organic papers

Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

Kazuma Gotoh,^a Youhei Tabuchi,^a Haruo Akashi^b and Hiroyuki Ishida^a*

^aDepartment of Chemistry, Faculty of Science, Okayama University, Okayama 700-8530, Japan, and ^bResearch Institute of Natural Sciences, Okayama University of Science, Okayama 700-0005, Japan

Correspondence e-mail: ishidah@cc.okayama-u.ac.jp

Key indicators

Single-crystal X-ray study T = 298 KMean σ (C–C) = 0.002 Å R factor = 0.036 wR factor = 0.092 Data-to-parameter ratio = 13.8

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

 $\ensuremath{\mathbb{C}}$ 2006 International Union of Crystallography All rights reserved

4-Carboxypyridinium hydrogen chloranilate monohydrate

The title compound (systematic name: 4-carboxypyridinium 2,5-dichloro-4-hydroxy-3,6-dioxocyclohexa-1,4-dien-1-olate monohydrate), $C_6H_6NO_2^+ \cdot C_6HCl_2O_4^- \cdot H_2O$, is a monohydrate salt of chloranilic acid (2,5-dichloro-3,6-dihydroxy-1,4-benzo-quinone) with isonicotinic acid (pyridine-4-carboxylic acid), in which an acid-base interaction involving a proton transfer is observed from the chloranilic acid to the pyridine group of isonicotinic acid. In the crystal structure, the 4-carboxy-pyridinium cation, the hydrogen chloranilate anion and the water molecule are held together through N-H···O, O-H···O and C-H···O hydrogen bonds, forming a chain. The chains are further linked by O-H···O and C-H···O hydrogen-bond network.

Comment

The title compound, (I), was prepared in order to extend our study on $D-H\cdots A$ hydrogen bonding (D = N, O, or C; A = N, O or Cl) in chloranilic acid-amine 1:1 and 1:2 systems (Tabuchi *et al.*, 2005). Chloranilic acid is attractive as a template for generating tightly bound self-assemblies with polarizable bases, as well as a model compound for investigating proton-transfer motions in intermolecular hydrogen bonds by ¹H NMR and ³⁵Cl NQR techniques (Ikeda *et al.*, 2005).



The asymmetric unit in the title compound, (I), contains a 4carboxypyridinium cation, a hydrogen chloranilate anion and a water molecule; an acid-base interaction involving a proton transfer is observed between the chloranilic acid and the isonicotinic acid through the water molecule and these three molecules are held together by N1-H2···O7, O7-H8···O4 and C11-H6···O1 hydrogen bonds (Fig. 1 and Table 1). The three components are further connected by three O-H···O hydrogen bonds [O2-H1···O7ⁱ, O5-H7···O3ⁱⁱ and O7-H9···O6ⁱⁱⁱ; symmetry codes (i)-(iii) are given in Table 2], resulting in a hydrogen-bonded chain running along the [110] direction (Fig. 2). Atom H1 is also involved in an intramolecular hydrogen bond with O3. Neighboring chains related Received 4 September 2006 Accepted 8 September 2006 by an *n*-glide plane to each other are linked through the water molecule, forming a three-dimensional hydrogen-bond network. Besides the $O-H \cdots O$ hydrogen bonds, there are $C-H \cdots O$ hydrogen bonds between the chains.

Experimental

Crystals were obtained by slow evaporation of an ethanol solution of chloranilic acid with isonicotinic acid in a 1:1 molar ratio (0.200 and 0.118 g for chloranilic acid and isonicotinic acid, respectively).

Z = 4

 $D_x = 1.687 \text{ Mg m}^{-3}$

10144 measured reflections

3041 independent reflections

2728 reflections with $I > 2\sigma(I)$

Mo $K\alpha$ radiation

 $\mu = 0.51 \text{ mm}^{-1}$

Prism, brown $0.50 \times 0.40 \times 0.30 \text{ mm}$

 $R_{\rm int} = 0.017$

 $\theta_{\rm max} = 27.5^{\circ}$

T = 298 K

Crystal data

 $C_6H_6NO_2^+ \cdot C_6HCl_2O_4^- \cdot H_2O$ $M_r = 350.11$ Monoclinic, $P2_1/n$ a = 12.9472 (3) Å b = 7.7206 (2) Å c = 13.8128 (3) Å $\beta = 93.4766$ (11)° V = 1378.19 (6) Å³

Data collection

Rigaku R-AXIS-IV diffractometer ω scans Absorption correction: multi-scan (ABSCOB: Uicaschi 1005)

(ABSCOR; Higashi, 1995) $T_{min} = 0.779, T_{max} = 0.859$

Refinement

Refinement on F^2 $w = 1/[\sigma^2(F_0^2) + (0.0445P)^2]$ $R[F^2 > 2\sigma(F^2)] = 0.036$ + 0.6445P] $wR(F^2) = 0.092$ where $P = (F_0^2 + 2F_c^2)/3$ S = 1.08 $(\Delta/\sigma)_{\rm max} = 0.001$ $\Delta \rho_{\rm max} = 0.25$ e Å -3 3041 reflections $\Delta \rho_{\rm min} = -0.49 \text{ e} \text{ Å}^{-3}$ 220 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Hydrogen-bond geometry (Å, $^{\circ}$).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
N1-H2···O7	0.89 (3)	1.90 (2)	2.7286 (19)	154 (2)
$O2-H1\cdots O3$	0.84 (3)	2.10(3)	2.6073 (16)	119 (2)
$O2-H1\cdots O7^{i}$	0.84 (3)	2.08 (3)	2.8175 (17)	146 (2)
O5-H7··· $O3$ ⁱⁱ	0.89 (3)	1.68 (3)	2.5633 (17)	175 (3)
O7−H8···O4	0.80(3)	1.97 (3)	2.7542 (18)	166 (3)
O7−H9···O6 ⁱⁱⁱ	0.88 (3)	2.02 (3)	2.8799 (18)	165 (3)
$C7-H3\cdots O4^{iv}$	0.93	2.31	3.168 (2)	153
$C10-H5\cdots O2^{v}$	0.93	2.40	3.3063 (19)	164
C11−H6···O1	0.93	2.36	2.9989 (19)	126

Symmetry codes: (1) $x - \frac{1}{2}, -y + \frac{1}{2}, z - \frac{1}{2};$ (1) x + 1, y - 1, z; (11) $x - \frac{1}{2}, -y - x + \frac{1}{2}, y - \frac{1}{2}, -z + \frac{3}{2};$ (v) $-x + \frac{1}{2}, y - \frac{1}{2}, -z + \frac{1}{2}.$

H atoms attached to O and N atoms were found in a difference Fourier map and refined isotropically (refined distances given in Table 1). Other H atoms were treated as riding, with C-H = 0.93 Å and $U_{iso}(H) = 1.2U_{eq}(C)$.

Data collection: *PROCESS-AUTO* (Rigaku/MSC, 2004); cell refinement: *PROCESS-AUTO*; data reduction: *CrystalStructure*



Figure 1

The asymmetric unit of (I), with the atom numbering. Displacement ellipsoids of non-H atoms are drawn at the 50% probability level. N– $H\cdots$ O, O– $H\cdots$ O and C– $H\cdots$ O hydrogen bonds are indicated by dashed lines.



Figure 2

A partial packing diagram, viewed approximately along the *b* axis, showing the hydrogen-bonded chain and hydrogen-bonding scheme around the water molecule. Dashed lines show N-H···O, O-H···O and C-H···O hydrogen bonds [symmetry codes: (ii) 1 + x, y - 1, z; (vi) $\frac{1}{2} + x, \frac{1}{2} - y, z - \frac{1}{2}$].

(Rigaku/MSC, 2004); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *CrystalStructure* and *PLATON* (Spek, 2003).

This work was supported by a Grant-in-Aid for Scientific Research (C) (No. 16550014) from the Japan Society for the Promotion of Science.

References

- Altomare, A., Cascarano, G., Giacovazzo, C., Guagliardi, A., Burla, M. C., Polidori, G. & Camalli, M. (1994). J. Appl. Cryst. 27, 435.
- Farrugia, L. J. (1997). J. Appl. Cryst. 30, 565.
- Higashi, T. (1995). ABSCOR. Rigaku Corporation, Tokyo, Japan.
- Ikeda, R., Takahashi, S., Nihei, T., Ishihara, H. & Ishida, H. (2005). Bull. Chem. Soc. Jpn, 78, 1241–1245.
- Rigaku/MSC (2004). *PROCESS-AUTO* and *CrystalStructure* (Version 3.7.0). Rigaku/MSC Inc., The Woodlands, Texas, USA.
- Sheldrick, G. M. (1997). SHELXL97. University of Göttingen, Germany.
- Spek, A. L. (2003). J. Appl. Cryst. 36, 7–13.
- Tabuchi, Y., Takahashi, A., Gotoh, K., Akashi, H. & Ishida, H. (2005). Acta Cryst. E**61**, 04215–04217.