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Molecular Recognition Involving an Interplay of O–H ··· O, C–H ··· O and π ··· π Interactions. The Anomalous Crystal Structure of the 1:1 Complex 3,5-Dinitrobenzoic Acid–4-(*N,N*-Dimethylamino)benzoic Acid

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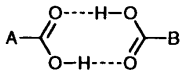
The crystal structure of the 1:1 donor–acceptor complex of 3,5-dinitrobenzoic acid and 4-(*N,N*-dimethylamino)benzoic acid contains the uncommon O–H ··· O hydrogen-bonded carboxy homodimers rather than the heterodimers found in nine other related complexes. The formation of these homodimers contradicts the general principle that in hydrogen-bonded networks, the strongest proton donor hydrogen bonds to the strongest proton acceptor. This unusual homodimer is obtained because of difficulties in C–H ··· O hydrogen bond formation, the consequent importance of π ··· π stacking interactions and the enhanced stability of homodimer stacks over heterodimer stacks. Additionally, it is concluded that: (i) O–H ··· O hydrogen bonds can act as a conduit for charge transfer and may alter the polarization of atoms; (ii) C–H ··· O bonds can be used for molecular recognition and C–H ··· O patterns are sensitive to molecular stoichiometry and substituent positioning; (iii) stacking interactions influence the nature of hydrogen bonding and *vice versa*. This study shows that for precise supramolecular construction, strong and weak intermolecular interactions must be considered together.

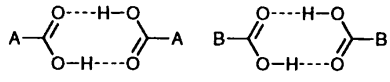
Supramolecular assembly is a central theme in the design of advanced materials (conducting, electronic, magnetic, optical) and is based on the mutual recognition of molecules.[1] This field has progressed with an increasing knowledge of intermolecular interactions, a variety of which have been exploited and utilized. However, the ever-growing demand for the construction of supramolecules with high precision, that is with a control of secondary and tertiary structural features, has been largely unfulfilled because such construction requires a subtle and simultaneous manipulation of strong and weak intermolecular interactions.[2] This is quite a difficult task, at least at present, because our knowledge of weak† intermolecular interactions has not yet reached a stage where they may be used reliably for molecular recognition.



Scheme 1

The conventional or strong O–H ··· O and N–H ··· O hydrogen bond has, in contrast, been successfully used for molecular recognition[1a,e,3] and a spate of recent articles on strong hydrogen bonds have improved our understanding of bonding patterns, and has led to the formulation of empirical rules.[3c,4] For example, aromatic carboxylic acids crystallize as centrosymmetric O–H ··· O mediated dimers, but a 1:1 mixed crystal obtained from a pair of acids **A** and **B** with substituents of different electronegativities contains only carboxy heterodimers **AB** (Scheme 1).[3c,4] Such heterodimers are stable because of the variation in the proton donating and accepting capabilities of the two acids, which leads to the two hydrogen bonds in the ring being of unequal strengths. Such a structural motif is supposed to be robust and not perturbed by other interactions[4a] since it is formed in accordance with the principle that the strongest proton donor hydrogen bonds to the strongest proton acceptor, followed by a matching of the next strongest proton donor and acceptor.[3c,4c,5] Therefore, the formation of this asymmetrical heterodimer has been tacitly assumed to be one of the guaranteed first steps in the overall objective of, say, designing a non-centrosymmetric crystal.

Do all carboxylic acid mixed crystals follow this principle? In a study of several complexes of nitro- and amino-substituted benzoic and cinnamic acids, we have found a case, namely the 1:1 complex, **1**, of 3,5-dinitrobenzoic acid, **1a**, and 4-(*N,N*-dimethylamino)benzoic acid, **1c**, where the structure is made up exclusively of homodimers **AA** and **BB** instead of **AB** heterodimers (Scheme 2). This observation suggests that a



Scheme 2

consummate understanding of all crystal packing forces is required even in the prediction of strongly hydrogen bonded structures. This is where the art of crystal engineering enters—how does one balance intermolecular interactions in crystals?

Besides strong hydrogen bonding, π ··· π interactions have received the attention of researchers in this area,[1f,6] even as the nature of these interactions is becoming clearer. Further, weak hydrogen bonds such as C–H ··· O[7] and C–H ··· N[8] are being increasingly implicated in crystal structures. Recently, we reported the use of C–H ··· O interactions in selective binding.[1k] All these three types of interactions, O–H ··· O, C–H ··· O and π ··· π, require special attention in the area of molecular recognition because of their omnipresence in most organic and biological structures. Traditionally, these interactions have been studied independently and there are no collective studies of them, in other words on how these three

† The terms 'weak' and 'strong' are defined with respect to conventional O–H ··· O and N–H ··· O hydrogen bonds which are considered strong.

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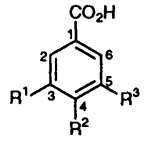
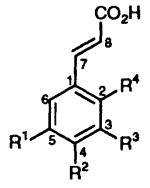
Table 1 Crystallographic data

Compound	1	3	4	7
Formula	$C_{16}H_{15}N_3O_8$	$C_{18}H_{17}N_3O_8$	$C_{20}H_{19}N_3O_8$	$C_{20}H_{18}N_2O_{10}$
M	377.32	403.36	429.39	446.38
Crystal system	Monoclinic	Triclinic	Triclinic	Triclinic
Space group	$P2_1/c$	$P\bar{1}$	$P\bar{1}$	$P\bar{1}$
a/Å	14.442(2)	7.974(1)	8.422(4)	9.008(3)
b/Å	6.969(3)	8.342(1)	15.854(6)	10.088(3)
c/Å	16.952(2)	15.045(1)	7.623(3)	11.874(2)
α/°	90.0	85.32(1)	85.20(3)	97.51(2)
β/°	99.58(1)	85.95(1)	102.76(3)	97.51(2)
γ/°	90.0	67.60(1)	91.73(3)	103.17(3)
U/Å^3	1682.4(4)	921.3(2)	989.2(6)	1027.1(5)
Z	4	2	2	2
$F(000)$	784	420	448	464
D_c/g cm^{-3}	1.489	1.454	1.442	1.443
λ/Å	0.7107	0.7107	0.7107	0.7107
μ/cm^{-1}	0.78	0.74	0.72	0.75
Crystal size	0.14 × 0.19 × 0.30	0.10 × 0.25 × 0.34	0.40 × 0.50 × 0.10	0.13 × 0.23 × 0.35
Diffractometer	P3	P3	P3	P3
Radiation	MoKα	MoKα	MoKα	MoKα
2θ range/°	2–50	2–50	2–50	2–50
h	−14–14	−9–9	−10–10	−10–10
k	0–9	−9–9	−20–20	−12–12
l	0–17	0–17	0–9	0–14
Total reflections	2781	3234	4804	3603
Unique reflections	2492	2569	4524	2511
Non-zero reflections	1635	1725	2173	1561
σ-Level	3.0	3.0	3.0	3.0
R	0.040	0.040	0.050	0.046
R_w	0.041	0.041	0.053	0.044
Min. electron density /e Å^{-3}	−0.15	−0.21	−0.24	−0.26
Max. electron density /e Å^{-3}	0.17	0.17	0.32	0.16

types of interactions co-adjust or coexist.* Our objective in this paper is precisely this—to study the interplay between O–H ··· O, C–H ··· O and $\pi \cdots \pi$ interactions in a series of benzoic and cinnamic acid donor–acceptor complexes **1–10** (Scheme 3).



1a $R^1 = R^3 = NO_2$; $R^2 = H$
b $R^1 = R^3 = H$; $R^2 = NO_2$
c $R^1 = R^3 = H$; $R^2 = N(CH_3)_2$
d $R^1 = R^3 = H$; $R^2 = NH_2$



2a $R^1 = R^3 = NO_2$; $R^2 = R^4 = H$
b $R^1 = R^3 = H$; $R^2 = R^4 = NO_2$
c $R^1 = R^3 = R^4 = H$; $R^2 = N(CH_3)_2$
d $R^1 = R^4 = OCH_3$; $R^2 = R^3 = H$
e $R^1 = R^2 = OCH_3$; $R^3 = R^4 = H$

1, 1a•1c; 2, 1a•1d; 3, 2a•1c; 4, 2a•2c; 5, 2a•2d; 6, 2b•2e; 7, 2b•2d; 8, 1b•1c; 9, 1b•2c; 10, 1a•2c

Scheme 3

Experimental

Acid Monomers.—These were either purchased (**1a–d**) or prepared (**2a–e**) from the corresponding aldehydes by Knoevenagel condensation. 3,5-Dinitrobenzaldehyde was synthesized by reducing 3,5-dinitrobenzoic acid with diborane/THF at 0 °C to 3,5-dinitrobenzyl alcohol, which was further oxidized by PCC/dichloromethane to give the aldehyde.

X-Ray Crystallographic Studies on Acid Complexes.—Complexes **1**, **3–10** were prepared by recrystallization from an equimolar MeOH solution of the two components or by grinding. The samples obtained by either method were identical. Crystals suitable for X-ray work were obtained by recrystallization from MeOH (**1** and **3**), EtOH (**4** and **7**) or 1 : 1 MeOH–toluene (**9**). Data were collected for all the complexes at the University of Milan on a Nicolet-Siemens P3 diffractometer. The structure solution of all complexes was carried out with SHELXS86[10] and the refinements were carried out with SHELX76.[11] Crystal structures of complexes **1**, **3**, **4**, **7** and **9** were determined in this study and the details of structures **1**, **3**, **4** and **7** are presented here (Table 1). Details of structure **9** will be presented elsewhere. The crystal structures of complexes **5**,[12] **6**[13] and **8**[1k] have been already reported by us, and complex **2** has been discussed briefly by Etter.[4a] Complex **10** formed twinned crystals and only an approximate structural analysis was possible. In complex **1**, the carboxyl proton in acid **1a** is disordered and was refined with 0.5 occupancy. In complex **7**, one of the oxygen atoms of the nitro group is disordered. Hydrogen atoms were located by difference Fourier maps. All non-hydrogen atoms were refined anisotropically and the final R-factors and other crystallographic information are presented in Table 1.†

* Strong hydrogen bonding and stacking have previously been considered jointly[9] but we believe that the present work is the first where both strong and weak hydrogen bonds are considered along with stacking interactions. In any case, these previous studies dealt with phenomena in solution.

† Full lists of bond lengths and angles, atomic coordinates, thermal parameters, hydrogen bonding schemes and F_o/F_c values have been deposited at the Cambridge Crystallographic Data Centre. For details of the deposition scheme, see 'Instructions for Authors', *J. Chem. Soc., Perkin Trans. 2*, 1993, issue 1.

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Results and Discussion

All these complexes consist of acid dimers which are themselves stacked so as to optimize π ··· π donor–acceptor interactions (Fig. 1). Therefore, two stacked heterodimers are related by an inversion centre (except in complex **2** which in non-centrosymmetric) while two stacked homodimers (complex **1**) are not crystallographically related, the inversion centres being located at the middle of each homodimer.

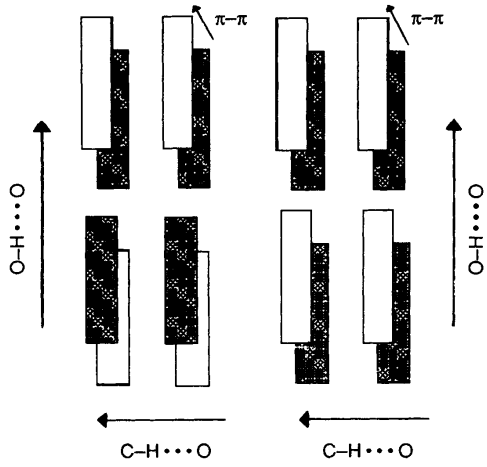

Fig. 1 Schematic diagram of carboxy hetero- (left) and homo- (right) dimers in the donor–acceptor complexes **1**–**10** showing the directional nature of the three interactions (O–H ··· O, C–H ··· O and π–π) important in these complexes. Donor monomer represented by an unshaded rectangle, acceptor monomer by a shaded rectangle.

Inspection of the carboxy dimer motif in these ten structures shows that while complexes **2**–**10** contain the 'expected' heterodimer, the crystal structure of **1** contains dinitrobenzoic and dimethylaminobenzoic homodimers (Fig. 2). This is an unusual result and the absence of such homodimers in other systems was verified with the Cambridge Structural Database (CSD).[14] We obtained 32 mixed acid crystals from the CSD, but none contained homodimers. AM1 calculations performed by Dannenberg show that the heterodimers AB for any given (aromatic) acid pair A and B are more stable than either of the homodimers AA or BB by around 1.0 kcal mol^{-1}.[15] We repeated these calculations on the acid pairs contained in complexes **1**–**10** and obtained very similar results. Even in complex **1**, the AM1 heterodimer energy obtained was −7.02 kcal mol^{-1} while the two homodimer energies were −6.27 kcal mol^{-1} (dinitro) and −6.15 kcal mol^{-1} (dimethylamino). Though AM1 methods do not consider electronic correlation effects and underestimate the hydrogen bond energy, their use in hydrogen bonded systems is well documented and it is believed that the calculations permit a relative comparison of hydrogen bond energies. Therefore, we concluded that our calculations of relative O–H ··· O bond energies were all reasonably accurate. Accordingly, the formation of homodimers in complex **1** is exceptional; the stabilization of heterodimer over homodimer to the extent of *ca.* 1.0 kcal mol^{-1} must be compensated by other (weaker) interactions in the crystal if the homodimer is to be obtained.

Complex **1** is a good example of molecular recognition because from a mixture of heterodimers, homodimers and

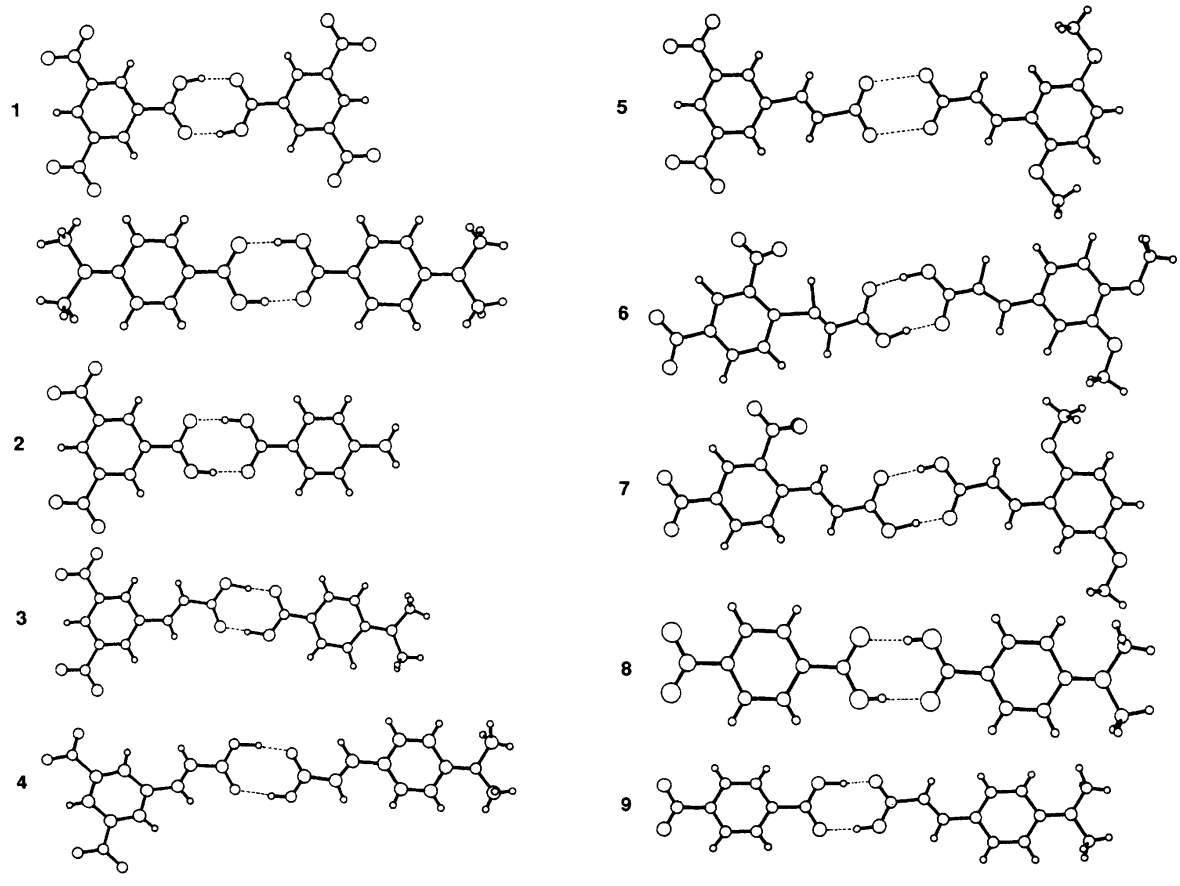

Fig. 2 O–H ··· O dimers in donor–acceptor complexes **1**–**9**. Only **1** has homodimers (**1a**–**1a**, **1c**–**1c**) in the crystal structure, all the others form the more common heterodimer. O–H ··· O bonds shown as (– – –).

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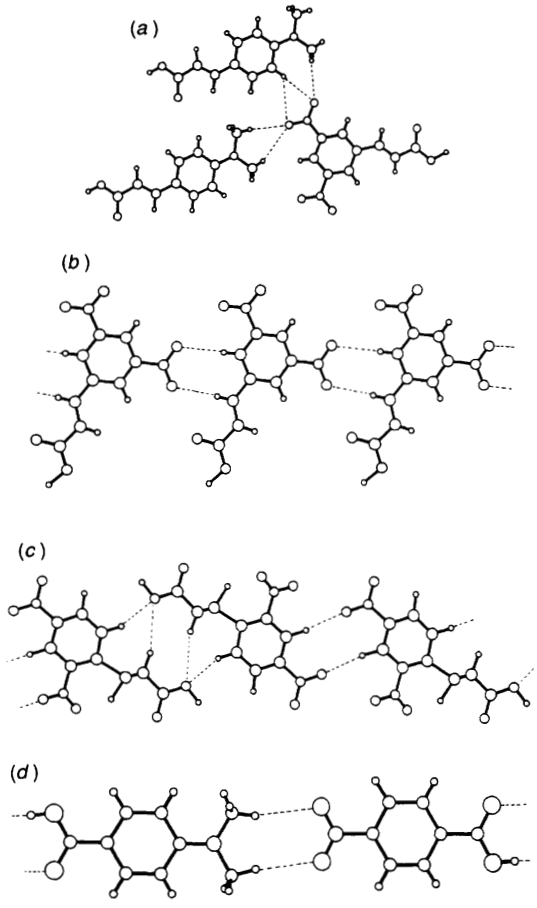

Fig. 3 Four types of C–H ··· O bonding patterns observed in **1**, **3**–**9**: (*a*) recognition pattern of 3,5-dinitro to 4-NMe_2 in **1**, **3** and **4**; (*b*) self-assembly of **2a** molecules in **3**, **4**, **5** and in acid **2a**; (*c*) self-assembly of **2b** molecules with two types of motifs in **6** and **7**; (*d*) C–H ··· O dimers between $-NO_2$ and $-NMe_2$ groups in **8** and **9**. C–H ··· O bonds shown as (– – –)

monomers in solution with a heterodimer–homodimer ratio of approximately 3:1,* only the minor component (homodimer) is obtained in the crystal. It is clear from the calculations and from structures **2**–**10** that the isolated heterodimer is more stable than the isolated homodimers. The occurrence of only homodimers in the crystal of **1**, obtained by either recrystallation or grinding, is therefore indicative of the importance of other factors.

Three weaker forces, van der Waals, C–H ··· O and π ··· π interactions, were identified as possible perturbing factors which cause the tilt towards homodimer formation in **1**. It has been held by Hunter and Sanders[6a] that van der Waals or isotropic forces cannot in themselves determine the crystal packing of donor–acceptor complexes.† This is because these forces are proportional to the extent of overlap between two stacked molecules. If these forces were structure determining, the overlap between stacked molecules would be maximized. This is never so, because π ··· π repulsions dominate at large overlaps. Thus, van der Waals forces are important only within the framework of the more electrostatic π ··· π interactions. Therefore, attention was shifted to C–H ··· O and π ··· π interactions in complexes **1**–**10**.

C–H ··· O Hydrogen Bonding in Complexes **3**–**9**.—It is known that C–H ··· O hydrogen bonds play a major role in stabilizing crystal structures and molecular conformations.[7a] The $-NO_2$ group is particularly suited for the formation of these bonds and, in general, we note the manifestation of four distinct patterns of C–H ··· O bonds in complexes **3**–**9**. Complex **2** was found not to contain any characteristic C–H ··· O bonds because the $-NO_2$ group of **1a** is involved in strong N–H ··· O hydrogen bonds with the $-NH_2$ group of **1d**. This is not surprising. Complex **1** is discussed later.

The choice between these four C–H ··· O patterns seems to depend on the stoichiometry and arrangement of the functional groups (mostly $-NO_2$) in the respective complexes **3**–**9**. The first pattern [Fig. 3(*a*)] is found in complexes of 3,5-dinitro substituted benzoic or cinnamic acids with 4-(*N*,*N*-dimethylamino) substituted benzoic or cinnamic acids and is characteristic of the nitro to dimethylamino approach. The C–H ··· O bonds in this first pattern involve mainly sp^3 H atoms of the $-N(CH_3)_2$ groups and $-NO_2$ O atoms (complex **4**: C ··· O: 3.68, 3.50, 3.79, 3.60, 3.37 Å; C–H ··· O: 157, 161, 132, 166, 132°).

The second pattern is a self-motif found in all complexes containing 3,5-dinitrocinnamic acid **2a** [Fig. 3(*b*)]. This pattern is characterized by an 8.3 to 8.4 Å translation and involves linear C–H ··· O bonds between both O atoms of a particular $-NO_2$ group with the styryl and aromatic H atoms of the translated neighbour (complex **3**: C ··· O: 3.50, 3.50 Å; C–H ··· O: 173, 167°). This pattern is also found in the crystal structure of the free acid **2a**[12] and can be considered to be a molecular ribbon obtained by self-assembly.

That the arrangement of $-NO_2$ groups in a molecule is also critical in determining the C–H ··· O pattern is clear on inspection of Fig. 3(*c*) which illustrates the third C–H ··· O pattern in these complexes, a pattern characteristic of the isomer 2,4-dinitrocinnamic acid **2b** (complex **6**: C ··· O: 3.52 Å; C–H ··· O: 162°). The 2,4-arrangement of $-NO_2$ groups results in a different C–H ··· O pattern than is obtained for the 3,5-arrangement shown in Fig. 3(*b*). In fact, there are two motifs, but both involve inversion-related molecules. One of the motifs involves an O atom of the 4-NO_2 group and the H(3) atom while the other involves the carboxyl O and H(6) and H(8).

The final C–H ··· O pattern is obtained in complexes containing the mononitro acid **1b** and either of the two $-N(CH_3)_2$ acids **1c** or **2c**. This linear dimer motif is shown in Fig. 3(*d*) and has been discussed earlier by us (complex **8**: C ··· O: 3.66, 3.74 Å; C–H ··· O: 164, 172°).[1k]

These four patterns are exclusive to each of the four substitutional categories described above and it is noteworthy that the particular pattern obtained depends not only on the stoichiometry (one or two $-NO_2$ groups) but also on the arrangement of groups (2,4-dinitro or 3,5-dinitro). C–H ··· O networks in complexes **3**–**9** are therefore predictable and consequently C–H ··· O bonds can be well utilized for molecular recognition and self-assembly in related organic solids. The non-centrosymmetric nature of some of these C–H ··· O patterns [Figs. 3(*a*), (*b*) and (*d*)] may also be exploited for the deliberate design of non-centrosymmetric crystals leading to NLO materials. These recognition patterns also highlight an interesting common feature; this is that the more acidic protons on the nitro-substituted acids (especially acids **2a** and **2b**) are the ones actively involved in the molecular recognition process, supporting arguments that H atom acidity is more important than O atom basicity in the formation of C–H ··· O bonds.[17]

* Assuming an energy difference of 0.80 kcal mol^{-1} between hetero- and homo-dimers.

† However, van der Waals forces can distort N–H ··· O hydrogen bond patterns in other cases, as is seen in the unusual crystal structure of adipamide.[16]

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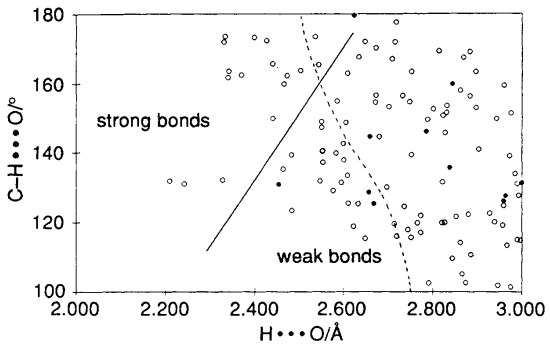


Fig. 4 Scatterplot of C–H • • • O angle *versus* H • • • O distance (normalized to 1.08 Å) for all C–H • • • O bonds in **1**–**9**. Bonds in **1** are shown as ●. C–H • • • O bonds in **1** are weak according to either our prescription (——) or Saenger's[7b] (– – –). Excepting **1**, all the complexes have contributors in the strong bonds region.

C–H • • • O Bonds in Complex **1**.—Unlike complexes **3**–**9**, which display rich and distinctive C–H • • • O patterns, complex **1** contains only a few C–H • • • O bonds and even these are of marginal significance. Fig. 4 is a plot of C–H • • • O angle *versus* the H • • • O distances for all C–H • • • O bonds in structures **1**–**9**. In these plots, normalized H atom positions are used with the C–H distance taken to be 1.08 Å. C–H • • • O bonds in complex **1** are shown as ●. It is very clear from the plot that the C–H • • • O bonds in **1** are neither the shortest nor the most linear in the group. The solid line in the plot appears to be a natural separation between two regions which contain strong and weak C–H • • • O bonds. The dashed line is drawn according to the prescription of Steiner and Saenger[7b] and makes allowance for elliptically-shaped H atoms. Whatever the type of demarcation, C–H • • • O contacts in complex **1** are feeble* and, unlike in **3**–**9**, probably do not play a key role in the stabilization of the structure. Could this observation correlate with the presence of homodimers in **1** and heterodimers in **3**–**9**?

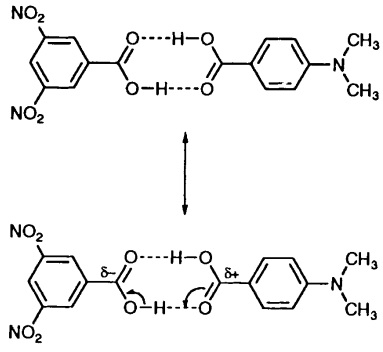
Inspection of the molecular formulae of **1a** and **1c** suggests probable reasons for the lack of C–H • • • O bonds in **1**. While **1a** has three acidic C–H protons, they are sterically inaccessible to O atoms. The only C–H • • • O pattern possible is the nitro-dimethylamino recognition motif [Fig. 3(*a*)] which makes weak bonds of 3.59, 3.41, 3.71 and 3.68 Å. Therefore H(4) of acid **1a**, which is the most acidic H atom in the system, is blocked. Atoms H(2) and H(6) of acid **1a** are also blocked by the flanking substituents. Most critically, the absence of styryl H atoms, which are invariably involved in C–H • • • O bonding in a large number of α,β-unsaturated carbonyl and nitro compounds[12,17b,18] [Figs. 3(*b*), (*c*)], means that there is just not enough C–H • • • O bond forming propensity here. In turn, it may be stated that the presence of such styryl H atoms as in acids **2a**–**2d** leads to C–H • • • O bonding which causes layering or sheet formation of molecules. This is depicted schematically in Fig. 1. The structures of complexes **3**–**9** (especially cinnamic acid-containing complexes **3**–**7**) may be understood as being formed by a stacking of layers which are themselves composed of C–H • • • O networked O–H • • • O heterodimers. Conversely, complex **1**, which has only weak C–H • • • O bonds, has no layer structure. Fig. 5 shows columns of stacked molecules which are inclined to one another at an angle of 23°, to optimize a few weak C–H • • • O bonds and close-packing aromatic • • • aromatic herringbone interactions. We believe that it is the lack of C–H • • • O bond-forming ability in complex **1** which causes it to adopt the anomalous homodimer structure.

* Further evidence for the weakness of the C–H • • • O bonds in complex **1** is provided by the disordered carboxyl group in acid **1a**. Complexes **3**–**9**, however, contain ordered carboxyl groups.

This absence of C–H • • • O bonds compelled us to consider the third variety of weak interactions in these structures, namely π • • • π stacking.

π • • • π Stacking in Complex **1** *and Elsewhere*.—We now consider π • • • π stacking interactions in the donor–acceptor complexes **1**–**10** and their possible role in stabilizing the homodimer structure in **1**. Hunter and Sanders have shown that the nature of these interactions is dependent on the intermolecular contacts between the relevant atoms rather than on the overall redox properties of the molecules.[6a] We will analyse π • • • π interactions according to this concept.

The electronic properties of atoms in carboxy homo- and hetero-dimers in complexes **1**–**10** are conveniently differentiated because the substituents on the aromatic rings are either powerful electron donors or acceptors. Let us consider complex **1**. The atoms in the aromatic ring and carboxyl group in the isolated **1a** molecule possess δ^+ charge and, correspondingly in **1c**, δ^- charge because of the presence of $-NO_2$ and $-N(CH_3)_2$ groups, respectively. If acids **1a** and **c** were to form a heterodimer, there would be a flow of charge from **1c** to **a** through the dimer ring (Scheme 4) *via* resonance assisted hydrogen bonding.[19] As a result, the δ^+ and δ^- charges in the aromatic rings of **1a** and **c** would be diminished in the heterodimer relative to the isolated monomers.



Scheme 4

If, however, **1a** and **c** were instead to form homodimers, as are observed, the δ^+ and δ^- charges on the rings would be enhanced. In other words, homodimer formation leads to a greater polarization or charge separation in **1a** and **c** molecules relative to the isolated monomers. The AM1 charges obtained for homo- and hetero-dimers of **1a** and **c** corroborate this statement but the magnitudes of all the charges are very small and the difference in charges for corresponding atoms between homo- and hetero-dimers is less than 0.02 e. However, the direction of change in charge is always so as to support the hypothesis above. More satisfactory evidence for this hypothesis is obtained from the O–H • • • O bond lengths in homodimers and heterodimers of some of the acids in the study (Table 2). The crystal structure of the pure acid is a model for the homodimer when no homodimers are obtained in the acid complexes (all acids other than **1a** and **1c**). Table 2 shows that both the O • • • O distances in a heterodimer are always less than the O • • • O distance in either of the two corresponding homodimers. These figures argue convincingly for a net flow of charge across the hydrogen-bonded ring in heterodimers and, conversely, for an accentuation of charge in a homodimer.

According to this argument, the polarization of C and O atoms in the **1a** • • • **1a** and **1c** • • • **1c** homodimers will be greater than in the **1a** • • • **1c** heterodimer. So, if one considers stacking interactions, these should be more favourable for homodimers

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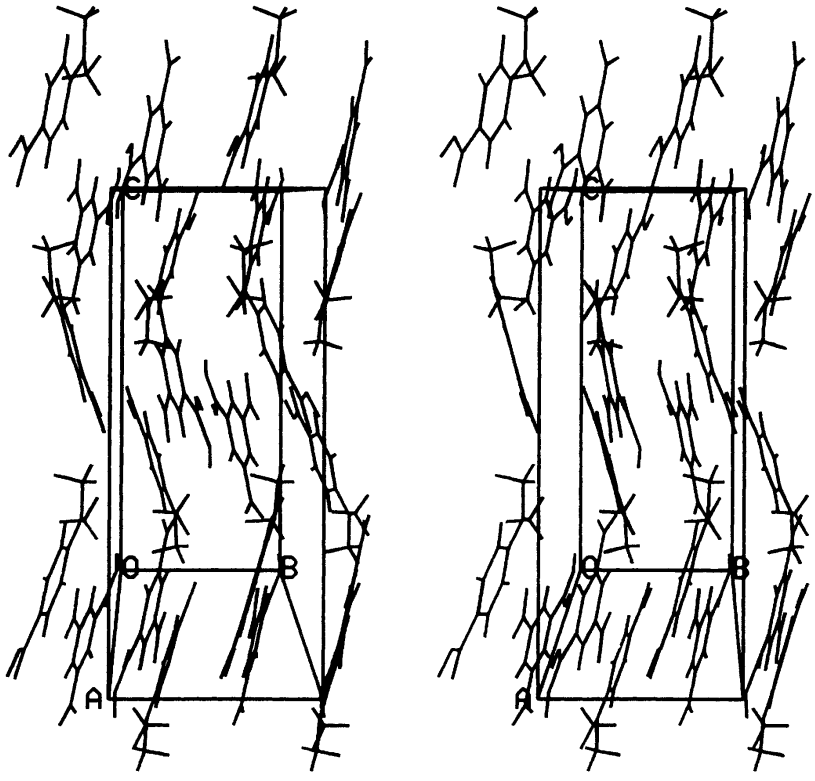

Fig. 5 Stereoview of the crystal structure of **1**. Adjacent stacked columns of **1a** and **c** make an angle of 23° indicating the stabilization of stacks by herringbone interactions.

Table 2 O···O distances (Å) in the hydrogen-bonded rings in some of the pure acids and complexes in this study

Compound	Pure	Complex[a]		
1a	2.636	2.655 (**1**)[b]	2.616 (**2**)	
1b	2.660	2.632 (**8**)		
1c	2.627	2.625 (**1**)[b]	2.608 (**3**)	2.606 (**4**)
1d	2.642	2.616 (**2**)		
2a	2.661	2.628 (**3**)	2.627 (**5**)	2.643 (**4**)
2b	2.657	2.632 (**6**)	2.638 (**7**)	
2e	2.632	2.619 (**6**)		

[a] Except **1**, all the complexes are heterodimers and have O···O distances less than those found in the pure acids. [b] Homodimers.

than those for heterodimers (Fig. 6). It is possible to verify the approximate strengths of these π···π interactions in complexes **1–9** by examining the donor–acceptor aryl···aryl stacking distances. This is best seen in Fig. 7 which is a plot of centroid-to-centroid *versus* average perpendicular interplanar distances for the stacked aromatic rings in these complexes. It is clear from this Fig. that complex **1** is a striking outlier. The short interplanar and centroid-to-centroid distances in complex **1** (C···O: 3.38, 3.22, 3.41 Å; C···C: 3.38, 3.35, 3.40, 3.41, 3.42 Å) are not found in any of the heterodimer structures **2–9** and show that the overlap of aromatic rings in **1** is very effective. Further, there is a significant overlap of the carboxyl hydrogen-bonded rings (Fig. 6), a structural feature which is absent in all the heterodimer structures studied here, and one which argues convincingly in favour of enhanced atomic charges throughout the homodimer framework. We feel that the combined aromatic and carboxyl π···π/electrostatic interactions obtained *via* overlap are a critical source of stabilization of the homodimer structure in complex **1**, and they are more than sufficient to compensate for the lack of O–H···O heterodimer stabilization (*ca.* 0.80 kcal mol^{-1}) and the unsatisfactory C–H···O situation.

A Possible Sequence for Crystallization of Complex **1**.—In MeOH solution, component acid molecules are likely to exist as hydrogen-bonded and solvated monomers, heterodimers and homodimers. If it is assumed that in all cases the energy difference between heterodimers and homodimers in solution is around 0.80 kcal mol^{-1}, this means that the heterodimer–homodimer ratio in solution is around 3 : 1. Either type of dimer can form crystal nuclei by aggregation with other dimers either laterally or along a stack. It is suggested that in the majority of cases (**3–10**), crystal nuclei develop by a lateral organization of O–H···O dimers *via* C–H···O bonding, the interaction of next importance (Fig. 1). These lateral interactions are equally easy for hetero- and homo-dimers because of the presence of favourable features in the molecular structures of the monomers (styrenic H atoms, *etc.*). Accordingly, the more abundant heterodimers form crystal nuclei more easily. These nuclei must also involve stacked molecules but the exact nature of this stacking is probably not critical, the growing nuclei having already obtained adequate stability from the O–H···O (hetero) and C–H···O interactions.

In the case of complex **1**, however, neither homodimers nor heterodimers can nucleate properly *via* lateral C–H···O bonds. Therefore, both these types of dimers aggregate primarily *via* stacking interactions. In this event, the homodimers are distinctly favoured as detailed above. Growing homodimer stacks are formed in spite of an unfavourable heterodimer–homodimer ratio in solution and they aggregate *via* weak van der Waals forces to achieve close packing (Fig. 5). The exclusive formation of the homodimer structure of **1** indicates that the stabilization gained from π···π interactions

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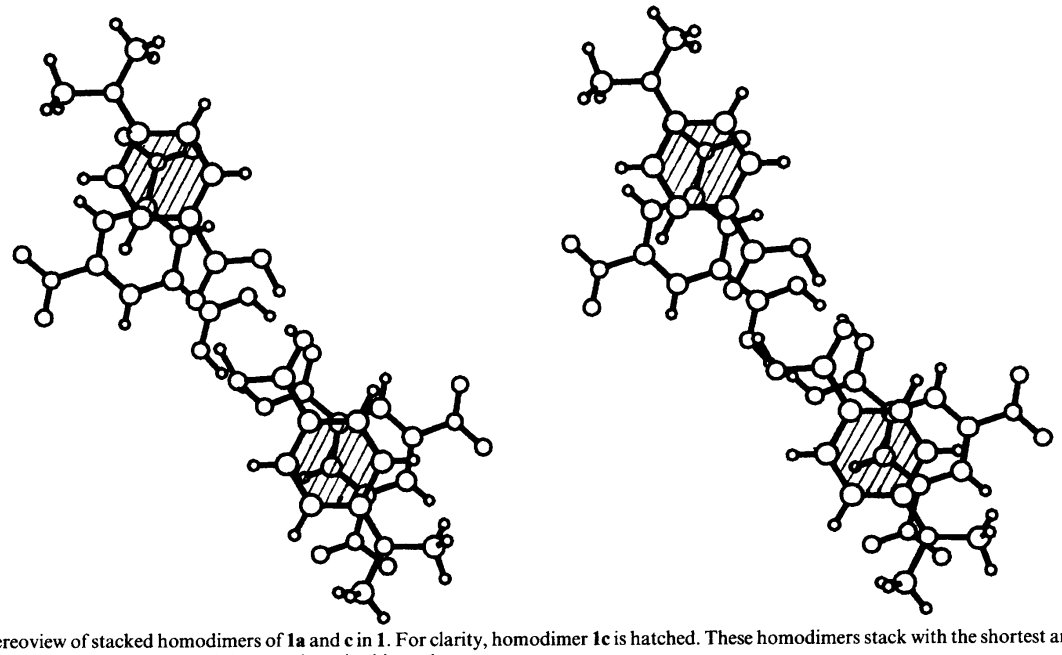

Fig. 6 Stereoview of stacked homodimers of **1a** and **c** in **1**. For clarity, homodimer **1c** is hatched. These homodimers stack with the shortest aryl–aryl and carboxy–carboxy distances of all the complexes in this study.

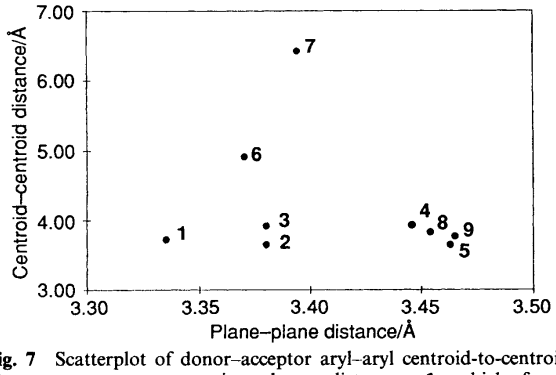

Fig. 7 Scatterplot of donor–acceptor aryl–aryl centroid-to-centroid distances *versus* average interplanar distances. **1**, which forms homodimers, is an outlier.

more than offsets the loss in O–H • • • O stability in avoiding the heterodimer alternative.

As crystallization progresses, the heterodimer $\rightleftharpoons$ homodimer equilibrium in solution shifts towards homodimer. It is remarkable that very slight energetic preferences dictate an almost completely unequivocal crystallization pathway. This, in general, has been observed by us and others and augurs well for future experiments in molecular recognition and crystal engineering.

Conclusions

The homodimer complex **1** is a good case study to examine stacking interactions *vis-à-vis* weak and strong hydrogen bonding. These interactions which are sometimes in competition and sometimes in consonance are of great importance in biological molecules where the nature of the stacking may dictate the type of hydrogen bonding (Watson–Crick and Hoogsteen). The interplay between these two types of interactions has also been studied in the binding of Kemp's acid derivations with adenines.[9] However, these studies are involved with changes in the exposed surface area between stacked molecules, whereas the present example considers mainly changes in the atomic charges in stacked molecules brought about by different kinds of hydrogen bonding. The assumption of charge transfer through hydrogen bonding involves a new perception in studies of hydrogen bonding and $\pi \cdots \pi$ interactions.

The analysis of complexes **1**–**10** in this study addresses three salient points which are of current interest: (i) O–H • • • O hydrogen bonds can act as channels for charge transfer; (ii) C–H • • • O hydrogen bonds can be used in molecular recognition and self-assembly; (iii) stacking interactions influence the nature of hydrogen bonding and *vice versa*.

The anomalous structure of complex **1** shows that a strong interaction alone need not always dictate the crystal geometry if other weaker interactions are of special significance. This result cautions one to keep track of weak interactions while designing novel structures of new materials and suggests that without a proper appreciation of both strong and weak interactions, the prediction and design of crystal structures may often turn out to be an elusive objective.

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