Adenosinium 3,5-dinitrosalicylate

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Key indicators

Single-crystal X-ray study

T = 298 K

Mean $\sigma(\text{C}-\text{C}) = 0.005 \text{ \AA}$

R factor = 0.036

wR factor = 0.122

Data-to-parameter ratio = 7.6

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

The crystal structure of adenosinium 3,5-dinitrosalicylate, $\text{C}_{10}\text{H}_{14}\text{N}_5\text{O}_4^+ \cdot \text{C}_7\text{H}_3\text{N}_2\text{O}_7^-$, shows the presence of a primary chain structure formed through homomeric head-to-tail cyclic $R_2^2(10)$ hydrogen-bonding interactions between hydroxy O- and both purine and amine N-donor and acceptor groups of the furanose and purine moieties of the adenosinium species. These chain structures are related by crystallographic 2_1 symmetry. Secondary hetero-ionic hydrogen bonding, involving the 3,5-dinitrosalicylate anion, including a cyclic $R_2^2(8)$ interaction between the carboxylate group and the protonated purine and amine groups of the adenosinium cation are also present, together with heteromolecular π - π interactions giving a three-dimensional hydrogen-bonded polymer structure.

Comment

The nucleoside adenosine (6-amino-9 β -D-ribofuranosyl-9H-purine) is an essential biological molecule, which in its 5'-di- and triphosphorolated forms (ADP, ATP) is associated with energy-transfer processes in muscle tissue (Wilson *et al.*, 1991), where the ATP levels in mammals are commonly 350–400 mg per 100 g (Stecher, 1968). Also as its 3',5'-cyclic monophosphate ester (cAMP) it is associated with G proteins in second messenger systems for a number of hormones (Wilson *et al.*, 1991). Adenosine is also involved in a number of other biological processes involving RNA where it is present with high frequency among the structural motifs (Portmann *et al.*, 1996; Ortoleva-Donnelly *et al.*, 1998), while it has also been a targeted molecule for derivatization for enzyme pro-drug therapy (Vogt *et al.*, 2000; Bressi *et al.*, 2000; Qiu *et al.*, 2002; Costanzi *et al.*, 2003). The structures of many simple neutral adenosine analogues have been reported, including the parent [Lai & Marsh, 1972 (X-ray); Klooster *et al.*, 1991 (neutron, 123 K)], adenosine-5'-phosphate (Kraut & Jensen, 1963), adenosine-3'-phosphate dihydrate (adenylic acid b) (Brown *et al.*, 1953; Sundaralingam, 1966), deoxyadenosine monohydrate (Watson *et al.*, 1965), adenosine-5'-O-methylphosphate (Hoogendorp *et al.*, 1978), 3'-O-acetyladenosine (Rao & Sundaralingam, 1970), and α -D-2'-deoxyadenosine monohydrate (Rohrer & Sundaralingam, 1970). The stereochemistry of 3'-N-substituted 3'-deoxyadenosines has also been reviewed (Sheldrick & Morr, 1980) and the structure of the Na salt of deoxyadenosine-5'-phosphate hexahydrate has been determined (Reddy & Viswamitra, 1975). The di- and trinucleoside phosphate esters β -adenosine-2'- β -uridine-5'-phosphate (Shefter *et al.*, 1969) and adenylyl-(3',5')-adenylyl-(3',5')-adenosine (Suck *et al.*, 1976) are also known. The structures of neutral adducts of adenosine with 5-bromouridine (Haschemeyer & Sobell, 1965), 5-bromouracil (Aiba *et*

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al., 1978) and proflavine (Swaminathan *et al.*, 1982) have been reported, and in this 1:2 proflavine structure, stability is enhanced by the presence of heteromolecular π - π ring interactions, as well as the expected conventional hydrogen-bonding interactions.

As a base, adenosine will react with the stronger carboxylic acids, resulting in protonation at the N1 position of the purine ring, giving salts with enhanced crystallinity due to hydrogen-bonding interactions, such as in the adenosinium chloride structure (Shikata *et al.*, 1973) and the structural aspects of protonated and complexed adenosine have also been reviewed (Hauser & Keese, 2002). One such compound, adenosinium picrate has been known for some time (Stecher, 1968), but its crystal structure has only recently been reported (Goto *et al.*, 2004).

We report here the crystal structure of a proton-transfer compound formed from the reaction of adenosine with an acid similar to picric acid, 3,5-dinitrosalicylic acid (DNSA)–adenosinium 3,5-dinitrosalicylate, (I). We have previously completed the structures of more than 40 charge-transfer compounds of DNSA with both aliphatic and aromatic Lewis bases (Smith *et al.*, 2002; Smith *et al.*, 2003, 2004). In these,

Figure 3

The crystal packing of (I), viewed down the *c* axis, showing cation–anion hydrogen-bonding associations and partial inter-species ring superimposition with π – π stacking.

membered DNSA anion benzene rings with the five-membered (N72–C82) portions of the adenosinium cation rings down the *c* axis [minimum ring centroid separation = 3.61 (1) Å]. The overall result is a three-dimensional polymer structure.

The conformation of the adenosinium cation appears to be influenced in (I) by the presence of an intramolecular C–H...O interaction between H82 of the purine ring and the O51 hydroxy group [3.278 (5) Å]. However, the resultant torsion angle C82–N92–C11–C21 [–71.4 (4)°] is a value which is extremely variable among the adenosine analogues.

Within the DNSA anion, the structural features vary from those of the majority of the proton-transfer compounds (Smith *et al.*, 2002, 2003) mainly in the conformation of the nitro substituent groups. The proximal nitro group at C3 is more commonly involved in hydrogen bonding and therefore shows a greater rotation out of the plane of the ring than the C5 group. However, in (I), where both O5A and O5B are associated, C5 rotation is greater than usual but C3 rotation is also significant, despite being unassociated [torsion angles: C4–C5–N5–O5B = 152.6 (4)° and C2–C3–N3–O5B = 146.8 (4)°]. By comparison, the torsion angle C2–C1–C7–O7A, associated with the intramolecularly hydrogen-bonded carboxylate group, is –177.7 (4)°. This hydrogen bond [O2...O7B = 2.438 (5) Å] has the proton located on the phenol O atom rather than the carboxyl group, such as is

found in *ca* 70% of the proton-transfer compounds of DNSA (Smith *et al.*, 2002, 2003).

Experimental

The title compound was synthesized by heating under reflux for 10 min, 1 mmol quantities of adenosine and 3,5-dinitrosalicylic acid (DNSA) in 50 ml of 50% ethanol/water. After concentration to *ca* 30 ml, partial room temperature evaporation of the hot-filtered solution gave thin pale-yellow crystal plates (m.p. 487.2–488.5 K).

Crystal data

$C_{10}H_{14}N_5O_4^+ \cdot C_7H_3N_2O_7^-$
 $M_r = 495.38$
 Monoclinic, $P2_1$
 $a = 15.297$ (2) Å
 $b = 8.8543$ (14) Å
 $c = 7.2805$ (8) Å
 $\beta = 92.32$ (1)°
 $V = 985.3$ (2) Å³
 $Z = 2$

$D_x = 1.670$ Mg m^{–3}
 Mo $K\alpha$ radiation
 Cell parameters from 25 reflections
 $\theta = 12.5$ – 16.9 °
 $\mu = 0.14$ mm^{–1}
 $T = 298$ (2) K
 Plate, pale yellow
 $0.40 \times 0.35 \times 0.03$ mm

Data collection

Rigaku AFC-7R diffractometer
 ω – 2θ scans
 Absorption correction: ψ scan
 (TEXSAN for Windows;
 Molecular Structure
 Corporation, 1999)
 $T_{\min} = 0.945$, $T_{\max} = 0.995$
 2690 measured reflections
 2406 independent reflections

1873 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.018$
 $\theta_{\max} = 27.5$ °
 $h = -8 \rightarrow 19$
 $k = 0 \rightarrow 11$
 $l = -9 \rightarrow 9$
 3 standard reflections
 frequency: 150 min
 intensity decay: none

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.037$
 $wR(F^2) = 0.122$
 $S = 0.88$
 2406 reflections
 317 parameters
 H-atom parameters not refined

$w = 1/[\sigma^2(F_o^2) + (0.1P)^2 + 2.5029P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.003$
 $\Delta\rho_{\max} = 0.20$ e Å^{–3}
 $\Delta\rho_{\min} = -0.24$ e Å^{–3}
 Extinction correction: SHELXL97
 Extinction coefficient: 0.013 (3)

Table 1

Hydrogen-bonding geometry (Å, °).

<i>D</i> –H... <i>A</i>	<i>D</i> –H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> –H... <i>A</i>
O2–H2...O7B	0.92	1.61	2.438 (5)	147
N12–H12...O7A ⁱ	0.90	1.87	2.763 (4)	170
N62–H62B...O7B ⁱ	0.88	1.92	2.785 (5)	167
O21–H21A...O7A ⁱⁱ	0.91	1.90	2.782 (4)	163
O51–H51C...O5B ⁱⁱⁱ	0.80	2.42	2.955 (5)	125
O31–H31A...N72 ⁱⁱⁱ	0.93	1.93	2.785 (4)	152
O51–H51C...O5A ^{iv}	0.80	2.45	3.164 (5)	149
N62–H62A...O21 ^v	0.84	2.12	2.886 (4)	152
C22–H22...O2 ^{vi}	0.96	2.22	3.041 (5)	142
C82–H82...O51	0.97	2.42	3.278 (5)	148

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

H atoms potentially involved in hydrogen-bonding interactions were located by difference methods, while others were included in the refinement at calculated positions (C–H = 0.96 Å). All were treated as riding, with $U_{\text{iso}}(\text{H})$ fixed at 1.2 $U_{\text{eq}}(\text{attached atom})$. The absolute configuration was not determined but was assumed from that known for the parent adenosine [C1'(R), C2'(R), C3'(S) and C4'(R)]. Friedel pairs were merged before refinement.

Data collection: MSC/AFC Diffractometer Control Software (Molecular Structure Corporation, 1999); cell refinement: MSC/AFC

Diffraction Control Software; data reduction: *TEXSAN for Windows* (Molecular Structure Corporation, 1999); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON for Windows* (Spek, 1999); software used to prepare material for publication: *PLATON for Windows*.

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