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(\pm)-cis-10-Carboxymethyl-2-decalone: Catemeric Hydrogen Bonding in an ε -Keto Acid

DANIEL ZEWGE, ANDREW P. J. BRUNSKILL, ROGER A. LALANCETTE* AND HUGH W. THOMPSON

Carl A. Olson Memorial Laboratories, Department of Chemistry, Rutgers University, Newark, NJ 07102, USA. E-mail: lalancette@hades.rutgers.edu

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Abstract

The crystal structure of the title compound, (\pm) -*cis*-2-oxoperhydronaphthalene-4a-acetic acid, $C_{12}H_{18}O_3$, involves hydrogen-bonding catemers. Hydrogen bonds progress from the carboxyl group of one molecule to the ketone group of a translationally related neighbor $[O \cdots O \ 2.715 \ (3) \text{ Å}]$. Eight parallel hydrogen-bonding chains proceed in the *a* direction through the chosen cell. Two C=O \cdots H-C close contacts were found, involving the acid carbonyl group.

Comment

Our continuing interest in the crystal structures of keto carboxylic acids lies in the elucidation of their hydrogen-bonding behavior, which is more elaborate than in unadorned acids. Most often, the ketone fails to participate in the hydrogen bonding, giving typical carboxyl dimers, but less commonly, intermolecular carboxylto-ketone hydrogen bonds occur, yielding a catemer. A third, rare arrangement has an internal hydrogen bond, and instances are known of acid-to-ketone dimerization and acid-to-acid catemerization, while several cases are known of hydrates with more complex hydrogen-bonding patterns. We have previously referenced and discussed numerous examples of these hydrogenbonding modes (Thompson *et al.*, 1992, 1998; Coté *et al.*, 1996; Lalancette *et al.*, 1998). To denote the handedness of the intrachain units, we have further categorized such catemers as either hetero- or homochiral, and the latter grouping contains subcategories for screw-related and translational types. Most of the previously reported keto-acid catemers have screw-related components, but a sizable minority are translational. In addition to these necessarily homochiral catemer types, a small minority display a glide relationship between adjacent members and are thus heterochiral (Thompson *et al.*, 1998).

The title compound, (I), is an ε -keto acid, a category that includes dimers and at least one instance each of an internal hydrogen bond and a carboxyl-toketone catemer [refcodes KENROK (Abell et al., 1990) and FAXWOQ (Vanderhoff et al., 1986), respectively; Cambridge Structural Database, 1998]. Compound (I) was of interest to us as a one-carbon homolog of a dimerically hydrogen-bonded keto acid whose structure and hydrogen-bonding behavior we had previously reported (Lalancette et al., 1991). Our experience has led us often to anticipate similar hydrogen-bonding behavior among structurally similar compounds, especially in certain small cyclic or polycyclic systems with specific skeletal features, including some present in (I). We report here that (I), rather than dimerizing, forms carboxyl-to-ketone catemers.



The asymmetric unit of (I) with its numbering is shown in Fig. 1. The decalone system crystallizes in the 'non-steroidal' conformation, in which the angular substituent is axial to the ketone ring, as has been found in some similar angularly substituted decalone acids [refcodes VILZIZ (Lalancette et al., 1991) and OCBDCX (Chadwick & Dunitz, 1979); Cambridge Structural Database, 1998]. The only options available for full rotation in (I) involve bonds C4a-C9 and C9-C10. The former adopts a staggered arrangement, with C9-C10 anti to C4-C4a, while the carboxyl is rotated about C9-C10 so that it lies in a plane close to that of the ketone [dihedral angle C1/C2/C3/O1 versus C9/C10/O2/O3 is $16.7(1)^{\circ}$, with the carboxyl C=O aimed toward the ketone. The result is a linearopposed arrangement of ketone O=C and carboxyl C-O or O-H, of the sort that often allows the formation of translational catemers (Lalancette et al., 1997; Brunskill et al., 1997). This spatial arrangement is shown formally in the 'octant-rule' depiction of the conformation (Moffitt et al., 1961), alongside the usual schematic structure for (I). An alignment normal to \mathbf{c} ,



Fig. 1. The asymmetric unit of (I), with the atomic numbering scheme. Ellipsoids are set at the 30% probability level.

but rotated by 20.5° from the *a* direction, provides exactly such a view of the asymmetric unit.

Averaging of C—O bond lengths and C—C—O angles by disorder, which is common in carboxyl dimers (Leiserowitz, 1976), is not observed in catemers, whose geometry cannot support the mechanisms underlying the averaging processes involved. In (I), these C—O bond lengths are 1.205 (3) and 1.321 (3) Å, with angles of 124.5 (3) and 114.2 (2)°. Our survey of 28 catemeric keto-acid structures gives average values of 1.20 (1) and 1.32 (1) Å, and 124.5 (10) and 112.8 (14)° for these lengths and angles, in accord with typical values of 1.21 and 1.31 Å, and 123 and 112° cited for highly ordered dimeric carboxyls (Borthwick, 1980).

The packing arrangement for (I) is shown in Fig. 2. Carboxyl-to-ketone catemers having an $O \cdots O$ distance of 2.715 (3) Å are formed by hydrogen bonds that progress among molecules translationally related in the *a* direction, and each molecule in the cell participates in a separate chain. These eight parallel chains are centrosymmetrically arrayed around $\frac{1}{2}, \frac{1}{2}, \frac{1}{2}$, and represent all the permutations of handedness, chain direction and up-down orientation of the asymmetric unit. Due to the translational nature of the catemer, the dihedral angle between the carboxyl and ketone planes in adjacent hydrogen-bonded molecules is the same as that between the carboxyl and ketone within a molecule [16.7 (1)°].

Two C=O···H-C close contacts are found to the acid carbonyl (O2), both involving the same neighboring molecule, related by a *b* glide perpendicular to **a**. The participating H atoms are H4*B* (2.66 Å) and H9*B* (2.69 Å), and the contacts may represent polar attractions contributing materially to the packing forces (Jönsson, 1972; Leiserowitz, 1976; Berkovitch-Yellin & Leiserowitz, 1982).

The solid-state (KBr) IR spectrum of (I) has C=O absorptions at 1721 cm^{-1} for the carboxyl, and at 1687



Fig. 2. A partial packing diagram for (I), with extracellular molecules, illustrating the counterdirectional pairs of parallel hydrogen-bonding chains. For clarity, all carbon-bound H atoms have been omitted and only four of the eight chains centrosymmetrically related around $\frac{1}{3}, \frac{1}{2}, \frac{1}{3}$ are shown. Ellipsoids are set at the 30% probability level.

and 1680 cm^{-1} for the ketone. These positions conform to the shifts seen typically in catemers, due to removal of hydrogen bonding from carboxyl C=O and addition of hydrogen bonding to the ketone (Coté *et al.*, 1997). In CHCl₃ solution, all these absorptions coalesce to a single broader peak centered at 1709 cm^{-1} , consistent with a dimerically hydrogen-bonded carboxyl group.

Experimental

Ethoxycarbonylmethylcyclohexanone (Stork *et al.*, 1963) was subjected to Robinson annelation and the purified product was hydrogenated under basic conditions, as described by Gula & Spencer (1980). Saponification provided (I) (m.p. 401 K), which was purified and finally crystallized from 50% ethanol (after seeding with small crystals grown from 10% ethanol).

Crystal data

$C_{12}H_{18}O_3$	Mo $K\alpha$ radiation
$M_r = 210.26$	$\lambda = 0.71073 \text{ Å}$
Orthorhombic	Cell parameters from 27
Pbca	reflections
a = 9.182(2) Å	$\theta = 3.45 - 15.02^{\circ}$
b = 10.917 (2) Å	$\mu = 0.090 \text{ mm}^{-1}$
c = 21.955 (4) Å	T = 293 (2) K
$V = 2200.8 (7) \text{ Å}^3$	Parallelepiped
Z = 8	$0.76 \times 0.40 \times 0.20 \text{ mm}$
$D_x = 1.269 \text{ Mg m}^{-3}$	Colorless
$D_m = 1.269 (1) \text{ Mg m}^{-3}$	
D_m measured by flotation in	
CCl ₄ /p-xylene	

$R_{\rm int}=0.060$
$\theta_{\rm max} = 25.05^{\circ}$
$h = -10 \rightarrow 1$
$k = -13 \rightarrow 1$
$l = -26 \rightarrow 26$
3 standard reflections
every 97 reflections
intensity decay: 1.84%

Refinement

Refinement on F^2	$(\Delta/\sigma)_{\rm max} < 0.001$
$R[F^2 > 2\sigma(F^2)] = 0.054$	$\Delta \rho_{\rm max} = 0.182 \ {\rm e} \ {\rm \AA}^{-3}$
$wR(F^2) = 0.135$	$\Delta \rho_{\rm min}$ = -0.132 e Å ⁻³
S = 1.001	Extinction correction: none
1942 reflections	Scattering factors from
147 parameters	International Tables for
H atoms: see below	Crystallography (Vol. C)
$w = 1/[\sigma^2(F_o^2) + (0.055P)^2]$	
where $P = (F_o^2 + 2F_c^2)/3$	

Table 1. Selected geometric parameters (Å, °)

O1—C2 O2—C10	1.214 (3) 1.205 (3)	O3—C10	1.321 (3)
O2-C10-C9	124.5 (3)	O3-C10-C9	114.2 (2)

Table 2. Hydrogen-bonding geometry $(Å, \circ)$

D—H···A	D—H	$\mathbf{H} \cdot \cdot \cdot \mathbf{A}$	$D \cdot \cdot \cdot A$	D — $\mathbf{H} \cdots \mathbf{A}$		
O3—H3· · ·O1'	0.94 (3)	1.78(3)	2.715(3)	174 (1)		
C4—H4 <i>B</i> · · ·O2"	0.97	2.66	3.566 (3)	155		
C9—H9 <i>B</i> ···O2 ¹¹	0.97	2.69	3.537 (3)	146		
Symmetry codes: (i) $r = 1$ $y = r$ (ii) $1 = r + y = r$						

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

All non-carboxyl H atoms were found in electron-density difference maps, but were replaced in calculated positions and allowed to refine as riding models on their appropriate C atoms. Displacement parameters for methylene H-atom pairs were allowed to refine independently, as was the single methine H atom. The carboxyl H atom was found in an electron-density difference map, but was replaced in a calculated position, and the O—H distance and displacement parameter allowed to refine.

Data collection: XSCANS (Fait, 1991). Cell refinement: XSCANS (Siemens, 1996). Data reduction: XSCANS (Siemens, 1996). Program(s) used to solve structure: SHELXTL/PC (Sheldrick, 1994). Program(s) used to refine structure: SHELXTL/PC. Molecular graphics: SHELXTL/PC. Software used to prepare material for publication: SHELXTL/PC.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: FG1471). Services for accessing these data are described at the back of the journal.

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Amaryllidaceae Alkaloids: (+)-Tazettine, (+)-3-*O*-Demethylcriwelline and (+)-3-Epimacronine at 173 K

Anthony Linden,^{*a*} Gülnur Akineri,^{*b*} Seda Noyan,^{*b*} Tekant Gözler^{*b*} and Manfred Hesse^{*a*}

^aInstitut of Organic Chemistry, University of Zürich, Winterthurerstrasse 190, CH-8057 Zürich, Switzerland, and ^bFaculty of Pharmacy, Ege University, Bornova 35100, Izmir, Turkey. E-mail: alinden@oci.unizh.ch

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Abstract

The Amaryllidaceae alkaloids (+)-tazettine [(+)-(3S,4aS,-6aS,13bS)-3-methoxy-5-methyl-3,4,4a,5,6,6a-hexahydro-8H,11H-[1,3]dioxolo[6,7][2]benzopyrano[3,4-c]indol-