Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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#### Key indicators

Single-crystal X-ray study T = 298 KMean  $\sigma$ (C–C) = 0.004 Å R factor = 0.063 wR factor = 0.192 Data-to-parameter ratio = 16.4

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

# Redetermination of phenylbiguanide hydrochloride

The crystal structure of the title compound, *N*-phenylimidocarbonimidic diamide hydrochloride (phenylbiguanide hydrochloride),  $C_8H_{12}N_5^+ \cdot Cl^-$ , (BIGH)<sup>+</sup> · Cl<sup>-</sup>, has been redetermined with higher precision and with the location and free refinement of all H atoms. Received 2 June 2004 Accepted 8 June 2004 Online 12 June 2004

## Comment

The rational design of supramolecular structures can be realised through crystal engineering based on relatively weak intermolecular forces (Desiraju, 1995). Among these forces, hydrogen bonding is by far the most common (HDA, hydrogen donor–acceptor complexation). Multiple-hydrogenbonding systems offer more possibilities for forming stronger networks than common double-hydrogen-bonding systems. Hence biguanide derivatives, characterized by multiplehydrogen-bond donor sites, are good candidates to be associated in the crystal structure with carefully selected molecules having multiple hydrogen bond acceptor sites.



With this aim, phenylbiguanide hydrochloride, (I), poorly analysed some twenty years ago (Amigó *et al.*, 1985) with a high R value (0.115) and without location of the H atoms, has been more precisely redetermined.

The asymmetric unit of  $(BIGH)^+ \cdot Cl^-$  consists of a monoprotonated phenylbiguanidium cation and a chloride anion; protonation occurs at the N atom (N1) attached to the phenyl ring (Fig. 1). The biguanidinium group is not planar; the planes defined by atoms N1, N2 and N3 and by atoms N2, N4 and N5 are inclined to each other by an angle of 51.9 (3)°. Nevertheless, the equivalence of the C–N bond lengths (Table 1) suggests some degree of delocalization of  $\pi$ -electron density through this fragment. The biguanidinium group is rotated with respect to the phenyl ring by the rotation angle  $\tau =$ 52.4 (5)° (the angle  $\tau$  is defined as;  $\tau = |\omega 1 + \omega 2 \pm \pi|/2$ , the torsion angles  $\omega 1$  and  $\omega 2$  being respectively C6–C1–N1–C7 and C2–C1–N1–C7), in agreement with the corresponding angle in phenylbiguanide [59.0 (6)°; Dalpiaz *et al.*, 1996].

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#### Figure 1

A drawing of the title compound, showing the atom labelling and the hydrogen-bonding scheme (dashed lines). Displacements ellipsoids are drawn at the 50% probability level.

The hydrogen-bonding scheme involves all H atoms of the  $(BIGH)^+$  cation (Table 2). It consists almost entirely of N- $H \cdots CI^-$  interactions and accounts for the rather high melting point of the compound (517–520 K). An N- $H \cdots N$  intermolecular hydrogen bond connects two centrosymmetrically related molecules, just forming a well known  $R_2^2(8)$  (Etter *et al.*, 1990) supramolecular synthon (Fig. 1).

## **Experimental**

The title compound (purchased from Sigma Aldrich at 98% purity) was recrystallized from water by slow evaporation of the solvent.

#### Crystal data

$C_{8}H_{12}N_{5}^{+} \cdot CI^{-}$ $M_{r} = 213.68$ Monoclinic, $P2_{1}/c$ $a = 9.3421 (14) \text{ Å}$ $b = 6.6804 (11) \text{ Å}$ $c = 17.297 (6) \text{ Å}$ $\beta = 106.82 (2)^{\circ}$ $V = 1033.3 (4) \text{ Å}^{3}$ $Z = 4$ Data collection	$D_x = 1.374 \text{ Mg m}^{-3}$ Mo K $\alpha$ radiation Cell parameters from 30 reflections $\theta = 10.0-21.0^{\circ}$ $\mu = 0.34 \text{ mm}^{-1}$ T = 298 (2)  K Tablet, colourless $0.30 \times 0.30 \times 0.10 \text{ mm}$
Huber CS four-circle diffractometer $\omega$ scans Absorption correction: none 5323 measured reflections 2672 independent reflections 2659 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.043$	$\theta_{\text{max}} = 35.0^{\circ}$ $h = 0 \rightarrow 14$ $k = 0 \rightarrow 10$ $l = -26 \rightarrow 25$ 3 standard reflections every 97 reflections intensity decay: <3%
Refinement Refinement on $F^2$ $R[F^2 > 2\sigma(F^2)] = 0.063$ $wR(F^2) = 0.192$ S = 1.14 2672 reflections 163 parameters Only coordinates of H atoms refined	$\begin{split} &w = 1/[\sigma^2(F_o{}^2) + (0.122P)^2 \\ &+ 0.6386P] \\ &\text{where } P = (F_o{}^2 + 2F_c{}^2)/3 \\ (\Delta/\sigma)_{\text{max}} = 0.001 \\ \Delta\rho_{\text{max}} = 0.36 \text{ e } \text{\AA}{}^{-3} \\ \Delta\rho_{\text{min}} = -0.38 \text{ e } \text{\AA}{}^{-3} \end{split}$

Table	1
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Selected geometric parameters (Å, °).

N1-C7	1.357 (3)	C1-C6	1.387 (3)
N1-C1	1.422 (3)	C1-C2	1.391 (4)
N2-C7	1.335 (3)	C2-C3	1.394 (4)
N2-C8	1.336 (3)	C3-C4	1.385 (5)
N3-C7	1.337 (3)	C4-C5	1.385 (5)
N4-C8	1.332 (3)	C5-C6	1.392 (4)
N5-C8	1.333 (3)		
C7-N1-C1	123.6 (2)	C4-C5-C6	119.9 (3)
C7-N2-C8	122.1 (2)	C1-C6-C5	119.8 (3)
C6-C1-C2	120.3 (2)	N2-C7-N3	124.9 (2)
C6-C1-N1	119.0 (2)	N2-C7-N1	118.2 (2)
C2-C1-N1	120.7 (2)	N3-C7-N1	116.8 (2)
C1-C2-C3	119.7 (3)	N4-C8-N5	118.1 (2)
C4-C3-C2	119.9 (3)	N4-C8-N2	117.6 (2)
C5-C4-C3	120.4 (3)	N5-C8-N2	124.2 (2)
C7 N1 C1 C(	129.2 (2)		152.0.(2)
C/-NI-CI-C6	128.2 (3)	C8 - N2 - C7 - N1	153.0 (2)
C/-NI-CI-C2	-52.9 (4)	CI = NI = C/ = N2	-10.9(4)
N1 - C1 - C2 - C3	179.4 (3)	CI - NI - C/ - N3	172.5 (2)
N1 - C1 - C6 - C5	180.0 (2)	C/-N2-C8-N4	151.8 (3)
C8-N2-C7-N3	-30.8(4)	C7-N2-C8-N5	-31.7 (4)

Table 2		
Hydrogen-bonding geometry	(Å,	°).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
N1-H11···Cl1	0.91 (3)	2.57 (3)	3.373 (2)	148 (3)
N3-H31···Cl1	0.84 (4)	2.49 (4)	3.273 (3)	156 (3)
$N3-H32\cdots Cl1^{i}$	0.86 (4)	2.54 (4)	3.353 (3)	157 (3)
$N4-H41\cdots Cl1^{ii}$	0.93 (4)	2.51 (4)	3.387 (3)	157 (3)
$N4 - H42 \cdot \cdot \cdot N2^{iii}$	0.85 (4)	2.41 (4)	3.243 (4)	164 (3)
N5-H51···Cl1 <sup>ii</sup>	0.81 (4)	2.55 (4)	3.324 (3)	160 (3)
$N5-H52\cdots Cl1^{iv}$	0.87 (4)	2.62 (4)	3.432 (3)	155 (3)

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

All the H atoms were located in a difference synthesis and their coordinates were refined;  $U_{iso}(H)$  was constrained to be equal to  $U_{eq}$  of the parent atom.

Data collection: XCS (Colapietro *et al.*, 1992); cell refinement: XCS; data reduction: XCS; program(s) used to solve structure: SIR97 (Altomare *et al.*, 1999); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP-3 (Farrugia, 1997); software used to prepare material for publication: SHELXL97.

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