The molecular structure of acyclic aralkyl compounds studied by a crystallographic database survey. Relevance of the intramolecular CH/π hydrogen bond to conformation

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A database study was carried out, by the use of the Cambridge Structural Database, to investigate the conformation of aralkyl compounds $ArCH_2XCH_2Y$ 1 and $ArCHCH_3XCH$ 2 in crystals. The structure bearing R (R: any group) and Ar in the *syn* relationship has often been found in these compounds. The proportion of crystal structures bearing R and Ar in the *syn* relationship relative to the *anti* conformation ($r_{syn/anti}$) varied from 0.55 for 1 to 3.68 for 2. The logarithm of $r_{syn/anti}$ was plotted against the difference in Gibbs energy $\Delta G_{syn-anti}$ obtained by MO calculations of model compounds at the MP2/6-311G(d,p)//MP2/6-31G(d) level: $C_6H_5CH_2XCH_3$ and $C_6H_5CHCH_3XCH_3$. A linear correlation has been shown between $lnr_{syn/anti}$ and $\Delta G_{syn-anti}$. The CH/π interaction is suggested to operate in controlling the R/Ar-folded crystal structure of these aralkyl compounds.

Introduction

In 1996, Taylor and coworkers¹ analyzed the crystal conformation of a series of organic compounds in the Cambridge Structural Database (CSD) to investigate the effects of packing on the molecular structure.² They compared the crystal-structure conformer distributions of 12 substructures with MO data from the HF/6-31G*//HF/STO-3G level calculations. Least-squares regression showed that there was a statistically significant correlation between the crystal data and calculated potential-energy differences. It follows that the influence of the so-called packing force on the molecular structure is neither strong nor systematic.

Among the substructures they examined, there are compounds with an aromatic group at a terminus of the molecule, $ArCH_2XC$ and $ArXCH_2C$ (X = CH_2 , O, S). It seemed interesting that the Ar/C syn conformation was frequently found by their database search. Recently we studied, by ab initio calculations [MP2/6-311G(d,p)//MP2/6-31G(d)], the conformation of a series of benzylic compounds $C_6H_5CH_2XR$ (X = O, CH₂, CO, S, SO, SO₂). The most stable conformation has been shown to bear R and Ph in the syn relationship, with exceptions for several tert-butyl analogues. The conformation of 1-phenylethyl compounds $C_6H_5CHCH_3XR$ (X = CO, SO,⁵ CHOH,⁶ S and SO₂⁷) was also studied. These molecules have been shown to prefer the conformation whereby the alkyl group (R) is syn to $C_6H_5(Ph)$ and anti to the benzylic methyl group. The computational results agreed well with those obtained by NMR studies.8

Here, we examined crystal structures deposited in the CSD with our own hypothesis that such a R/Ar-folded motif is

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encountered, generally, in organic crystals since we felt the above result to be a consequence of the CH/π interaction. The CH/π interaction is the weakest extreme of non-conventional hydrogen bonds. The CH/π hydrogen bond occurs between soft acids and soft bases, in contrast to the ordinary hydrogen bond that is the interaction between hard acids and hard bases. Recent molecular orbital calculations have established the theoretical basis of the CH/π interaction. The same stable is the interaction.

Method

Database study

The CSD version 5.24 (January 2003 release, 272 066 entries) was used. The torsion angle ϕ defined by the Ar-C¹-X-C³ sequence in substructures ArCH₂XCH₂Y 1 and ArCH-CH₃XC₃p₃H 2 (Fig. 1) was inspected for organic crystals in the CSD. Only error-free structures with no disorder and R<10% were accepted. Groups X and Y were any atoms in the initial survey and were replaced by an atom or group in the individual searches. X, Y and C₃p₃ in 2 were constrained not in a cyclic environment. Structures were inverted where necessary so that the torsion angle ϕ fell in the range $0\sim180^\circ$. The C–H bond length was normalized to the standard value of 1.083 Å.

Ab initio calculations

A detailed description of the method is given in our previous papers.^{3–7} Briefly, the geometry of C₆H₅CH₂NHCH₃,

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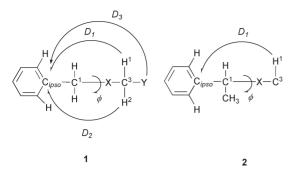


Fig. 1 Substructures to be surveyed.

C6H5CHCH3CH2CH3, C6H5CHCH3NHCH3 and C6H5CH-CH₃OCH₃ was optimized at the MP2/6-31G(d) level of approximation. Using these geometries, single point calculations were performed at the MP2/6-311G(d,p) level to estimate the energies of the conformers. Vibrational frequencies were calculated using the analytical second derivatives at the same level of the geometry optimization; all the eigenvalues were real for each conformer. Using these results, the thermal energy corrections were added to the total energy at 298.15 K and 1 atmosphere of pressure, with the principal isotope for each element type. All the calculations were performed by Gaussian 98 program. ¹⁴

Results and discussion

First, organic crystals with substructures ArCH₂XCH₂Y 1 were surveyed. 195 entries (268 fragments) were obtained from this search. Fig. 2 gives a histogram; the number of fragments is plotted against the torsion around the Ar-C¹-X-C³ sequence. The peak at ϕ 180° (Ar/C³ anti) is sharp but the cluster corresponding to the Ar/C³ syn structure is broad. The number of fragments with the syn conformation (ϕ $0 \sim 90^{\circ}$, 95 structures) is smaller than that of the *anti* conformation (ϕ 90 ~ 180°, 173 structures). The ratio of the syn vs. anti conformation ($r_{syn/anti}$) is 0.55.

Fig. 3 shows a scattegram plotted for H^1/C_{ipso} distance (D^1) against the Ar/C³ torsion angle (ϕ). Three clusters, centred at D^1 ca. 2.7, 3.3 and 4.0 Å, are found for the syn conformations. These correspond, in part, to the nearest, the second nearest

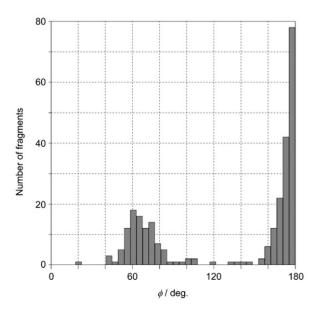


Fig. 2 Histogram obtained from a search of the substructure ArCH₂XCH₂Y 1. VISTA ver. 2.0.

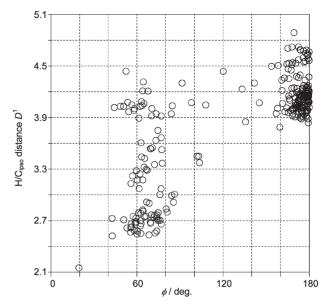


Fig. 3 Scattegram from a search of the substructure ArCH₂XCH₂Y 1 plotted for H/C_{ipso} distance (D^1) against Ar/C³ torsion angle (ϕ). VÎSTA ver. 2.0.

and the remotest CH of a methyl group in CH₂Y, interacting with the aromatic ring, respectively. Superimposed on these clusters are CHs of other groups such as methylene or methine in CH₂Y. Fig. 4 is a scattegram plotted for H/C_{ipso} distances D^1 and D^2 . It is noted that either D^1 or D^2 is in a short distance range with respect to C_{ipso} .

The above syn 95 fragments were analyzed to seek structure with at least one 5-member CH/π intramolecular distance D shorter than 3.05 Å [= 2.9 Å (1.2 Å for H and 1.7 Å for sp^2 C) \times 1.05]¹⁵ for entries with ϕ < 90, 80, 70 and 60°. Many short H/C_{inso} distances have been noted at the relevant atoms. Table 1 shows that almost every structure bears a CH/π contact shorter than 3.05 Å. A similar result was obtained for D^2 .

Next, we surveyed the CSD by replacing group X with CH₂, NH, O and S. Table 2 summarizes the results. For $X = CH_2$, only 6 are in the syn conformation, whereas 61 fragments are anti with respect to Ar and C^3 . For X = O, 21 and 40 are found syn and anti among 61 fragments, respectively. Figs. 5 and 6 give histograms for these surveys.

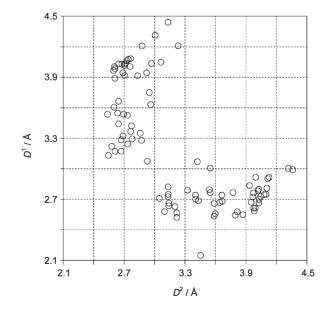


Fig. 4 Scattegram from a search of the substructure ArCH₂XCH₂Y 1 plotted for H/C_{ipso} distances D^1 vs. D^2 ($\phi < 90^{\circ}$).

Table 1 Number and proportion of structures with the *syn* conformation of ArCH₂XCH₂Y 1 (X, Y: any atom), bearing 5-member CH/ π intramolecular distances (H/C_{ipso}) shorter than 3.05 Å^a

	$\phi/^\circ$	Fragment ^b	Ratio (%)	$D_{ m atm}/{ m \AA}^c$
1	$0 \sim 90$	91	96	2.72 ± 0.14
	$0 \sim 80$	84	88	2.70 ± 0.13
	$0 \sim 70$	60	63	2.68 ± 0.13
	$0 \sim 60$	24	25	2.63 ± 0.13

^a The C–H bond length was normalized to the standard value of 1.083 Å. ^b Number of observations with CH/C_{ipso} distance shorter than 3.05 Å. ^c Mean atomic distance \pm SD.

Table 2 Crystal data of (a) ArCH₂XCH₂Y and (b) ArCHCH₃XCH^a

(a) ArCH ₂ XCH ₂ Y (Y: any atom)	$Fragment^b$	syn ^c	$anti^d$	$r_{syn/anti}^{e}$
X				
Any atom	268	95	173	0.55
Any C	109	27	82	0.33
CH_2	67	6	61	0.10
NH	2	0	2	_
O	61	21	40	0.53
S	14	6	8	0.75

X				
Any atom	159	125	34	3.68
Any C	41	34	7	4.86
CH_2	7	7	0	_
NH	13	12	1	12.00
O	4	2	2	1.00
S	0	0	0	_

 $[^]a$ The C–H bond length was normalized to 1.083 Å. b Number of observations. c ϕ $0 \sim 90^\circ$. d ϕ $90^\circ \sim 180^\circ$. e Ratio of the syn vs. anti conformation.

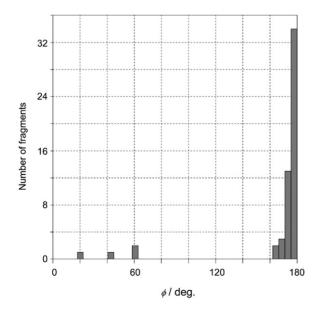


Fig. 5 Histogram obtained from a search of the substructure $ArCH_2$ - CH_2CH_2Y .

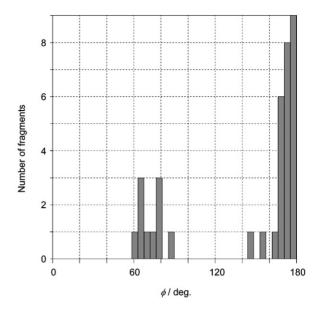


Fig. 6 Histogram obtained from a search of the substructure ArCH₂OCH₂Y.

For arylethyl compounds ArCHCH₃XCH₂Y **2** (X, Y: any atom), only 14 entries were found in the database. We therefore surveyed, instead, the substructure ArCHCH₃-XC_{sp3}H. Fig. 7 gives a histogram of this survey. The number of fragments with the *syn* conformation (ϕ 0~90°, 125 fragments) is larger than that of the *anti* conformation (ϕ 90~180°, 34 fragments). The ratio of the *syn vs. anti* conformation ($r_{syn/anti}$) is 3.68. Introduction of an alkyl group α to the aromatic ring greatly increased the abundance of the R/Ar-folded structure. This is reasonable in view of the unfavourable steric interaction, which may occur between the benzylic methyl group and R.

In Table 3 are listed the number of fragments and mean interatomic distances $D_1 \sim D_3$ in the crystal structure of Ar/C³ syn-conformation. We note that the distance from the *ipso* carbon is shorter (around 1 Å) when the atom attached to C₃ is hydrogen than in the other cases. This is much shorter than might be expected by replacement of a C-H (bond length *ca.* 1.09 Å) to C-C (1.54 Å). The contribution from

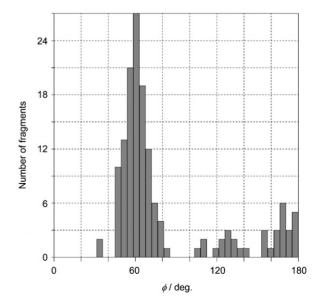
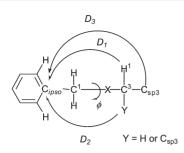


Fig. 7 Histogram obtained from a search of the substructure $ArCHCH_3XC_{sp3}H$ 2.

 $Y = C_{sp3}$

Table 3 Number of fragments and mean interatomic $(C_{ipso}/H^1, C_{ipso}/Y \text{ and } C_{ipso}/C_{sp3})$ distances (Å)in the crystal structure of Ar/C^3 synconformation^a



(a) $ArC^1H_2XC^3H_2C_{sp3}$				
	Fragment ^b	D_1	D_2	D_3
$X = AA^c$				
Y: AA	95	3.20 ± 0.58	3.25 ± 0.55	4.16 ± 0.38
Y: Any C _{sp3}	58	3.21 ± 0.58	3.18 ± 0.53	4.18 ± 0.36
$X = CH_2$				
Y: AA	6	3.02 ± 0.51	2.96 ± 0.29	4.28 ± 0.42
Y: Any C _{sp3}	4	2.81 ± 0.50	3.10 ± 0.26	4.19 ± 0.51
X = O				
Y: AA	21	3.07 ± 0.44	3.17 ± 0.48	4.27 ± 0.32
Y: Any C _{sp3}	10	2.98 ± 0.36	3.13 ± 0.35	4.40 ± 0.08
X = S				
Y: AA	6	3.63 ± 0.72	3.16 ± 0.60	4.26 ± 0.34
Y: Any C _{sp3}	4	3.32 ± 0.67	3.27 ± 0.73	4.43 ± 0.22
(b) $ArC^{1}H_{2}XC^{3}H(C_{sp3})_{2}$				
$(Y = C_{sp3})$				
	Fragment	D_1	D_2	D_3
X = AA				
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 $^a{\rm The}$ C–H bond length was normalized to 1.083 Å. $^b{\rm Number}$ of observations. $^c{\rm Any}$ atom.

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 2.66 ± 0.30 4.07 ± 0.29 4.11 ± 0.26

the CH/π bond in making these conformations favorable seems apparent.

Comparison of the crystallographic data with the conformational energies calculated by the *ab initio* method

Table 4 compares the logarithm of syn/anti- ratio $(\ln r_{syn/anti})$ and the difference in the conformational energies $(\Delta G_{syn-anti})$. The greater the $\Delta G_{syn-anti}$, the greater the proportion of the syn conformation. A least-squares regression analysis shows a linear correlation to exist between $\ln r_{syn/anti}$ and $\Delta G_{syn-anti}$ (Fig. 8). This is consistent with the result reported by Taylor et~al.

Table 4 Crystal conformer distributions $(\ln r_{syn/anti})$ and difference in the conformational energies $(\Delta G_{syn-anti}, \ker \log^{-1})$ calculated by the *ab initio* method for the *syn* and *anti* conformations of methyl benzyl and methyl 1-phenylethyl compounds

	$\ln r_{syn/anti}$	$\Delta G_{syn-anti}$	Reference
C ₆ H ₅ CH ₂ CH ₂ CH ₃	-2.30^{a}	0.04	3
C ₆ H ₅ CH ₂ NHCH ₃	_	-0.35	this work
C ₆ H ₅ CH ₂ OCH ₃	-0.63^{a}	0.79	3
C ₆ H ₅ CH ₂ SCH ₃	-0.29^{a}	0.97	3
C ₆ H ₅ CHCH ₃ CH ₂ CH ₃		1.09	this work
C ₆ H ₅ CHCH ₃ NHCH ₃	2.48^{b}	3.60^{c}	this work
C ₆ H ₅ CHCH ₃ OCH ₃	0.00^{b}	2.05	this work
C ₆ H ₅ CHCH ₃ SCH ₃	_	1.54	7

^a ArCH₂XCH₂Y. ^b ArCH(CH₃)XC_{sp3}H. ^c threo isomer.

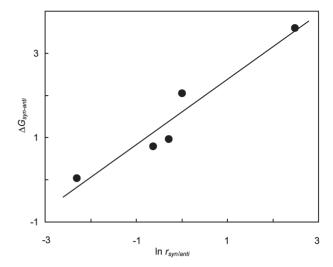


Fig. 8 Plot of $\ln r_{syn/anti}$ against calculated Gibbs energy difference $\Delta G_{syn-anti}$.

Conclusion

To summarize, crystal structures bearing CH and Ar in the syn relationship are often found in aralkyl compounds. Correlation of the crystal-structure conformer distribution with the computed conformational energy difference is statistically significant. As to the origin of the favoured syn R/Ar conformation, contribution from the CH/ π hydrogen bond is suggested.

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