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Bis(melaminium) DL-malate tetrahydrate

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The crystal structure of the title melaminium salt, $bis(2,4,6-triamino-1,3,5-triazin-1-ium)$ DL -malate tetrahydrate, $2C_3H_7N_6^+ \cdot C_4H_4O_5^2$ ⁻⁻ \cdot 4H₂O, consists of singly protonated melaminium residues, DL-malate dianions and water molecules. The melaminium residues are connected into chains by four $N-H\cdots N$ hydrogen bonds, and these chains form a stacking structure along the c axis. The DL-malate dianions form hydrogen-bonded chains and, together with hydrogenbonded water molecules, form a layer parallel to the (100) plane. The conformation of the malate ion is compared with an ab initio molecular-orbital calculation. The oppositely charged moieties, i.e. the stacks of melaminium chains and hydrogenbonded DL-malate anions and water molecules, form a threedimensional polymeric structure, in which $N-H\cdots O$ hydrogen bonds stabilize the stacking.

Comment

The present study is a continuation of our investigations characterizing the hydrogen bonds formed by triazine derivatives in the solid state (Janczak & Kubiak, 1999; Janczak & Perpétuo, 2001a,b,c,d; Janczak & Perpétuo, 2002a,b; Perpétuo & Janczak, $2002a,b$). Melamine and its organic and inorganic complexes or salts can develop well defined supramolecular structures via multiple hydrogen bonds by self-assembly of components that contain complementary arrays of hydrogenbonding sites (Desiraju, 1990; MacDonald & Whitesides, 1994; Row, 1999; Krische & Lehn, 2000; Sherrington & Taskinen, 2001). To expand our understanding of the solid-state physical±organic chemistry of compounds containing multiple hydrogen-bonding systems, we present here the solid-state structure of the title compound, bis(2,4,6-triamino-1,3,5 triazin-1-ium) DL-malate tetrahydrate, (I). Additionally, the geometries of the oppositely charged parts, i.e. the singly protonated melaminium cation and the DL-malate dianion, are compared with ab initio fully optimized parameters calculated

at the HF/6-31 $G(d,p)$ level (Frisch et al., 1995). The ab initio molecular-orbital calculations were carried out on isolated ions, and the results are illustrated in Fig. 1.

The asymmetric unit of (I) consists of two melaminium cations, singly protonated at one of the ring N atoms, a p_L-malate dianion and four water molecules (Fig. 2). The sixmembered rings of the singly protonated melaminium residues exhibit significant distortions from the ideal hexagonal form (Table 1). The internal $C-N-C$ angle at the protonated N atom in both independent melaminium cations is greater than the other two $C-N-C$ angles within the ring. This difference is a result of the steric effect of a lone-pair electron, as predicted by the valence-shell electron-pair repulsion theory (Gillespie, 1963, 1992). As a result of the protonation of the melamine ring at one of the three N atoms, the internal $N C-N$ angle involving only the non-protonated N atoms is significantly greater than the $N - C - N$ angles involving both protonated and non-protonated N atoms. The ab initio opti-

Figure 1

The results of the optimized molecular-orbital calculations (\mathring{A}, \degree) for (a) the melaminium cation and (b) the malate(2–) ion.

mized geometry calculated for the singly protonated melaminium residue shows a correlation between the $C-N-C$ and $N-C-N$ angles within the ring that is similar to the correlation seen in the crystal. Thus, the ring distortion of the singly protonated melaminium residue results mainly from the protonation and, to a lesser degree, from the hydrogenbonding system and the crystal packing. The $C-N$ bond lengths in the optimized melaminium residue are slightly shorter than those in the crystal. The lengthening of these $C-\frac{1}{2}$ N bonds in the crystal is likely to be due to the interaction of the $\pi-\pi$ clouds between the rings in the stacks and the hydrogen-bonding system. A similar correlation between the internal $C-N-C$ and $N-C-N$ angles within the melaminium ring is reported for crystals of barbituric acid with melamine (Zerkowski et al., 1994), melaminium phthalate (Janczak & Perpétuo, 2001a), melaminium chloride hemihydrate (Janczak & Perpétuo, 2001c), bis(melaminium) sulfate dihydrate (Janczak & Perpétuo, 2001d), melaminium acetate (Perpétuo & Janczak, 2002a), melaminium glutarate monohydrate (Janczak & Perpétuo, 2002a) and melaminium phosphate (Janczak & Perpétuo, 2002b), *i.e.* those singly protonated melaminium salts that have been previously structurally characterized.

Each melaminium residue is involved in nine hydrogen bonds; in seven of these it acts as a donor and in the remaining two it acts as an acceptor. Two pairs of almost linear $N H \cdot \cdot N$ hydrogen bonds link the melaminium moieties into chains, which in turn form stacks along the [001] direction. Within one stack, the melaminium residues are separated by 3.196 (3) \AA . This distance is shorter than that between the π -aromatic ring systems (3.4 Å; Pauling, 1960) and indicates

Figure 2

A view of the molecular structure of (I), showing displacement ellipsoids at the 50% probability level and H atoms as spheres of arbitrary radii.

Figure 3

A view of the crystal packing, showing the stacking structure of hydrogenbonded melaminium residues that stabilize the $N-H\cdots O$ hydrogen bonds, and the layer of $O-H\cdots O$ hydrogen-bonded malate ions and water molecules. Dashed lines represent hydrogen bonds and H atoms have been omited for clarity.

 π - π interactions between the melaminium rings in the stack. The remaining five $N-H\cdots O$ hydrogen bonds (see Table 2), which are more bent, link the chains of melaminium residues with DL-malate ions and water molecules (see Fig. 3). These $N-H\cdots$ O hydrogen bonds stabilize the stacking structure. One of the melaminium moieties forms three hydrogen bonds with two malate ions (with atoms O1 and O2 of one malate ion and with atom O5 of the other malate ion), while the other melaminium residue forms only two hydrogen bonds with two malate ions (with atom O3 of one malate ion and with atom O5 of the second). Atom H12 on the protonated N atom of one melamine residue is involved in a hydrogen bond with atom $O1$ of the $COO⁻$ group, while atom H22 on the protonated N atom of the second melaminium residue forms a hydrogen bond with atom $O3$ of the other $COO⁻$ group. Additionally, the first melaminium residue is involved in hydrogen bonds with two water molecules (O2W and O4W), and the other melaminium cation is involved in hydrogen bonds with three water molecules (O2W, O3W and O4W).

The C1–C2–C3–C4 (ψ) , O4–C4–C3–O5 (φ) and $C3-C2-C1-O1$ (χ) torsion angles describe well the conformation of the malate ion and the conformation of malic acid (Sluis & Kroon, 1985; 1989). The conformation of the carbon skeleton of the malate anion is extended $[\psi = -170.5 \,(3)^{\circ}]$, with the C3-carboxyl group almost coplanar with atoms C3 and O5 $[\varphi_2 = 7.3 \text{ (4)}^\circ]$, because of the intramolecular $O5 - H5 \cdots O4$ hydrogen-bonding interaction, with a relatively short $O5 \cdots O4$ distance. The conformation of the C2-carboxyl group (COO^-) around the C $-C$ bond is clinal $[\chi = 17.3 \ (4)^{\circ}]$. In the optimized malate dianion, the values of ψ , φ_2 and χ are -166.3, 4.2 and 36.9°, respectively. The

greatest difference between the angles in the optimized ion and those in the crystal malate ion is found for angle χ , which describes the orientation of the $COO⁻$ group at atom C2; the difference results from the formation of relatively strong $O \cdot \cdot H - N$ hydrogen bonds with the melaminium moiety. The optimized $O - C - O$ angles in both dissociated carboxyl groups are greater than those in the crystal, probably because of the diminishing steric effect of lone pairs of electrons on the O atoms, due to the $O \cdot H-N$ and $O \cdot H-O$ hydrogenbonding interactions. The C -O bonds in both $COO[–]$ groups are intermediate between single Csp^2 – O (1.308–1.320 A) and double Csp^2 = O bonds (1.214–1.224 Å; Allen *et al.*, 1987; Allen, 2002) indicating delocalization of the charge on both O atoms of the $COO⁻$ groups. The slight differences between the $C1 - O1$ and $C1 - O2$ bonds in one $COO⁻$ group, and between the $C4-\overline{O3}$ and $C4-\overline{O4}$ bonds in the other $C\overline{O}\overline{O}$ group, correlate well with the strength of the hydrogen bonds in which the O atoms are involved (Table 2). The $C3-O5$ bond length is slightly longer in the crystal than in the ab initio calculation, since, in the crystal, the hydroxyl group is involved in four hydrogen bonds, viz. in two as a donor and in two as an acceptor. Thus, hydroxyl atom H5 of the malate ion forms a bifurcated hydrogen bond. The malate ions form hydrogenbonded chains *via* O5–H5 \cdots O2(*x*, 2 – *y*, $z - \frac{1}{2}$) interactions and, together with hydrogen-bonded water molecules, form a two-dimensional layer parallel to the (100) plane.

Two pairs of water molecules (O1W and O4W) related by an inversion centre form a hydrogen-bonded cyclic tetramer in which atom O4W is a donor and atom O1W is an acceptor. Additionally, water molecule O3W interacts as an acceptor with atom H21W, and water molecule O2W interacts via atom H22W to form an O2W–H22W \cdots O4W($\frac{3}{2} - x$, $y - \frac{1}{2}$, $\frac{1}{2} - z$) hydrogen bond.

Experimental

Melamine was added to a solution of DL -malic acid (10%) and the resulting solution was evaporated slowly. After several days, colourless crystals of (I) appeared.

> D_m measured by flotation in dichloroethane/dibromoethane

Parallelepiped, colourless $0.28 \times 0.24 \times 0.16$ mm

Mo $K\alpha$ radiation Cell parameters from 3878

reflections $\theta = 3.2 - 28.4^{\circ}$ $\mu = 0.13$ mm⁻¹ $T = 293 (2) K$

Crystal data

Data collection

Refinement

Table 1

Selected geometric parameters (\AA, \degree) .

Symmetry codes: (i) $x, y - 1, z$; (ii) $1 - x, 2 - y, -z$; (iii) $x - \frac{1}{2}, y - \frac{1}{2}, z$; (iv) $x - \frac{1}{2}$, $\frac{1}{2} + y$, z; (v) x, 1 + y, z; (vi) x, 2 - y, z - $\frac{1}{2}$; (vii) $\frac{3}{2} - x$, $\frac{5}{2} - y$, -z; (viii) $\frac{3}{2} - x$, $\frac{3}{2} - y$, -z; (viii) $\frac{3}{2} - x$, $\frac{3}{2} - y$, -z; (viii)

Data collection: KM-4 Software (Kuma, 2000); cell refinement: KM-4 Software; data reduction: KM-4 Software; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Sheldrick, 1990); software used to prepare material for publication: SHELXL97.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: NA1613). Services for accessing these data are described at the back of the journal.

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