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Key indicators

Single-crystal X-ray study T = 100 KMean σ (C–C) = 0.002 Å R factor = 0.037 wR factor = 0.082 Data-to-parameter ratio = 14.6

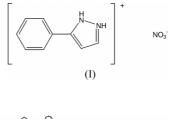
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

3-Phenylpyrazolium nitrate

The title compound, $C_9H_9N_2^+ \cdot NO_3^-$, is composed of discrete 3-phenylpyrazolium cations and nitrate anions. The crystal packing is stabilized by $N-H\cdots O$ and $C-H\cdots O$ hydrogen bonds.

Comment

Recently, we have reported the X-ray crystal structure analysis of 3-phenylpyrazole, (2) (Haghiri *et al.*, 2002; Haghiri *et al.* 1993). We describe here the X-ray crystal structure analysis of 3-phenylpyrazolium nitrate, (I). Tris(1-pyrazolyl)borates ('scorpinates'), (1), were invented by Trofimenko more than 30 years ago and are today well established as ligands in coordination chemistry (Trofimenko, 2003), but only a limited number of transition metal complexes with 3-phenylpyrazole, (2), as ligand have been structurally characterized.



 $HB \xrightarrow{N = N} N \xrightarrow{(2)} (1)$

Therefore, we are interested in the synthesis of Fe^{III} complexes with (2) as ligand. Surprisingly, only protonation of (2) takes place in the reaction of $Fe(NO_3)_3$ with (2). Fe^{III} reacts as an acid in solution.



Figure 1

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Perspective view of the title compound, with the atom numbering. Displacement ellipsoids are drawn at the 50% probability level.

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The crystal structure of (I) is composed of discrete 3phenylpyrazolium cations and nitrate anions (Fig. 1). Geometric parameters are as expected. The dihedral angle between the phenyl ring and the pyrazole ring is $15.50 (7)^{\circ}$. Anions and cations are connected by bifurcated N-H···O hydrogen bonds. In addition, the crystal packing is stabilized by C-H···O hydrogen bonds (Fig. 2).

Experimental

X-ray quality crystals of (I) were obtained from a solution of 0.04 g (0.10 mmol) $Fe(NO_3)_3$ ·9H₂O and 0.04 g (0.28 mmol) 3-phenylpyrazole in 5 ml CH₃OH at ambient temperature.

> $D_x = 1.462 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation Cell parameters from 5297

reflections $\theta = 3.7-27.2^{\circ}$ $\mu = 0.11 \text{ mm}^{-1}$ T = 100 (2) K

Plate, colourless

 $0.22 \times 0.16 \times 0.12 \text{ mm}$

Crystal data

$C_9H_9N_2^+\cdot NO_3^-$
$M_r = 207.19$
Monoclinic, C2/c
a = 16.8447 (16) Å
b = 13.392 (2) Å
c = 8.3779(8) Å
$\beta = 95.211 \ (8)^{\circ}$
V = 1882.2 (4) Å ³
Z = 8

Data collection

Stoe IPDS-II two-circle	1502 reflections with $I > 2\sigma(I)$
diffractometer	$R_{\rm int} = 0.058$
ω scans	$\theta_{\rm max} = 27.3^{\circ}$
Absorption correction: none	$h = -21 \rightarrow 21$
8471 measured reflections	$k = -14 \rightarrow 17$
2106 independent reflections	$l = -10 \rightarrow 10$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.037$	H atoms treated by a mixture of independent and constrained
$wR(F^2) = 0.082$	refinement
S = 0.90	$w = 1/[\sigma^2(F_o^2) + (0.0427P)^2]$
2106 reflections	where $P = (F_o^2 + 2F_c^2)/3$
144 parameters	$(\Delta/\sigma)_{\rm max} < 0.001$
	$\Delta \rho_{\rm max} = 0.18 \ {\rm e} \ {\rm \AA}^{-3}$
	$\Delta \rho_{\rm min} = -0.27 \ {\rm e} \ {\rm \AA}^{-3}$

Table 1

Hydrogen-bonding geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$N4-H4\cdots O1$ $N4-H4\cdots O1^{i}$ $N5-H5\cdots O2$ $N5-H5\cdots O1$	0.90 (2) 0.90 (2) 0.91 (2) 0.91 (2)	2.40 (2) 1.83 (2) 1.90 (2) 2.297 (18)	2.9019 (17) 2.7233 (16) 2.8060 (17) 2.8802 (16)	115.0 (16) 169 (2) 177.0 (17) 121.7 (14)
$C16-H16\cdots O2$	0.95	2.51	3.3643 (17)	149

Symmetry code: (i) -x, 1 - y, -z.

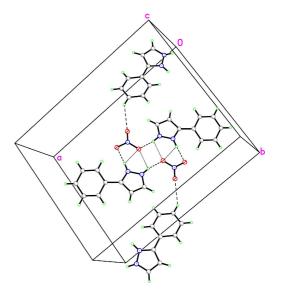


Figure 2

Hydrogen bonds (dashed lines) in the crystal structure of the title compound. Atom codes: C shaded black circles, H small open green circles, N blue shaded circles and O cross-hatched red circles.

H atoms bonded to C atoms were refined with fixed individual displacement parameters $[U_{iso}(H) = 1.2U_{eq}(C)]$, using a riding model, with C-H = 0.95 Å. The H atoms bonded to N atoms were refined isotropically.

Data collection: X-AREA (Stoe & Cie, 2001); cell refinement: X-AREA; data reduction: X-AREA; program(s) used to solve structure: SHELXS97 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: XP in SHELXTL-Plus (Sheldrick, 1991); software used to prepare material for publication: SHELXL97 and PLATON (Spek, 2003).

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