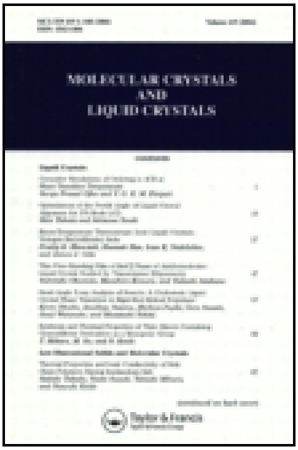

Molecular Crystals and Liquid Crystals Science and Technology. Section A. Molecular Crystals and Liquid Crystals
Publication details, including instructions for authors and subscription information:
http://www.tandfonline.com/loi/gmcl19

Effect of Alkyl Chain Length on Acid - Amide Hydrogen Bonding

John King [a] & William Jones [a]
[a] Department of Chemistry, University of Cambridge, Lensfield Road, Cambridge, CB2 1EW, U.K.

Version of record first published: 24 Sep 2006.

To cite this article: John King & William Jones (1994): Effect of Alkyl Chain Length on Acid - Amide Hydrogen Bonding, Molecular Crystals and Liquid Crystals Science and Technology. Section A. Molecular Crystals and Liquid Crystals, 240:1, 225-230

To link to this article: http://dx.doi.org/10.1080/10587259408029733

Mol. Cryst. Liq. Cryst. 1994, Vol. 240, pp. 225–230
Reprints available directly from the publisher

Printed in the United States of America

EFFECT OF ALKYL CHAIN LENGTH ON ACID - AMIDE HYDROGEN BONDING

JOHN KING AND WILLIAM JONES
Department of Chemistry, University of Cambridge, Lensfield Road, Cambridge, CB2 1EW, U.K.

Abstract The hydrogen bonding motifs in four families of carboxyl acid amides — p-amido benzoic, phenylamido carboxylic, benzoylamino carboxylic, and phthalimido carboxylic acids — are examined. Available structural data suggested that the dominant factor in motif determination might be alkyl chain length. Additional representative structures were determined to investigate this hypothesis, revealing that, although important, chain length alone is not responsible for the observed hydrogen bond motif.

INTRODUCTION

The rôle of hydrogen bonding in influencing the crystal packing, and hence many solid state properties, of organic molecules is well known. An understanding of the factors, often very subtle, influencing the selection of hydrogen bond motif is therefore a very useful tool in the field of crystal engineering. Here, we examine the extent to which a single structural factor, that of alkyl chain length, influences the hydrogen bonding in four families of carboxyl acid amides. These families of molecules are illustrated in figure 1.

I p-Amidobenzoic acids (**p-ABA**) II Phenylamido carboxylic acids (**PA**)

III Benzoylamino carboxylic acids (**BA**) IV Phthalimido carboxylic acids (**PI**)

FIGURE 1 Families of molecules considered

Although structural knowledge of these families is far from complete, sufficient structures with moderately short chain lengths, ($n \leq 7$), have been determined to permit some generalisation. Of specific interest to this study is the type of hydrogen bonding adopted. Two very distinct types have been observed. In the first of these, dimers are formed by the familiar cyclic acid–acid interaction, with these dimers packed together in one of several ways to form the complete structure. In the second, no acid dimers are found; instead, the acid acts as a donor in a hydrogen bond to the oxygen atom of an amide group, forming an infinite chain of molecules along one of the crystallographic axes.

The crystal structures so far determined[1] for these families are indicated in table 1, along with the type of hydrogen bonding adopted.

Family	n	Hydrogen bonding
p-ABA	0-7	Acid dimers
PA	4-5	Acid dimers
BA	1-2	Acid — Amide
PI	1-2	Acid — Amide
	3-5	Acid dimers

TABLE 1 Known structures with hydrogen bond type

It is now generally accepted that, for structures containing more than one type of hydrogen bond donor or acceptor, the most favourable hydrogen bonding motif will be that which involves the strongest donor interacting with the strongest acceptor[2]. In a typical acid – amide molecule, the strongest donor will be the carboxyl group and the strongest acceptor the amide oxygen. Therefore, the BA family appears to exhibit idealised hydrogen bonding, whilst the p-ABA and PA families adopt a less favourable hydrogen bond motif.

Table 1 suggests there may be a very simple explanation, based on alkyl chain length, for the differing behaviour of the PA and BA families. For the PA family, the only structures known are for relatively long chain lengths, whereas the reverse is the case for the BA family, where the known structures are for the very shortest chain lengths. In the PI family, which is the only one in which both hydrogen bond types have been observed, the acid – amide interaction is seen for the shorter chains, whilst longer chains produce acid dimers. One might therefore hypothesise that the single most important factor in determining the type of hydrogen bonding is the length of the alkyl chain. The p-ABA family would not be expected to conform to this pattern, since, in this family, the alkyl chain is terminal, and does not separate acid and amide groups, which are linked through a fairly rigid unit.

To investigate this hypothesis, we undertook the determination of further structures in the PA and BA families.

RESULTS

Four further crystal structures have been determined, two in each of the PA and BA families. For the PA family, molecules with chain lengths shorter than those already studied were selected ($n = 2,3$), whilst for the BA family, molecules with chain lengths longer than those already studied were chosen ($n = 3,4$). Details of the structure solution and refinement will be reported elsewhere.

For the present study, the fine details of the structures are not important; more significant is the hydrogen bonding type found in each instance. In the PA family, both of the shorter chain molecules were found to adopt the acid dimer motif. In the BA family, the molecule with n=3 was found to produce hydrogen bonding of the acid — amide type, whereas that with n=4 produced acid dimers. Representative packing diagrams are shown in figures 2-4.

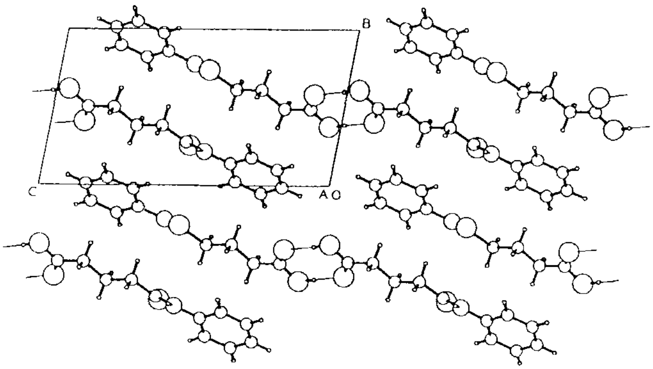

FIGURE 2 Packing of PA-butanoic acid (n=3), illustrating acid dimers. PA-propanoic acid (n=2) exhibits an identical H-bond topology.

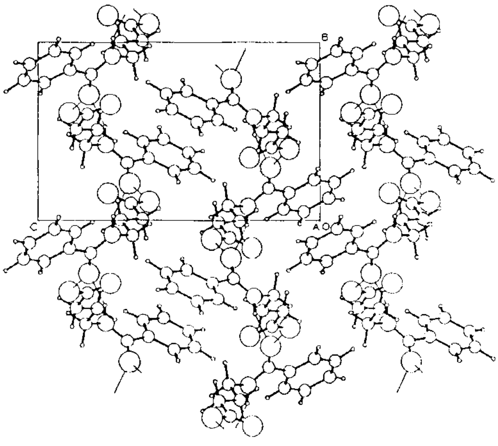

FIGURE 3 Packing of BA-butanoic acid (n=3), illustrating chains of molecules along b, linked by acid – amide hydrogen bonds.

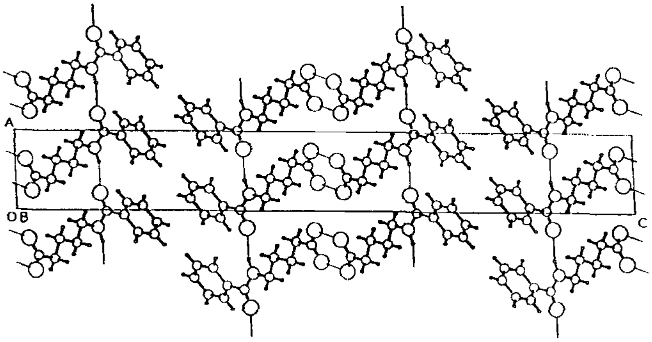

FIGURE 4 Packing of BA-pentanoic acid (n=4), illustrating acid dimers.

DISCUSSION

The behaviour observed in the BA family appears to parallel very closely that found in the PI family. For the shorter alkyl chains, the adoption of the most favourable hydrogen bond, from acid to amide, is possible. For the longer chains, it would appear that this hydrogen bonding would compromise the efficient packing of the molecules, and therefore is not observed. Instead, acid dimers are formed, which allow the long alkyl chains to adopt a trans conformation, and pack together in an efficient parallel fashion.

In the PA family, the failure of either of the shorter chain molecules to adopt the acid — amide hydrogen bond motif suggests that the requirements for adoption of this motif are more demanding than a simple chain length criterion, although the n=1 structure for PA remains to be determined. Several possible explanations for this behaviour can be suggested:

- The amide environment in PA either makes the oxygen atom of this group a weaker hydrogen bond acceptor than the carboxyl oxygen, or makes the amide nitrogen a stronger hydrogen bond donor than the carboxylic acid, such that acid dimers will yield the most favourable hydrogen bond energy.
- The molecular geometry of the PA molecules makes impossible the

formation of a hydrogen bond network containing acid — amide interactions, whilst preserving an energetically acceptable molecular conformation.

- The molecular geometry of the PA molecules is such that efficient close packing is not possible within the confines of a structure containing both acid — amide hydrogen bonds and an acceptable molecular conformation.

The first of these suggestions seems unlikely. Any weakening of amide acceptor strength by conjugation with the phenyl ring would appear more likely for the BA family, in which ring and carbonyl groups are adjacent, whilst a comparison of acid dissociation constants in DMSO (pKa(acetanilide)=21.5, pKa(benzamide)=23.4, pKa(benzoic acid)=23.4)[3] suggests that N-phenylation will not increase the donor strength of the amide sufficiently to surpass that of the acid. The remaining possibilities are currently under investigation, and will be discussed in a future communication.

ACKOWLEDGMENTS

The financial support of the SERC, (studentship for JK), and of Molecular Simulations Inc. is appreciated.

REFERENCES

1. All structures except (i) & (ii): N. Feeder and W. Jones, submitted for publication in Acta Cryst., (1993); (i) p-acetamidobenzoic acid (p-ABA, n=0): S. Kashino, T. Matsushita, T. Iwamoto, K. Yamaguchi, M. Haisa, Acta Cryst., C42, 457, (1986); (ii) hippuric acid (BA, n=1): H. Ringertz, Acta Cryst., B27, 285, (1971)
2. Z. Berkovitch-Yellin, S. Ariel, L. Leiserowitz, J. Am. Chem. Soc., 105, 765, (1983)
3. T. Cohen, D. A. Bennet, A. J. Mura Jr., J. Org. Chem., 41, 2507, (1976)