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You-Quan Zhu,^a Hai-Bin Song,^a Jian-Rong Li,^b Chang-Sheng Yao,^a Fang-Zhong Hu,^a Xiao-Mao Zou^a and Hua-Zheng Yang^a*

^aState Key Laboratory and Institute of Elemento-Organic Chemistry, Nankai University, Tianjin 300071, People's Republic of China, and ^bDepartment of Chemistry, Nankai University, Tianjin 300071, People's Republic of China

Correspondence e-mail: youquan_zhu@mail.nankai.edu.cn

Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.006 Å R factor = 0.059 wR factor = 0.131 Data-to-parameter ratio = 9.1

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. The title compound, $C_{18}H_{15}NO_3$, is a potent new herbicide containing the pyrrolidine-2,4-dione ring system. In the crystalline state, the molecular skeleton contains one enol hydrogen-bonded moiety, formed from benzoyl C==O isomer-

1-Benzyl-3-(α-hydroxybenzylidene)-

pyrrolidine-2,4-dione

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Comment

ization.

Many compounds containing the 3-acylpyrrolidine-2,4-dione moiety are novel heterocyclic compounds with antibiotic activity, such as tenuazonic (Sticking, 1959), streptolydigin (Rinehart et al., 1963), tirandamycin (Mackellar et al., 1971), malonomycin (Bann et al., 1978), α-cyclopiazonic acid (Sticking, 1959) and β -cyclopiazonic acid (Holzapfel et al., 1970). All these compounds possess a 3-acyltetramic acid moiety as a tricarbonylmethane structure and their hydrogen chemical shift of the enol hydroxy is about 11 p.p.m. (Wu et al., 2002). On the other hand, most of the excellent inhibitors of p-hydroxyphenylpyruvate dioxygenase also possess similar characteristics, which are crucial for their two kinds of bioactivity (Zhu et al., 2004). Up to now, we have synthesized a series of 3-(un)substituted benzoyl-1-benzylpyrrolidine-2,4dione compounds and some of them have high herbicidal activity. The structure reported here, (Ib), helps us to investigate the relationship between structure and herbicidal activity. To the best of our knowledge, this is the first reported crystal structure determination of a molecule with a 3benzoylpyrrolidine-2,4-dione ring system.



The molecular structure of (*Ib*) is shown in Fig. 1. The analysis of crystals grown from a solution of 3-benzoyl-1benzylpyrrolidine-2,4-dione, (*Ia*), showed that we had obtained crystals of the related tautomeric form 1-benzyl-3-(α -hydroxybenzylidene)pyrrolidine-2,4-dione, (*Ib*). Atom H1,



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View of the title compound, drawn with 40% probability ellipsoids.



Figure 2 Packing diagram showing the intra- and intermolecular hydrogen bonds.

involved in intramolecular hydrogen bonding between O1 and O2, was assigned to O1 rather than to O2, based on bond lengths. The C9–O2 distance is 1.268 (4) Å, which is longer than the normal carbonyl bond length (C11–O3) of 1.219 (5) Å. In contrast, the C1–O1 distance [1.326 (4) Å] is intermediate between the normal carbonyl bond and the C–O single bond length (Ibers & Hamilton, 1974). A similar situation has been found in 3-(1-hydroxyethylidene)-1-phenylpyrrolidine-2,4-dione, which contains the same pyrrolidine skeleton (Ellis & Spek, 2001). In addition, the X-ray data also indicates a weak hydrogen-bonding interaction between two adjacent molecules (see Fig. 2), with an O···C distance of 3.109 (6) Å.

Experimental

The title compound was obtained according to the similar reported procedure of Matsuo *et al.* (1980). Colorless single crystals were obtained by recrystallization of 3-benzoyl-1-benzylpyrrolidine-2,4-dione from petroleum ether and ethyl acetate.

Crystal data

C ₁₈ H ₁₅ NO ₃	Mo $K\alpha$ radiation
$M_r = 293.31$	Cell parameters from 765
Orthorhombic, $P2_12_12_1$	reflections
a = 5.569 (3) Å	$\theta = 2.6 - 19.6^{\circ}$
b = 15.062 (7) Å	$\mu = 0.09 \text{ mm}^{-1}$
c = 18.245 (9) Å	T = 293 (2) K
$V = 1530.3 (12) \text{ Å}^3$	Prism, colourless
Z = 4	$0.20 \times 0.18 \times 0.16 \text{ mm}$
$D_x = 1.273 \text{ Mg m}^{-3}$	
Data collection	
Bruker SMART CCD area-detector	1101 reflections with $I > 2\sigma(I)$
diffractometer	$R_{\rm int} = 0.060$
φ and ω scans	$\theta_{\rm max} = 26.4^{\circ}$
Absorption correction: none	$h = -6 \rightarrow 5$

 $k = -14 \rightarrow 18$

 $l = -22 \rightarrow 21$

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.059$	$w = 1/[\sigma^2(F_o^2) + (0.0612P)^2]$
$vR(F^2) = 0.131$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.07	$(\Delta/\sigma) = 0.001$
1830 reflections 200 parameters	$\Delta \rho_{\text{max}} = 0.17 \text{ e } \text{\AA}^{-3}$ $\Delta \rho_{\text{min}} = -0.12 \text{ e } \text{\AA}^{-3}$

Table 1

Selected geometric parameters (Å, °).

N1-C9	1.345 (4)	C2-C3	1.388 (5)
N1-C10	1.454 (5)	C2-C7	1.392 (6)
N1-C12	1.475 (4)	C8-C11	1.469 (5)
O1-C1	1.326 (4)	C8-C9	1.479 (5)
O2-C9	1.268 (4)	C10-C11	1.535 (5)
O3-C11	1.219 (5)	C12-C13	1.514 (6)
C1-C8	1.399 (5)	C13-C14	1.379 (6)
C1-C2	1.487 (5)		
C9-N1-C10	111.9 (3)	C1-C8-C9	118.5 (3)
C9-N1-C12	124.7 (3)	C11-C8-C9	105.8 (3)
C10-N1-C12	122.2 (3)	O2-C9-N1	124.1 (4)
C1-O1-H1	109.5	02-C9-C8	125.0 (3)
O1-C1-C8	118.0 (3)	N1-C9-C8	110.8 (3)
O1-C1-C2	112.2 (3)	N1-C10-C11	104.4 (3)
C8-C1-C2	129.8 (4)	N1-C10-H10A	110.9
C3-C2-C7	117.3 (4)	O3-C11-C8	131.3 (4)
C1-C8-C11	135.5 (4)	O3-C11-C10	121.8 (4)
01 - C1 - C2 - C3	86(5)	C1 - C8 - C9 - O2	12(5)
$C_{8}-C_{1}-C_{2}-C_{3}$	-1694(4)	$C_{11} - C_{8} - C_{9} - O_{2}^{2}$	177.0 (3)
01 - C1 - C2 - C7	-169.8(4)	C1 - C8 - C9 - N1	-177.9(3)
C8-C1-C2-C7	12.1 (6)	C11-C8-C9-N1	-2.1(4)
C1-C2-C3-C4	179.7 (4)	C9-N1-C12-C13	129.4 (4)
C10-N1-C9-O2	-178.4(3)	C10-N1-C12-C13	-63.9(4)
C12-N1-C9-O2	-10.5(5)	N1-C12-C13-C14	-60.2(5)
C10-N1-C9-C8	0.6 (4)	N1-C12-C13-C18	118.9 (4)
C12-N1-C9-C8	168.5 (3)		

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

$D - H \cdot \cdot \cdot A$	$D-{\rm H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$C10-H10B\cdots O3^{i}$	0.97	2.46	3.019 (5)	116
$O1-H1\cdots O2$	0.82	1.74	2.507 (4)	155
C3-H3···O1	0.93	2.32	2.669 (6)	102
C7-H7···O3	0.93	2.14	2.969 (6)	148
$C12-H12A\cdots O2$	0.97	2.52	2.908 (5)	104
			()	

Symmetry code: (i) $x - \frac{1}{2}, \frac{3}{2} - y, 1 - z$.

All H atoms were placed in calculated positions, with C-H = 0.93 or 0.97 Å and O-H = 0.82 Å, and included in the final cycles of refinement using a riding model, with $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm C})$ or $1.5U_{\rm eq}({\rm O})$. Friedel pairs were not merged.

Data collection: *SMART* (Bruker, 1999); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1999); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1999); software used to prepare material for publication: *SHELXTL*.

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8033 measured reflections

1830 independent reflections

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