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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.003 Å R factor = 0.033 wR factor = 0.103 Data-to-parameter ratio = 9.8

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

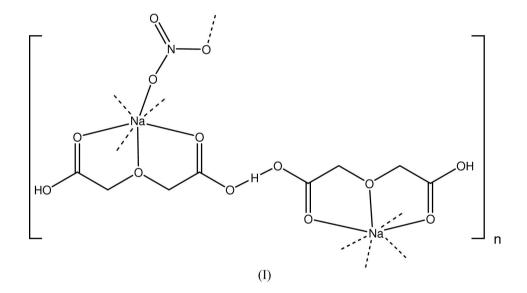
Possible strong symmetric hydrogen bonding in disodium trihydrogen bis(2,2'-oxydiacetate) nitrate

In the title compound, $2Na^+ \cdot C_8H_{11}O_{10}^- \cdot NO_3^-$, the Na^I atom is heptacoordinate with an approximately pentagonal-bipyramidal geometry. A possible strong symmetric hydrogen bond, with the H atom located at an inversion centre and an $O \cdot \cdot \cdot O$ distance of 2.450 (2) Å, is observed in the crystal structure.

Comment

The nature of short hydrogen-bonding interactions is still a subject of much interest and debate (Meot-Ner, 2005). It appears that, for O-H-O interactions where $O\cdots O$ is less than about 2.50 Å, examples can be found of truly symmetric hydrogen bonds (Catti & Ferraris, 1976), most of which have crystallographic equivalence between donor-acceptor atoms. The title sodium compound, (I), displays just such a short and possibly symmetric hydrogen-bonding interaction.

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The compound can be viewed as a mixed sodium salt containing two monoanionic components, *viz.* nitrate and trihydrogen bis(2,2'-oxydiacetate) (a hydrogen-bonded adduct formed by the loss of a single H atom from two of the dicarboxylic acid molecules). These 2,2'-oxydiacetate molecules adopt the fairly common planar all-*trans* configuration (Albertsson & Grenthe, 1973; Albertsson *et al.*, 1973*a,b*; Hatfield *et al.*, 1987). The Na^I cation in (I) is heptacoordinate with an approximately pentagonal–bipyramidal geometry (Fig. 1); Na–O distances range from 2.4075 (17) to 2.5861 (18) Å. A tridentate chelating 2,2'-oxydiacetate molecule occupies three of the equatorial sites bonding through the two carboxyl and one ether O atoms. Symmetry-equivalent carboxyl atoms O2ⁱⁱⁱ, O5^{iv} and O1^v [symmetry codes: (iii)

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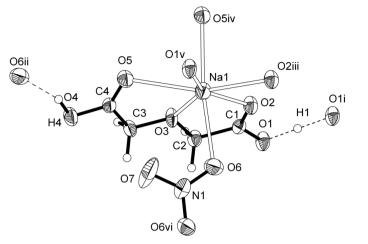


Figure 1

The molecular structure and sodium environment, with 50% probability displacement ellipsoids and the atom-labelling scheme. Dashed lines indicate hydrogen bonds. [Symmetry codes: (i) $\frac{3}{2} - x$, $\frac{3}{2} - y$, 1 - z; (ii) x, y - 1, z; (iii) 1 - x, 1 - y, 1 - z; (iv) 1 - x, -y, 1 - z; (v) $x - \frac{1}{2}$, $y - \frac{1}{2}$, z; (vi) 1 - x, y, $\frac{3}{2} - z$].

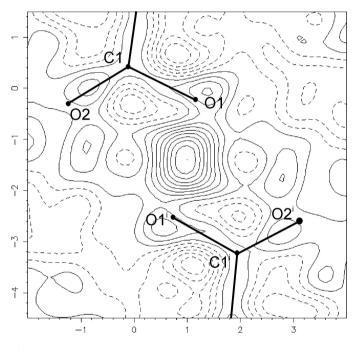


Figure 2

Difference Fourier map from a refined model where atom H1 is absent. The O1/C1/O2 plane is shown with the crystallographic inversion in the centre of the plot.

1 - x, 1 - y, 1 - z; (iv) 1 - x, -y, 1 - z; (v) $x - \frac{1}{2}$, $y - \frac{1}{2}$, z] from neighbouring 2,2'-oxydiacetate molecules and atom O6 of a bridging nitrate make up the rest of the coordination sphere.

The nitrate anion lies on the crystallographic twofold axis and links pairs of Na^I ions in an *anti–anti-*1,3-bridging coordination mode. The carboxyl O atoms act in a bis- μ -bridging capacity between Na^I ions, forming the polymeric structure.

In addition to these ionic interactions, the crystal structure is also held together by a network of two types of hydrogen

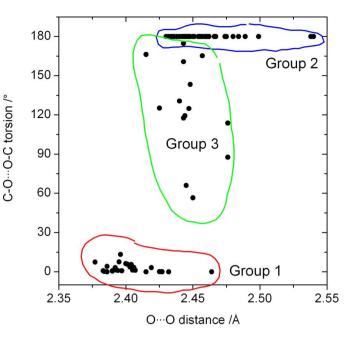
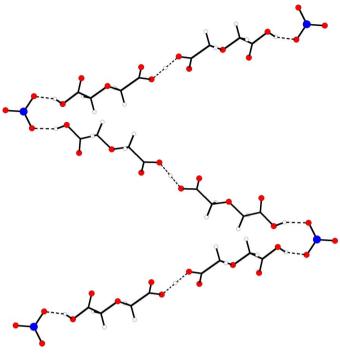


Figure 3

Graph showing the distribution of $C-O\cdots O-C$ torsion angles as a function of $O\cdots O$ interatomic separations for short hydrogen-bonded interactions between two carboxylic acid groups. Data taken from 78 structures in the CSD (Version 5.25; Allen, 2002).

bonds. The first is formed between the O4-carboxyl group and the nitrate anion (Table 1). This hydrogen bond is asymmetric and non-linear. The nature of the second type of hydrogen bond is ambiguous. Certainly there exists a short hydrogenbond interaction between the O1-carboxyl group and its crystallographically equivalent group; the O1···O1ⁱ distance of 2.450 (2) Å [symmetry code:(i) $\frac{3}{2} - x$, $\frac{3}{2} - y$, 1 - z] falls within the normal range for symmetric hydrogen bonds (Catti & Ferraris, 1976). A Fourier map section in the O1/C1/O2 plane (MAPVIEW; Farrugia, 1999) clearly indicates a peak of electron density centred on the crystallographic inversion (Fig. 2). Two alternative structural models have been studied. Placing atom H1 on the inversion centre gives a symmetric structure. Full-matrix least-squares refinement converged to a stable solution which is reported here. The residual difference Fourier map has a largest peak and hole of 0.16 and $-0.23 \text{ e} \text{ Å}^{-3}$, respectively. The crystallographic symmetry constrains the hydrogen-bond angle to 180° and the O1-H1 distance to 1.23 Å. A second structural model is one with the H1-atom site half occupied and displaced from the inversion centre towards O1. Free refinement of the x, y, z and U_{iso} parameters for the H1 atom (118 parameters in total) converged to give a sensible asymmetric hydrogen-bonding interaction; the crystallographic residuals are insignificantly different and the difference map shows essentially the same features. The limited data quality and resolution mean that we cannot unambiguously determine the nature of this hydrogenbonding interaction. The compound clearly merits further study, if only to resolve this issue. Despite this uncertainty in the H-atom position, such a linear hydrogen-bonding interaction linking two 2,2'-oxydiacetate molecules in a trans





The hydrogen-bonded network formed by both types of hydrogenbonding interaction (dashed lines).

fashion is not an unusual motif when an H atom is shared between two carboxylic acid groups (Nahringbauer, 1969; Longo & Richardson, 1982; Misaki et al., 1989).

An examination of the Cambridge Structural Database (CSD; Version 5.25; Allen, 2002) for short hydrogen bonds between two carboxylate groups reveals three distinct conformational/geometric groups (Fig. 3). Group 1 have a C- $O \cdots O - C$ torsion angles of about 0° and have $O \cdots O$ separations mostly in the range 2.38–2.43 Å. Group 2 have $C-O \cdots O-C$ torsion angles of 180° (invariably fixed by crystallographic symmetry) and $O \cdots O$ separations in the range 2.43–2.53 Å. Group 3 have intermediate torsion angles (unrestricted by symmetry) and have $O \cdots O$ distances all within the range 2.42-2.47 Å. The possibly symmetric hydrogen bond observed in (I) falls well within the known range for group 2 conformations, and this geometry is seen for many other dicarboxylate compounds (see, for example, Kalsbeek & Larsen, 1991; Leban & Rupnik, 1992; Flensburg et al., 1995) and also in other 2,2'-oxydiacetate salts (Albertsson & Grenthe, 1973; Albertsson et al., 1973a,b; Herbertsson & Hedman, 1982; Urbańczyk-Lipkowska, 2000).

We also note that the first hydrogen-bonding pattern (between the carboxylic acid and the nitrate anion), although asymmetric, seems to be a strong and important structural motif. In nine out of 14 reported structures that contain both a carboxylic acid and a nitrate anion, the acid is hydrogen bonded to the nitrate, and none of the structures displays the common $R_2^2(8)$ dimeric carboxylic acid motif (see, for example, Sridhar et al., 2002).

Together, these two hydrogen-bonded motifs form a network. Using the nomenclature for graph theoretical analysis developed by Etter et al. (1990), we can describe this system as $N_1 = D_2^2(4)D$; $N_2 = C_3^3(20)$, where the second-order net consists of infinite chains that zigzag through the crystal structure (Fig. 4).

Experimental

Crystals of (I) were grown by slow evaporation from a methanolic solution which contained the bis(2.2'-oxydiacetic acid), sodium hydroxide and aluminium nitrate nonahydrate.

Crystal data

-	
$2Na^{+} \cdot C_{8}H_{11}O_{10}^{-} \cdot NO_{3}^{-}$	$D_x = 1.808 \text{ Mg m}^{-3}$
$M_r = 375.16$	Mo $K\alpha$ radiation
Monoclinic, C2/c	Cell parameters from 101
a = 12.010 (2) Å	reflections
$b = 7.0290 (14) \text{\AA}$	$\theta = 3.2-24.8^{\circ}$
c = 16.382 (3) Å	$\mu = 0.22 \text{ mm}^{-1}$
$\beta = 94.84 \ (3)^{\circ}$	T = 293 (2) K
$V = 1378.0 (4) \text{ Å}^3$	Block, colourless
Z = 4	$0.16 \times 0.16 \times 0.06~\mathrm{mm}$

 $R_{\rm int}=0.016$

 $\theta_{\rm max} = 24.8^{\circ}$ $h = 0 \rightarrow 14$

 $k = -8 \rightarrow 8$

 $l = -19 \rightarrow 19$

Data collection

Rigaku R-AXIS-IIc diffractometer φ scans Absorption correction: none 1999 measured reflections 1124 independent reflections 996 reflections with $I > 2\sigma(I)$

Refinement

D-

01

O4

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0446P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.033$	+ 1.8079P]
$wR(F^2) = 0.103$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.17	$(\Delta/\sigma)_{\rm max} < 0.001$
1124 reflections	$\Delta \rho_{\rm max} = 0.16 \ {\rm e} \ {\rm \AA}^{-3}$
115 parameters	$\Delta \rho_{\rm min} = -0.23 \ {\rm e} \ {\rm \AA}^{-3}$
H atoms treated by a mixture of	
independent and constrained	
refinement	

Table 1		
Hydrogen-bonding geometry	(Å,	°).

$-H\cdots A$	<i>D</i> -H	Н∙∙∙А	$D \cdots A$	$D - \mathbf{H} \cdots A$
$-H1\cdots O1^{i}$ $-H4\cdots O6^{ii}$	1.225 0.92 (4)	1.225 1.82 (4)	2.450 (2) 2.703 (3)	180 160 (3)
mmatry and as (i)	3 x 3 y 1			

Symmetry codes: (i) $\frac{3}{2} - x, \frac{3}{2} - y, 1 - z$; (ii) x, y - 1, z.

All methylene H atoms were located in idealized positions and refined in riding mode. C-H distances were set at 0.97Å and $U_{iso}(H)$ values were constained to be $1.5U_{eq}$ of the parent C atom. Both H atoms involved in hydrogen bonding were found in a Fourier difference map and were refined, subject only to the inversion centre constraint.

Data collection: MSC R-AXIS-II Control Software; cell refinement: DENZO (Otwinowski & Minor, 1997); data reduction: SCALEPACK (Otwinowski & Minor, 1997); program(s) used to solve structure: SHELXS86 (Robinson & Sheldrick, 1988); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997) in WinGX (Farrugia, 1999); molecular graphics: DIAMOND (Brandenburg, 1999).

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