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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.005 Å R factor = 0.086 wR factor = 0.219 Data-to-parameter ratio = 13.4

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

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3-(3,7-Dimethylocta-2,6-dienyloxy)-1,8-dihydroxy-6-methyl-9,10-anthraquinone

The 9,10-anthraquinone ring system of the title compound, $C_{25}H_{26}O_5$, is essentially planar. The *O*-geranyl substituent is at the *meta* position with respect to the hydroxyl group. O- $H \cdots O$ intramolecular hydrogen bonds are observed in the molecular structure. The molecules form centrosymmetric hydrogen-bonded dimers *via* intermolecular C- $H \cdots O$ hydrogen bonds which generate rings of motif $R_2^2(10)$. The crystal structure is further stabilized by weak $\pi - \pi$ interactions.

Comment

Cratoxylum is a small genus belonging to the *Guttiferae* family and found mainly in Southeast Asia (Robson, 1974); it has been used in traditional medicine (Usher, 1984) and some species of this genus exhibit antimalarial and antiprotozoal properties and also are slightly cytotoxic against human L6 cells (Seo *et al.*, 2002; Zakaria, 2004). In the course of our studies involving bioactive compounds from medicinal plants, the structure determination of the title compound, (I), was undertaken. We have isolated (I) for the first time from *Cratoxylum formosum ssp. pruniflorum*, widely distributed in the northeastern part of Thailand. It was previously isolated from *Psorospermum febrifugum* (Botta *et al.*, 1983).



The 9,10-anthraquinone ring system in (I) is essentially planar (Fig. 1), with a maximum deviation of 0.068 (3) Å for atom C10. The *O*-geranyl substituent (O5/C15–C23) is at the *meta* position with respect to the C14 hydroxyl group and the C15–O5–C12–C11 torsion angle of 178.7 (3)° indicates a (+)-antiperiplanar conformation.

The bond lengths in (I) show normal values (Allen *et al.*, 1987). Intramolecular $O-H\cdots O$ and intermolecular $C-H\cdots O$ interactions are observed (Table 2). The molecules are linked together to form dimers by $C4-H4A\cdots O3^{i}$ interactions [symmetry code: (i) -x, -y, -z] (Fig. 2). In the molecular structure, both $O1-H1\cdots O2$ and $O4-H4\cdots O2$ intramolecular hydrogen bonds involving the hydroxyl groups generate $R_{2}^{1}(6)$ ring motifs (Etter *et al.*, 1990). The molecules, which are linked together to form dimers by $C-H\cdots O$

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Figure 1

The structure of the title compound, showing 50% probability displacement ellipsoids and the atom-numbering scheme. Dashed lines indicate hydrogen bonds.

interactions, generate $R_2^2(10)$ ring motifs (Bernstein *et al.*, 1995). The crystal packing is stabilized by weak π - π interaction between the anthraquinone ring system of the molecules translated by a unit along the *a* axis (Fig. 2). The ring system is stacked in such a way that the centroid-centroid distance between the C5-C10 ring at (x, y, z) and the C8-C13 ring at (1 + x, y, z) is 3.759 (2) Å, while the centroid-centroid separation between the C1-C6) ring at (x, y, z) and the C5-C10 ring at (x - 1, y, z) is 3.829 (2) Å.

Experimental

The air-dried bark of *Cratoxylum formosum ssp. pruniflorum* (4 kg) was ground and extracted with hexane and CH_2Cl_2 (2 × 20 l for each solvent for 5 d) at room temperature. The residue obtained after evaporation of the solvent was subjected to quick column chromatography (QCC) over silica gel and eluted with a gradient of hexane-ethyl acetate to afford 10 fractions (F1–F10). Fraction F2 (58.06 g) was further purified by QCC using a gradient of hexane-ethyl acetate as eluent to afford 25 fractions (17A–17Y). Fraction 17I was recrystallized from hexane-ethyl acetate (7:3 ν/ν) to give needle-shaped orange single crystals (m.p. 391–392 K; yield *ca* 0.10%).

Crystal data

$C_{25}H_{26}O_5$	Z = 2
$M_r = 406.46$	$D_x = 1.279 \text{ Mg m}^{-3}$
Triclinic, P1	Mo $K\alpha$ radiation
a = 4.6082 (1) Å	Cell parameters from 1719
b = 12.965 (4) Å	reflections
c = 18.105 (5) Å	$\theta = 1.0-28.1^{\circ}$
$\alpha = 100.074 \ (5)^{\circ}$	$\mu = 0.09 \text{ mm}^{-1}$
$\beta = 92.978 \ (5)^{\circ}$	T = 293 (2) K
$\gamma = 96.526 \ (5)^{\circ}$	Needle, orange
$V = 1055.3 (4) \text{ Å}^3$	$0.28 \times 0.05 \times 0.05 \text{ mm}$



The packing of (I), viewed down the *a* axis. Hydrogen bonds are shown as dashed lines.

Data collection

Bruker SMART CCD area-detector diffractometer ω scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996) $T_{\min} = 0.995, T_{\max} = 0.996$ 9919 measured reflections

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.086$
$wR(F^2) = 0.219$
S = 1.07
3693 reflections
275 parameters
H-atom parameters constrained

5095 maependent reflections
2097 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.044$
$\theta_{\rm max} = 25.0^{\circ}$
$h = -5 \rightarrow 5$
$k = -15 \rightarrow 15$
$l = -21 \rightarrow 21$

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$w = 1/[\sigma^2(F_o^2) + (0.0885P)^2]$
+ 0.4977P]
where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\rm max} < 0.001$
$\Delta \rho_{\rm max} = 0.22 \text{ e } \text{\AA}^{-3}$
$\Delta \rho = -0.21 \text{ e} \text{ Å}^{-3}$

Table 1

Selected geometric parameters (Å, °).

O1-C1	1.346 (4)	O5-C12	1.353 (4)
O2-C7	1.260 (4)	O5-C15	1.446 (4)
O3-C10	1.223 (4)	C16-C17	1.314 (5)
O4-C14	1.346 (3)	C20-C21	1.299 (6)
C15-O5-C12-C11	178.7 (3)	C16-C17-C18-C19	1.1 (7)
C12-O5-C15-C16	-161.6(3)	C17-C18-C19-C20	-175.7(4)
O5-C15-C16-C17	-114.2(4)	C18-C19-C20-C21	126.5 (6)
C15-C16-C17-C18	177.9 (4)		

Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
O1−H1···O2	0.82	1.86	2.583 (4)	146
$O4-H4\cdots O2$ $C4-H4A\cdots O3^{i}$	0.82 0.93	1.84 2.54	2.563 (3) 3.393 (5)	146 153

Symmetry code: (i) -2 - x, -y, -z.

H atoms were placed in calculated positions, with O-H distances of 0.82 Å and C-H distances in the range 0.93–0.97 Å. The $U_{\rm iso}$

values were constrained to be $1.5U_{eq}$ of the carrier atom for hydroxyl and methyl H atoms and $1.2U_{eq}$ for the remaining H atoms.

Data collection: *SMART* (Siemens, 1996); cell refinement: *SAINT* (Siemens, 1996); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Sheldrick, 1997); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL* and *PLATON* (Spek, 2003).

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