organic papers

Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

Xin-Dong Guo,^a Cheng-Zhu Liao,^b Lin Ma^a and Lian-Quan Gu^a*

^aThe School of Chemistry and Chemical Engineering, Sun Yat-Sen (Zhongshan) University, Guangzhou 510275, People's Republic of China, and ^bInstrumentation Analysis and Research Center, Sun Yat-Sen (Zhongshan) University, Guangzhou 510275, People's Republic of China

Correspondence e-mail: cep00gxd@student.zsu.edu.cn

Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.004 Å R factor = 0.053 wR factor = 0.148 Data-to-parameter ratio = 9.5

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

© 2003 International Union of Crystallography Printed in Great Britain – all rights reserved 4-Hydroxy-3,6,9-trimethyl-2,3-dihydrobenzo[*d*e]chromene-7,8-dione

The title compound, $C_{15}H_{14}O_4$, also known as mansonone H, crystallizes in the space group $P2_12_12$ with two molecules in the asymmetric unit. In both molecules, the tetrahydropyran ring adopts an envelope conformation and the attached methyl group occupies an axial position. In the crystal structure, symmetry-related molecules are linked by $O-H\cdots O$ and $C-H\cdots O$ hydrogen bonds, to form chains along the *a* and *b* axes. They are interlinked by $C-H\cdots O$ hydrogen bonds to form a network.

Comment

Mansonone H, (I), was isolated from the roots of *Helicteres* angustifolia (Sterculiaceae), which is a known anti-inflammatory and antitumour medicine (Jiangsu New Medical Colleges, 1986). This cadinane sesquiterpenoid quinone has been previously isolated from the wood sawdust of *Mansonia* altissima Chev (Tanaka et al., 1966), the root bark of Ulmus davidiana (Kim et al., 1996) and the heartwood of Mansonia gagei Drumm (Tiew et al., 2002). The structure of (I) was previously elucidated on the basis of spectroscopic analysis. Here we report the crystal structure of (I).



The X-ray study of (I) confirms the previously proposed molecular structure based on spectroscopic data (Fig. 1). The asymmetric unit of (I) consists of two independent molecules, A and B, linked by a C13B-H13D···O3A hydrogen bond (Table 1). Bond lengths and angles observed in these two molecules agree with each other. The C8A-C9A [1.523 (4) Å] and C8B-C9B [1.536 (4) Å] bond lengths are longer than the mean value of 1.478 (12) Å reported for unconjugated Cs p^2 -Cs p^2 bonds by Allen *et al.* (1987). In both molecules, the tetrahydropyran ring adopts an envelope conformation and the attached methyl group occupies an axial position.

In the crystal structure, symmetry-related A molecules are linked by $O1A-H1A\cdots O3A^{i}$ and $C2A-H2A\cdots O3A^{ii}$ hydrogen bonds, forming chains along the b axis. Similarly, symmetry-related B molecules are linked by $O1B-H1B\cdots O3B^{i}$ and $C2B-H2B\cdots O3B^{ii}$ hydrogen bonds, forming chains along the a axis (symmetry codes are as in Table 1). The chains formed by molecules A and B are linked Received 4 March 2003 Accepted 18 March 2003 Online 31 March 2003



Figure 1

View of the molecules in the asymmetric unit of (I), with ellipsoids drawn at the 50% probability level.



Figure 2 The molecular packing of (I), viewed down the c axis.

into a network by $C13B-H13D\cdots O3A$ hydrogen bonds (Fig. 2).

Experimental

Dried powder, obtained from the roots of Helicteres angustifolia, was extracted with EtOH. The extract was concentrated in vacuo, and the residue was extracted with EtOAc. The soluble portion of the EtOAc extract was subjected to silica-gel column chromatography, eluting with chloroform/methanol, to yield the title compound, mansonone H, (I). The compound identity was confirmed by the NMR spectra. Crystals of (I) were obtained from chloroform/methanol by solvent diffusion. ¹H NMR (500 MHz, DMSO- d_6): δ 6.78 (s, H5), 3.19 (m,

Crystal data

$C_{15}H_{14}O_4$	Mo $K\alpha$ radiation		
$M_r = 258.26$	Cell parameters from 25		
Orthorhombic, $P2_12_12$	reflections		
a = 17.917 (1) Å	$\theta = 25-31^{\circ}$		
b = 18.126(1) Å	$\mu = 0.10 \text{ mm}^{-1}$		
c = 7.668 (1) Å	T = 293 (2) K		
V = 2490.3 (4) Å ³	Plate, red		
Z = 8	$0.28 \times 0.20 \times 0.12 \text{ mm}$		
$D_x = 1.378 \text{ Mg m}^{-3}$			
Data collection			
Bruker SMART CCD	2108 reflections with $I > 2\sigma(I)$		
diffractometer	$R_{\rm int} = 0.056$		
ω scans	$\theta_{\rm max} = 28.3^{\circ}$		
Absorption correction: none	$h = -23 \rightarrow 22$		

 $k = -15 \rightarrow 23$ $l = -10 \rightarrow 10$

H-atom parameters constrained $w = 1/[\sigma^{2}(F_{o}^{2}) + (0.0879P)^{2}]$ where $P = (F_{o}^{2} + 2F_{c}^{2})/3$ $(\Delta/\sigma)_{\rm max} < 0.001$ $\Delta \rho_{\rm max} = 0.23 \text{ e} \text{ Å}^{-3}$ $\Delta \rho_{\rm min} = -0.21 \ {\rm e} \ {\rm \AA}^{-3}$

Table 1

3275 reflections

344 parameters

Refinement

S = 1.00

Refinement on F^2

 $R[F^2 > 2\sigma(F^2)] = 0.053$ $wR(F^2) = 0.148$

14655 measured reflections

3275 independent reflections

Hydrogen-bonding geometry (Å, °).

$D-\mathrm{H}\cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$\overline{\begin{array}{c} O1A - H1A \cdots O3A^{i} \\ O1B - H1B \cdots O3B^{ii} \\ C2A - H2A \cdots O3A^{i} \end{array}}$	0.82	1.97	2.785 (3)	169
	0.82	2.13	2.892 (3)	154
	0.93	2.37	3.099 (4)	136
$C2B - H2B \cdots O3B^{ii}$ $C13B - H13D \cdots O3A$	0.93	2.29	3.074 (4)	141
	0.97	2.43	3.311 (5)	150

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

The H atoms were positioned geometrically and were treated as riding on their parent C and O atoms, with C-H distances in the range 0.93–0.98 Å and an O–H distance of 0.82 Å. The reflections (001) and (110) were omitted during the refinement as they fit very badly. One of the anisotropic displacement parameters (U_{33}) for the carbonyl atom O4A is large, indicating a possible disorder. Owing to a large fraction of weak data at higher angles, the completeness of the data is rather low. The Friedel opposites were merged during the refinement.

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1999); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Bruker, 1998); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

This work is supported by The National Natural Science Foundation (No. 20272085) and Guangdong Provincial Natural Science Foundation of China (No. 021770).

References

Allen, F. H., Kennard, O., Watson, D. G., Brammer, L., Orpen, A. G. & Taylor, R. (1987). J. Chem. Soc. Perkin Trans. 2, pp. S1-19.

- Bruker (1998). *SMART* (Version 5.0) and *SHELXTL* (Version 5.1). Bruker AXS Inc., Madison, Wisconsin, USA.
- Bruker (1999). SAINT-Plus. Version 6. Bruker AXS Inc., Madison, Wisconsin, USA.
- Jiangsu New Medical Colleges (1986). Zhong-yao-da-ci-dian, pp. 178–179. Shanghai: Shanghai Science and Technology Publisher.
- Kim, J. P., Kim, W. G., Koshino, H., Jung, J. & Yoo, I. D. (1996). *Phytochemistry*, **43**, 425–430.
- Tanaka, N., Yasue, M. & Imamura, H. (1966). *Tetrahedron Lett.* 24, 2767–2773.
- Tiew, P., Puntumchai, A., Kokpol, U. & Chavasiri, W. (2002). *Phytochemistry*, **60**, 773–776.