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Anion-controlled networks of intermolecular interactions in the crystal structure of 9-aminoacridinium salts

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This paper is dedicated to Professor Jerzy Błażejowski on his 65th birthday

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ABSTRACT

A series of salts, with the 9-aminoacridinium cation (9-AA) and aromatic carboxylic acid: benzoate (**1**), *ortho*-phthalate (**2**), and salicylate (**3**) anions have been synthesized and characterized using X-ray diffraction. In the crystal packing, the ions are linked via N–H···O, O–H···O, and C–H···O hydrogen bonds. Analysis of the hydrogen bonds in the crystal lattices of the title compounds shows that the cations and anions form tetramers. The ions in these tetramers are linked via N(amino)–H···O(carboxy) hydrogen bonds forming $R_2^2(8)$ (**1** and **3**) or $R_2^4(15)$ (**2**) hydrogen bond ring motifs. The cations interact through π–π interactions in the ABBA (**1**), AB (**2**) or ABA (**3**) arrangement to form columns (**1** and **2**) or chains (**3**).

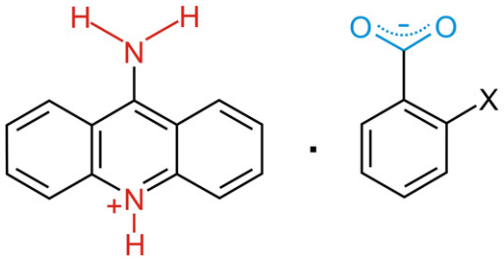
1. Introduction

9-Aminoacridine (9-AA) and its derivatives present a very interesting object of research. This group of compounds exhibits a wide spectrum of biological activities: antiamoebic, antibacterial, antiprion, antitumor, antiinflammatory, antiimplantation, hypertensive, and mutagenic.[1] The potency of acridines as agents is due to their ability to bind DNA through intercalation.[2] 9-AA is also used as a ΔpH-probe in a variety of biological systems.[3]

X-ray crystallographic investigations have been carried out on the salts of 9-aminoacridine derivatives with different kind of acids in attempts to understand their specific properties.[4]

In this communication we report the synthesis and X-ray characterization of a series of salts with the 9-aminoacridine cation and the anions of aromatic carboxylic acids—benzoic (**1**), *ortho*-phthalic (**2**), and salicylic (**3**).

9-AA is one of the simplest representatives of the group of organic bases able to interact with biomolecules. The 9-AA cation consists of three conjugated aromatic rings with an extended π system and contains two basic sites situated in the heterocyclic (in the acridine skeleton) and exocyclic (in the amino-group) N atoms (Scheme 1).



Scheme 1. Donor–acceptor system in the 9-aminoacridinium–aromatic carboxylic acid anion salts, where X=–H (**1**), –COOH (**2**), and –OH (**3**).

With such a structure, this cation can interact with different kinds of anions via strong N–H···X or weak C–H···X, N–H···π, C–H···π hydrogen bonds, and π–stacking interactions. On the other hand, aromatic carboxylic acid anions have two O atoms that are strong hydrogen bonding acceptors and an aromatic ring, which may interact through a C–H···X hydrogen bond or play a π–electron donor/acceptor role. In this context, an understanding of how these ions aggregate in crystal structures may provide some interesting insight into the influences of different kind anions on the geometry and packing of the 9-AA cation in the crystal lattice.

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2. Results and discussion

2.1. 9-Aminoacridiniun benzoate (1)

Single-crystal X-ray diffraction measurements show that compound **1** crystallizes in the triclinic *P*–1 space group with two 9-AA cations, benzoic acid anions, and water molecules in the asymmetric unit (Fig. S1, Table S1, Supplementary data).

In the packing of the molecules in **1**, the crystal structure is stabilized by N–H···O, O–H···O, and C–H···O hydrogen bonds (Table S2, Supplementary data) and π–π interactions (Table S3, Supplementary data). Analysis of the hydrogen bonds in the structure of **1** has shown that the ions form tetramers in the crystal lattice. In these tetramers the ions are inverted via crystallographic inversion center, and both cations A and B and the anions from the asymmetric unit are involved in the formation of the $R_2^2(8)$ hydrogen bond ring motif (Fig. 1). In this motif, amino groups from the cations and one O-atom of the carboxy-group from the anions participate in the hydrogen bonds. Additionally, the O(carboxy)-atoms engaged in the formation of this motif also take part in weak C(acridine)–H···O (carboxy) hydrogen bonds. The water molecules in the crystal lattice of **1** act as linkers between the tetramers. The tetramers in **1** are connected by N(acridine)–H···O(water) hydrogen bonds, where the O-atoms from the water molecules are acceptors for H-atoms bonded to endocyclic N-atoms from the acridine skeleton. The tetramers of **1** are additionally linked via an O(water)–H···O(carboxy) hydrogen bond, where the O-atoms from the carboxy-groups do not participate in tetramer formation. The water molecules also interact with each other via O–H···O hydrogen bonds (O···O=2.804 Å) (Fig. 1a). Analysis of the π–π interactions in **1** shows that the

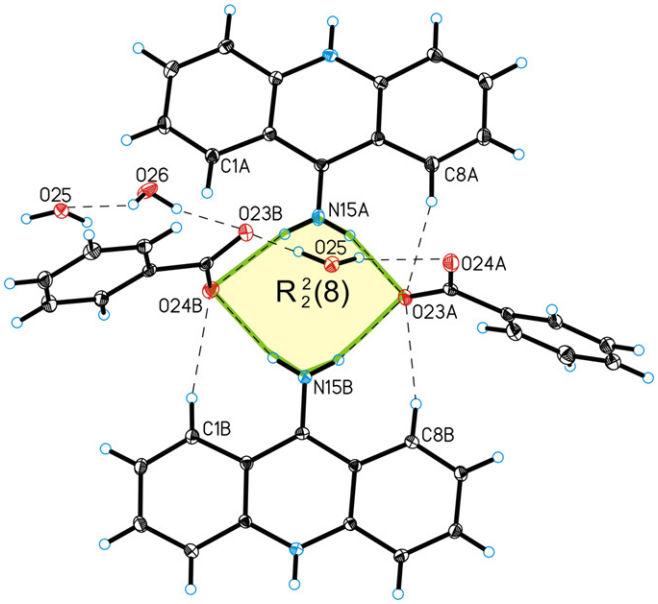

Fig. 1. Network the hydrogen bonds in the structure of **1** ($R_2^2(8)$ hydrogen bond ring motif is highlighted in yellow).

adjacent 'head to tail' oriented acridine skeletons are linked via π-stacking interactions in the *ABBA* arrangement to form columns (Fig. 2). All the aromatic rings from the acridine skeletons participate in π–π interactions and form a *zigzag* motif with centroid···centroid

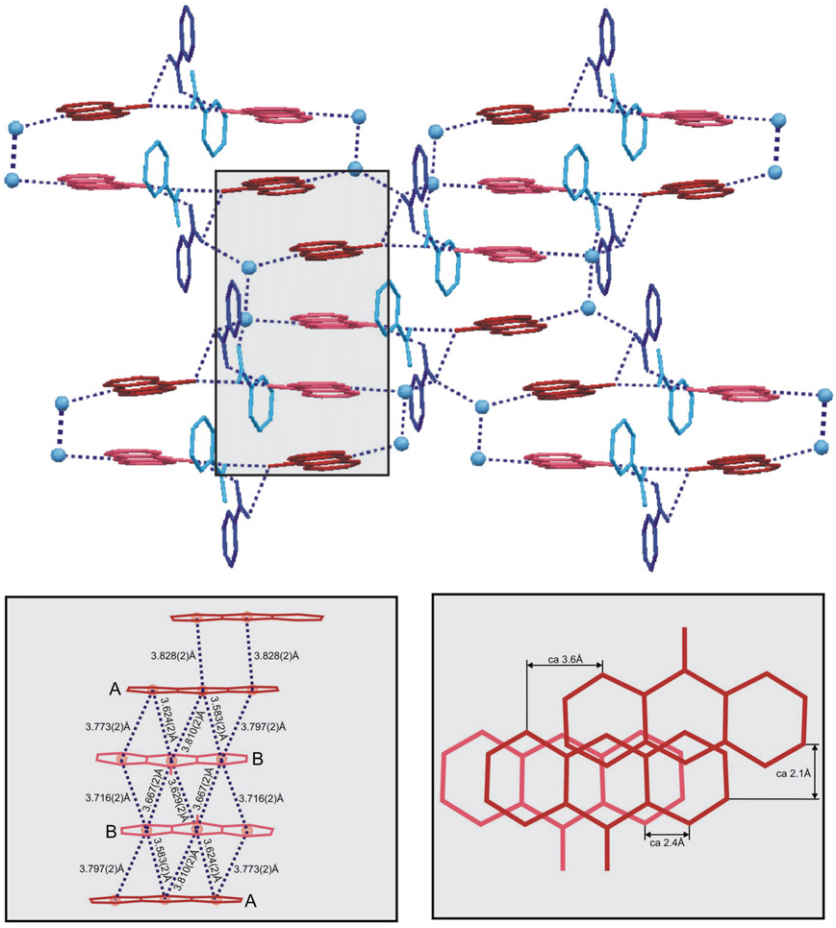

Fig. 2. π–π interactions in **1** (the column of acridine skeletons has shown as shadowed rectangle).