 1990). Program(s) used to refine structure: *SHELXL93* (Sheldrick, 1993). Molecular graphics: *PLUTON* (Spek, 1994), *ZORTEP* (Zsolnai & Pritzkow, 1996). Software used to prepare material for publication: *SHELXL93*.

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Supplementary data for this paper are available from the IUCR electronic archives (Reference: KH1129). Services for accessing these data are described at the back of the journal.

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## Characterization of Quinoline Derivatives. I. 6,7-Dihydro-8-(4-methyl-1-piperaziny)[1]-benzoxepino[4,5-c]quinoline 0.13-Hydrate

GIANLUCA GIORGI,<sup>a</sup> ANDREA CAPPELLI,<sup>b</sup> MAURIZIO ANZINI,<sup>b</sup> SALVATORE VOMERO<sup>b</sup> AND FABIO MARCHETTI<sup>c</sup>

<sup>a</sup>Centro Interdipartimentale di Analisi e Determinazioni Strutturali, Università di Siena, via A. Moro, 53100 Siena, Italy, <sup>b</sup>Dipartimento Farmaco Chimico Tecnologico, Università di Siena, via Banchi di Sotto 55, 53100 Siena, Italy, and <sup>c</sup>Dipartimento di Chimica, Università di Pisa, via Risorgimento 35, 56126 Pisa, Italy. E-mail: ciads@unisi.it

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**Abstract**

The title compound,  $\text{C}_{22}\text{H}_{23}\text{N}_3\text{O} \cdot 0.13\text{H}_2\text{O}$ , is a novel potent and selective serotonin 5-HT<sub>3</sub> receptor antagonist. Three independent molecules constitute the asymmetric unit. While two of these molecules show only small differences in their metric and conformational parameters, the third differs from the other two, mainly as a result of the conformation of the oxepine ring. The conformations of the seven-membered ring determine quite different orientations of the oxepine-fused benzene ring, whose role is important in the exploitation of biological activity.