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Key indicators

Single-crystal X-ray study
 T = 295 K
 Mean $\sigma(C-C) = 0.004 \text{ \AA}$
 R factor = 0.031
 wR factor = 0.072
 Data-to-parameter ratio = 12.8

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

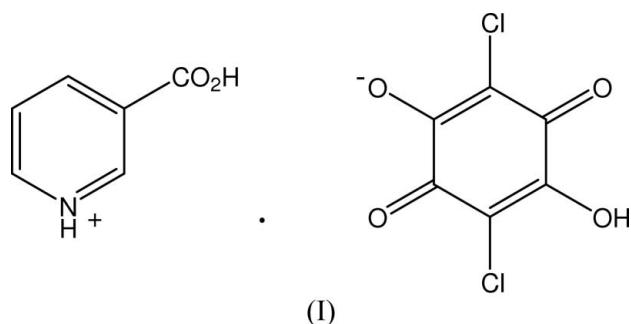
2-Carboxypyridinium hydrogen chloranilate

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The title compound, $C_6H_6NO_2^+ \cdot C_6HCl_2O_4^-$, is the salt of chloranilic acid with nicotinic acid (2-carboxypyridine), where an acid–base interaction involving a proton transfer is observed from the chloranilic acid to the pyridine group of nicotinic acid. In the crystal structure, the hydrogen chloranilate anion and the 2-carboxypyridinium cation are linked by N—H···O and O—H···O hydrogen bonds to form a zigzag chain. The chains are further linked by O—H···O hydrogen bonds to form a three-dimensional hydrogen-bond network.

Comment

The title compound, (I), was prepared in order to extend our study on D—H···A hydrogen bonding (D = N, O or C; A = N, O or Cl) in chloranilic acid–amine 1:1 and 1:2 systems (Fukunaga & Ishida, 2003; Fukunaga *et al.*, 2003; Ishida, 2004*a,b,c,d,e*). Chloranilic acid (2,5-dichloro-3,6-dihydroxy-1,4-benzoquinone) is a strong dibasic acid endowed with hydrogen-bond donor and acceptor groups, and appears particularly attractive as a template for generating tightly bound self-assemblies with polarizable bases (Ishida & Kashino, 1999*a,b,c*, 2000, 2001, 2002; Zaman *et al.*, 1999, 2000), as well as a model compound for investigating proton-transfer motions in intermolecular hydrogen bonds by ¹H NMR and ³⁵Cl NQR techniques (Nihei *et al.*, 2000*a,b*; Ikeda *et al.*, 2005).



In (I), the asymmetric unit is composed of $C_6H_6NO_2^+ \cdot C_6HCl_2O_4^-$; an acid–base interaction involving a proton transfer is observed between chloranilic acid and nicotinic acid (Fig. 1). The cations and anions are stacked in columns along the *b* axis. The two components are linked by a bifurcated hydrogen bond (N1—H2···O1 and N1—H2···O4) and an O2—H1···O6ⁱ hydrogen bond (Table 2) to form a zigzag chain running along the [111] direction. Atom H1 is also involved in an intramolecular hydrogen bond with O3. The dihedral angle between the C1–C6 plane of the anion and the pyridinium ring is 84.18 (15) $^\circ$. Neighboring chains related

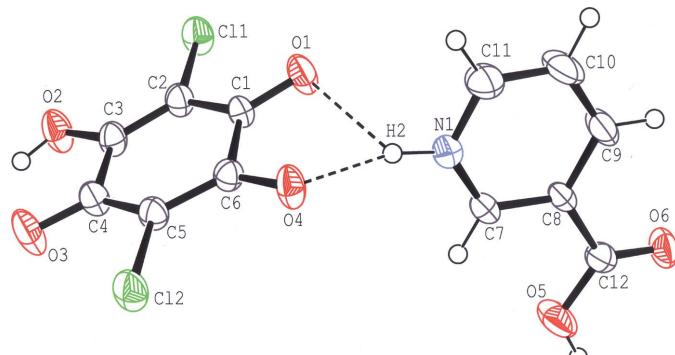


Figure 1
ORTEP-3 (Farrugia, 1997) drawing of (I), with the atom numbering. Displacement ellipsoids of non-H atoms are drawn at the 50% probability level. N—H···O hydrogen bonds are indicated by dashed lines.

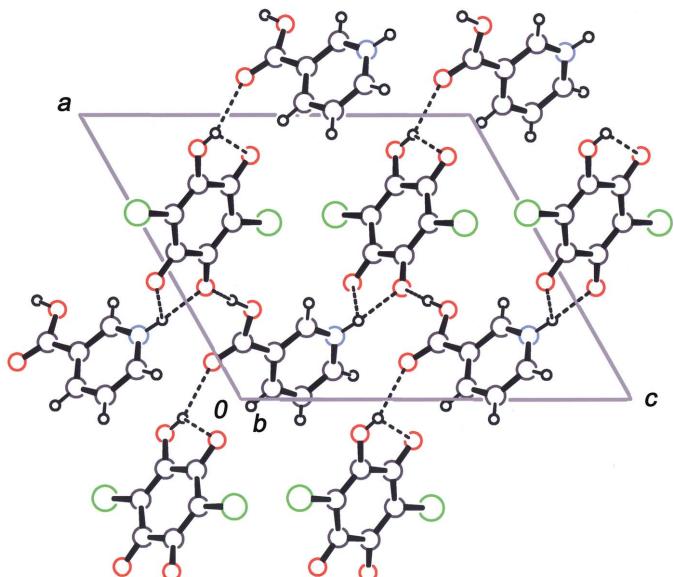


Figure 2
Packing diagram, viewed down the *b* axis. Dashed lines show N—H···O and O—H···O hydrogen bonds.

to each other by a *c*-glide plane are connected by an O5—H7···O4ⁱⁱ hydrogen bond (Table 2) to form a three-dimensional hydrogen-bond network (Fig. 2). Besides the O—H···O and N—H···O hydrogen bonds, there are C—H···O hydrogen bonds between neighboring chains (Table 2).

Experimental

Crystals were obtained by slow evaporation from a methanol solution of chloranilic acid with nicotinic acid in a 1:1 molar ratio.

Crystal data

| | |
|------------------------------------|---|
| $C_6H_6NO_2^+ \cdot C_6HCl_2O_4^-$ | $D_x = 1.679 \text{ Mg m}^{-3}$ |
| $M_r = 332.10$ | Mo $K\alpha$ radiation |
| Monoclinic, Pc | Cell parameters from 2638 reflections |
| $a = 10.7715 (10) \text{ \AA}$ | $\theta = 4.2\text{--}27.4^\circ$ |
| $b = 5.4301 (5) \text{ \AA}$ | $\mu = 0.52 \text{ mm}^{-1}$ |
| $c = 12.9139 (12) \text{ \AA}$ | $T = 295 \text{ K}$ |
| $\beta = 119.580 (7)^\circ$ | Prism, brown |
| $V = 656.89 (11) \text{ \AA}^3$ | $0.25 \times 0.25 \times 0.20 \text{ mm}$ |
| $Z = 2$ | |

Data collection

Rigaku R-Axis IV diffractometer
 ω scans
Absorption correction: multi-scan (*ABSCOR*; Higashi, 1995)
 $T_{\min} = 0.835$, $T_{\max} = 0.901$
4509 measured reflections
2602 independent reflections

2312 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.021$
 $\theta_{\text{max}} = 27.5^\circ$
 $h = -13 \rightarrow 13$
 $k = -6 \rightarrow 6$
 $l = -16 \rightarrow 16$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.031$
 $wR(F^2) = 0.072$
 $S = 1.01$
2602 reflections
204 parameters
H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0438P)^2 + 0.0699P]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.002$
 $\Delta\rho_{\text{max}} = 0.21 \text{ e \AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.19 \text{ e \AA}^{-3}$
Absolute structure: Flack (1983), 1100 Friedel pairs
Flack parameter: 0.54 (6)

Table 1
Selected bond lengths (Å).

| | | | |
|--------|-----------|--------|-----------|
| Cl1—C2 | 1.729 (3) | O4—C6 | 1.277 (3) |
| Cl2—C5 | 1.740 (3) | O5—C12 | 1.308 (3) |
| O1—C1 | 1.217 (3) | O6—C12 | 1.211 (3) |
| O2—C3 | 1.337 (3) | C1—C6 | 1.544 (4) |
| O3—C4 | 1.227 (4) | C3—C4 | 1.504 (4) |

Table 2
Hydrogen-bond geometry (Å, °).

| $D—H \cdots A$ | $D—H$ | $H \cdots A$ | $D \cdots A$ | $D—H \cdots A$ |
|---------------------------|----------|--------------|--------------|----------------|
| O2—H1···O3 | 0.84 (4) | 2.09 (4) | 2.598 (3) | 118 (4) |
| O2—H1···O6 ⁱ | 0.84 (4) | 2.11 (5) | 2.847 (3) | 146 (4) |
| O5—H7···O4 ⁱⁱ | 1.00 (5) | 1.59 (5) | 2.576 (3) | 169 (5) |
| N1—H2···O1 | 0.96 (4) | 2.39 (4) | 2.921 (3) | 114 (3) |
| N1—H2···O4 | 0.96 (4) | 1.81 (4) | 2.743 (3) | 164 (3) |
| C7—H3···O1 ⁱⁱⁱ | 0.93 | 2.36 | 3.080 (3) | 134 |
| C9—H4···O3 ^{iv} | 0.93 | 2.45 | 3.037 (3) | 121 |
| C10—H5···C11 ^v | 0.93 | 2.81 | 3.728 (4) | 168 |
| C11—H6···O2 ^v | 0.93 | 2.55 | 3.232 (4) | 131 |

Symmetry codes: (i) $x + 1, y - 1, z + 1$; (ii) $x, -y + 1, z - \frac{1}{2}$; (iii) $x, y + 1, z$; (iv) $x - 1, y, z - 1$; (v) $x - 1, -y - 1, z - \frac{1}{2}$.

H atoms attached to O and N atoms were found in a difference Fourier map and refined isotropically (refined distances given in Table 2). Other H atoms were treated as riding, with C—H = 0.93 Å and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$. The value of the Flack (1983) parameter indicates that the crystal is an inversion twin with almost equal contributions of the two components.

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

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