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Key indicators

Single-crystal X-ray study T = 297 KMean σ (C–C) = 0.003 Å R factor = 0.043 wR factor = 0.107 Data-to-parameter ratio = 13.9

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

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14-Deoxy-11,12-didehydro-3,19-isopropylideneandrographolide

The title compound, (E)-3-[2-(3,3,6a,10*b*-tetramethyl-8-methyleneperhydronaphtho[2,1-*d*][1,3]dioxin-7-yl)vinyl]furan-2(5*H*)-one, C₂₃H₃₂O₄, an andrographolide analogue, was semi-synthesized from 14-deoxy-11,12-didehydroandrographolide. All the six-membered rings in the structure adopt chair conformations. The crystal structure is stabilized by C— H···O interactions, which form a two-dimensional network parallel to the *ab* plane

Comment

Andrographis paniculata Nees (Acanthaceae) is a very popular herb commonly used in Indian Ayurvedic and Chinese traditional medicine for the treatment of a variety of illnesses. Extracts of this plant have been shown to possess anti-inflammatory (Shen *et al.*, 2002), antiviral (Chang *et al.*, 1991; Calabrese *et al.*, 2000), immunostimulatory (Puri *et al.*, 1993; See *et al.*, 2002), hypoglycaemic (Zhang & Tan, 2000), hypotensive (Zhang & Tan, 1996) and anticancer (Siripong *et al.*, 1992; Stanslas *et al.*, 2001; Kumar *et al.*, 2004) activities. The main labdane type diterpenoid constituents of this plant are andrographolide, neoandrographolide, 14-deoxyandrographolide and 14-deoxy-11,12-didehydroandrographolide.



During the course of developing andrographolide analogues with significant pharmacological activities, the title compound, (II), was semi-synthesized by reacting compound (I) with 2,2-dimethoxypropane under reflux. The X-ray crystal structure analysis of (II) was undertaken in order to establish its molecular structure and stereochemistry.

A molecular view of (II) is shown in Fig. 1. Bond lengths and angles display normal values (Allen *et al.*, 1987), comparable with related structures (Smeets *et al.*, 1987; Spek *et al.*, 1987; Fujita *et al.*, 1984). The five-membered lactone ring is planar, with a maximum deviation of 0.014 (2) Å for atom Received 3 January 2006 Accepted 6 January 2006



Figure 1

The structure of (II), showing 30% probability displacement ellipsoids and the atomic numbering.



Figure 2

The crystal packing of (II), viewed along the *a* axis. Hydrogen bonds are shown as dashed lines.

C15. The orientation of the five-membered ring with respect to the fused ring system is illustrated by the torsion angles C9-C8-C13-C14 [126.2 (2)°], C8-C13-C14-C15 [172.5 (2)°] and C13-C14-C15-C18 [171.7 (2)°]; the corresponding torsion angles for neoandrographolide monohydrate $[164.3 (5), -171.8 (5) \text{ and } 83.3 (7)^{\circ}; \text{ Smeets et al., } 1987]$ and andrographolide [170.6 (2), 158.2 (2) and 175.9 (2)°; Spek et al., 1987] indicate different orientations.

The six-membered rings adopt chair conformations; the Cremer & Pople (1975) puckering parameters Q, θ and φ are 0.531 (2) Å, $12.3 (2)^{\circ}$ and $204.3 (10)^{\circ}$, respectively, for the C3– C4/C9–C12 ring, 0.590 (2) Å, 170.3 (2)° and 148.1 (12)°, respectively, for the C4–C9 ring, and 0.515 (2) Å, 164.5 (2) $^{\circ}$ and $18.7 (8)^\circ$, respectively, for the O1/C1/O2/C2-C3/C12 ring.

The crystal structure is stabilized by $C-H \cdots O$ interactions (Table 1), which form a two-dimensional network parallel to the *ab* plane (Fig. 2).

Experimental

A mixture of 14-deoxy-11,12-didehydroandrographolide (100 mg, 0.3 mmol), 2,2-dimethoxypropane (312 mg, 3.0 mmol) and a catalytic amount of pyridinium p-toulenesulfonate in benzene/dimethyl sulfoxide (5.0 ml/0.5 ml) was refluxed for 1 h. After completion of the reaction (checked by thin-layer chromatography), the reaction mixture was cooled to room temperature. The remaining catalyst was quenched with excess triethylamine (a few drops). The reaction mixture was diluted with benzene and washed with water. The organic layer was dried over anhydrous Na₂SO₄ and concentrated. The final residue was purified by silica gel column chromatography with dichloromethane/methanol (98:2 v/v) as an eluting solvent system. After slow evaporation of the solvent, compound (II) (90 mg, 62%) formed as colourless crystals.

Crystal data

$C_{23}H_{32}O_4$	Mo $K\alpha$ radiation
$M_r = 372.49$	Cell parameters from 7069
Orthorhombic, $P2_12_12_1$	reflections
a = 9.1528 (2) Å	$\theta = 1.9 - 30.0^{\circ}$
b = 10.3440 (2) Å	$\mu = 0.08 \text{ mm}^{-1}$
c = 22.0663 (4) Å	T = 297 (2) K
V = 2089.16 (7) Å ³	Rod, colourless
Z = 4	$0.54 \times 0.21 \times 0.21 \text{ mm}$
$D_x = 1.184 \text{ Mg m}^{-3}$	

Data collection

Bruker SMART APEX2 CCD area-	3452 independent reflections
detector diffractometer	2173 reflections with $I > 2\sigma(I)$
w scans	$R_{\rm int} = 0.034$
Absorption correction: multi-scan	$\theta_{\rm max} = 30.0^{\circ}$
(SADABS; Bruker, 2005)	$h = -12 \rightarrow 12$
$T_{\min} = 0.825, \ T_{\max} = 0.984$	$k = -14 \rightarrow 14$
27503 measured reflections	$l = -31 \rightarrow 31$
Refinement	
,	

$w = 1/[\sigma^2(F_o^2) + (0.0499P)^2]$
+ 0.0866P]
where $P = (F_0^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\rm max} = 0.001$
$\Delta \rho_{\rm max} = 0.12 \text{ e } \text{\AA}^{-3}$
$\Delta \rho_{\rm min} = -0.13 \text{ e } \text{\AA}^{-3}$

Table 1

Hyd	lrogen-	bond g	eomet	try	(A,	Č)	

$D - H \cdots A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - \mathbf{H} \cdots A$
C16 $-$ H16 \cdots O1 ⁱ C17 $-$ H17 $4\cdots$ O4 ⁱⁱ	0.93	2.42	3.273 (2) 3.302 (3)	153 155
<u> </u>	0.97	2.40	3.302 (3)	155

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

H atoms were placed in calculated positions, with C-H distances in the range 0.93–0.98 Å. The U_{iso} values were constrained to be $1.5U_{eq}$ of the carrier atom for methyl H atoms and $1.2U_{eq}$ for the remaining H atoms. Owing to the absence of any significant anomalous dispersion in the molecules, Friedel pairs were merged before the final refinement.

Data collection: *APEX2* (Bruker, 2005); cell refinement: *APEX2*; data reduction: *SAINT* (Bruker, 2005); program(s) used to solve structure: *SHELXTL* (Sheldrick, 1998); 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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