Monoclinic	Cell parameters from 20 reflections
$P2_1/a$	θ = 19.80–20.03°
a = 13.323 (2) Å	μ = 0.713 mm^{-1}
b = 7.8005 (9) Å	T = 293 (2) K
c = 15.324 (2) Å	Block
β = 110.499 (8)°	0.6 × 0.4 × 0.1 mm
V = 1491.7 (3) Å^3	Colorless
Z = 4	
D_x = 1.181 Mg m^{-3}	
D_m not measured	

Data collection

Rigaku AFC-5*R* diffractometer	R_{int} = 0.018
$2\theta-\omega$ scans	θ_{max} = 63.18°
Absorption correction: none	$h = 0 \rightarrow 15$
2533 measured reflections	$k = -9 \rightarrow 0$
2413 independent reflections	$l = -17 \rightarrow 16$
1783 reflections with $I > 2\sigma(I)$	3 standard reflections every 100 reflections
	intensity decay: −0.7%

Refinement

Refinement on F^2	$(\Delta/\sigma)_{max} < 0.001$
$R[F^2 > 2\sigma(F^2)]$ = 0.068	$\Delta\rho_{max}$ = 0.281 e Å^{-3}
$wR(F^2)$ = 0.183	$\Delta\rho_{min}$ = −0.458 e Å^{-3}
S = 1.176	Extinction correction: *SHELXL*93
2365 reflections	Extinction coefficient: 0.0038 (8)
176 parameters	Scattering factors from *International Tables for Crystallography* (Vol. C)
H atoms constrained	
$w = 1/[\sigma^2(F_o^2) + (0.1062P)^2 + 0.6150P]$ where $P = (F_o^2 + 2F_c^2)/3$	

Scan widths were (1.628 + 0.3tanθ)° in ω, with a background/scan time ratio of 0.5. The data were corrected for Lorentz and polarization effects. The Laue group assignment, systematic absences and intensity statics were consistent with centrosymmetric space group $P2_1/a$. Intensities were measured to the mechanical limit of the diffractometer; the θ_{max} was set approximately at 65°. H atoms were calculated at idealized positions and refined with fixed isotropic displacement parameters (U_{iso} = 1.2U_{eq} for the associated C atom or 1.5U_{eq} for methyl C atoms).

Data collection: *MSC/AFC Diffractometer Control Software* (Molecular Structure Corporation, 1991). Cell refinement: *MSC/AFC Diffractometer Control Software*. Data reduction: *MSC/AFC Diffractometer Control Software*. Program(s) used to solve structure: *SHELXS*86 (Sheldrick, 1985). Program(s) used to refine structure: *SHELXL*93 (Sheldrick, 1993). Molecular graphics: *ORTEP*III (Burnett & Johnson, 1996). Software used to prepare material for publication: *PARST* (Nardelli, 1983).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: SX1067). Services for accessing these data are described at the back of the journal.

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9-Deoxy-15-hydroxy- and 9-Deoxy-19-hydroxycotylenol†

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Abstract

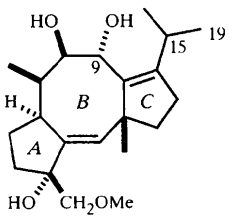
The title analogs (both $C_{21}H_{34}O_4$) of cotylenol, a plant-growth regulator, both have a chair–sofa eight-membered ring, which has been recognized as important for the biological activity of this class of compounds.

Comment

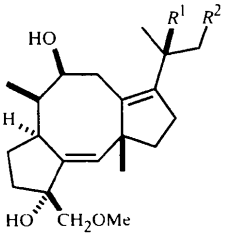
Cotylenol, (I) (Sassa *et al.*, 1975), is a common aglycon of cotylenins and is known to have potent plant hormone-like activity, similar to fusicoccin. Since the binding protein of fusicoccin has recently been identified as a member of the 14–3–3 proteins (Korthout & De Boer, 1994), these fusicoccane diterpenoids have at-

† Alternative nomenclature: (1*R*,3a*S*,4*R*,5*S*,9a*R*)-1,2,3,3a,4,5,6,8,9,9a-decahydro-7-(1-hydroxy-1-methylethyl)-1-(methoxymethyl)-4,9a-dimethyldicyclopenta[*a*,*d*]cyclooctene-1,5-diol and (1*R*,3a*S*,4*R*,5*S*,9a*R*)-1,2,3,3a,4,5,6,8,9,9a-decahydro-7-[(*S*)-2-hydroxy-1-methylethyl]-1-(methoxymethyl)-4,9a-dimethyldicyclopenta[*a*,*d*]cyclooctene-1,5-diol.

tracted much attention. In the course of our synthetic studies on this class of compounds, we observed that 9-deoxy-15-hydroxycotylenol, (II*a*), and 9-deoxy-19-hydroxycotylenol, (II*b*), retain biological activity and, therefore, the 9α-hydroxyl group of (I) is not essential (Li *et al.*, 1997). Furthermore, compound (II*b*) had a greater stimulating activity on seed germination than (II*a*). It had been reported that the conformation of the central eight-membered ring is quite important for biological activity (Ballio *et al.*, 1991). We present here the molecular structures of (II*a*) and (II*b*) in connection with these points.



(I)



(II*a*) R^1=OH, R^2=H
(II*b*) R^1=H, R^2=OH

The structures of (II*a*) and (II*b*) are shown in Figs. 1 and 2, respectively. The disorder ratios in the two independent fragments of (II*a*) are 0.812 (8):0.188 (8) and 0.681 (9):0.319 (9). Except for these values, the fragments do not differ noticeably in their molecular structures.

It is clear that the eight-membered ring (C1, C2, C6–C11) of both (II*a*) and (II*b*) has a chair–sofa conformation, which is believed to be important for biological activity, the conformation being very similar to that in fusicoccin *p*-iodobenzenesulfonate (Brufani *et al.*, 1971). Although both of (II*a*) and (II*b*) retained the stimulating activity on the germination of lettuce seeds, that of (II*b*) was much greater than that of (II*a*). The most significant difference in the conformations of these two compounds was the C2—C3—C16—O2 torsion angle. In the major conformers of the two fragments of (II*a*), the torsion angles are 63.5 (5) and 67.7 (6)°, while that of (II*b*) is −78.0 (4)°. However, this fact should not be correlated with the discrepancy of the biological nature. Since the corresponding value in the fusicoccin derivative has been reported to be 166°, energy differences between three *gauche* rotamers of the methoxymethyl group must be very small. In fact, the values of the minor contributions of (II*a*) are 156.0 (18) and 156.0 (13)°. Therefore, only the small structural difference of (II*a*) and (II*b*), *i.e.* the substitution pattern of the C_3 unit on the *C* ring, must affect the degree of biological activity. It is interesting that (II*a*) was less active, even though the C15-hydroxyl group is in a similar location to the 9α-hydroxyl group of fusicoccin *p*-iodobenzenesulfonate. In other words, elaborate structural analyses, including the direction of the C—O bond, will be necessary to understand the relationship between biological activity and *B*/*C* ring structure in this class of compounds.

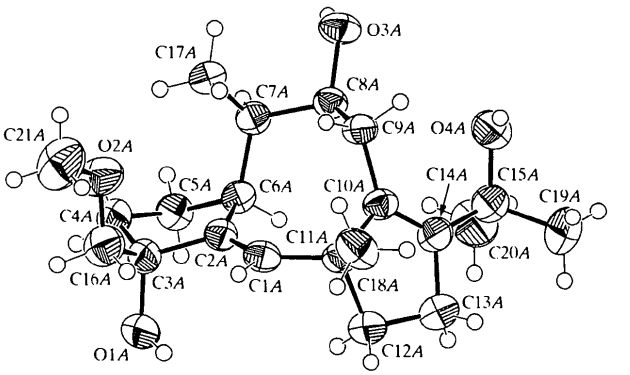


Fig. 1. The molecular structure of (II*a*) showing 50% probability displacement ellipsoids. Although there are two independent fragments, and both fragments have disordered contributions with regard to the rotational conformers of the methoxymethyl group (C16—O2—C21), only the major contribution of one selected fragment is shown for clarity.

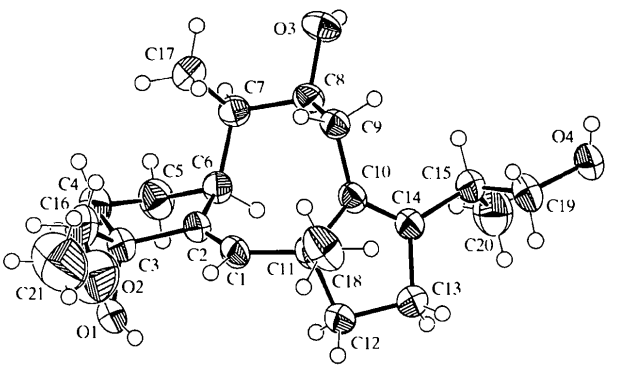


Fig. 2. The molecular structure of (II*b*) showing 50% probability displacement ellipsoids.

Experimental

Compounds (II*a*) and (II*b*) were totally synthesized by us (Li *et al.*, 1997) and recrystallized from *n*-hexane.

Compound (II*a*)

Crystal data

$C_{21}H_{34}O_4$
M_r = 350.50
Orthorhombic
$P2_12_12_1$
a = 11.898 (3) Å
b = 29.390 (5) Å
c = 11.634 (2) Å
V = 4068.2 (14) Å^3
Z = 8
D_x = 1.144 Mg m^{-3}
D_m not measured

Cu $K\alpha$ radiation
λ = 1.54184 Å
Cell parameters from 25 reflections
θ = 40.2–46.2°
μ = 0.615 mm^{-1}
T = 296 (2) K
Prism
0.55 × 0.45 × 0.25 mm
Colorless

Data collection

Enraf–Nonius FR590 diffractometer
ω–2θ scans
Absorption correction: empirical *via* ψ scans (North *et al.*, 1968)
T_{min} = 0.706, T_{max} = 0.857
4320 measured reflections
4320 independent reflections
3438 reflections with $I > 2\sigma(I)$
θ_{max} = 69.94°
$h = 0 \rightarrow 14$
$k = 0 \rightarrow 35$
$l = 0 \rightarrow 14$
3 standard reflections
frequency: 120 min
intensity decay: 2.9%

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.061$
$wR(F^2) = 0.189$
$S = 1.055$
4320 reflections
496 parameters
H atoms riding
$w = 1/[\sigma^2(F_o^2) + (0.1251P)^2 + 0.7301P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.442 e Å^{-3}
$\Delta\rho_{min}$ = −0.307 e Å^{-3}
Extinction correction: *SHELXL*93
Extinction coefficient: 0.0014 (2)
Scattering factors from *International Tables for Crystallography* (Vol. C)

Table 1. *Selected torsion angles (°)*

C11*A*—C1*A*—C2*A*—C6*A*	−6.3 (7)
C1*A*—C2*A*—C6*A*—C7*A*	−77.6 (5)
C2*A*—C6*A*—C7*A*—C8*A*	91.6 (4)
C6*A*—C7*A*—C8*A*—C9*A*	−65.4 (4)
C7*A*—C8*A*—C9*A*—C10*A*	83.0 (4)
C8*A*—C9*A*—C10*A*—C11*A*	−111.4 (4)
C2*A*—C1*A*—C11*A*—C10*A*	25.4 (6)
C9*A*—C10*A*—C11*A*—C1*A*	49.9 (5)
C2*A*—C3*A*—C16*A*—O2*A*	63.5 (5)
C2*A*—C3*A*—C16*A*—O2*A*′	156.0 (18)
C11*B*—C1*B*—C2*B*—C6*B*	−5.0 (8)
C1*B*—C2*B*—C6*B*—C7*B*	−77.4 (6)
C2*B*—C6*B*—C7*B*—C8*B*	93.4 (4)
C6*B*—C7*B*—C8*B*—C9*B*	−66.7 (4)
C7*B*—C8*B*—C9*B*—C10*B*	82.2 (4)
C8*B*—C9*B*—C10*B*—C11*B*	−111.3 (4)
C2*B*—C1*B*—C11*B*—C10*B*	20.5 (7)
C9*B*—C10*B*—C11*B*—C1*B*	54.3 (5)
C2*B*—C3*B*—C16*B*—O2*B*	67.7 (6)
C2*B*—C3*B*—C16*B*—O2*B*′	156.0 (13)

Compound (II*b*)

Crystal data

$C_{21}H_{34}O_4$
M_r = 350.50
Orthorhombic
$P2_12_12_1$
a = 12.703 (3) Å
b = 17.141 (3) Å
c = 9.203 (1) Å
V = 2003.9 (6) Å^3
Z = 4
D_x = 1.162 Mg m^{-3}
D_m not measured
Cu $K\alpha$ radiation
λ = 1.54184 Å
Cell parameters from 25 reflections
θ = 40.37–46.17°
μ = 0.624 mm^{-1}
T = 296 (2) K
Prism
0.45 × 0.40 × 0.18 mm
Colorless

Data collection

Enraf–Nonius FR590 diffractometer
ω–2θ scans
Absorption correction: empirical *via* ψ scans (North *et al.*, 1968)
T_{min} = 0.779, T_{max} = 0.894
4150 measured reflections
3785 independent reflections
3500 reflections with $I > 2\sigma(I)$
R_{int} = 0.024
θ_{max} = 69.92°
$h = -15 \rightarrow 15$
$k = -20 \rightarrow 0$
$l = -11 \rightarrow 0$
3 standard reflections
frequency: 120 min
intensity decay: 1.1%

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.060$
$wR(F^2) = 0.182$
$S = 1.067$
3785 reflections
230 parameters
H atoms riding
$w = 1/[\sigma^2(F_o^2) + (0.1200P)^2 + 0.5649P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.567 e Å^{-3}
$\Delta\rho_{min}$ = −0.367 e Å^{-3}
Extinction correction: *SHELXL*93
Extinction coefficient: 0.0090 (12)
Scattering factors from *International Tables for Crystallography* (Vol. C)

Table 2. *Selected torsion angles (°)*

C11—C1—C2—C6	−2.6 (5)	C8—C9—C10—C11	−106.7 (3)
C1—C2—C6—C7	−78.0 (3)	C2—C1—C11—C10	24.7 (4)
C2—C6—C7—C8	91.2 (3)	C9—C10—C11—C1	47.3 (3)
C6—C7—C8—C9	−67.1 (3)	C2—C3—C16—O2	−78.0 (4)
C7—C8—C9—C10	82.6 (3)		

For both compounds, all H atoms were located at ideal positions and were included in the refinement, but restrained to ride on their parent atoms. The isotropic displacement parameters of the H atoms were held at 1.2 times or 1.5 times (for methyl and hydroxyl groups) U_{eq} of the riding atoms. In the case of (II*a*), *A* and *B* were used to designate the two independent fragments. The disorder ratios in both fragments were independently refined, being treated as free variables in *SHELXL*93 (Sheldrick, 1993).

For both compounds, data collection: *CAD*-4 *Software* (Enraf–Nonius, 1989); cell refinement: *CAD*-4 *Software*; data reduction: *MolEN* (Fair, 1990); program(s) used to solve structures: *SIR*92 (Altomare *et al.*, 1994); program(s) used to refine structures: *SHELXL*93; molecular graphics: *Xtal_GX* (Hall & du Boulay, 1995); software used to prepare material for publication: *SHELXL*93.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: OA1053). Services for accessing these data are described at the back of the journal.

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5,5-Diphenyl-2-thiohydantoin

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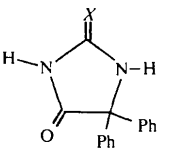
Abstract

The molecular structure of the title compound, 5,5-diphenyl-2-thioxoimidazolidin-4-one, $C_{15}H_{12}N_2OS$, resembles that of 5,5-diphenylhydantoin (phenytoin). The C=S distance is 1.648 (2) Å. The crystal structure consists of ribbon-like infinite sheets of molecules bonded by N—H···O and N—H···S hydrogen bonds. The packing of sheets is governed by van der Waals forces only.

Comment

Phenytoin, 5,5-diphenylhydantoin, (I), is one of the main well established anti-epileptic drugs effective against various forms of partial and generalized seizures (Ramsay *et al.*, 1983). Although the mode of action of phenytoin is still not fully elucidated, it is believed to work mainly by blockade of sodium channels (McLean & Macdonald, 1983). Structure–activity relationship studies for some 80 hydantoin derivatives suggest that the –N3—C4(=O)—C5–phenyl segment of phenytoin (numbering as in Fig. 1) defines its anticonvulsant pharmacophore ('bioactive fragment'), while the –C2(=O)—N3(H)–amide 'face' of the imidazolidine-2,4-dione ring is most likely involved in its mutagenic and teratogenic effects (Weaver, 1992). It is postulated that alterations of this 'face' do not remove anticonvulsant activity, but may result in decreased toxicity in terms of mutagenic potential (Weaver, 1992). The 2-thio analog of phenytoin, 5,5-diphenyl-2-thiohydantoin, (II), was found to have the same spectrum of activity as phenytoin (Kozelka *et al.*, 1942); on the other hand, it was expected to display a different range of toxicity from phenytoin, namely, some undesired antithyroid effects (Gesler *et al.*, 1961). This reinforces the notion that the –C2(=O)—N3(H)–amide 'face' facilitates the differentiation of efficacy from toxicity. The crystal structure of (II) was solved as part of a program of structural analyses of phenytoin analogs with alterations in the 'biotoxic face' of the imidazolidinedione ring (Weaver, 1992) and of the metal complexes of phenytoin (Roszak *et al.*, 1995).



(I) X = O
(II) X = S

The molecular structure of (II) (Fig. 1) is very similar to the structure of 5,5-diphenylhydantoin, (I) (Camerman & Camerman, 1971; Chattopadhyay *et al.*, 1993), despite the different keto function at C2. The imidazolidine ring in (II) is planar, with the thioketone sulfur out of this plane by 0.036 (2) Å and the carbonyl oxygen by −0.013 (2) Å; the geometry of the ring equals that in (I) within 3σ. The spatial arrangement of the two phenyl rings *versus* the imidazolidine ring is slightly different in (I) and (II). The phenyl rings in 5,5-diphenyl-2-thiohydantoin form dihedral angles of 83.66 (7) (ring C51–C56) and 67.50 (7)° (ring C61–C66) with the plane of the five-membered ring, and an

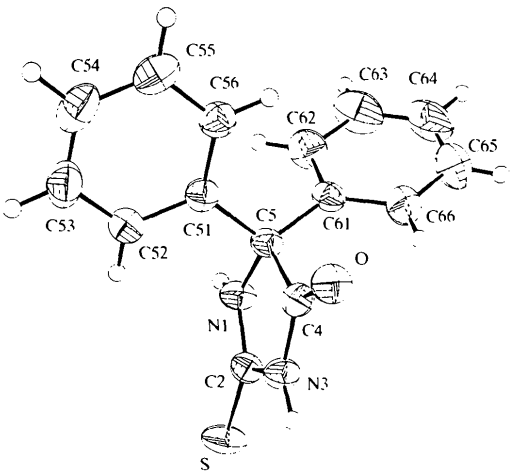


Fig. 1. The molecular structure of the title compound showing the atom-numbering scheme. Displacement ellipsoids are shown at the 50% probability level and H atoms are drawn as unlabelled spheres of arbitrary size.

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