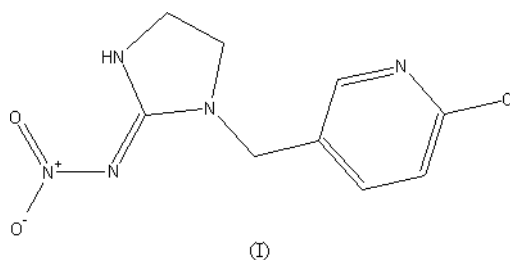


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Key indicators

Single-crystal X-ray study
T = 293 K
Mean σ (C–C) = 0.004 Å
R factor = 0.058
wR factor = 0.162
Data-to-parameter ratio = 12.2For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.(2*E*)-1-[(6-Chloropyridin-3-yl)methyl]-*N*-nitro-
imidazolidin-2-imine (imidachloprid)The title compound (also known as imidachloprid), C₉H₁₀ClN₅O₂, is an active agrochemical possessing insecticidal activity. The dihedral angle between the mean planes passing through the pyridine ring and the imidazolidine ring is 76.9 (1)°. There are intramolecular and intermolecular N—H···O hydrogen bonds and C—H···O intermolecular interactions.Received 9 November 2004
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Comment

An important aspect in the rational design of bioactive molecules involves relating chemical structure to biological activity (Lewis *et al.*, 1991). The conformation of the molecule is found to influence the levels of biological activity. Correlation of the results obtained from X-ray crystallography with biological activity has aided in the chemical design of few active agrochemicals. The activity of a series of triazolyl ketone herbicides (Anderson *et al.*, 1983) has been investigated along with the fungicidal activities of *N*-phenylsuccinamides (Zenei *et al.*, 1988). In this paper, we report the structure of the title compound, (I).

In (I), the five-membered ring N2/C7/C8/N3/C9 is approximately planar and the dihedral angle it makes with the pyridine ring (N1/C1–C5) is 76.9 (1)° (Fig. 1). An intramolecular N—H···O hydrogen bond (Table 2) forms a pseudo-

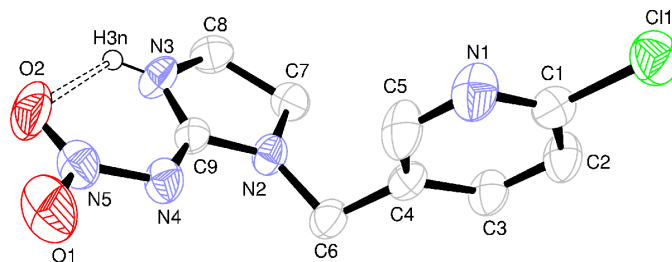


Figure 1

The molecular structure of (I), showing 50% probability ellipsoids. H atoms have been omitted for clarity, except for that involved in the N—H···O hydrogen bond (broken lines).

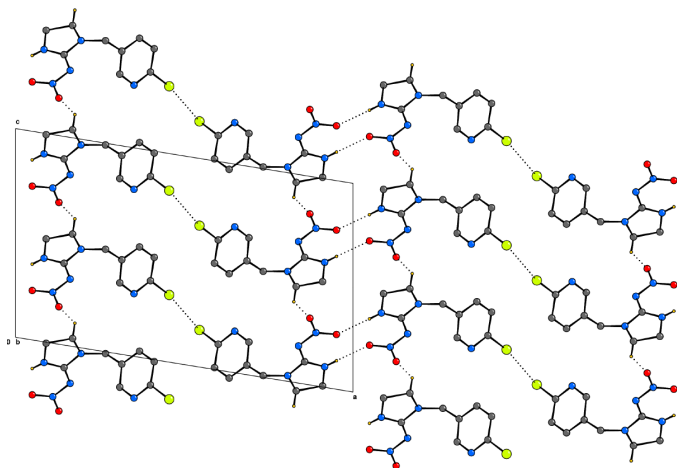


Figure 2
Packing diagram of (I), showing the N—H...O and C—H...O hydrogen bonds (dashed lines), forming molecular chains; Cl...Cl short contacts are also shown.

six-membered ring [Etter symbol $S(6)$; Bernstein *et al.*, 1995], which restricts the conformational freedom. Intermolecular N—H...O hydrogen bonds also further stabilize the packing of molecules [Etter symbol $C(6)$]. In addition, a C—H...O intermolecular interaction generates molecular chains [Etter symbol $C(7)$] parallel to the c axis, forming a sheet-like structure (Fig. 2), and further held together by a Cl...Cl intermolecular contact that links molecules, forming a zigzag chain along the b axis (Fig. 3).

Experimental

Compound (I) was obtained from Rallis India, Bangalore. Single crystals were grown by slow evaporation of a methanol/dichloromethane solution at 278 K.

Crystal data

$C_9H_{10}ClN_5O_2$	$D_x = 1.564 \text{ Mg m}^{-3}$
$M_r = 255.67$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 865 reflections
$a = 19.290(8) \text{ \AA}$	$\theta = 1.4\text{--}25.7^\circ$
$b = 4.839(2) \text{ \AA}$	$\mu = 0.35 \text{ mm}^{-1}$
$c = 11.784(5) \text{ \AA}$	$T = 293(2) \text{ K}$
$\beta = 99.220(6)^\circ$	Prism, colorless
$V = 1085.8(8) \text{ \AA}^3$	$0.51 \times 0.18 \times 0.14 \text{ mm}$
$Z = 4$	

Data collection

Bruker SMART CCD area detector diffractometer	2364 independent reflections
φ and ω scans	1822 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	$R_{\text{int}} = 0.035$
$T_{\text{min}} = 0.842$, $T_{\text{max}} = 0.953$	$\theta_{\text{max}} = 27.8^\circ$
8430 measured reflections	$h = -24 \rightarrow 24$
	$k = -6 \rightarrow 6$
	$l = -14 \rightarrow 14$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0928P)^2 + 0.1346P]$
$R[F^2 > 2\sigma(F^2)] = 0.058$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.162$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.12$	$\Delta\rho_{\text{max}} = 0.45 \text{ e \AA}^{-3}$
2364 reflections	$\Delta\rho_{\text{min}} = -0.32 \text{ e \AA}^{-3}$
194 parameters	
All H-atom parameters refined	

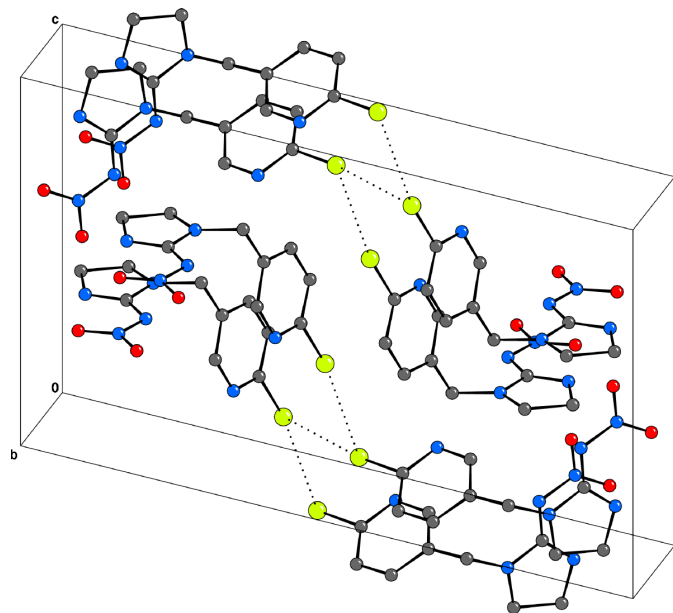


Figure 3
Intermolecular Cl...Cl contacts (dashed lines), forming a zigzag chain along the b axis.

Table 1

Selected geometric parameters (\AA , $^\circ$).

N2—C9	1.328 (3)	N4—C9	1.336 (3)
N3—C9	1.304 (3)		
N2—C6—C4	112.8 (2)		
C8—N3—C9—N2	0.8 (3)	C5—C4—C6—N2	63.0 (3)
C7—N2—C6—C4	69.6 (3)	C9—N2—C7—C8	−6.9 (3)

Table 2

Hydrogen-bonding geometry (\AA , $^\circ$).

$D\text{—}H\cdots A$	$D\text{—}H$	$H\cdots A$	$D\cdots A$	$D\text{—}H\cdots A$
N3—H3N...O2	0.77 (3)	2.12 (3)	2.572 (3)	118 (3)
N3—H3N...O2 ⁱ	0.77 (3)	2.25 (3)	2.903 (4)	143 (2)
C7—H7B...O1 ⁱⁱ	0.90 (3)	2.42 (3)	3.015 (4)	123 (2)

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

All H atoms were located in difference Fourier maps and refined isotropically. The C—H bond lengths are in the range 0.91 (3)–1.00 (3) \AA .

Data collection: SMART (Bruker, 2000); cell refinement: SAINT (Bruker, 2000); data reduction: SAINT; program(s) used to solve structure: SIR92 (Altomare *et al.*, 1993); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP-3 for Windows (Farrugia, 1997) and CAMERON (Watkin *et al.*, 1993); software used to prepare material for publication: PLATON (Spek, 2003).

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