Structural Studies of Curcuminoids. VI. Crystal Structure of 1,7-Bis(4-hydroxyphenyl)-1,6-heptadiene-3,5-dione Hydrate

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The crystal and molecular structure of 1,7-bis(4-hydroxyphenyl)-1,6-heptadiene-3,5-dione hydrate (BISDEM) has been determined at low temperature (122 K) by X-ray crystallographic methods using 1746 reflections. The crystals are monoclinic, space group $P2_1/c$ with unit cell dimensions a = 6.971(1), b = 7.503(1), c = 30.807(5) Å and β = 91.66(2)°. The structure was refined to a conventional R-factor of 0.041. The molecular structure as well as the molecular packing in the crystals of the title compound are found to be almost identical to those reported for the methanol solvate of the curcumin derivative.

The title compound is a natural product that has been studied previously in this laboratory in the form of a methanol solvate.[1] In an effort to exclude solvent molecules from the crystals, different solvents were used for recrystallization; crystals which appeared to be promising were obtained from ethanol. It subsequently turned out that the crystals contained water molecules, but the hydrate presented an opportunity to study the curcuminoid molecules in a crystal environment different from that of the methanol solvate. A structural study was therefore carried out.

Experimental

Orange-yellow crystals of the title compound were obtained by recrystallisation from ethanol. Crystal and experimental data are given in Table 1. Three test reflections were measured periodically at intervals of 135 measurements during the intensity data collection; no loss of intensity was found. Standard deviations in the measured intensities were calculated as $\sigma(I) = [C_T + (0.02C_N)^2]^{1/2}$, where C_T is the total number of counts and C_N is the scan count minus the background count. Corrections were made for Lorentz and polarisation effects. Unit cell dimensions were determined from diffractometer setting angles of 25 reflections. The coordinates of all non-hydrogen atoms were determined by di-

Table 1. Crystal and experimental data.

Compound	$C_{19}H_{16}O_4\ H_2O$
Diffractometer	NICOLET P-3/F
Crystal size/mm	0.35×0.25×0.15
Radiation	Mo$K\alpha$
Crystal system	Monoclinic
a/Å	6.970(1)
b/Å	7.503(1)
c/Å	30.807(5)
β/°	91.66(2)
V/Å^3	1610.5
Temp./K	122
Space group	$P2_1/c$
M	326.2
Z	4
F(000)	688
D_x/g cm^{-3}	1.345
μ(Mo$K\alpha$)/cm^{-1}	1.0
Scan mode	ω
Scan speed (2θ)/°min^{-1}	3.0
Scan range (2θ)/°	1.1
Maximum sinθ/λ/Å^{-1}	0.59
No. of indep. meas.	3129
No. with $I > 3\sigma(I)$	1740
Method used to solve structure	MITHRIL
No. of parameters refined	304
$R=\Sigma\lvert F_o-F_c\rvert/\Sigma F_o$	0.040
$R_w=[\Sigma w(F_o-F_c)^2/\Sigma wF_o^2]^{1/2}$ [a]	0.039
$S=[\Sigma w(F_o-F_c)^2/(n-m)]^{1/2}$	1.5

[a] w is the inverse of the variance of the observed structure factors.

Table 2. Fractional atomic coordinates for BISDEM. Estimated standard deviations in parentheses.

Atom	*x*	*y*	*z*	U_{eq} [a]
O1	1.7987(3)	−0.3793(3)	0.5107(1)	0.042
O2	0.7861(2)	0.1141(3)	0.5913(1)	0.033
O3	0.5052(2)	0.1545(3)	0.6394(1)	0.035
O4	−0.1626(2)	−0.0020(3)	0.8563(1)	0.040
O5	1.0022(3)	0.3966(3)	0.5652(1)	0.039
C1	1.6297(4)	−0.3151(4)	0.5261(1)	0.034
C2	1.5923(4)	−0.3214(4)	0.5703(1)	0.036
C3	1.4240(4)	−0.2492(4)	0.5850(1)	0.034
C4	1.2897(4)	−0.1705(4)	0.5563(1)	0.031
C5	1.3320(4)	−0.1682(4)	0.5124(1)	0.036
C6	1.5002(4)	−0.2410(4)	0.4972(1)	0.037
C7	1.1141(4)	−0.0864(4)	0.5706(1)	0.035
C8	1.0433(4)	−0.0803(4)	0.6105(1)	0.033
C9	0.8617(4)	0.0079(4)	0.6192(1)	0.030
C10	0.7697(4)	−0.0270(4)	0.6589(1)	0.031
C11	0.5954(4)	0.0470(4)	0.6680(1)	0.030
C12	0.4972(4)	0.0163(4)	0.7083(1)	0.031
C13	0.3280(4)	0.0925(4)	0.7164(1)	0.031
C14	0.2127(4)	0.0720(4)	0.7549(1)	0.029
C15	0.229(4)	0.1345(4)	0.7532(1)	0.031
C16	−0.0989(4)	0.1101(4)	0.7872(1)	0.032
C17	−0.0336(4)	0.0233(4)	0.8245(1)	0.031
C18	0.1565(4)	−0.0346(4)	0.8278(1)	0.030
C19	0.2780(3)	−0.0104(4)	0.7935(1)	0.031
H2	1.693(4)	−0.378(3)	0.593(1)	0.043(7)
H3	1.401(3)	−0.262(3)	0.615(1)	0.038(7)
H5	1.241(3)	−0.116(3)	0.493(1)	0.032(7)
H6	1.526(3)	−0.242(3)	0.464(1)	0.039(7)
H7	1.038(3)	−0.030(3)	0.548(1)	0.029(6)
H8	1.109(3)	−0.142(3)	0.634(1)	0.034(7)
H10	0.826(3)	−0.103(3)	0.679(1)	0.025(6)
H12	0.562(3)	−0.065(3)	0.729(1)	0.029(6)
H13	0.274(3)	0.175(3)	0.693(1)	0.030(7)
H15	−0.024(3)	0.195(3)	0.726(1)	0.040(7)
H16	−0.232(3)	0.149(3)	0.785(1)	0.028(7)
H18	0.202(3)	−0.096(3)	0.854(1)	0.023(6)
H19	0.414(3)	−0.055(3)	0.798(1)	0.038(7)
H21	1.864(4)	−0.441(4)	0.531(1)	0.10(1)
H30	0.595(4)	0.160(4)	0.615(1)	0.076(9)
H40	−0.099(4)	−0.055(5)	0.884(1)	0.13(1)
H51	0.934(4)	0.291(4)	0.569(1)	0.075(9)
H52	1.086(4)	0.378(5)	0.544(1)	0.11(1)

[a] $U_{eq} = (U_{11} + U_{22} + U_{33})/3$.

rect methods.[2] Refinements were performed by least-squares calculations. Hydrogen atomic positions were calculated and included in the refinements, which proceeded with anisotropic temperature factors for the heavier atoms and isotropic temperature factors for hydrogen atoms. Computer programs employed are described in Refs. 3 and 4. Final figures of merit are included in Table 1. Positional parameters are given in Table 2. Lists of anisotropic thermal parameters and structure factors may be obtained from the authors on request.

Description and discussion

A drawing of the molecule is shown in Fig. 1, where the numbering of the atoms is also indicated. Bond lengths and angles are given in Table 3 together with the corresponding values in the methanol solvate. The packing of the molecules and the hydrogen bonding is illustrated in Fig. 2. It is interesting to note that the packing of the molecules in the crystals of the monohydrate is almost identical to that found in the methanol solvate. Van der Waals contacts between molecules related by screw axes are the same in both structures; between two molecules related by a screw axis in the *y*-direction there are equal distances of 2.8 Å from the oxygen atoms O2 and O3 in one molecule to the atom H18 in the next, and about 3.0 Å from atoms C15 and C16 to H10; the distance between O4 and H3 is 2.6 Å. In the methanol solvate the molecules are linked together by three hydrogen bonds all involving the methanol oxygen atom. The water molecule in the hydrate structure is found to be engaged in the corresponding three hydrogen bonds and, in addition, one directed to the O1 atom. Thus, there is a slight difference in the hydrogen bond system in the two structures; in the hydrate structure there is water-linked hydrogen bonding between the layers of molecules which in the methanol solvate are connected only through van der Waals forces. As in the methanol solvate, there are no direct hydrogen bonds between the BISDEM molecules; all hydrogen bonds involve water molecules. Each water molecule is surrounded by two hydrogen donors and two hydrogen acceptors positioned in the corners of a distorted tetrahedron. Thus, the water molecule acts as a hydrogen donor to the O2 atom, and to the O1 atom in a molecule displaced by a center of symmetry. It also acts as an acceptor from O1 in a molecule translated one unit down the *x*-axis and one unit along the *y*-axis, and finally as an acceptor from O4 in a molecule acted upon by a screw axis. The geometry of the hydrogen bond-

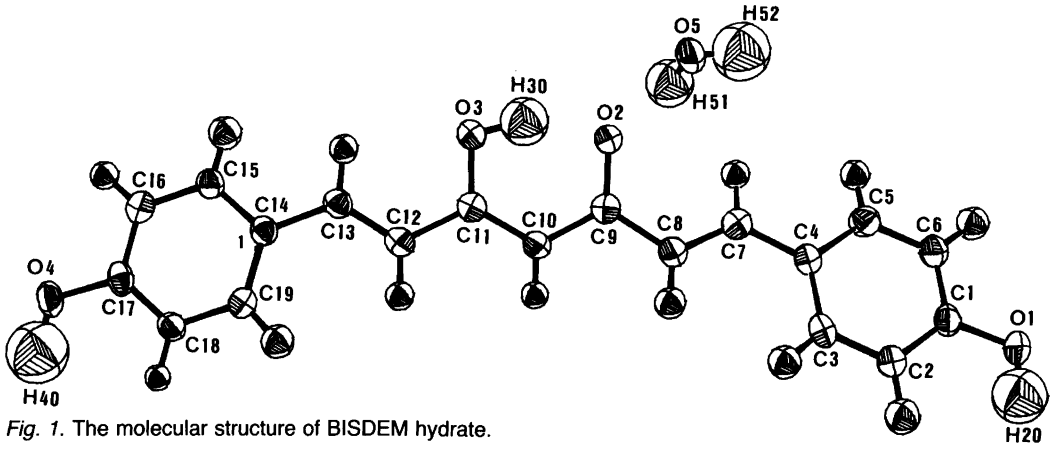

Fig. 1. The molecular structure of BISDEM hydrate.

Table 3. Bond lengths (Å) and angles (°) in BISDEM in the present study (H_2O) and in the methanol solvate (Meth.). Estimated standard deviations in bond lengths are 4×10^{-3} Å (H_2O) and 3×10^{-3} Å (Meth.), and in angles 0.3° (H_2O) and 0.2° (Meth.). The C–H distances are all between 0.89 and 1.06 Å in the hydrate structure.

	H_2O	Meth.		H_2O	Meth.
Bond lengths					
O1–C1	1.370	1.357	O2–C9	1.275	1.283
O3–C11	1.336	1.337	O4–C17	1.364	1.359
C1–C2	1.396	1.394	C1–C6	1.367	1.386
C2–C3	1.380	1.377	C3–C4	1.399	1.400
C4–C5	1.391	1.395	C4–C7	1.456	1.455
C5–C6	1.388	1.380	C7–C8	1.341	1.337
C8–C9	1.460	1.457	C9–C10	1.424	1.421
C10–C11	1.375	1.372	C11–C12	1.453	1.448
C12–C13	1.341	1.336	C13–C14	1.461	1.459
C14–C15	1.403	1.404	C14–C19	1.403	1.403
C15–C16	1.380	1.377	C16–C17	1.386	1.388
C17–C18	1.395	1.394	C18–C19	1.385	1.382
Angles					
O1–C1– C2	120.8	122.2	O1–C1 –C6	118.5	118.0
C2–C1 –C6	120.7	119.8	C1–C2 –C3	119.4	120.1
C2–C3 –C4	121.3	121.1	C3–C4 –C5	117.5	117.6
C3–C4 –C7	123.1	123.3	C5–C4 –C7	119.4	119.1
C4–C5 –C6	122.0	121.9	C1–C6 –C5	119.2	119.5
C4–C7 –C8	128.8	128.8	C7–C8 –C9	121.8	121.6
O2–C9 –C8	120.2	120.2	O2–C9 –C10	120.7	120.4
C8–C9 –C10	119.1	119.3	C9–C10–C11	121.3	121.8
O3–C11–C10	121.0	120.9	O3–C11–C12	115.7	116.0
C10–C11–C12	123.3	123.1	C11–C12–C13	122.1	122.4
C12–C13–C14	127.9	127.9	C13–C14–C15	118.3	118.0
C13–C14–C19	124.2	124.6	C15–C14–C19	117.5	117.3
C14–C15–C16	121.8	121.8	C15–C16–C17	119.8	119.9
O4–C17–C16	117.0	117.1	O4–C17–C18	123.2	123.2
C16–C17–C18	119.7	119.7	C17–C18–C19	120.2	120.1
C14–C19–C18	120.9	121.3			

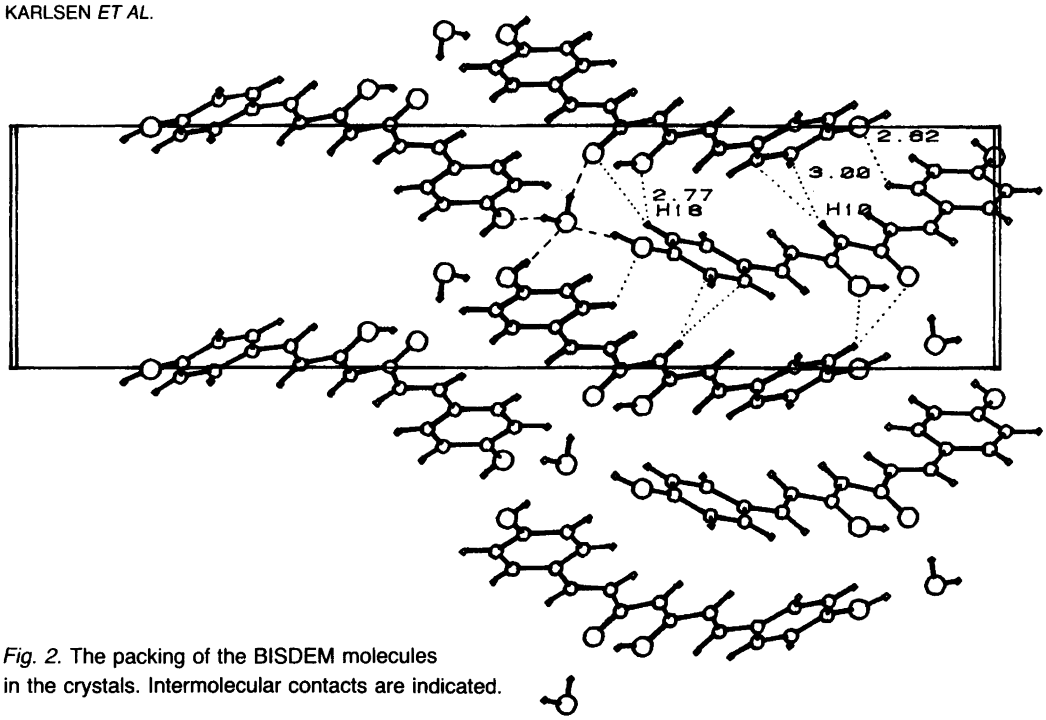

Fig. 2. The packing of the BISDEM molecules in the crystals. Intermolecular contacts are indicated.

Table 4. Geometry of the hydrogen bonds in BISDEM. Distances in Å, angles in °.

D	A		D–A	H···A	D–H···A	C–O–H	C–O···A
O1	O5	(1+*x*,−1+*y*,*z*)	2.742	1.86	170	112	116
O4	O5	(1−*x*,−1/2+*y*,3/2−*z*)	2.741	1.71	168	112	114
O5	O2	(*x*,*y*,*z*)	2.734	1.82	163	–	–
O5	O1	(3−*x*,−*y*,1,−*z*)	2.758	1.88	170	–	–
O3	O2	(*x*,*y*,*z*)	2.510	1.57	154	103	–

ing is summarized in Table 4. The similarity in the molecular packing in the hydrate and the methanol solvate is mirrored in the molecular geometry. The conformation of the BISDEM molecule is the same in the two crystal structures, as can be seen from the conformational angles in Table 5. The only significant differences is in the torsion angle about the C4–C7 bond, where the difference is found to be 2.8(4)°. Moreover, it is seen from Table 3 that all the bond angles are practically identical except for the O1–C1–C2 angle, where the difference is 1.4(4)°. Finally, there is also good agreement between bond lengths in the two structures, and the only significant differences are in the O1–C1 and C1–C6 distances. It may be noted that all the significant

Table 5. Comparison of torsion angles (°) in BISDEM hydrate and methanol solvate. Estimated standard deviations are 0.3°.

Torsion angle	H_2O	Meth.
C5 –C4 –C7 –C8	176.9	179.7
C4 –C7 –C8 –C9	−178.9	−179.6
C7 –C8 –C9 –O2	−15.3	−14.4
C7 –C8 –C9 –C10	164.1	165.8
O2 –C9 –C10–C11	1.6	1.5
C8 –C9 –C10–C11	−177.8	−178.7
C9 –C10–C11–O3	0.8	0.7
C9 –C10–C11–C12	−179.2	−178.9
O3 –C11–C12–C13	−0.6	−1.1
C10–C11–C12–C13	179.4	178.5
C11–C12–C13–C14	179.2	178.9
C12–C13–C14–C19	11.1	9.9

differences occur in, or in connection with, the aromatic ring which is involved, via the O1 atom, in the extra hydrogen bond (relative to the methanol solvate). On the other hand, all the differences except for that in the torsion angle may be explained by a displacement of the C1 atom.

References

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