Table 5. Close intermolecular contacts (Å)

Orange G/Adenine		Orange G/Cytosine	
O(1)…N(4)	2.742 (4)	O(1)…O(8W)	2.920 (2)
$D(2) \cdots N(3)$	2.809 (4)	O(2)…N(6)	2.857 (2)
$O(3) \cdots O(12W)$	2.850 (5)	O(3)N(7)	2.740 (2)
O(3)O(10W)	2.988 (5)	O(4)N(6 ^{iv})	2.803 (2)
O(4)…O(12W)	2.778 (5)	O(5)…N(4 ^{vii})	2.971 (2)
O(5)…N(3")	2.824 (5)	O(6)…N(3)	2.837 (2)
O(6)O(10W)	2.774 (4)	O(7)…N(5 ^{viii})	2.740 (2)
O(7)O(11W ^{/iii})	2.928 (4)	O(8W)N(8ix)	2.761 (2)
O(8W)N(6)	2.873 (4)	O(8W)O(9ix)	2.873 (2)
O(9W)N(11)	2.760 (5)	O(10)N(4)	2.699 (2)
O(9W)…N(5 ^{iv})	2.878 (5)	O(10)…N(3)	2.915 (3)
O(10W)N(8)	2.855 (4)	.,	
$O(11W) \cdots O(12W)$	2.635 (7)		
O(11W)…N(9)	2.694 (4)		
N(8)…N(12 ^{vi})	2.882 (5)		

Symmetry codes: (i) 1 + x, y, z; (ii) x, 1 + y, z; (iii) -x, 1 - y, -z; (iv) -1 + x, -1 + y, z; (v) x, -1 + y, z; (vi) -1 - x, 1 - y, 1 - z; (vii) -x, 2 - y, 2 - z; (viii) 1 + x, y, -1 + z; (ix) 1 - x, 3 - y, 2 - z.

In both structures, H atoms bonded to C atoms were placed in calculated positions and were not refined. H atoms bonded to N atoms in Orange G/adenine were located in difference maps and their positional parameters were refined. Peaks were also found near the water O atoms, but their positions were not considered chemically reasonable and were left unassigned. H atoms bonded to N atoms and to the water O atom in Orange G/cytosine were located and their positional parameters were refined. Refinement of a secondary extinction coefficient (Zachariasen, 1963) was considered warranted only in the case of Orange G/cytosine. Data collection and cell determination were carried out using Enraf-Nonius CAD-4 software. Data reduction and structure refinement used the TEXSAN software package (Molecular Structure Corporation, 1985). Structure solution was accomplished using SHELXS86 (Sheldrick, 1985). Molecular graphics were prepared using ORTEPII (Johnson, 1976) and PLUTO (Motherwell & Clegg, 1978).

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Lists of structure factors, anisotropic displacement parameters, H-atom coordinates and complete geometry have been deposited with the IUCr (Reference: BK1002). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

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Sorbic Acid

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Abstract

The crystal and molecular structure of sorbic acid [(E,E)-2,4-hexadienoic acid], $C_6H_8O_2$, has been determined. There appears to be no delocalization of the C_{sp^2} — C_{sp^2} bonds, arranged in an *E,E* configuration, which have lengths of 1.328 (2) and 1.335 (2) Å (double) and 1.442 (2)–1.487 (2) Å (single). Dimers are formed in the crystal with an intermolecular O…O separation of 2.632 (2) Å; O—H 0.99 (2), H…O 1.65 (2) Å, O—H…O 174 (2)°.

Comment

Sorbic acid, (I), exhibits antibacterial and antifungal properties (Martindale, 1993) and has been used to prevent spoilage of syrup by moulds (Richards, 1972). The structures of numerous simple carboxylic acids have been determined and many involve intermolecular hydrogen bonding (Speakman, 1972; CSSR, 1993). It is difficult to obtain well formed crystals of sorbic acid and attempts to determine the cell dimensions by X-ray powder diffraction from a commercial crystalline sample (99 + %, Sigma) were unsuccessful. After repeated crystallizations from ethanol only one specimen was considered suitable for data collection.



The study shows that dimers form in the crystal with intermolecular hydrogen bonding around a centre of symmetry. The short O…O separation is achieved by transposing the coordinates of O(2) in Table 1 by 1 - x, -y, 1 - z. The planar nature of the molecule is shown by the torsion angles and the C_{sp^2} — C_{sp^2} bond lengths compare favourably with values for formal single (1.46 Å) and double bonds (1.34 Å) (Ladd & Palmer, 1993). The crystal structures of several compounds similar to sorbic acid, where the molecules differ only at C(1), have been studied and show very similar intermolecular hydrogen-bonding patterns. These include monomethyl trans, trans-muconate (Rabinovich & Schmidt, 1967), trans, trans-muconic acid (Bernstein & Leiserowitz, 1972) and 5-phenyl-2,4-pentadienoic acid (Kashino & Haisa, 1980).



Fig. 1. The atomic arrangement in the molecule.



Fig. 2. The crystal packing viewed on the (010) plane.

Experimental

Crystal data	
$C_6H_8O_2$ $M_r = 112.12$ Monoclinic C2/c a = 19.749 (3) Å b = 3.9355 (5) Å c = 15.649 (2) Å $\beta = 101.66$ (1)° V = 1191.2 (3) Å ³ Z = 8 $D_x = 1.250$ Mg m ⁻³	Mo $K\alpha$ radiation $\lambda = 0.71069$ Å Cell parameters from 250 reflections $\theta = 2.1-25.2^{\circ}$ $\mu = 0.093$ mm ⁻¹ T = 150 K Square plate $0.25 \times 0.25 \times 0.05$ mm Colourless

Data collection

Delft Instruments FAST diffractometer Area detector Absorption correction: none 1744 measured reflections 908 independent reflections 658 observed reflections $[I > 2\sigma I]$

Refinement

Refinement on F^2	$(\Delta/\sigma)_{\rm max} < 0.01$
R(F) = 0.039	$\Delta \rho_{\rm max} = 0.20 \ {\rm e} \ {\rm \AA}^{-3}$
$wR(F^2) = 0.096$	$\Delta \rho_{\rm min} = -0.16 \ {\rm e} \ {\rm \AA}^{-3}$
S = 0.508	Extinction correction: none
908 reflections	Atomic scattering factors
35 parameters	from SHELXL93
$w = 1/[\sigma^2(F_o^2) + (0.0132P)^2]$	(Sheldrick, 1993)
where $P = (F_0^2 + 2F_c^2)/3$	

 $R_{\rm int} = 0.048$

 $\theta_{\rm max} = 25.2^{\circ}$ $h = -19 \rightarrow 21$

 $k = -3 \rightarrow 4$

 $l = -17 \rightarrow 9$

Standard reflections not

applicable to FAST area

detection data collection

Table 1. Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å²)

 U_{iso} for H atoms; $U_{eq} = (1/3)\sum_i \sum_j U_{ij} a_i^* a_i^* a_i a_j$ for others.

	x	у	Z	$U_{\rm iso}/U_{\rm eq}$
D(1)	0.4644 (1)	0.2581 (3)	0.4074(1)	0.036(1)
D(2)	0.4164(1)	-0.0584 (3)	0.4985(1)	0.034(1)
2(1)	0.0880(1)	0.1738 (5)	0.3066(1)	0.033 (1)
C(2)	0.1573 (1)	0.0909 (4)	0.3597(1)	0.029(1)
C(3)	0.2171 (1)	0.2111 (4)	0.3460(1)	0.026(1)
C(4)	0.2839(1)	0.1218 (4)	0.3970(1)	0.026(1)
C(5)	0.3442 (1)	0.2344 (4)	0.3819(1)	0.027 (1)
C(6)	0.4106(1)	0.1308 (4)	0.4348(1)	0.027(1)
H(1)	0.5074 (12)	0.1804 (50)	0.4458 (16)	0.068 (7)
H(1A)	0.0590	0.2708	0.3443	0.069 (7)
H(1 <i>B</i>)	0.0664	-0.0336	0.2790	0.041 (5)
H(1C)	0.0930	0.3389	0.2614	0.045 (6)
H(2)	0.1590	-0.0606	0.4073	0.032 (5)
H(3)	0.2156	0.3670	0.2993	0.024 (4)
H(4)	0.2852	-0.0282	0.4448	0.018 (4)
H(5)	0.3439	0.3878	0.3349	0.025 (4)

Table 2. Selected geometric parameters (Å, °)

O(1)—C(6)	1.322 (2)	C(3)—C(4)	1.442 (2)
O(2)C(6)	1.231 (2)	C(4)C(5)	1.335 (2)
C(1) - C(2)	1.487 (2)	C(5)-C(6)	1.460 (2)
C(2)C(3)	1.328 (2)		.,
C(3) - C(2) - C(1)	125.4 (2)	O(2)-C(6)-O(1)	122.8 (2)
C(2)-C(3)-C(4)	124.6 (2)	O(2)C(6)C(5)	123.7 (2)
C(5) - C(4) - C(3)	124.8 (2)	O(1)-C(6)-C(5)	113.5 (2)
C(4)—C(5)—C(6)	122.5 (2)		
C(1)—C(2)—C(3)—C(4)	-178.5 (2)	C(4)-C(5)-C(6)-O(2)	-2.3 (3)
C(2)-C(3)-C(4)-C(5)	178.0 (2)	C(4)-C(5)-C(6)-O(1)	177.32 (14)
C(3) - C(4) - C(5) - C(6)	-178.89 (14)		

Atom H(1) was freely refined with all other H atoms riding. All H-atom U's were refined. Computer programs used were SHELXS86 (Sheldrick, 1990), SHELXL93 (Sheldrick, 1993) and SNOOPI (Davies, 1983).

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Lists of structure factors and anisotropic displacement parameters have been deposited with the IUCr (Reference: LI1092). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

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γ -Resorcylic Acid, its Monohydrate and its Pyridinium Complex

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Abstract

The crystal structures of γ -resorcylic acid (2,6dihydroxybenzoic acid), C₇H₆O₄, (I), γ -resorcylic acid monohydrate, C₇H₆O₄.H₂O, (II), and pyridinium γ resorcylate, C₅H₆N⁺.C₇H₅O₄⁻, (III), have been determined. In (I) and (II), the carboxyl group of the γ resorcylic acid molecule is in an *anti* conformation and the carboxylic OH group is involved as a donor in an O—H···O intramolecular hydrogen bond. This bond is part of an infinite hydrogen-bonded chain with mixed σ - and π -bond cooperativity. Structure (II) is disordered and may be considered to result from the superposition of two lower-symmetry structures related by a mirror plane. Structure (III) consists of discrete complex units formed from the anion and cation by means of an N— $H \cdots O$ hydrogen bond.

Comment

 γ -Resorcylic acid is one of the strongest carboxylic acids (p $K_a = 1.3$). It is also an interesting example of a molecule with two possible intramolecular hydrogenbond systems, one with two phenolic OH groups and another with one phenolic and one carboxylic OH group involved as donors in intramolecular hydrogen bonds; these two forms, A and B, are shown in the scheme below.



Solution ¹H NMR studies of this acid in the presence of bases of different proton-acceptor ability show that structure A prevails and that an intermolecular hydrogen-bond interaction with the base occurs through the carboxylic OH group (Golubev & Denisov, 1992). Some strengthening of the intramolecular hydrogen bonds was observed as the proton-acceptor ability of the base increased. In order to study the hydrogen-bond interactions of γ -resorcylic acid in the solid state, it was recrystallized from solvents of different proton-acceptor and proton-donor ability. The only forms obtained were anhydrous γ -resorcylic acid, γ -resorcylic acid monohydrate and, where a strong base was present in the crystallization mixture, an $A^- \cdots H - B^+$ complex. This paper presents X-ray structure analyses of γ -resorcylic acid (I), its monohydrate (II) and its pyridinium salt (III).

The carboxyl group of the γ -resorcylic acid molecule in (I) is in an anti conformation as a result of the intramolecular hydrogen bond with the hydroxyl group at O4. Unlike the structure in solution, the molecular structure in the crystal corresponds to form B, in which one phenolic OH group acts as an intra- and the other as intermolecular hydrogen-bond donor. The molecules are linked by hydrogen bonds to form infinite chains along [011]. Intra- and intermolecular hydrogen bonds form a chain with alternating σ - and π -bond cooperativity (Jeffrey & Saenger, 1991) (Fig. 1). The energy of the H atoms involved in the hydrogen bonds along this chain can be considered to be characterized by double-minimum potentials. A concerted protontransfer process induced along this chain would cause a transformation from form B to form A. The two minima are of different energies and only molecules of form B