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## Guadalupe Hernández,<sup>a</sup> Sylvain Bernès,<sup>b</sup>\* Roberto Portillo<sup>a</sup> and René Gutiérrez<sup>a</sup>

<sup>a</sup>Laboratorio de Síntesis de Complejos, Facultad de Ciencias Químicas, Universidad Autónoma de Puebla, AP 1067, 72001 Puebla, Pue., Mexico, and <sup>b</sup>DEP Facultad de Ciencias Químicas, UANL, Guerrero y Progreso S/N, Col. Treviño, 64570 Monterrey, NL, Mexico

Correspondence e-mail sylvain\_bernes@hotmail.com

#### Key indicators

Single-crystal X-ray study T = 296 K Mean  $\sigma$ (C–C) = 0.003 Å R factor = 0.043 wR factor = 0.116 Data-to-parameter ratio = 19.2

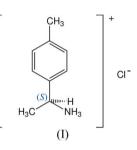
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

In the chiral title salt,  $C_9H_{14}N^+ \cdot Cl^-$ , cations and anions are held together by N-H···Cl hydrogen bonds, forming a onedimensional network in the crystal structure.

(S)-(-)-1-(4-Methylphenyl)ethylammonium chloride

### Comment

Reactions in dry media or under solvent-free conditions are becoming an area of growing interest; they are especially appealing as they provide rapid reaction rates, clean reaction conditions and ease of manipulation (Tanaka & Toda, 2000; Jeon et al., 2005). As part of an ongoing program to develop benign and expeditious methods for organic transformations under solvent-free conditions, we have undertaken the preparation of chiral amides. The title salt, (I) (Fig. 1), was observed as a by-product in such reactions (see Experimental).

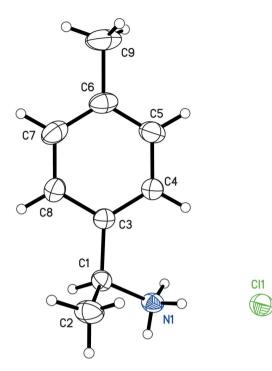


The (p-tolyl)ethylammonuim cation found in (I) has been crystallographically characterized with a number of anions (e.g. Bálint et al., 2004); however no halogenide salts have been reported so far. In contrast, the crystal structure of (R)-1phenylethylammonium bromide, (II), has been reported recently (Fischer, 2006); this is based on a layered network formed through  $N-H \cdots Br$  hydrogen bonds. Interestingly, the crystal structure of (I) is different from that observed for (R)-1-phenylethylammonium bromide, even though both compounds crystallize in the same space group with similar cell parameters. In (I), ammonium H atoms are involved in N-H···Cl hydrogen bonds (Table 1), forming R(8) motifs. Edge-sharing motifs propagate along [100], forming a onedimensional chain (Fig. 2). Differences in interionic contacts between (I) and (II) are reflected in a limited, but significant modification of the conformation of the cation: the dihedral angle between the benzene ring and Nammonium/Cmethine/Cmethyl plane (N1/C1/C2) is 66.02 (12)° in (I), versus 72.7° in (II).

### **Experimental**

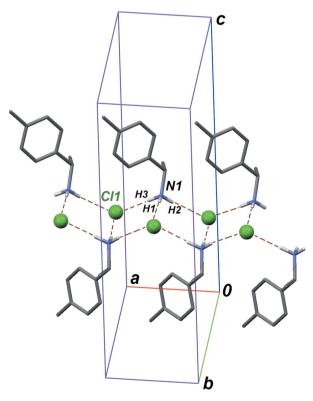
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Under solvent-free conditions, (S)-(-)-1-(4-methylphenyl)ethylamine (0.378 g, 2.8 mmol) and pyridine-2,6-dicarbonyl dichloride (0.286 g, 1.4 mmol) were mixed at 298 K. The resulting crude product



#### Figure 1

The structure of (I) with displacement ellipsoids drawn at the 30% probability level for non-H atoms.



#### Figure 2

Part of the crystal structure of (I), showing hydrogen bonds as dashed lines. C-bound H atoms have been omitted for clarity.

was recrystallized from ethanol, affording the expected diamide (96% yield) and (I) as a by-product (less than 2% yield).

#### Crystal data

$C_9H_{14}N^+ \cdot Cl^-$
$M_r = 171.66$
Orthorhombic, $P2_12_12_1$
$a = 5.4849 (9) \text{ Å}_{1}$
b = 9.1520 (13)Å
c = 19.867 (4)  Å
V = 997.3 (3) Å <sup>3</sup>

#### Data collection

Bruker P4 diffractometer  $2\theta/\omega$  scans Absorption correction:  $\psi$  scan (XSCANS; Siemens, 1996)  $T_{min} = 0.767, T_{max} = 0.929$ 2315 measured reflections 2128 independent reflections

#### Refinement

Refinement on  $F^2$   $R[F^2 > 2\sigma(F^2)] = 0.043$   $wR(F^2) = 0.116$  S = 1.032128 reflections 111 parameters H atoms treated by a mixture of independent and constrained refinement Z = 4  $D_x = 1.143 \text{ Mg m}^{-3}$ Mo K\alpha radiation  $\mu = 0.33 \text{ mm}^{-1}$  T = 296 (1) KPrism, colourless  $0.60 \times 0.40 \times 0.22 \text{ mm}$ 

1779 reflections with  $I > 2\sigma(I)$   $R_{int} = 0.039$   $\theta_{max} = 30.0^{\circ}$ 3 standard reflections every 97 reflections intensity decay: 5.3%

$$\begin{split} &w = 1/[\sigma^2(F_o^2) + (0.0642P)^2 \\ &+ 0.076P] \\ &where \ P = (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{max} < 0.001 \\ \Delta\rho_{max} = 0.30 \ e^{\Lambda^{-3}} \\ \Delta\rho_{min} = -0.24 \ e^{\Lambda^{-3}} \\ Absolute \ structure: \ Flack \ (1983), \\ &431 \ Friedel \ pairs \\ Flack \ parameter: \ 0.01 \ (9) \end{split}$$

# Table 1 Hydrogen-bond geometry (Å, $^{\circ}$ ).

$D - \mathbf{H} \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots \mathbf{A}$
N1-H1···Cl1 <sup>i</sup>	0.90 (3)	2.29 (3)	3.1552 (19)	160 (2)
$N1 - H2 \cdot \cdot \cdot Cl1^{ii}$	0.82 (4)	2.38 (4)	3.157 (2)	159 (3)
$N1 - H3 \cdots Cl1$	0.89 (4)	2.29 (4)	3.180 (2)	179 (3)

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

H atoms bonded to C atoms were placed in idealized positions and refined with a riding model approximation. Constrained C–H distances: 0.93 for aromatic CH, 0.96 for methyl CH<sub>3</sub> and 0.98 Å for methine CH. Isotropic displacement parameters:  $U_{\rm iso}(\rm H) = 1.2 U_{eq}(\rm C)$  for aromatic and methine (CH) and  $1.5 U_{eq}(\rm C)$  for methyl H atoms. Methyl groups were considered as rigid rotating groups. H atoms bound to N1 were found in a difference map and their coordinates refined freely, with  $U_{\rm iso}(\rm H) = 1.5 U_{eq}(\rm N1)$ .

Data collection: *XSCANS* (Siemens, 1996); cell refinement: *XSCANS*; data reduction: *XSCANS*; program(s) used to solve structure: *SHELXTL-Plus* (Sheldrick, 1998); program(s) used to refine structure: *SHELXTL-Plus*; molecular graphics: *SHELXTL-Plus*; software used to prepare material for publication: *SHELXTL-Plus*.

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