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Zai-Gang Luo,^a De-Qing Shi^a* and Xiang-Gao Meng^b

^aKey Laboratory of Pesticide and Chemical Biology of Ministry of Education, College of Chemistry, Central China Normal University, Wuhan 430079, Hubei, People's Republic of China, and ^bCollege of Chemistry, Central China Normal University, Wuhan 430079, Hubei, People's Republic of China

Correspondence e-mail: chshidq@yahoo.com.cn

Key indicators

Single-crystal X-ray study T = 292 KMean $\sigma(\text{C}-\text{C}) = 0.003 \text{ Å}$ R factor = 0.046 wR factor = 0.127 Data-to-parameter ratio = 17.7

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3-pyridylmethylamino)-1*H*-pyrazole-4-carboxylate

In the title compound, $C_{23}H_{26}Cl_2N_5O_5P$, the P atom adopts a distorted tetrahedral configuration. The carboxyl fragment of the ethylcarboxylate group is almost coplanar with the pyrazole ring. The dihedral angle between the pyrazole and pyridine rings is 82.7 (1)°. Intramolecular C-H···O, C-H···N and N-H··O hydrogen bonds contribute strongly to the stability of the molecular configuration. C-H···O intermolecular hydrogen bonds link inversion-related molecules into a centrosymmetric $R_2^2(10)$ dimer. In addition, C-H··· π hydrogen bonds are observed in the crystal structure.

cis-Ethyl 5-amino-1-[4-(4-chlorophenyl)-5,5-dimethyl-

2-oxo-1,3,2-dioxaphosphinan-1-yl]-3-(6-chloro-

Comment

Neonicotinioid insecticides as nicotinic acetylcholine receptor inhibitors have attracted increasing attention because of their safety, low toxicity and high activities (Shiokawa *et al.*, 1986). It is found that most biologically active nicotinic compounds contain the 3-aminomethylpyridine group (Yamamoto *et al.*, 1994). Pyrazole and phosphorus heterocyclic compounds appear to be very important owing to their biological activities (Tomcufcik *et al.*, 1985; Hirashima *et al.*, 1986). We report here the crystal structure of the title compound, (I), which was synthesized by introducing 1,3,2-dioxaphosphinane and 3aminomethylpyridine molecules into pyrazole.



Fig. 1 shows the molecular structure of (I). The P atom is in a slightly distorted tetrahedral geometry. The deformation of the tetrahedron can be described by the different bond types, *viz*. the P=O double bond, P-O single bond and P-N single bond, and associated angles (Table 1). The P1-O4 [1.5554 (15) Å], P1-O5 [1.5584 (13) Å] and P1=O3 [1.4581 (15) Å] distances are shorter than those observed in a related structure [1.586 (2), 1.572 (2) and 1.468 (2) Å; Liu *et al.*, 2005], but the P1-N4 distance of 1.6604 (17) Å is longer than that observed [1.605 (3) Å] in the above structure. The variation in the lengths may be a result of steric and electronic effects. The dioxaphosphinane ring adopts a chair conformaReceived 20 September 2005 Accepted 11 October 2005 Online 15 October 2005

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Figure 1

The structure of (I), showing 50% probability displacement ellipsoids and the atom-numbering scheme. For clarity, H atoms have been omitted.

tion, with puckering parameters Q = 0.495 (2) Å, $\theta = 25.6$ (2) and $\varphi = 180.8 (5)^{\circ}$ (Cremer & Pople, 1975).

The C9-C8-C10-O1 [6.1 (3) $^{\circ}$] and C7-C8-C10-O2 $[7.7 (3)^{\circ}]$ torsion angles indicate that the carboxyl fragment of the ethylcarboxylate group is almost coplanar with the pyrazole ring. This orientation results in an intramolecular N5-H5B···O1 hydrogen bond (Table 2), which forms a pseudosix-membered ring. The terminal carbon C12 is twisted substantially out of the plane of the pyrazole ring, the C12-C11-O2-C10 torsion angle being $-143.2 (2)^{\circ}$. The short C11-C12 bond distance [1.474 (4) Å] can probably be attributed to unresolved disorder of the terminal methyl group, as indicated by the unusual displacement parameters for atoms C11 and C12 (Patel et al., 2003).

Intramolecular C-H···O, C-H···N and N-H···O hydrogen bonds (Table 2) contribute strongly to the stability of the molecular configuration. As a result of the hydrogenbonding interactions, the benzene and pyridine rings lie on the same side of the pyrazole ring; the dihedral angle between the pyrazole and pyridine rings is $82.7 (1)^{\circ}$.

The crystal packing shows that the intermolecular C11-H11B···O1ⁱ [symmetry code: (i) 1 - x, 2 - y, 1 - z] hydrogen bond between inversion-related molecules leads to the formation of a centrosymmetric $R_2^2(10)$ dimer (Bernstein *et al.*, 1995) (Fig. 2). In addition, two C $-H \cdot \cdot \pi$ hydrogen bonds are observed in the crystal structure of (I). It is known that methyl groups can function as hydrogen-bond donors towards aromatic π systems (Desiraju, 2002). The C6 and C11 methylene groups are involved in $C-H\cdots\pi$ interactions with the C18-C23 benzene ring, with its centroid at Cg1 (Table 2).

Experimental

A solution of 3-(6-chloro-3-pyridylmethylamino)-4-ethoxycarbonyl-5-aminopyrazole (4 mmol) in anhydrous CH₃CN (20 ml) and NaOH powder (5 mmol) were placed in a three-necked flask; after vigorous stirring for 5 min, a solution of 2-chloro-4-chlorophenyl-5,5-dimethyl-1,3,2-dioxaphosphinane 2-oxide (4.5 mmol) in anhydrous acetonitrile (5 ml) was added dropwise while the mixture was cooled in an icebath. After the addition was finished, the mixture was stirred at room temperature until the reaction finished (monitored by thin layer chromatography). The workup involved removal of the solvent followed by addition of water and extraction of the product mixture into chloroform; after phase separation, drying over Na₂SO₄, filtration and evaporation, the crude product was purified by flash column chromatography on silica gel using petroleum ether/ethyl acetate (1:1 v/v) as eluant, giving a white solid (yield 45%, m.p. 433 K). Single crystals of (I) were obtained from an absolute ethanol solution.

Crystal data

C ₂₃ H ₂₆ Cl ₂ N ₅ O ₅ P	$D_x = 1.446 \text{ Mg m}^{-3}$
$M_r = 554.36$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 5782
a = 12.4196 (11) Å	reflections
b = 12.1995 (11) Å	$\theta = 2.4-22.9^{\circ}$
c = 17.5992 (15) Å	$\mu = 0.36 \text{ mm}^{-1}$
$\beta = 107.198 \ (2)^{\circ}$	T = 292 (2) K
V = 2547.3 (4) Å ³	Block, colourless
Z = 4	0.30 \times 0.20 \times 0.18 mm

5812 independent reflections 3999 reflections with $I > 2\sigma(I)$

 $= 1/[\sigma^2(F_0^2) + (0.0617P)^2]$

where $P = (F_0^2 + 2F_c^2)/3$

 $R_{\rm int} = 0.031$

 $\theta_{\rm max} = 27.5^{\circ}$

 $h = -16 \rightarrow 16$ $k = -15 \rightarrow 14$

 $l = -22 \rightarrow 22$

Data collection

Bruker SMART CCD area-detector
diffractometer
φ and ω scans
Absorption correction: multi-scan
(SADABS; Bruker, 2000)
$T_{\min} = 0.899, T_{\max} = 0.938$
21527 measured reflections

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.06)]$
$R[F^2 > 2\sigma(F^2)] = 0.046$	+ 0.368P]
$vR(F^2) = 0.127$	where $P = (F_0^2 + 2)$
S = 1.02	$(\Delta/\sigma)_{\rm max} = 0.001$
5812 reflections	$\Delta \rho_{\rm max} = 0.30 \text{ e } \text{\AA}^{-3}$
328 parameters	$\Delta \rho_{\rm min} = -0.27 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

Table 1 Selected bond angles (°).

O3-P1-O4	116.88 (9)	O3-P1-N4	109.80 (9)
O3-P1-O5	115.40 (9)	O4-P1-N4	103.86 (8)
O4-P1-O5	105.50 (7)	O5-P1-N4	104.06 (8)

l able 2			
Hydrogen-bond	geometry	(Å,	°).

$D - H \cdots A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$C11-H11B\cdots O1^{i}$	0.97	2.52	3.290 (3)	136
$C16 - H16A \cdots N3$ N2 - H2 4 O2	0.96	2.54	3.486 (3)	167 124
$N5 - H5A \cdots O3$	0.86	2.17	2.834 (2)	134
$N5-H5B\cdots O1$	0.86	2.36	2.909 (2)	122
$C6-H6A\cdots Cg1^{ii}$ $C11-H11A\cdots Cg1^{iii}$	0.97 0.97	2.80 2.89	3.680 (3) 3.753 (3)	152 149

Symmetry codes: (i) -x + 1, -y + 2, -z + 1; (ii) $-x + \frac{3}{2}, y - \frac{1}{2}, -z + \frac{1}{2};$ $x - \frac{1}{2}$, $-y + \frac{3}{2}$, $z + \frac{1}{2}$. Cg1 is the centroid of the C18–C23 ring.



Figure 2

Part of the crystal structure of (I), showing the formation of an $R_2^2(10)$ ring [centred at $(\frac{1}{2}, 1, \frac{1}{2})$]. Hydrogen bonds are shown as dashed lines. Atoms labelled with the suffix 'a' are at the symmetry position (1 - x, 2 - y, 1 - z). C-H··· π interactions are shown as dotted lines.

The H atoms were placed in calculated positions, with N–H = 0.86 Å and C–H = 0.93–0.98 Å, and included in the final cycles of refinement using a riding-model approximation, with $U_{\rm iso}({\rm H}) = 1.2-1.5U_{\rm eq}({\rm carrier atom})$. A rotating group model was used for the methyl groups.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINT* (Bruker, 2000); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

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